JOURNAL OF HEPATOLOGY

The Home of Liver Research

THE INTERNATIONAL LIVER CONGRESS™
Savour science together again

#ILC2022
Join our dynamic & forward-thinking community

+ Best education
+ Journal of Hepatology
+ Best research
+ JHEP Reports
+ Reduced fees for events
Open-access eLearning anytime, anywhere

2,000+ resources available
21 CME-accredited courses

• 19 CPG slide decks
• 20,300 registered users

• 4,100 ePosters
• 2,200 webcasts
Your weekly hepatology broadcast news
Every Wednesday
18:00 CET

Topics:
+ JHEP Live
+ YIs Choice
+ Nurses & AHPs Focus
+ and more...
Abstracts of The International Liver Congress™ 2022
22–26 June 2022, London, United Kingdom

Publication of this Abstract supplement was supported by the European Association for the Study of the Liver (EASL)
+ Premium hepatology journal
+ International Editorial team led by Prof. Paolo Angeli
+ 2020 Impact Factor: 25.1
## CONTENTS

### Oral Presentations

<table>
<thead>
<tr>
<th>Session/Topic</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>General Session I</td>
<td>S1</td>
</tr>
<tr>
<td>General Session II</td>
<td>S5</td>
</tr>
<tr>
<td>Late-Breaker</td>
<td>S10</td>
</tr>
<tr>
<td>Hepatitis C: Clinical aspects and therapy</td>
<td>S15</td>
</tr>
<tr>
<td>Cirrhosis and its complications: Other clinical complications except ACLF and critical illness</td>
<td>S18</td>
</tr>
<tr>
<td>Non-invasive assessment of liver disease except NAFLD</td>
<td>S22</td>
</tr>
<tr>
<td>Immune-mediated and cholestatic: Experimental and pathophysiology</td>
<td>S26</td>
</tr>
<tr>
<td>Non-invasive assessment/treatment and liver related outcomes in NAFLD/ALD</td>
<td>S29</td>
</tr>
<tr>
<td>Alcoholic liver disease</td>
<td>S33</td>
</tr>
<tr>
<td>Fibrosis</td>
<td>S36</td>
</tr>
<tr>
<td>NAFLD: Clinical aspects except therapy</td>
<td>S39</td>
</tr>
<tr>
<td>Viral hepatitis elimination</td>
<td>S42</td>
</tr>
<tr>
<td>Primary Liver Cancer: Experimental and pathophysiology</td>
<td>S45</td>
</tr>
<tr>
<td>Cirrhosis and its complications: ACLF and Critical illness</td>
<td>S48</td>
</tr>
<tr>
<td>Liver Immunology</td>
<td>S53</td>
</tr>
<tr>
<td>Rare liver diseases (including paediatric and genetic)</td>
<td>S58</td>
</tr>
<tr>
<td>Nurses and AHP</td>
<td>S63</td>
</tr>
<tr>
<td>Gut microbiota in liver disease and liver regeneration</td>
<td>S65</td>
</tr>
<tr>
<td>Hepatitis B emerging therapies</td>
<td>S69</td>
</tr>
<tr>
<td>NAFLD: Diagnostics and non-invasive assessment</td>
<td>S73</td>
</tr>
<tr>
<td>Liver tumours: Clinical aspects except therapy</td>
<td>S75</td>
</tr>
<tr>
<td>Public health</td>
<td>S80</td>
</tr>
<tr>
<td>Molecular and cellular biology</td>
<td>S83</td>
</tr>
<tr>
<td>NAFLD Therapy</td>
<td>S86</td>
</tr>
<tr>
<td>Cirrhosis and its complications: Portal Hypertension</td>
<td>S89</td>
</tr>
<tr>
<td>Immune-mediated and cholestatic disease: Clinical aspects</td>
<td>S93</td>
</tr>
<tr>
<td>Viral hepatitis basic science</td>
<td>S97</td>
</tr>
</tbody>
</table>
EASL’s first open-access journal

+ **Discoverability**
  Indexed by PubMed Central, Clarivate, and Scopus

+ **Speed**
  Time to first decision: 3.6 weeks
  Acceptance to online publication: 2.2 weeks

+ **Excellence**
  High-quality peer review guaranteed by an international Editorial team led by Prof. Jessica Zucman-Rossi

**First Impact Factor in 2022**
The EASL–Lancet Liver Commission

The EASL–Lancet Liver Commission has published a landmark report on liver diseases in Europe.
How to maximise your chances of getting your article accepted by the Journal of Hepatology
About the iconic EASL International Liver Congress™: Memories and motivations
Standing on the shoulders of giants: Our new Vice-Secretary
and much more...

easl.eu/easl-blog
## FUTURE EVENTS 2022–2023

### 2022

<table>
<thead>
<tr>
<th>Date</th>
<th>Month</th>
<th>Event</th>
<th>Location</th>
</tr>
</thead>
<tbody>
<tr>
<td>1–2 July</td>
<td>July</td>
<td>EASL School</td>
<td>London, UK</td>
</tr>
<tr>
<td>1–2 July</td>
<td>July</td>
<td>EASL School</td>
<td>Freiburg, Germany</td>
</tr>
<tr>
<td>15–17 Sep</td>
<td>September</td>
<td>EASL NAFLD Summit</td>
<td>Dublin, Ireland</td>
</tr>
<tr>
<td>15–17 Sep</td>
<td>September</td>
<td>EASL School</td>
<td>London, UK</td>
</tr>
<tr>
<td>10–11 Dec</td>
<td>December</td>
<td>AASLD-EASL Masterclass</td>
<td>Savannah, USA</td>
</tr>
</tbody>
</table>

### 2023

<table>
<thead>
<tr>
<th>Date</th>
<th>Month</th>
<th>Event</th>
<th>Location</th>
</tr>
</thead>
<tbody>
<tr>
<td>20–22 Apr</td>
<td>April</td>
<td>EASL Liver Cancer Summit</td>
<td>Estoril, Portugal</td>
</tr>
<tr>
<td>12–13 May</td>
<td>May</td>
<td>Monothematic Biliary Fibrosis</td>
<td>Florence, Italy</td>
</tr>
<tr>
<td>TBD</td>
<td>May</td>
<td>AASLD-EASL Endpoints</td>
<td>USA</td>
</tr>
<tr>
<td>21–25 Jun</td>
<td>June</td>
<td>EASL Congress 2023</td>
<td>Vienna, Austria</td>
</tr>
<tr>
<td>Summer</td>
<td></td>
<td>EASL Schools</td>
<td>Europe</td>
</tr>
<tr>
<td>7–9 Sep</td>
<td>September</td>
<td>EASL NAFLD Summit</td>
<td>Europe</td>
</tr>
<tr>
<td>19–21 Oct</td>
<td>October</td>
<td>EASL-AASLD Endpoints</td>
<td>Brussels, Belgium</td>
</tr>
<tr>
<td>30 Nov. – 2 Dec.</td>
<td></td>
<td>EASL-AASLD Masterclass</td>
<td>Madrid, Spain</td>
</tr>
</tbody>
</table>
Young Investigators
The future of hepatology

+ YIs Task Force
+ YIs webinars
+ EASL Schools & Masterclasses
+ Fellowships & Mentorships
+ EASL Emerging Leader Award
+ Abstracts & Bursaries at events
+ YIs newsletter
Nurses & AHPs
On the frontline of hepatology

+ Nurses & AHPs Task Force
+ Nurses & AHPs webinars
+ Nurses & AHPs Forum at ILC
+ Rising Star Award
+ Abstracts & Bursaries at events
Annual Patient Forum: Making the patient voice heard
QUIZ

+ Testing your guidelines knowledge since June 2020
+ Sharpening your skills

EARS Campus

+ Hear directly from authors and experts in the field
+ Get answers to your questions
+ Take part every month

EASL Campus

Earn up to two badges with gamification on EASL Campus
The A-TANGO project - featuring G-TAK, a novel combinatorial therapy for acute-on-chronic liver failure (ACLF)

**Expected Impact**

- More than **10 million people** suffer from **decompensated cirrhosis** worldwide.
- Effective treatment of ACLF is an urgent and unmet need.
- A-TANGO performs **Phase II clinical studies of G-TAK**, a novel and innovative therapeutic strategy that aims to **reduce inflammation** and improve hepatocyte proliferation.
- A-TANGO also strives to identify **reliable biomarkers** for better patient stratification and increased survival.

**14 partners, one goal: Helping cirrhosis patients in Europe!**

www.a-tango.eu
info@atango.eu

This project has received funding from the European Union’s Horizon 2020 research and innovation programme under grant agreement No 945096.
The objective of DECISION is to better understand the pathophysiology of decompensated cirrhosis leading to acute-on-chronic liver failure (ACLF) or death. This consortium will take advantage of already existing large and clinically well-characterised patient cohorts to develop reliable prognostic and response tests and combinatorial therapies tailored to the needs of individual patients to decrease the risk of short-term death.

- Pathophysiologic elucidation of acute decompensated cirrhosis at the systems level (genetics, epigenetics, transcriptomics, metabolomics, lipidomics, miR, and analysis of extracellular vesicles)

- Integration of existing clinical data and new multi-omics data from 2,200 patients with more than 8,600 measurements

- Development of new combinatorial therapies

- Optimization of therapies using existing and new animal models

- Development of novel and robust tests for prediction of outcome following traditional treatment versus response to new therapies

- Phase II clinical trials to test new combination therapies

- Creation of new guidelines for outcome prediction and personalized treatment of acute decompensated cirrhosis to prevent ACLF to death

This project has received funding from the European Union’s Horizon 2020 research and innovation programme under grant agreement No 847949.
Liver Investigation: Testing Marker Utility in Steatohepatitis

- 54 partners
- 14 countries for clinical recruitment
- True public-private co-funding model

The overarching aim of LITMUS is to develop, robustly validate and advance towards regulatory qualification biomarkers that diagnose, risk stratify and/or monitor NAFLD/NASH progression and fibrosis stage.

litmus-project.eu
imi.europa.eu

The LITMUS project has received funding from the Innovative Medicines Initiative 2 Joint Undertaking under grant agreement No. 777377. This Joint Undertaking receives support from the European Union’s Horizon 2020 research and innovation programme and EFPIA.
Screening for liver fibrosis population-based study across European Countries

A project that will change the paradigm of diagnosis of chronic liver diseases

AIM:

To assess the prevalence of liver fibrosis in the general population using Transient Elastography, with the objective of establishing criteria for screening for liver fibrosis in the population.
MICROBiome-based biomarkers to PREDICT decompensation of liver cirrhosis and treatment response

Project duration
6 ¼ years

Start
01 January 2019

Grant amount
15 million €

10 Countries
22 Partners

Follow-us on Twitter and LinkedIn:

MICROB-PREDICT

www.microb-predict.eu

This project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 825694.

MICROB-PREDICT will investigate the human microbiome to identify predictors and mechanisms associated with the development of decompensation of cirrhosis and progression to acute-on-chronic liver failure (ACLF) and death.

- New microbiome-based tests for better stratification of cirrhosis patients
- Personalized prediction and prevention of decompensation and ACLF
- Clinical trial to predict response to treatment
- Modern, effective nanobiosensors as clinical tools with improved specificity
- More personalized treatment
- Increased survival times
- Decreased costs for the health systems

@MicrobPredict

Follow-us on Twitter and LinkedIn:

MICROB-PREDICT

www.microb-predict.eu

This project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 825694.
Thursday 23 June

General Session I

GS001
Efficacy and safety of ALXN1840 versus standard of care in Wilson disease: primary results from an ongoing phase 3, randomized, controlled, rater-blinded trial
Karl Heinz Weiss¹, Michael Schilsky², Anna Członkowska³, Fred Askari⁴, Aftab Ala⁵, Peter Ferenci⁶, Peter Ott⁷, Dzhamal Abdurakhmanov⁸, Ferenc Szalay⁹, Piotr Socha¹⁰, Norikazu Shimizu¹¹, Jeff Bronstein¹², Danny Bega¹³, Sihoun Hahn¹⁴, Eugene Swenson¹⁵, Yi Chen¹⁵, Aurelia Poujois¹⁶, ¹Krankenhaus Salem der Evang. Stadtmission Heidelberg gGmbH, Heidelberg, Germany; ²Yale School of Medicine, New Haven, United States; ³Institute of Psychiatry and Neurology, Warsaw, Poland; ⁴University of Michigan Health System, Ann Arbor, United States; ⁵Royal Surrey County Hospital, Guildford, United Kingdom; ⁶Medical University of Vienna, Vienna, Austria; ⁷Aarhus University Hospital, Aarhus, Denmark; ⁸Sechenov First Moscow State Medical University, Moscow, Russian Federation; ⁹Semmelweis University, Budapest, Hungary; ¹⁰The Children’s Memorial Health Institute, Warsaw, Poland; ¹¹Toho University School of Medicine, Tokyo, Japan; ¹²Ronald Reagan UCLA Medical Center, Los Angeles, United States; ¹³Northwestern University Feinberg School of Medicine, Chicago, United States; ¹⁴University of Washington/Seattle Children’s Hospital, Seattle, United States; ¹⁵Alexion, AstraZeneca Rare Disease, Boston, United States; ¹⁶Rothschild Foundation Hospital, Paris, France
Email: karlheinz.weiss@stadtmission-hd.de

Abstract GS001 is under embargo until the start of the General Session I on Thursday 23 June 2022, 13:30 BST. It will be made publicly available on the congress website once the embargo has lifted.

Journalists, industry, investigators and/or study sponsors must abide by the embargo times set by EASL. Violation of the embargo will be taken seriously. Individuals and/or sponsors who violate EASL’s embargo policy may face sanctions relating to current and future abstract submissions, presentations and visibility at EASL Congresses. The EASL Governing Board is at liberty to ban attendance and/or retract data.

Copyright for abstracts (both oral and poster) on the website and as made available during The International Liver Congress™ 2022 resides with the respective authors. No reproduction, re-use or transcription for any commercial purpose or use of the content is permitted without the written permission of the authors. Permission for re-use must be obtained directly from the authors.
GS002
Anti-fibrotic effect of rifaximin in early alcohol-related liver disease: a double-blind, randomised, placebo-controlled trial
Mads Israelsen1, Bjørn Stehr Madsen1, Nikolaj Torp1,2, Stine Johansen1,2, Camilla Dalby Hansen1,2, Sönke Detlefsen1,2, Peter Andersen1, Johanne Kragh Hansen1,2, Katrine Prier Lindvig1,2, Ditlev Nytoft Rasmussen1, Katrine Thorhauge1,2, Maria Kjærgaard1,2, Manimozhiyan Arumugam1,3, Torben Hansen3, Jonel Trebicka1,4,5, Maja Thiele1,2, Aleksander Krag1,2, Odense University Hospital, Odense, Denmark; 2University of Southern Denmark, Faculty of Health Sciences; 3Copenhagen University, CBMR, København, Denmark; 4Goethe University Frankfurt, Gastroenterology, Frankfurt, Germany; 5European Foundation for the study of chronic liver failure, Barcelona, Spain
Email: mads.egerod.israelsen@rsyd.dk

Abstract GS002 is under embargo until the start of the General Session I on Thursday 23 June 2022, 13:30 BST. It will be made publicly available on the congress website once the embargo has lifted.

Journalists, industry, investigators and/or study sponsors must abide by the embargo times set by EASL. Violation of the embargo will be taken seriously. Individuals and/or sponsors who violate EASL’s embargo policy may face sanctions relating to current and future abstract submissions, presentations and visibility at EASL Congresses. The EASL Governing Board is at liberty to ban attendance and/or retract data.

Copyright for abstracts (both oral and poster) on the website and as made available during The International Liver Congress™ 2022 resides with the respective authors. No reproduction, re-use or transcription for any commercial purpose or use of the content is permitted without the written permission of the authors. Permission for re-use must be obtained directly from the authors.

GS003
The spatial distribution and detailed composition of infiltrating immune cells define autoimmune- and checkpoint-therapy associated hepatitis
Laurenz Krimmel1, Henrike Salie1, Saskia Killmer1, Marilyn Salvat Lago1, Nisha Rana1, Peter Bronsert2, David Rafei-Shamsabadi1, Frank Meiss2, Ursula Ehmer1, Angela Krackhardt2, Marius Schwabenland6, Marco Prinz1,7, Christoph Neumann-Haefelin1, Maike Hofmann1, Michael Schultheiss1, Robert Thimme1, Carolin Mogler1, Bertram Bengsch1,2, Freiburg University Medical Center, Department of Internal Medicine II (Gastroenterology, Hepatology, Endocrinology und Infectiology), Freiburg, Germany; 2Freiburg University Medical Center, Institute of Pathology, Freiburg, Germany; 3Freiburg University Medical Center, Department of Dermatology, Freiburg, Germany; 4Klinikum rechts der Isar Technical University Munich, Department of Internal Medicine II, Munich, Germany; 5Klinikum rechts der Isar Technical University Munich, Department of Internal Medicine III, Munich, Germany; 6Freiburg University Medical Center, Institute of Neuropathology, Freiburg, Germany; 7Signalling Research Centres BIOSS and CIBSS, Freiburg, Germany; 8Technical University Munich, Institute of Pathology, Munich, Germany
Email: bertram.bengsch@uniklinik-freiburg.de

Abstract GS003 is under embargo until the start of the General Session I on Thursday 23 June 2022, 13:30 BST. It will be made publicly available on the congress website once the embargo has lifted.

Journalists, industry, investigators and/or study sponsors must abide by the embargo times set by EASL. Violation of the embargo will be taken seriously. Individuals and/or sponsors who violate EASL’s embargo policy may face sanctions relating to current and future abstract submissions, presentations and visibility at EASL Congresses. The EASL Governing Board is at liberty to ban attendance and/or retract data.

Copyright for abstracts (both oral and poster) on the website and as made available during The International Liver Congress™ 2022 resides with the respective authors. No reproduction, re-use or transcription for any commercial purpose or use of the content is permitted without the written permission of the authors. Permission for re-use must be obtained directly from the authors.
GS004
Prospective randomized controlled trial of biomarkers for early detection of hepatocellular carcinoma
Hooman Farhang Zangneh1, Orlando Cerocchi1, Korosh Khalili2, Lima Awad El-Karim2, Mara Vecchio3, Jeffrey Winick3, Yasuhiro Mori4, Hiroyuki Yamada4, Harry Janssen1, Bettina Hansen1,5, Morris Sherman1, Jordan Feld1. 1University Health Network, Toronto General Hospital, Toronto Centre for Liver Disease, Toronto, Canada; 2University Health Network, Joint Department of Medical Imaging, Toronto, Canada; 3Fujifilm Healthcare Americas Corporation, United States; 4Fujifilm Wako Pure Chemical Corporation, Osaka, Japan; 5University of Toronto, Institute of Health Policy, Management and Evaluation, Toronto, Canada
Email: jordan.feld@uhn.ca
Abstract GS004 is under embargo until the start of the General Session I on Thursday 23 June 2022, 13:30 BST. It will be made publicly available on the congress website once the embargo has lifted.
Journalists, industry, investigators and/or study sponsors must abide by the embargo times set by EASL. Violation of the embargo will be taken seriously. Individuals and/or sponsors who violate EASL's embargo policy may face sanctions relating to current and future abstract submissions, presentations and visibility at EASL Congresses. The EASL Governing Board is at liberty to ban attendance and/or retract data.
Copyright for abstracts (both oral and poster) on the website and as made available during The International Liver Congress™ 2022 resides with the respective authors. No reproduction, re-use or transcription for any commercial purpose or use of the content is permitted without the written permission of the authors. Permission for re-use must be obtained directly from the authors.

GS005
Development and validation of the gender-equity model for liver allocation (GEMA) to prioritize liver transplant candidates
Manuel Rodríguez-Perálvarez1, Antonio M. Gómez-Orellana2, Avik Majumdar2, Geoff McCaughan2, Paul Gow4, David Guigo-Rubio2, César Hervás2, Michael Bailey2, Emmanuel Tsochatzis6. 1Hospital Universitario Reina Sofia, University of Córdoba, IMIBIC, CIBERehd, Department of Hepatology and Liver Transplantation, Córdoba, Spain; 2University of Córdoba, Department of Computer Science and Numerical Analysis, Córdoba, Spain; 3Royal Prince Alfred Hospital, Morrow Gastroenterology and Liver Centre and Australian National Liver Transplant Unit, Sydney, Australia; 4The University of Melbourne, Austin Health, Victorian Liver Transplant Unit, Melbourne, Australia; 5Australian and New Zealand Intensive Care Research Centre (ANZIC RC), Department of Epidemiology and Preventive Medicine, Melbourne, Australia; 6Royal Free Hospital and University College London (UCL), Sheila Sherlock Liver Unit and UCL Institute for Liver and Digestive Health, London, United Kingdom
Email: ropeml@hotmail.com
Abstract GS005 is under embargo until the start of the General Session I on Thursday 23 June 2022, 13:30 BST. It will be made publicly available on the congress website once the embargo has lifted.
Journalists, industry, investigators and/or study sponsors must abide by the embargo times set by EASL. Violation of the embargo will be taken seriously. Individuals and/or sponsors who violate EASL’s embargo policy may face sanctions relating to current and future abstract submissions, presentations and visibility at EASL Congresses. The EASL Governing Board is at liberty to ban attendance and/or retract data.
Copyright for abstracts (both oral and poster) on the website and as made available during The International Liver Congress™ 2022 resides with the respective authors. No reproduction, re-use or transcription for any commercial purpose or use of the content is permitted without the written permission of the authors. Permission for re-use must be obtained directly from the authors.
GS006
Efficacy and safety of bulevirtide monotherapy given at 2 mg or 10 mg dose level once daily for treatment of chronic hepatitis delta: week 48 primary end point results from a phase 3 randomized, multicenter, parallel design study
Heiner Wedemeyer1, Soo Aleman2, Maurizia Brunetto3,4, Antje Blank5, Pietro Andreone6, Pavel Bogomolov7, Vladimir Chulano8, Nina Mamonova9, Natalia Geyvandova9, Morozov Viacheslav10, Olga Sagalova11, Tatyana Stepanova12, Dmitry Manuilov13, Vithika Suri13, Qi An13, John F. Flaherty13, Anu Osinusi13, Julian Schulze zur Wiesch14, Markus Cornberg1, Stefan Zeuzem15, Pietro Lampertico16,17. 1Medizinische Hochschule Hannover, Klinik für Gastroenterologie, Hepatologie und Endokrinologie, Hannover, Germany; 2Karolinska University Hospital/Karolinska Institutet, Department of Infectious Diseases, Stockholm, Sweden; 3University Hospital of Pisa, Hepatology Unit, Reference Center of the Tuscany Region for Chronic Liver Disease and Cancer, Pisa, Italy; 4University of Pisa, Department of Clinical and Experimental Medicine, Pisa, Italy; 5Heidelberg University Hospital, Clinical Pharmacology and Pharmacoepidemiology, Heidelberg, Germany; 6University of Modena and Reggio Emilia, Internal Medicine, Modena, Italy; 7State budgetary institution of health care of Moscow region “Moscow regional research clinical institute after M.F. Vladimirsky”, Moscow, Russian Federation; 8FSBI National Research Medical Center for Phthisiopulmonology and Infectious Diseases of the Ministry of Health of the Russian Federation, Moscow, Russian Federation; 9FSBI National Research Medical Center for Phthisiopulmonology and Infectious Diseases of the Ministry of Health of the Russian Federation, Moscow, Russian Federation; 10Stavropol Regional Hospital, Stavropol, Russian Federation; 11 LLC Medical Company “Hepatolog,” Samara, Russian Federation; 12Federal state-funded institution of higher education “Southern Ural State Medical University of Ministry of Health of the Russian Federation”, Chelyabinsk, Russian Federation; 13Limited liability company “Clinic of Modern Medicine,” Moscow, Russian Federation; 14Gilead Sciences, Foster City, United States; 15Universitätsklinikum Hamburg-Eppendorf, Medizinische Klinik Studienambulanz Hepatologie, Hamburg, Germany; 16Limited liability company “Clinic of Modern Medicine,” Moscow, Russian Federation; 17CRC “A. M. and A. Migliavacca” Center for Liver Disease, University of Milan, Department of Pathophysiology and Transplantation, Milan, Italy Email: wedemeyer.heiner@mh-hannover.de

Abstract GS006 is under embargo until the start of the General Session I on Thursday 23 June 2022, 13:30 BST. It will be made publicly available on the congress website once the embargo has lifted. Journalists, industry, investigators and/or study sponsors must abide by the embargo times set by EASL. Violation of the embargo will be taken seriously. Individuals and/or sponsors who violate EASL’s embargo policy may face sanctions relating to current and future abstract submissions, presentations and visibility at EASL Congresses. The EASL Governing Board is at liberty to ban attendance and/or retract data. Copyright for abstracts (both oral and poster) on the website and as made available during The International Liver Congress™ 2022 resides with the respective authors. No reproduction, re-use or transcription for any commercial purpose or use of the content is permitted without the written permission of the authors. Permission for re-use must be obtained directly from the authors.
General Session II

GS007
Transcatheter arterial chemoembolization (TACE) followed by conformal radiotherapy versus TACE alone for hepatocellular carcinoma: a western controlled trial
Cyrille Feray¹, Loic Campion², Isabelle Mahile-Arachambeaud³, Philippe Mathurin⁴, Xavier Mirabel⁵, Emmanuel Rio⁶, Jean-Pierre Bronowicki⁶, Yann Touchefeu³, Jérôme Gournay³, Agnès Rode⁷, Françoise Mornex⁸, Philippe Merle⁹. ¹Centre Hepato Biliaire, Villejuif, France; ²CRLCC, Nantes, France; ³IMAD, Nantes, France; ⁴Hepatology, Lille, France; ⁵CRLCC, Lille, France; ⁶Hepatology, Nancy, France; ⁷Radiology, Lyon, France; ⁸Radiotherapy, Lyon, France; ⁹Hepatology, Lyon, France
Email: cyrille.feray@gmail.com

Abstract GS007 is under embargo until the start of the General Session II on Friday 24 June 2022, 13:40 BST. It will be made publicly available on the congress website once the embargo has lifted. Journalists, industry, investigators and/or study sponsors must abide by the embargo times set by EASL. Violation of the embargo will be taken seriously. Individuals and/or sponsors who violate EASL’s embargo policy may face sanctions relating to current and future abstract submissions, presentations and visibility at EASL Congresses. The EASL Governing Board is at liberty to ban attendance and/or retract data. Copyright for abstracts (both oral and poster) on the website and as made available during The International Liver Congress™ 2022 resides with the respective authors. No reproduction, re-use or transcription for any commercial purpose or use of the content is permitted without the written permission of the authors. Permission for re-use must be obtained directly from the authors.

GS008
The global burden of liver cancer (LC) and chronic liver diseases (CLD) is driven by non-alcoholic steatohepatitis (NASH) and alcohol liver disease (ALD)
James Paik¹,², Linda Henry¹,²,³, Youssef Younossi³, Janus Ong³,⁴ Saleh Alqahtani¹,³,⁵,⁶, Zobair Younossi¹,²,⁷, Inova Health System, Center for Liver Diseases, Department of Medicine; ³Betty and Guy Beatty Center for Integrated Research, IHS; ⁴Center for Outcomes Research in Liver Disease; ⁵University of the Philippines, College of Medicine; ⁶Johns Hopkins Medical Center; ⁷King Faisal Specialist Hospital and Research Center; ⁸Inova Health System, Medicine Service Line
Email: zobair.younossi@inova.org

Abstract GS008 is under embargo until the start of the General Session II on Friday 24 June 2022, 13:40 BST. It will be made publicly available on the congress website once the embargo has lifted. Journalists, industry, investigators and/or study sponsors must abide by the embargo times set by EASL. Violation of the embargo will be taken seriously. Individuals and/or sponsors who violate EASL’s embargo policy may face sanctions relating to current and future abstract submissions, presentations and visibility at EASL Congresses. The EASL Governing Board is at liberty to ban attendance and/or retract data. Copyright for abstracts (both oral and poster) on the website and as made available during The International Liver Congress™ 2022 resides with the respective authors. No reproduction, re-use or transcription for any commercial purpose or use of the content is permitted without the written permission of the authors. Permission for re-use must be obtained directly from the authors.
GS009
Is there a murine model that fully recapitulates human NASH? An unbiased bioinformatics approach to rank pre-clinical models based on proximity to human disease

Michele Vaccar1,2, Ioannis Kamzolash,3 Lea March Harde4, Fiona Oakley4, Christian Trautwein5, Maximilian Hatting6, Trenton Ross7, Barbara Bernardo8, Anouk Oldenburg9, Sara Toftegard Hjuler4, Iwona Ksiazek10, Daniel Linden11,12, Detlef Schuppan13, Sergio Rodriguez-Cuenca1, Maria Manuela Tonini4, Aimo Kanno5,16, Tamara Rodriguez-Castanedas13, Cecilia M. P. Rodrigues17, Simon Cockell18, Olivier Govaere19, Ann K. Daly20, Michael Allison20, Kristian Honnens de Lichtenberg4, Yong Ook Kim13, Anna Lindblom11, Stephanie Oldham9, Anne-Christine Andréasson21, Franklin Schlerman22, Jonathon Marionenaxes23, Arun Sanyal24, Marta B. Alonso27, Anthony Kinaldi27, Yuichiro Amano25, Valérie Paradis26, Alastair Burt10, Davies Susan27, Ann Driessen28, Hiroaki Yashiro29, M. Julia Brosnan, Carla Yunis10, Pierre Bedossa30, Dina Tiniaatos31,32, Quentin Anstee31,33, Evangelia Petsalaki, Peter Davidsen4, Jim Perfield34, Antonio Vidal-Puig1, University of Cambridge, WT/MRC Institute of Metabolic Science, United Kingdom; 2University of Bari Aldo Moro, Interdisciplinary Department of Medicine, Bari, Italy; 3European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI), European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI), Wellcome Genome Campus, Hinxton, UK, Hinxton, Cambridge, United Kingdom; 4Nordov Nordisk, Research and Early Development, Novo Nordisk A/S, Denmark, Måløv, Copenhagen, Denmark; 5Newcastle University, Newcastle Fibrosis Research Group, Biosciences Institute, Faculty of Medical Sciences, Newcastle University, Newcastle upon Tyne, UK, Newcastle, United Kingdom; 6Aachen University Hospital, Department of Medicine III, Aachen; 7Pfizer IMRU, Internal Medicine Research Unit, Pfizer Worldwide Research and Development, Cambridge Massachusetts, United States; 8Pfizer, Internal Medicine, Pfizer Worldwide Research and Development, 558 Eastern Point Road, Groton, CT, 06340, USA, Groton, United States; 9Boehringer Ingelheim Pharma GmbH and Co. KG, CardioMetabolic Diseases Research, Boehringer Ingelheim Pharma GmbH and Co. KG, Biberach a.d. Riß, Germany; 10Novartis Pharma AG, Novartis Institutes for BioMedical Research, Novartis Pharma AG, 4056 Basel, Switzerland, Basel, Switzerland; 11AstraZeneca, Bioscience Metabolism, Research and Early Development Cardiovascular, Renal and Metabolism (CVRM), BioPharmaceuticals R&D, AstraZeneca, Gothenburg, Sweden, Gothenburg, Sweden; 12University of Gothenburg, Division of Endocrinology, Department of Neuroscience and Physiology, Sahlgrenska Academy, University of Gothenburg, Sweden, Gothenburg, Sweden; 13Institute of Translational Immunology and Research Unit for Immunotherapy, Johannes Gutenberg University Medical Center, Mainz, Germany; 14Integrated Biobank of Luxembourg (IBBL), Luxembourg Institute of Health, Translational Medicine Operations Hub, Luxembourg, Dudelange, Luxembourg; 15Sanofi-Aventis Deutschland GmbH, RandD Diabetes, Sanofi-Aventis Deutschland GmbH, Industriepark Hoechst, 65926 Frankfurt, Germany, Frankfurt am Main, Germany; 16Fraunhofer Institute for Translational Medicine and Pharmacology ITMP, Fraunhofer Institute for Translational Medicine and Pharmacology ITMP, Theodor-Stern-Kai 7, 60566 Frankfurt, Germany, Frankfurt am Main, Germany; 17University of Lisbon, Research Institute for Medicines, Faculty of Pharmacy, Universidade de Lisboa, Lisbon, Portugal, Lisbon, Portugal; 18Newcastle University, Bioinformatics Support Unit, Faculty of Medical Sciences, Newcastle University, Newcastle upon Tyne, United Kingdom, Newcastle upon Tyne, United Kingdom; 19Newcastle University, Translational and Clinical Research Institute, Faculty of Medical Sciences, Newcastle University, Newcastle upon Tyne, United Kingdom, Newcastle upon Tyne, United Kingdom; 20Cambridge University Hospitals NHS Foundation Trust, Liver Unit, Cambridge NIHR Biomedical Research Centre, Cambridge, United Kingdom; 21AstraZeneca, Bioscience Metabolism, Research and Early Development Cardiovascular, Renal and Metabolism (CVRM), BioPharmaceuticals R&D, AstraZeneca, Gothenburg, MD, USA, Gothenburg, MD, United States; 22Pfizer, Inflammation and Immunology Research Unit, Pfizer Worldwide Research and Development, Cambridge Massachusetts, Cambridge Massachusetts, United States; 23Sanyel Biotechnology LLC, Sanyel Biotechnology LLC, Norfolk, Virginia, USA, Virginia, United States; 24Virginia Commonwealth University, Department of Internal Medicine, Virginia Commonwealth University, Richmond, VA, United States; 25Takeda Pharmaceuticals International AG, Takeda Pharmaceuticals International AG, Takeda Pharmaceutical Company Limited, Fujisawa, Japan, Fujisawa, Japan; 26Université Paris-Diderot, Department of Imaging and Pathology, Hôpital Beaujon, Paris, France; 27Cambridge University Hospitals NHS Foundation Trust, Department of Cellular Pathology, Cambridge University Hospitals NHS Foundation Trust, Cambridge, United Kingdom; 28University of Antwerp, Department of Pathology, University of Antwerp, Antwerp, Belgium, Antwerp, Belgium; 29Takeda Pharmaceuticals International AG, Takeda Pharmaceutical Company Limited, Cambridge, Massachusetts, Cambridge, Massachusetts, United States; 30Newcastle University, LiverPat, Paris, France and Translational and Clinical Research Institute, Newcastle University, UK, France; 31Newcastle University, Translational and Clinical Research Institute, Faculty of Medical Sciences, Newcastle University, Newcastle upon Tyne, UK, Newcastle upon Tyne, United Kingdom; 32National and Kapodistrian University of Athens, Department of Pathology, Aretaieion Hospital, Medical School, National and Kapodistrian University of Athens, Greece, Athens, Greece; 33Newcastle University, Newcastle NIHR Biomedical Research Centre, Newcastle upon Tyne Hospitals NHS Trust, Newcastle upon Tyne, United Kingdom, Newcastle upon Tyne, United Kingdom; 34Eli Lilly and Company, Lilly Research Laboratories, Eli Lilly and Company, Indianapolis, Indiana, Indianapolis, United States

Email: ajv22@medschl.cam.ac.uk

Abstract GS009 is under embargo until the start of the General Session II on Monday 20 June 2022, 13:40 BST. It will be made publicly available on the congress website once the embargo has lifted. Journalists, industry, investigators and/or study sponsors must abide by the embargo times set by EASL. Violation of the embargo will be taken seriously. Individuals and/or sponsors who violate EASL’s embargo policy may face sanctions relating to current and future abstract submissions, presentations and visibility at EASL Congresses. The EASL Governing Board is at liberty to ban attendance and/or retract data. Copyright for abstracts (both oral and poster) on the website and as made available during The International Liver Congress™ 2022 resides with the respective authors. No reproduction, re-use or transcription for any commercial purpose or use of the content is permitted without the written permission of the authors. Permission for re-use must be obtained directly from the authors.
GS010
Efficacy and safety of finite 48-week treatment with the siRNA JNJ-3989 and the capsid assembly modulator (CAM-N) JNJ-6379 in HBeAg negative virologically suppressed (VS) chronic hepatitis B (CHB) patients: results from REEF-2 study
Kosh Agarwal1, Maria Buti2, Florian van Bömmel3, Pietro Lampertico4, Ewa Janczewska5, Marc Bourliere6, Thomas Vanwolleghem7,8, Oliver Lenz9, Thierry Verbinnen9, Thomas Kakuda9, Cristina Mayer9, John Jerzorowski9, Maria Beumont-Mauviel9, Ronald Kalmeijer9, Michael Biermer9, Isabelle Lonjon-Domanec9. 1Institute of Liver Studies, King’s College Hospital; 2Hospital Universitario Valle de Hebrón; 3University Hospital Leipzig; 4Fondazione IRCCS Ca’ Granda, Ospedale Maggiore Policlinico, University of Milan; 5Medical University of Silesia; 6Hôpital Saint Joseph; 7Antwerp University Hospital (UZA); 8Viral Hepatitis Research Group, Laboratory of Experimental Medicine and Pediatrics, University of Antwerp; 9Janssen Research and Development
Email: kosh.agarwal@nhs.net

Abstract GS010 is under embargo until the start of the General Session II on Friday 24 June 2022, 13:40 BST. It will be made publicly available on the congress website once the embargo has lifted. Journalists, industry, investigators and/or study sponsors must abide by the embargo times set by EASL. Violation of the embargo will be taken seriously. Individuals and/or sponsors who violate EASL’s embargo policy may face sanctions relating to current and future abstract submissions, presentations and visibility at EASL Congresses. The EASL Governing Board is at liberty to ban attendance and/or retract data.

Copyright for abstracts (both oral and poster) on the website and as made available during The International Liver Congress™ 2022 resides with the respective authors. No reproduction, re-use or transcription for any commercial purpose or use of the content is permitted without the written permission of the authors. Permission for re-use must be obtained directly from the authors.
GS011
Microbial produced ethanol: an underestimated burden on the liver
Stijn Meijnikman1, Mark Davids2, Hilde Herrema1, Omrum Aydin1, Valentina Tredaoli3, Joanne Verheij1, Maurits De Brauw4, Sven Francque3, Christophe De Block2, Fredrik Backhed1, Victor Gerdes1, Bert Groen1, Max Nieuwdorp1. 1Amsterdam UMC, locatie AMC, Amsterdam, Netherlands; 2Amsterdam UMC, locatie AMC, Vascular Medicine, Amsterdam, Netherlands; 3Gothenburg University, Gothenburg, Sweden; 4Sparnae Hospital Hoofddorp, Hoofddorp, Netherlands; 5Antwerp University Hospital, Edegem, Belgium
Email: a.s.meijnikman@amc.uva.nl

Abstract GS011 is under embargo until the start of the General Session II on Friday 24 June 2022, 13:40 BST. It will be made publicly available on the congress website once the embargo has lifted. Journalists, industry, investigators and/or study sponsors must abide by the embargo times set by EASL. Violation of the embargo will be taken seriously. Individuals and/or sponsors who violate EASL’s embargo policy may face sanctions relating to current and future abstract submissions, presentations and visibility at EASL Congresses. The EASL Governing Board is at liberty to ban attendance and/or retract data. Copyright for abstracts (both oral and poster) on the website and as made available during The International Liver Congress™ 2022 resides with the respective authors. No reproduction, re-use or transcription for any commercial purpose or use of the content is permitted without the written permission of the authors. Permission for re-use must be obtained directly from the authors.

GS012
A non-calorie restricted low carbohydrate high fat diet improves non-alcoholic fatty liver disease (NAFLD) activity score (NAS) and HbA1c in type 2 diabetes: a six-month randomised controlled trial
Camilla Dalby Hansen1,2, Eva-Marie Gram-Kampmann1,2, Johanne Kragh Hansen1,2, Mie Balle Hugger1, Bjørn Stæhr Madsen1, Jane Jensen1, Sara Olesen2, Nikolaj Torp1, Ditte Nytoft Rasmussen1, Maria Kjærgaard1,2, Stine Johansen1,2, Katrine Prier Lindvig1,2, Peter Andersen1, Katrine Thorhauge1,2, Jan Christian Brønd2, Pernille Hermann2, Henning Beck-Nielsen3, Sönke Detlefsen2,4, Torben Hansen3, Kurt Højlund3, Maja Thiele1,2, Mads Israelsen1, Aleksander Krag1,3,1 Odense University Hospital, Gastroenterology and Hepatology, Odense, Denmark; 2University of Southern Denmark, Clinical Institute, Odense, Denmark; 3Odense University Hospital, Endocrinology, Odense, Denmark; 4Odense University Hospital, Pathology, Odense, Denmark; 5The Novo Nordisk Foundation Center for Basic Metabolic Research, København, Denmark
Email: aleksander.krag@rsyd.dk

Abstract GS012 is under embargo until the start of the General Session II on Friday 24 June 2022, 13:40 BST. It will be made publicly available on the congress website once the embargo has lifted. Journalists, industry, investigators and/or study sponsors must abide by the embargo times set by EASL. Violation of the embargo will be taken seriously. Individuals and/or sponsors who violate EASL’s embargo policy may face sanctions relating to current and future abstract submissions, presentations and visibility at EASL Congresses. The EASL Governing Board is at liberty to ban attendance and/or retract data. Copyright for abstracts (both oral and poster) on the website and as made available during The International Liver Congress™ 2022 resides with the respective authors. No reproduction, re-use or transcription for any commercial purpose or use of the content is permitted without the written permission of the authors. Permission for re-use must be obtained directly from the authors.
Saturday 25 June

Late-Breaker

LB001
Semaglutide 2.4 mg once weekly improved liver and metabolic parameters, and was well tolerated, in patients with non-alcoholic steatohepatitis-related cirrhosis: a randomised, placebo-controlled phase 2 trial
Rohit Loomba¹, Manal F. Abdelmalek², Matthew Armstrong³, Maximilian Jara⁴, Mette Kjaer⁴, Niels Krarup⁴, Eric Lawitz⁵, Vlad Ratziu⁶, Arun Sanyal⁷, Jörn Schattenberg⁸, Philip N. Newsome³.
¹University of California at San Diego, NAFLD Research Center, Division of Gastroenterology, La Jolla, CA, United States; ²Duke University, Durham, United States; ³University of Birmingham and University Hospitals Birmingham NHS Foundation Trust, Birmingham, United Kingdom; ⁴Novo Nordisk A/S, Søborg, Denmark; ⁵Texas Liver Institute, University of Texas Health San Antonio, San Antonio, TX, United States; ⁶Sorbonne Université, Hôpital Pitié-Salpêtrière, Paris, France; ⁷Virginia Commonwealth University School of Medicine, Richmond, VA, United States; ⁸Metabolic Liver Research Program, I. Department of Medicine, University Medical Centre, Mainz, Germany
Email: roloomba@ucsd.edu

The late breaker abstracts are under embargo until the start of the session on Saturday 25 June 2022 at 14:00 BST. They will be made publicly available on the congress website once the embargo has lifted.
Journalists, industry, investigators and/or study sponsors must abide by the embargo times set by EASL. Violation of the embargo will be taken seriously. Individuals and/or sponsors who violate EASL's embargo policy may face sanctions relating to current and future abstract submissions, presentations and visibility at EASL Congresses. The EASL Governing Board is at liberty to ban attendance and/or retract data.
Copyright for abstracts (both oral and poster) on the website and as made available during The International Liver Congress™ 2022 resides with the respective authors. No reproduction, re-use or transcription for any commercial purpose or use of the content is permitted without the written permission of the authors. Permission for re-use must be obtained directly from the authors.
LB002
Genetic variation in TERT modifies the risk of hepatocellular carcinoma in alcohol-related cirrhosis: results form a genome-wide case-control study
Stephan Buch1, Hamish Innes2, Philipp Lutz3, Hans Dieter Nischalke4, Jacob Nattermann5, Jens U. Marquardt6, Janett Fischer6, Karl Heinz Weiss7, Jonas Rosendahl8, Astrid Marot9, Marcin Krawczyk10, Markus Casper10, Frank Lammert10, Florian Eyer11, Arndt Vogel12, Silke Marhenke12, Johann von Felden13, Rohini Sharma14, Stephen Atkinson15, Andrew McQuillan15, Clemens Schafmayer16, Christian Strassburg17, Heidi Altman1, Stefan Sulik1, Veera Raghavan Thangapandi1, Mario Brosch1, Carolin Lackner18, Rudolf E. Stauber19, Ali Canbay19, Alexander Link20, Thomas Reiberger21, Mattias Mandorfer21, Georg Semmler21, Bernhard Schinegger21, Christian Datz21, Stefano Romeo21, Stefano Ginanni Corradini24, Luca Valent25, Sascha Müller26, Marsha Morgan15, Jean-François Dufour28, Josel Trebicka28, Thomas Berg29, Pierre Deltenre29, Sebastian Mueller29, Jochen Hanpe1, Felix Stiekel31, University Hospital Dresden, Medical Department 1, Dresden, Germany; 2Glasgow Internal Medicine and Metabolic Diseases, Milan, Italy; 3Department of Gastroenterology, Hepatology and Endocrinology, Hannover, Germany; 4Leipzig University Medical Center, Division of Hepatology, Department of Medicine II, Leipzig, Germany; 5Saale Medical Center Heidelberg, Department of Internal Medicine, Heidelberg, Germany; 6University Hospital Halle/Saale, Department of Gastroenterology, Halle/Saale, Germany; 7Université Catholique de Louvain, Department of Gastroenterology and Hepatology, CHU UCL Namur, Belgium; 8Saarland University, Department of Medicine II, Saarland University Medical Center, Homburg, Germany; 9Technical University of Munich, Department of Clinical Toxicology, Klinikum Rechts der Isar, München, Germany; 10Hannover Medical School, Department of Gastroenterology, Hepatology and Endocrinology, Hannover, Germany; 11University Medical Center Hamburg-Eppendorf, First Department of Medicine, Hamburg, Germany; 12Imperial College London, London, United Kingdom; 13University College London, UCL Institute for Liver and Digestive Health, Division of Medicine, London, United Kingdom; 14Rostock University Medical Center, Department of General, Visceral, Vascular and Transplant Surgery, Rostock, Germany; 15Universitätsklinikum Bonn, Medical Department I, Bonn, Germany; 16Medical University of Graz, Institute of Pathology, Graz, Austria; 17University Hospital, Ruhr University Bochum, Department of Medicine, Bochum, Germany; 18Otto-von-Guericke University, Department of Gastroenterology, Hepatology and Infectious Diseases, Magdeburg, Germany; 19Medical University of Vienna, Division of Gastroenterology and Hepatology, Department of Internal Medicine III, Vienna, Austria; 20Teaching Hospital of the Paracelsus Medical University Salzburg, Department of Internal Medicine, General Hospital Oberndorf, Oberndorf, Austria; 21University of Gothenburg, Department of Molecular and Clinical Medicine, Institute of Medicine, Sahlgrenska Academy, Wallenberg Laboratory, Gothenburg, Sweden; 22Sapienza University of Rome, Division of Gastroenterology, Department of Translational and Precision Medicine, Gastroenterology Unit, Rome, Italy; 23Fondazione IRCCS Ca’Granda Ospedale Maggiore Policlinico, Internal Medicine and Metabolic Diseases, Milan, Italy; 24Clinic Beaufour, Department of Surgery, Berne, Switzerland; 25UCL Institute for Liver and Digestive Health, Department of Medicine, Royal Free Campus, London, United Kingdom; 26University of Bern, Hepatology, Department of Biomedical Research, Bern, Switzerland; 27Goethe University Frankfurt, Department of Internal Medicine I, Frankfurt, Germany; 28Leipzig University Medical Center, Division of Hepatology, Leipzig, Germany; 29Centre Hospitalier Universitaire Vaudois, Division of Gastroenterology and Hepatology, Switzerland; 30Semel Medical Center, Center for Alcohol Research, University of Heidelberg and Medical Department, Heidelberg, Germany; 31University Hospital of Zurich, Department of Gastroenterology and Hepatology, Zurich, Switzerland

The late breaker abstracts are under embargo until the start of the session on Saturday 25 June 2022 at 14:00 BST. They will be made publicly available on the congress website once the embargo has lifted. Journalists, industry, investigators and/or study sponsors must abide by the embargo times set by EASL. Violation of the embargo will be taken seriously. Individuals and/or sponsors who violate EASL’s embargo policy may face sanctions relating to current and future abstract submissions, presentations and visibility at EASL Congresses. The EASL Governing Board is at liberty to ban attendance and/or retract data. Copyright for abstracts (both oral and poster) on the website and as made available during The International Liver Congress™ 2022 resides with the respective authors. No reproduction, re-use or transcription for any commercial purpose or use of the content is permitted without the written permission of the authors. Permission for re-use must be obtained directly from the authors.

LB003
Reprogramming necroptosis limits immune responses and prevents liver cancer development
Mihael Vucur1, Ahmed Ghallab2, Anne Schneider3, Jakob Kather4, Olivier Govaere4, Augusto Villanueva5, Achim Weber6, Thomas Longerich7, Frank Tacke8, Christoph Roderburg9, Johannes Bode1, Fabian Geisler9, Ulf Neumann10, Jan G. Hengstler11, Mathias Heikenwälder11, Tom Lüdde1. University Hospital Duesseldorf, Department of Gastroenterology, Hepatology and Infectious Disease, Germany; 2Leibniz Research Centre for Working Environment and Human Factors (IfADo) at the Technical University Dortmund, Germany; 3Department of Medicine III, University Hospital RWTH Aachen, Germany; 4Translational and Clinical Research Institute, Faculty of Medical Sciences, Newcastle University; 5Division of Liver Diseases, Department of Medicine, Ichin School of Medicine at Mount Sinai, United States; 6Department of Pathology and Molecular Pathology, University Hospital Zurich, Switzerland; 7Institute of Pathology, University Hospital Heidelberg, Germany; 8Department of Hepatology and Gastroenterology, Charité-Universitätsmedizin, Berlin, Germany; 9Second Department of Internal Medicine, Klinikum rechts der Isar, Technische Universität München, Germany; 10Visceral and...
LB004A
Efficacy and safety of bepirovirsen in patients with chronic hepatitis B virus infection not on stable nucleos (t)ide analogue therapy: interim results from the randomised phase 2b B-Clear study
Seng Gee Lim¹, Cristina Pojoga²,³, Harry Janssen⁴, Denis Gusev⁵, Robert Plesniak⁶, Keiji Tsuji⁷, Ewa Janczewska⁸, Corneliu Petru Popescu⁹, Pietro Andreone¹⁰, Jinlin Hou¹¹, Manuela Arbune¹², Adrian Gadano¹³, Diana Petrova¹⁴, Jun Inoue¹⁵, Teerha Piratsvisuth¹⁶, Young-Suk Lim¹⁷, Apinya Leerapun¹⁸, Masanori Atsukawa¹⁹, Ji-Dong Jia²⁰, Eternity Labio²¹, Jennifer Cremer²², Robert Elston²², Tamara Lukic²⁴, Geoff Quinn²³, Stuart Kendrick²³, Punam Bharania²³, Fiona Campbell²³, Melanie Paff²³, Dickens Theodore²³, ¹National University Health System, Singapore; ²Regional Institute of Gastroenterology and Hepatology, Romania; ³Babes-Bolyai University, Department of Clinical Psychology and Psychotherapy, International Institute for Advanced Study of Psychotherapy and Applied Mental Health, Romania; ⁴Toronto General Hospital, Canada; ⁵Center for Prevention and Control of AIDS and Infectious Diseases, Russian Federation; ⁶University of Rzeszow Centrum Medyczne w Lancucie Sp. z o.o., Poland; ⁷Hiroshima Red Cross Hospital, Japan; ⁸Faculty of Health Sciences in Bytom, Medical University of Silesia, ID Clinic, Poland; ⁹Dr Victor Babes Clinical Hospital of Infectious and Tropical Diseases, Carol Davila University of Medicine and Pharmacy, Romania; ¹⁰Azienda Ospedaliero-Universitaria di Modena, Italy; ¹¹Nanfang Hospital, Southern Medical University, China; ¹²Sf.Cuv. Parascheva Infectious Diseases Clinical Hospital, Romania; ¹³Hospital Italiano de Buenos Aires, Argentina; ¹⁴Diagnostic Consultative Centre Alexandrovska, Bulgaria; ¹⁵Tohoku University Hospital, Japan; ¹⁶NKC Institute of Gastroenterology and Hepatology, Thailand; ¹⁷Asan Medical Center, University of Ulsan College of Medicine, Korea, Rep. of South; ¹⁸Chiang Mai University, Thailand; ¹⁹Department of Internal Medicine, Division of Gastroenterology and Hepatology, Nippon Medical School, Japan; ²⁰Beijing Friendship Hospital, Capital Medical University, China; ²¹Makati Medical Center, Philippines; ²²GloxoSmithKline, United States; ²³GloxoSmithKline, United Kingdom; ²⁴GloxoSmithKline, United Arab Emirates
Email: jennifer.x.cremer@gsk.com

The late breaker abstracts are under embargo until the start of the session on Saturday 25 June 2022 at 14:00 BST. They will be made publicly available on the congress website once the embargo has lifted.

Violations of the embargo will be taken seriously. Individuals and/or sponsors who violate EASL's embargo policy may face sanctions relating to current and future abstract submissions, presentations and visibility at EASL Congresses. The EASL Governing Board is at liberty to ban attendance and/or retract data.

Copyright for abstracts (both oral and poster) resides with the respective authors. No reproduction, re-use or transcription for any commercial purpose or use of the content is permitted without the written permission of the authors. Permission for re-use must be obtained directly from the authors.
Efficacy and safety of bepirovirsen in patients with chronic hepatitis B virus infection on stable nucleos (t)ide analogue therapy: interim results from the randomised phase 2b B-Clear study


1Queen Mary Hospital, China; 2University of Rzeszow, College of Medicine, Centrum Medyczne w Lancucie Sp. z o.o., Poland; 3National University Health System, Singapore; 4Hiroshima Red Cross Hospital, Japan; 5Spitalul Clinic de Boli Infectioase si Pneumoftiziologie, Romania; 6Hospital Italiano de Buenos Aires, Argentina; 7Department of Gastroenterology, Gachon University Gil Medical Center, Korea, Rep. of South; 8Hôpital Beaujon, France; 9Korea University Ansan Hospital, Korea, Rep. of South; 10College of Medicine, Pusan National University and Biomedical Research Institute, National University Hospital, Korea, Rep. of South; 11Luigi Sacco Hospital, Italy; 12Toronto General Hospital, Canada; 13Dr Victor Babes Clinical Hospital of Infectious and Tropical Diseases, Carol Davila University of Medicine and Pharmacy, Romania; 14Alexandrovsk, Bulgaria; 15Department of Medicine, University of Saskatchewan, Canada; 16UMHAT Sofiaemed, Bulgaria; 17Regional Institute of Gastroenterology and Hepatology, Romania; 18Kumamoto University, Japan; 19Center for Prevention and Control of AIDS and Infectious Diseases, Russian Federation; 20Ig Clinic, Poland; 21GlaxoSmithKline, United States; 22GlaxoSmithKline, United Kingdom; 23GlaxoSmithKline, United Arab Emirates

Email: jennifer.x.cremer@gsk.com

The late breaker abstracts are under embargo until the start of the session on Saturday 25 June 2022 at 14:00 BST. They will be made publicly available on the congress website once the embargo has lifted.

Journalists, industry, investigators and/or study sponsors must abide by the embargo times set by EASL. Violation of the embargo will be taken seriously. Individuals and/or sponsors who violate EASL’s embargo policy may face sanctions relating to current and future abstract submissions, presentations and visibility at EASL Congresses. The EASL Governing Board is at liberty to ban attendance and/or retraction of any commercial purpose or use of the content is permitted without the written permission of the authors. Permission for re-use must be obtained directly from the authors.
Primary data analyses of MAESTRO-NAFLD-1 a 52 week double-blind placebo-controlled phase 3 clinical trial of resmetirom in patients with NAFLD
Stephen Harrison1, Rebecca Taub2, Guy Neff3, Sam Moussa4, Naim Alkhouri5, Mustafa Bashir6. 1Pinnacle, Clinical Research, San Antonio, United States; 2Madrigal Pharmaceuticals, RandD, Conshohocken, United States; 3Covenant Research, Sarasota, United States; 4Adobe Gastroenterology, Tucson, United States; 5Arizona Liver Institute, Phoenix, United States; 6Duke University, Radiology, Raleigh, United States.
Email: rebeccataub@yahoo.com

Reduction of intra-hepatic Z-AAT synthesis by fazirsiran decreases globule burden and improves histological measures of liver disease in adults with alpha-1 antitrypsin deficiency
Pavel Strnad1, Mattias Mandorfer2, Gourab Choudhury3, Griffiths Bill4, Christian Trautwein5, Rohit Loomba6, Romil Saxena6, Thomas Schluep7, Ting Chang7, Min Yi7, Bruce Given7, James Hamilton7, Javier San Martin7, Jeffrey Teckman8. 1RWTH University Hospital Aachen, Aachen, Germany; 2Medical University of Vienna, Wien, Austria; 3The University of Edinburgh, United Kingdom; 4Cambridge University Hospitals, United Kingdom; 5University of California San Diego, La Jolla, United States; 6Emory University Hospital, Pathology and Laboratory Medicine, Atlanta, United States; 7Arrowhead Pharmaceuticals, Inc., Pasadena, United States; 8Saint Louis University, Pediatrics, St. Louis, United States.
Email: pstrnad@ukaachen.de

The late breaker abstracts are under embargo until the start of the session on Saturday 25 June 2022 at 14:00 BST. They will be made publicly available on the congress website once the embargo has lifted. Journalists, industry, investigators and/or study sponsors must abide by the embargo times set by EASL. Violation of the embargo will be taken seriously. Individuals and/or sponsors who violate EASL’s embargo policy may face sanctions relating to current and future abstract submissions, presentations and visibility at EASL Congresses. The EASL Governing Board is at liberty to ban attendance and/or retract data.
Copyright for abstracts (both oral and poster) on the website and as made available during The International Liver Congress™ 2022 resides with the respective authors. No reproduction, re-use or transcription for any commercial purpose or use of the content is permitted without the written permission of the authors. Permission for re-use must be obtained directly from the authors.
Thursday 23 June

Hepatitis C: Clinical aspects and therapy

OS001
Results of a ten year prospective observational study on acute hepatitis C in HCV-mono- and HIV/HCV-coinfected patients
Christiana Graf1, Lara Fuhrmann2,3, Lutz Thomas4, Christoph Stephan1, Gaby Knecht4, Peter Gute4, Markus Bickel4, Kai-Henrik Peiffer1, Fabian Finkelmeier1, Georg Dultz1, Nils Wetzstein1, Natalie Filmann5, Eva Herrmann5, Stefan Zeuzem1, Niko Beerenwinkel2,3, Julia Dietz1, Christoph Sarrazin1, 7, Goethe University Hospital Frankfurt, Department of Internal Medicine I, Frankfurt, Germany; ETH Zurich, Department of Biosystems Science and Engineering, Basel, Switzerland; SIB Swiss Institute of Bioinformatics, Basel, Switzerland; Infektiologikum, Frankfurt, Germany; Goethe University Hospital, Department of Infectious Diseases, Frankfurt, Germany; Goethe University Frankfurt, Institute of Biostatistics and Mathematical Modeling, Frankfurt, Germany; St. Josef-Hospital, Medizinische Klinik II, Wiesbaden, Germany
Email: christianagraf@kgu.de

Background and aims: Over the last two decades, a persistent epidemic of acute Hepatitis C virus (HCV) infections has been observed in HIV-positive men who have sex with men (MSM) in several metropolitan areas worldwide. In this study, epidemiological and clinical parameters as well as phylogenetic analyses were conducted to characterize HCV transmission among MSM.

Method: This prospective observational study analysed clinical and epidemiological parameters of patients with confirmed acute HCV infection between 2009 and 2019 from 3 centers in Frankfurt. NS5B population-based sequencing was performed at the time of diagnosis to determine HCV genotype (GT) and for phylogenetic analyses.

Results: A total of n = 161 patients diagnosed with acute HCV-infection were included in the study, of whom n = 140 (87%) were HIV-positive and n = 145 (90%) were MSM. We observed a different distribution of HCV genotypes over time. In the first eight years, HCV infection were included in the study, of whom n = 140 (87%) were MSM and n = 145 (90%) were HIV-positive. In contrast, HCV GT were almost equally distributed in non-MSM patients. Here, 36% were infected with HCV GT1a, 21% each with GT1b or GT3a and 16% had GT2. Phylogenetic analyses in NS5B showed a diverse sequence pattern in patients with HCV GT1b and GT3a. In contrast, HCV strains among MSM infected with HCV GT1a and 4d were more closely related. Based on the comparison of HCV GT or NS5B sequences, 24 patients (15%) were diagnosed with an HCV reinfection. The incidence rate in MSM for a first HCV infection declined in the period between 2017 and 2019 (3.6/1000PY) compared to the DAA era between 2013 and 2017 (6.8/1000 PY) and to the interferon era (2008–2013; 10.1/1000 PY). Conversely, the incidence of HCV reinfections among MSM increased slightly from 1.9/1000PY to 2.8/1000PY over time.

Conclusion: During the last 5 study years the prevalence of GT4 infections increased, while annual acute hepatitis C incidences decreased. HCV reinfection is an issue of major concern in HIV-positive MSM and may have implications for HCV elimination.

OS002
Multicenter prospective study for the use of shortened preemptive therapy with Glecaprevir/Pibrentasvir (G/P) and Ezetimibe in hepatitis C (HCV) seronegative non-liver solid organ transplant recipients of HCV viremic grafts
Bashar Aqel1, Surakit Pungpapong2, Adyr Moss1, Rolland Dickson1
Mayo Clinic, Gastroenterology, Hepatology and Liver Transplant, Phoenix, United States; Mayo Clinic, Jacksonville, United States
Email: aqelbashar@mayo.edu

This abstract is under embargo until Thursday 23 June 2022, 13:30 BST. This abstract has been selected to be highlighted during official EASL Press Office activities or in official EASL Press Office materials that will be made publicly available on the congress website at 13:30 (BST). Journalists, industry, investigators and/or study sponsors must abide by the embargo times set by EASL. Violation of the embargo will be taken seriously. Individuals and/or sponsors who violate EASL’s embargo policy may face sanctions relating to current and future abstract submissions, presentations and visibility at EASL Congresses. The EASL Governing Board is at liberty to ban attendance and/or retract data. Copyright for abstracts (both oral and poster) on the website and as made available during The International Liver Congress™ 2022 resides with the respective authors. No reproduction, re-use or transcription for any commercial purpose or use of the content is permitted without the written permission of the authors. Permission for re-use must be obtained directly from the authors.
OS003
Effectiveness of voxilaprevir/velpatasvir/sofosbuvir in hepatitis C patients previously treated with direct-acting antiviral agents (DAA)

Christiana Graf, Julia Dietz, Beat Müller, Peter Buggisch, Jörn Schattenberg, Christoph Antoni, Stefan Mauss, Elena Durmashkina, Claus Niederau, Thomas Discher, Julian Schulze zur Wiesch, Tobias Müller, Thomas Berg, Christoph Neumann-Haefelin, Christoph Berg, Stefan Zeuzem, Christoph Sarrazin

Background and aims: Oral DAA therapy has been available in New Zealand since mid-2016 for treatment of chronic hepatitis C. Over the last 5 years, more than 10,000 New Zealanders have had virologic failure. Retreatment of patients with confirmed antiviral resistance requires a triple DAA combination of a polymerase, a protease and an NS5A inhibitor. Method: In an open-labelled, ethics-approved study, 100 New Zealanders who had failed DAA therapy with confirmed NS5A resistance will be retreated with glecaprevir/pibrentasvir (GLE/PIB) from Feb 2019 plus sofosbuvir for 16 weeks. Patients with decompensated cirrhosis or hepatocellular carcinoma or post-transplant are excluded.

Results: To-date, 57 patients have been enrolled in the study. Median age was 56 years (38–80), 78% were male and 44% had established cirrhosis. Thirty-five patients had previously failed GLE/PIB, 19 failed ombitasvir, paritaprevir, dasabuvir, and ritonavir (PrOD) and 1 each failed grazoprevir/elbasvir (GRZ/ELB), ledipasvir/sofosbuvir (LDV/SOF) and sofosbuvir/velpatasvir (SOF/VEL). Six patients had failed multiple regimens. Most frequently detected NS5A resistance-associated substitutions (RASs) were Y93H (57%), A30 K (26%), M28 T/F/V (11%). Multiple NS5A RASs were detected associated substitutions within NS3, NSSA, and NS5B genes. One patient died from opioid overdose during treatment. There were no other SAEs or AE-related treatment discontinuations. Treatment effectiveness was not significantly affected by the type of previous DAA regimen, by liver cirrhosis, HCV GT 1a and baseline HCV-RNA viral load. Virologic relapse was observed in 20 patients (10% GT1a, 15% GT1b, 75% in GT3a). The presence of resistance-associated substitutions within NS3, NSSA, and NS5B genes did not impact SVR12 (p = 0.06).

Conclusion: VOX/VEL/SOF is an effective retreatment for patients with HCV who have failed on a previous DAA course in a real-life setting. We identified HCV GT 3a and HCC as the main predictors of VOX/VEL/SOF failure.
Conclusion: Glicaprevir/pibrentasvir plus sofosbuvir for 16 weeks is a safe and highly effective retreatment regimen for patients who have previously failed GLE/PIB and other DAA regimens regardless of cirrhosis status, or NS5A RAS profile. There is no indication for adding ribavirin.

**OS005**

Excess mortality risk among hepatitis C patients after being “cured” in the interferon-free era: results from three population-based cohorts

Victoria Hamill1,2, Stanley Wong3, Jennifer Bensel4,5, Mel Krajden6,7, Peter Hayes8, David Mutimer9, Amanda Yu10, John Dillon11, Will Gelson12, Hector Velasquez13,14, Philip Johnson12, Stephen Barclay15, Maria Alvarez16, Hidenori Toyoda17, Kosh Agarwal18, Andrew Fraser19,20, Sofia Bartlett21,22, Mark Aldersley23, Andrew Bathgate24, Mawuena Binka25,26, Paul Richardson27, Joanne Morling28,29, Stephen Ryder4, Douglas Macdonald21, Sharon Hutchinson1,2, Eleanor Barne22, Neil Guha3,5, William Irving4,5, Naveed Janju3,20,23, Hamish Innes1,2,20, 1Glasgow Caledonian University, School of Health and Life Sciences, Glasgow, United Kingdom; 2Public Health Scotland, Glasgow, United Kingdom; 3British Columbia Centre for Disease Control, Vancouver, British Columbia, Canada; 4Nottingham University Hospitals NHS Trust and the University of Nottingham, NIHR Nottingham Biomedical Research Centre, Nottingham, United Kingdom; 5University of Nottingham, School of Medicine, Nottingham Digestive Diseases Centre, Nottingham, United Kingdom; 6The University of British Columbia, Department of Pathology and Laboratory Medicine, Vancouver, British Columbia, Canada; 7Royal Infirmary of Edinburgh, Edinburgh, United Kingdom; 8Queen Elizabeth Hospital Birmingham, Liver and Hepatobiliary Unit, Birmingham, United Kingdom; 9University of Dundee, School of Medicine, Division of Molecular and Clinical Medicine, Dundee, United Kingdom; 10Cambridge University Hospitals NHS Foundation Trust, Cambridge Liver Unit, Cambridge, United Kingdom; 11University of British Columbia, School of Population and Public Health, Vancouver, British Columbia, Canada; 12University of Liverpool, Department of Molecular and Clinical Cancer Medicine, Liverpool, United Kingdom; 13Glasgow Royal Infirmary, Glasgow, United Kingdom; 14Ogaki Municipal Hospital, Department of Gastroenterology, Ogaki, Japan; 15King’s College Hospital NHS Foundation Trust, Institute of Liver Studies, London, United Kingdom; 16Aberdeen Royal Infirmary, Aberdeen, United Kingdom; 17Queen Elizabeth University Hospital, Glasgow, United Kingdom; 18St James’s University Hospital, Leeds Liver Unit, Leeds, United Kingdom; 19Royal Liverpool and Broadgreen University Hospitals NHS Trust, Liverpool, United Kingdom; 20University of Nottingham, Lifespan and Population Health, Nottingham, United Kingdom; 21Royal Free London NHS Foundation Trust, Gastroenterology and Hepatology, London, United Kingdom; 22University of Oxford, Nuffield Department of Medicine and the Oxford NIHR Biomedical Research Centre, Oxford, United Kingdom; 23St Paul’s Hospital Vancouver, Centre for Health Evaluation and Outcome Sciences, British Columbia, Canada

Email: victoria.hamill@gcu.ac.uk

**Background and aims:** Although the number of people living with a hepatitis C sustained viral response (SVR) has increased dramatically, mortality rates in this patient group remain poorly understood. Here, our goal was to assess excess mortality after SVR achievement in the interferon (IFN)-free era.

**Method:** We performed data analysis on patients achieving SVR in the IFN-free era (2014–2018/19) from three population-based cohorts in Scotland (SC), England (EN), and British Columbia (BC). Patients were divided into three disease stage groups: no cirrhosis (SC and BC only); compensated cirrhosis; and end stage liver disease (ESLD). Age-standardised mortality rates were calculated to take account of different age/sex structures between cohorts and disease stage groups. Further, we calculated standardised mortality ratios (SMRs) to compare the frequency of mortality in SVR patients to the general population (GP). We also quantified the proportion of excess death attributable to: a) death from liver cancer; b) death from liver disease unrelated to cancer; and c) death from drug-related causes. Finally, Poisson regression was used to identify factors associated with excess mortality.

**Results:** Our analysis included 20,031 patients, of which 1,402 (7%) died during follow-up. Mean follow-up duration was 2.2–3.9 years, and mean age ranged from 46.3 (SC) to 56.7 (BC). Mortality rates varied considerably according to disease stage. For example, the age-standardised mortality rate ranged from 12 to 23, 27–38, and 62–118 deaths per 1000 person-years in non-cirrhosis, compensated cirrhosis and ESLD patients, respectively. SMRs indicated that all-cause mortality was 3.4–3.5 times higher than the GP in non-cirrhosis patients, 4.2–5.9 times higher in compensated cirrhosis patients, and 8.7–15.3 times higher in ESLD patients. For non-cirrhosis patients, drug-related causes were responsible for the greatest proportion of excess death (77% SC; 41% BC). Conversely, for cirrhosis patients, liver-related causes were the key driver, responsible for 30–95% of excess deaths. In the regression analysis, younger age, drug use and comorbidities were associated with greater excess mortality (see figure).

**Conclusion:** In the largest study performed to-date, we show that individuals achieving SVR in the interferon-free era have a considerably higher mortality risk than the GP, driven mainly by drug-related mortality (in non-cirrhosis patients) and liver-related causes (in cirrhosis patients).

**OS006**

Impact of direct-acting antiviral treatment for hepatitis C on cardiovascular diseases and extrahepatic cancers

Laurent Lam1, Helene Fontaine2, Nathanaël Lapidus1,2, Celine Dorival1, Jonathan Bellet1, Dominique Larrey2,4, Pierre Nahon2,4, Alpha Diallo5, Carole Cagnot6, Clovis Lusivka-Nzinga7, Françoise Teoule1, Gilles Hejblum1, Marc Bourliere6,7, Stanislas Pol2,8, Fabrice Carrat1,2,1 Sorbonne Université, INSERM, Institut Pierre Louis d’Épidémiologie et de Santé Publique, IPE ashamed, Paris, France; 1 Assistance Publique-Hôpitaux de Paris, France; 1 Hôpital Saint Eloi et IBB, INSERM, Montpellier, France; 1 Insmer, UMR-1162, “Génomique fonctionnelle des tumeurs solides”, Paris, France; 1 ANRS, Emerging Infectious Diseases, Paris, France; 1 Hôpital Saint Joseph, Marseille, France; 1 INSERM, UMR 1252 IRD SESTIM, Aix Marseille Université, Marseille, France; 1 Université de Paris, Paris, France

Email: laurentlam@hotmail.fr

**Background and aims:** The impact of direct-acting antivirals (DAAs) on extrahepatic complications in chronic hepatitis C (CHC) patients remains poorly described. We estimated the association of DAAs with cardiovascular events and extrahepatic cancers.

---

**ORAL PRESENTATIONS**

**Journal of Hepatology 2022 vol. 77(S1) | S1–S118**

S17
Cirrhosis and its complications: Other clinical complications except ACLF and critical illness

OS007
Etiological cure prevents further decompensation and mortality in cirrhotic patients with ascites as the single first decompensating event

Marta Tonon1, Lorenz Balcar2,3, Georg Semmler2,3, Valeria Calvino1, Bernhard Scheiner2,3, Simone Incico1, Rafael Paternostro2,3, Carmine Gabriele Gambino1, David JM Bauer2,3, Antonio Accetta1, Lukas Hartl2,3, Alessandra Brocca1, Mathias Jachs2,3, Michael Trauner2,3, Mattias Mandorfer2,3, Paolo Angeli1, Thomas Reiberger2,3, Salvatore Piano1. 1University of Padua, Department of Medicine, Padova, Italy; 2Medical University of Vienna, Division of Gastroenterology and Hepatology, Department of Internal Medicine III, Vienna, Austria; 3Medical University of Vienna, Vienna Hepatic Hemodynamic Laboratory, Division of Gastroenterology and Hepatology, Department of Internal Medicine III, Vienna, Austria. Email: salvatorepiano@gmail.com

Background and aims: Etiologic treatment reduces the risk of decompensation and mortality in compensated cirrhosis. However, in the setting of decompensated cirrhosis the impact of etiologic treatment is less predictable, in particular in patients with ascites, who remain at high risk of developing further decompensating events and death. The aim of the study was to evaluate the impact of etiologic treatment in decompensated patients with cirrhosis and ascites as the single index decompensating event. The end points were the occurrence of further decompensation (i.e. refractory ascites, spontaneous bacterial peritonitis [SBP], hepatorenal syndrome [HRS-AKI], variceal bleeding [VB] and hepatic encephalopathy [HE]) and mortality.

Method: Cirrhotic patients with ascites as single first decompensation event at the University Hospital of Padova or the Vienna General Hospital between 2003–2021 were included and followed until death, liver transplantation or September 2021. The etiology was considered as “cured” in case of removal of the primary etiological factor (e.g. HCV: virological cure, HBV: virological suppression, ALD: alcohol abstinence) and as “controlled” in case of partial removal of etiologic factor (e.g. HBV: partial suppression of HBV-DNA, ALD: mostly abstinent but with drinking episodes).

Results: We included 622 patients (mean age: 57 ± 11 years, male 68%, mean MELD 15 ± 6); the most common etiology were ALD (59%) and HCV (23%). Etiology was “cured” in 146 patients (24%), “controlled” in 170 (27%) and uncontrolled in 306 (49%). During a median follow-up of 33 months, 350 patients (56%) developed further decompensation (33%refractory ascites, 29% HE, 17% SBP, 13% HRS-AKI, 9% VB). The incidence of further decompensation at 5 years was significantly lower in patients with “cured” vs “controlled” or uncontrolled etiology (38% vs 64% vs 72%, respectively; p = 0.001; Fig. 1A). Multivariable analysis (adjusted for age, varices, etiology, Child Pugh class, creatinine and sodium), “cured” (aHR = 0.52; p < 0.001) and “controlled” etiology (aHR = 0.60; p < 0.001) were both independently associated with a lower risk of further decompensation.

Conclusion: Further decompensation at 5 years was significantly lower in patients with “cured” vs “controlled” or uncontrolled etiology. Considering response to etiologic treatment as time-dependent covariates, 5-year cumulative incidence of survival was significantly higher in patients with cured vs controlled vs uncontrolled etiology (83% vs 58% vs40%, respectively; p < 0.001; Fig. 1B). In multivariable analysis, etiological cure (aHR = 0.35, p < 0.001) and controlled etiology (aHR = 0.61, p = 0.003) were independently associated with lower mortality.

Method: The prospective ANRS CO22 HEPATHER cohort was enriched with individual data until December 2018 from the French National Health Insurance Database (SNDS), which contains medical information regarding ambulatory care and hospital admissions. CHC patients were enrolled between August 2012 and December 2015 in 32 French hepatology centers. A total of 8148 CHC adults were selected. Cardiovascular events (stroke, acute coronary syndrome, pulmonary embolism, heart failure, arrhythmias and conduction disorders [ACD], peripheral arterial disease [PAD]) and cancers (colorectal, bladder, prostate, kidney, lung, pancreas, thyroid, head/neck, breast) were derived from the SNDS. Associations between DAAAs and extrahepatic events were estimated using marginal structural models, with adjustments for clinical confounders and medications.
Conclusion: In cirrhotic patients with ascites as single first decompensating event, the cure or control of etiology of liver disease reduces the risk of further decompensations and mortality.

OS008
Risk factors for short-term post discharge clinical outcomes in patients hospitalized with decompensated chronic liver disease: interim results from Global CLEARED study

Jasmohan S. Bajaj1, Patrick S. Kamath2, Florence Wong3, Peter Hayes4, Ramazan Idiliman5, Aldo Torre6, Mark Topazian7, Jacob George8, Mario Reis Álvares-da-Silva9, Qing Xie10, Shiv Kumar Sarin11, Abha Nagral12, Sumeet Asrani13, Mohammad Amin Fiałahazadeh14, Somaya Alblahi15, CE Eapen16, Ashish Goel17, Ajay Kumar Duseja18, Anoop Saraya19, Jatin Yegurla20, Mohd. Rela21, Dinesh Jothimani22, Marie Jeanne Loboses23, Belmi Hilal Alah24, Ricardo Cabello25, Ruveena Bhavani26, Nik MA Nik Arsyad27, Sambat Treeprasertsuk28, Salisa Wejnaruemarn29, Jose Luis Perez Hernandez30, Godolfino Miranda Zazueta31, Neil Rajoriya32, Rosemary Faulkes33, Tahmim Islam34, Suresh Vasan Venkatachalapathy35, Amey Sonavane36, Abdullah Emre Yildirim37, Sezgin Barutcu38, Anand Kulkarni39, Zubirán40, Mexico; 26Instituto Nacional de Ciencias Médicas y Nutrición Salvador Zubirán, Mexico; 27Queen Elizabeth University Hospitals, Birmingham, United Kingdom; 28Queen Elizabeth University Hospitals, United Kingdom; 29Gaziantepe, Turkey; 30Asian Institute of Gastroenterology, Hyderabad, India; 31Upenn (University of Pennsylvania), United States; 32Pereleman School of Medicine at the University of Pennsylvania, United States; 33Royal Berkshire Hospital, United Kingdom; 34Marmara University, Turkey; 35xx, Turkey; 36Sir Ganga Ram Hospital, Delhi, India; 37Jbn. Sina Hospital, Khartoum, Sudan, Sudan; 38Centro Médico la Raza, Mexico; 39Singapore General Hospital, Gastroenterology and Hepatology, Singapore, Singapore; 40Singapore General, Singapore; 41Mayo Scottsdale, United States; 42Mercy Medical Centre, United States; 43Jaslok Hospital, Delhi, India; 44Mayo Jacksonville, United States; 45VA Richmond, United States; 46xx, South Africa; 47xx, United Kingdom; 48xx, India; 49xx, Ethiopia; 50xx, Canada; 51xx, United States; 52Centro Medico Isseym, Gastroenterology, Mexico; 53Department of infectious disease, Ruijin hospital, Shanghai jiao Tong university school of medicine, Shanghai, China; 54xx, Israel; 55xx, Chile; 56xx, Argentina

Email: doctor.ashokchoudhury@gmail.com

Background and aims: Decompensated chronic liver disease (DCLD) is associated with poor outcomes, but no global study has addressed this after hospitalization. We prospectively evaluated non-elective hospitalized patients with DCLD to determine disease profile, predictors of readmission and 30 days mortality post discharge following index hospital admission under Chronic Liver Disease Evolution And Registry for Events and Decompensation (CLEARED) consortium.

Method: Data were prospectively collected from 49 centres from 6 continents of non-elective admissions in DCLD patients with or without cirrhosis, aged ≥18 years. We performed an interim analysis to predict readmission and mortality within 30 days following index hospital discharge. World Bank data were used to stratify countries according to income.

Results: 1383 patients, mean age 54.97 ± 13.55 years; 64% male; diverse ethnicity [White 39%, Asian 30%, Hispanic 10%, Black 9%] were analyzed. Alcohol was the most common etiology (46%), followed by NASH (23%), HBV (13%) and HCV (11%). Admissions were almost exclusively for liver related complications i.e. GI bleed (30%), HE (34%), AKI (33%), and anasarca (24%). Mean admission CTP was 10 (5-14) and MELD-Na 23 (6-40). Only 11% were listed for transplant. 51% had hospitalization in previous six months. 24% were infected at admission and another 13% developed infections subsequently. During hospitalization, organ failures were: AKI 46%; as brain 16%; a high discharge MELD-Na ≥ 6 M (p = 0.006). The most significant independent factors predicting readmission within 30 days were being in low/ lower middle income country (p < 0.0001), a high discharge MELD-Na (p = 0.0005), and hospitalization ≤6 M (p = 0.006). The most significant independent predictors of 30-day-mortality post index discharge were age, discharge MELD-Na (p < 0.0001 for both), and various organ failures during index admission (p < 0.01).

Conclusion: The clinical outcomes of patients with DCLD following index hospital admission vary widely around the world. Mortality within 30 days post discharge is largely dependent on patient and disease factors. Readmission post discharge, however, is variable across continents and inversely correlates socio-economic status. Global characterization of patients at high risk of readmission should include further study of socio-economic factors in addition to severity of liver disease.
Dyserythropoiesis is underrecognized and contributes to severe anemia in liver cirrhosis

Chhagan Bihari1, Sumit Garg1, Shiv Kumar Sarin2. 1Institute of Liver and Biliary Sciences, Pathology and Hepatology, Delhi, India; 2Institute of Liver and Biliary Sciences, Hepatology, Delhi, India

Email: shivsarin@gmail.com

Background and aims: Moderate to severe anemia is one of the common complication in liver cirrhosis and is often multifactorial. Contribution of dyserythropoiesis (DE) in cirrhosis related anemia is often neglected and has not been studied. We aimed to investigate the prevalence, severity and mechanisms of dyserythropoiesis in cirrhosis patients.

Method: We studied the bone marrows (BM) of cirrhosis patients (n = 517), who underwent a BM aspiration/biopsy between Jan 2014–Dec 2018, for investigation of anemia, hypersplenism or other clinical indications. Cases of haematological or non-hematological neoplasias, chronic kidney disease, chronic or acute drug injury, acute and chronic hepatitis and granulomatous pathology were excluded. Morphological analysis of BM aspirate, biopsies, erythroid colony assessment were done. A >5% dyserythropoiesis in erythroid lineage was considered and categorized as mild: 5–10%; moderate: 10–15% and marked: >15%.

Results: A 68/517 (13.2%) cirrhosis patients had dyserythropoiesis and none from control group. Of them 44% had mild; 35.4% moderate and 20.6% marked dyserythropoiesis in the BM. Cirrhosis patients with DE had significantly lower hemoglobin than those without DE (7.6 ± 1.4 gm/dl vs 8.9 ± 1.9 gm/dl, p < 0.001), but comparable serum iron (83.7 ± 42 vs 90.2 ± 46.6 mcg/dl, p = 0.997); total iron binding capacity (243.2 ± 85.1 vs 231 ± 87.2 mcg/dl, p = 0.291); and transferrin saturation (50.9 ± 27.9 vs 55.6 ± 30.8 %, p = 0.206) and serum folate (16 ± 3.8 vs 15.8 ± 4.4 ng/ml) levels. The former however, had higher saturation (50.9 ± 27.9 vs 55.6 ± 30.8 %, p = 0.206) and serum folate (16 ± 3.8 vs 15.8 ± 4.4 ng/ml) levels. The former however, had higher vitamin B12 (2339.2 ± 1406 vs 1842 ± 1411.9 pg/ml, p = 0.010) levels. (16 ± 3.8 vs 15.8 ± 4.4 ng/ml) levels. The former however, had higher vitamin B12 (2339.2 ± 1406 vs 1842 ± 1411.9 pg/ml, p = 0.010) levels. The former however, had higher vitamin B12 (2339.2 ± 1406 vs 1842 ± 1411.9 pg/ml, p = 0.010) levels. The former however, had higher vitamin B12 (2339.2 ± 1406 vs 1842 ± 1411.9 pg/ml, p = 0.010) levels.

Conclusion: Approximately 13.2% patients with cirrhosis with severe anemia show dyserythropoiesis. Standard hematological and iron studies fail to identify it and bone marrow examination is merited. Alternations in the erythroid colonies, HSP70 localization and diminished GATA.1 in BM are associated with dyserythropoiesis.

Effect of recruitment and selection policies on the volume of outcome of patients transplanted with ACLF-3

Baptiste Michard1, Thierry Artzner1, Pietro Addeo1, Philippe Bachelier1, Camille Besch1, Vincent Castelain1, Raphael Clerc-Jehl1, Mathilde Deridder1, Max Guillot1, Jean-Étienne Herbrecht1, Ralf Janssen-Langenstein1, Maleka Schenck1, Francis Schneider1, François Faitot1, 1Hopitaux Universitaires de Strasbourg

Email: baptiste.michard@chru-strasbourg.fr

Background and aims: Liver transplantation (LT) for critically ill cirrhotic patients is a debated issue, which raises complex medical, surgical and ethical challenges. In particular, it is crucial to achieve high post-LT survival in order to justify allocating livers to these patients, especially given the current organ shortage. To date, there is no granular data concerning the 3-year post-LT outcome of ACLF-3 patients.

Method: This study describes the three-year post-LT survival of a single center granular cohort of patients with ACLF-3 at the time of LT and compares it to the post-LT survival of all the patients who were transplanted without ACLF-3 in the same center between 2007 and 2018. Over this period of time, two policies were gradually implemented in this center: (i) developing a network of peripheral centers that transferred critically ill cirrhotic patients for LT assessment and (ii) increasing use of the transplantation for ACLF-3 model (TAM) score criteria to identify the optimal transplantability window.

Results: A total of 828 first time single LTs were performed over the study period. 91 patients had ACLF-3 at the time of LT and compares it to the post-LT survival of all the patients who were transplanted without ACLF-3 in the same center between 2007 and 2018. Over this period of time, two policies were gradually implemented in this center: (i) developing a network of peripheral centers that transferred critically ill cirrhotic patients for LT assessment and (ii) increasing use of the transplantation for ACLF-3 model (TAM) score criteria to identify the optimal transplantability window.

A. 3-year post-transplant survival of patients transplanted with ACLF-3 (red) and without (black)

B. Number of patients transplanted with AC (blue) and 3-year post-LT survival (red line)
patients transplanted with ACLF-3 and their 3-year post-LT survival increased over time: 2007–2009: 7 patients, 43% survival; 2010–2012: 20 patients, 60% survival; 2013–2015: 28 patients, 54% survival; 2016–2018: 36 patients, 83% survival (no significant difference in survival between the ACLF-3 and the non ACLF-3 group in the last period). This increase in the number of patients transplanted and in their post-LT three-year survival was not observed in the general population of patients transplanted without ACLF-3 (cf. Figure). A total of 12 ACLF-3 patients were transplanted with TAM scores>2. However, in the last period (2016–2018), in which both the number of patients transplanted with ACLF-3 and the post-LT survival were the highest, no patient was transplanted with a TAM score>2.

Conclusion: This study, which originates from the largest single center cohort of patients transplanted with ACLF-3, illustrates how gradually building a network of peripheral centers to refer critically ill cirrhotic patients to an expert ICU and LT center can lead to a dramatic increase in the number of patients transplanted with ACLF-3. It also shows that there is a learning curve when transplanting patients with ACLF-3 and that the implementation of the TAM score to help identify the optimal transplantability window at the time of organ proposal contributes to optimizing post-LT outcomes. The combination of these strategies can help centers increase the number of patients transplanted with ACLF-3 while reaching post-LT outcomes for these patients that are similar to those of non ACLF-3 patients.

OS011
Real-world evidence on long-term albumin treatment in patients with decompensated liver cirrhosis in Italy
Wim Laleman1, Jonel Trebicka2, Alastair O2, Wim Laleman1, Jonel Trebicka2, Alastair O

1University Hospitals Leuven, Department of Gastroenterology and Hepatology, Section of Liver and Biliopancreatic Medicine and Hepatology, Padova, Italy

OS012
Impact of cirrhotic cardiomyopathy and severity of liver cirrhosis on the development of acute kidney injury
Simona Bota1, Marcel Razpotnik1, Philipp Wimmer2, Michael Hackl2, Gerald Lesnik3, Hannes Alber2, Markus Peck-Radosavljevic1, Simona Bota1, Marcel Razpotnik1, Philipp Wimmer2, Michael Hackl2, Gerald Lesnik3, Hannes Alber2, Markus Peck-Radosavljevic1

1Klinikum Klagenfurt am Wörthersee, Department of Internal Medicine and Gastroenterology (IMuG) and Emergency Medicine (ZAE), Klagenfurt, Austria; 2Klinikum Klagenfurt am Wörthersee, Department of Internal Medicine and Cardiology (IMuK), Klagenfurt, Austria; 3Klinikum Klagenfurt am Wörthersee, Institut für diagnostische und interventionelle Radiologie, Klagenfurt, Austria

Email: bota_simona1982@yahoo.com

Background and aim: New criteria of cirrhotic cardiomyopathy (CCM) were published from a multidisciplinary consortium (Izzy et al. Hepatology 2019 Nov 11. doi: 10.1002/hep.31034) and define systolic dysfunction of the left ventricle as ejection fraction (EF) ≤50% and/or global longitudinal strain (GLS) <−18%, while the diastolic dysfunction is diagnosed when three of the following conditions are present: average E/e’ >14, peak tricuspid regurgitation velocity >2.8 m/s, septal e’<7 cm/s, left atrial volume index >34 ml/m². Our aim was to assess the influence of CCM, severity and etiology of liver cirrhosis on the development of acute kidney injury.

Method: Our prospective study included consecutive patients with liver cirrhosis without structural heart disease, arterial hypertension, HCC outside Milan criteria, portal vein thrombosis, presence of TIPS and with optimal acoustic echocardiography window. The patients were evaluated between 12/2018–11/2021 in our in- and out-patient Department. Conventional and speckle-tracking echocardiography (Vendors GE, EchoPAC PC software) were performed by a single investigator (EACVI TTE certified).

Acute kidney injury (AKIN) was defined according to the International Ascites Club as increase to serum creatinine of 0.3 mg/dL in <48 h or 50% increase in serum creatinine from baseline value within ≤3months.

The follow-up was performed until the patient was last seen or death.

Results: 412 cirrhotic patients were evaluated during the study period and 133 fulfilled the inclusion criteria and were included in the final analysis. The mean age of patients was 57.1 ± 10.2 years (60.1% males), 70.1% with alcoholic etiology and 48.1% with Child-Pugh A liver cirrhosis.

The median follow-up was 21 (0.5–36) months. Acute kidney injury was diagnosed in 26/133 (19.5%) of patients, while CCM (systolic and/or diastolic dysfunction) was present on 15% of patients.

The presence of acute kidney injury was correlated in univariate analysis with presence of CCM, Child-Pugh score, MELD score, alcoholic etiology of liver cirrhosis and prothrombin time (Table). In multivariate logistic regression analysis only CCM and alcoholic etiology remained significantly associated with AKIN: CCM –OR = 13.6 per patient per year) of other major complications was also reported in LTA patients: spontaneous bacterial peritonitis (0.19 vs 0.09), hepatorenal syndrome (0.28 vs 0.16) and hepatic encaphaleopathy (0.40 vs 0.31). Hospitalisations were 2.40 and 2.85 per patient per year in LTA and non-LTA groups, respectively. Differences were maintained when comparing patients within age groups (≤39, 40–59, ≥60 years).

Conclusion: These real-world data captured through an audit methodology indicate that Italian hepatologists consider LTA a valuable approach for the medical management of decompensated cirrhosis, as LTA is currently prescribed in a vast proportion of patients with ascites. Although the present study does not allow the comparison of the two groups, the lower incidence of paracentesis and complications observed in patients receiving LTA is consistent with the benefits documented by the ANSWER trial. Considering this, the cost-effectiveness of LTA and potential for reducing the economic burden upon healthcare systems should be assessed.
Non-invasive assessment of liver disease except NAFLD

OS013
Association of long term methotrexate therapy with liver fibrosis markers: a multi-centre prospective case-control study
Edmond Atallah1,2, Jane Grove1,4, Colin Crooks1,4, Esther Burden-teh3, Ruth Murphy1, Sulleman Moreea, Abhishek Abhishek6, Kelsey Jordan7, Aftab Ala1, David Hutchinson3, Richard Aspinal10, Guruprasad Athial1,2. 1University of Nottingham, Nottingham Digestive Diseases Centre, School of Medicine, Nottingham, United Kingdom; 2Nottingham University Hospitals NHS Trust and the University of Nottingham, National Institute for Health Research (NIHR) Nottingham Biomedical Research Centre, Nottingham, United Kingdom; 3University of Nottingham, Centre of Evidence Based Dermatology, School of Medicine, Nottingham, United Kingdom; 4Sheffield Dermatology Research, University of Sheffield, Sheffield, United Kingdom; 5Bradford Teaching Hospitals NHS Foundation Trust, Bradford, United Kingdom; 6Nottingham University Hospitals NHS Trust Queen's Medical Centre Campus, United Kingdom; 7Brighton and Sussex University Hospitals NHS Trust, Brighton, United Kingdom; 8Royal Surrey County Hospital, Surrey, United Kingdom; 9Royal Cornwall Hospitals NHS Trust, Cornwall, United Kingdom; 10Portsmouth Hospitals University NHS Trust, Portsmouth
Email: edmond.atallah@nottingham.ac.uk

Background and aims: Incidence of acute drug-induced liver injury due to methotrexate (MTX) reduces significantly after the first year of treatment. However, decompensated cirrhosis attributed to MTX might have been overestimated. The degree of inflammatory drugs was associated with ELF score ≥0.8, OR = 1.78 (1.22–2.60), p = 0.003.

Conclusion: Lack of association of MTX cumulative dose and duration with liver fibrosis in RA or PS indicates that the risk of liver fibrosis due to MTX itself might have been overestimated. The degree of inflammation in RA and PS may confuse ELF as a marker to detect fibrosis.

Table: Demographic and phenotypic features for cases and controls

<table>
<thead>
<tr>
<th>Characteristics</th>
<th>MTX group (n = 876)</th>
<th>Control group (n = 123)</th>
<th>p</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age (years), mean (SD)</td>
<td>61.6 (11.6)</td>
<td>55.6 (13.5)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Female, n (%)</td>
<td>560 (63.9)</td>
<td>62 (50.4)</td>
<td>&lt;0.01</td>
</tr>
<tr>
<td>Diagnosis, n (%)</td>
<td>100 (11.6)</td>
<td>21 (17.1)</td>
<td>NS</td>
</tr>
<tr>
<td>RA</td>
<td>615 (70.2)</td>
<td>67 (54.5)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>PS</td>
<td>241 (27.5)</td>
<td>1 (0.8)</td>
<td>NS</td>
</tr>
<tr>
<td>Both</td>
<td>20 (2.3)</td>
<td>25 (20.3)</td>
<td>0.001</td>
</tr>
<tr>
<td>Type 2 Diabetes</td>
<td>100 (11.5)</td>
<td>25 (20.3)</td>
<td>NS</td>
</tr>
<tr>
<td>Hypertension</td>
<td>225 (25.9)</td>
<td>25 (20.3)</td>
<td>NS</td>
</tr>
<tr>
<td>BMI (kg/m²), mean (SD)</td>
<td>29.9 (6.7)</td>
<td>30.9 (7.5)</td>
<td>NS</td>
</tr>
<tr>
<td>Alcohol &gt;14 units/week, n (%)</td>
<td>83 (9.5)</td>
<td>25 (20.3)</td>
<td>NS</td>
</tr>
<tr>
<td>Fibrosis markers</td>
<td>731 (85.5)</td>
<td>25 (20.3)</td>
<td>0.08</td>
</tr>
<tr>
<td>TE groups, n (%)</td>
<td>202 (25.7)</td>
<td>34 (27.5)</td>
<td>NS</td>
</tr>
<tr>
<td>Low risk &lt;9.8</td>
<td>202 (25.7)</td>
<td>34 (27.5)</td>
<td>NS</td>
</tr>
<tr>
<td>Moderate risk (≥9.8 to &lt;11.3)</td>
<td>23 (2.9)</td>
<td>3 (2.5)</td>
<td>NS</td>
</tr>
<tr>
<td>High risk ≥11.3</td>
<td>23 (2.9)</td>
<td>7 (5.7)</td>
<td>NS</td>
</tr>
</tbody>
</table>

NS: Not significant.

OS014
Development and validation of a machine learning-based model for varices screening in compensated cirrhosis (CHESS2001): an international multicenter study
Yifei Huang1, Jia Li1, Tian-lei Zheng2, Dong Ji4, Yu Jun Wong5, Hong You6, Ye Gu7, Musong Li8, Lili Zhao2, Sheng Geng3, Na Yang1, Guofeng Chen1, Yan Wang1, Manoj Kumar9, Ankur Jindal10, Qin Wei8, Zhenhuai Chen8, Yongning Xin10, Zicheng Jiang11, Xiaoling Chi12, Jilin Chen13, Mingxin Zhang14, Huan Liu14, Ming Lu15, Li Li15, Yong Zhang16, Chunwen Pu16, Deqi Yang17, Qin He18, Shanghong Tang19, ChunYan Wang19, Shiv Kumar Sarin3, Xiaolong Qi1. 1The First Hospital of Lanzhou University, CHESS Center, Institute of Portal Hypertension, Lanzhou, China; 2Tianjin Second People’s Hospital, Department of Gastroenterology and Hepatology, Tianjin; 3The Affiliated Hospital of Xuzhou Medical University, Artificial Intelligence Unit, Department of Medical Equipment, Xuzhou, China; 4The Fifth Medical Center of Chinese PLA General Hospital, Department of Liver Diseases, Beijing, China; 5Changji General Hospital, Duke-NUS Academic Clinical Program, SingHealth, Department of Gastroenterology and Hepatology, Singapore, Singapore; 6Beijing Friendship Hospital, Capital Medical University, Liver Research Center, Beijing Key Laboratory of Translational Medicine in Liver Cirrhosis, National Clinical Research Center of Digestive Diseases, Beijing, China; 7The Sixth People’s Hospital of Shenyang, Portal

Results: Of 999 patients included (mean age 60.8 ± 12 years, 622 females (62.3%)), 576 had valid TE values; 149 (15.3%) had liver stiffness ≥7.9 KPa. Of 892 with available ELF 262 had ELF score ≥9.8 (29.4%). Age and BMI were independently associated with elevated liver stiffness and ELF. Diabetes was associated with significant fibrosis defined by liver stiffness ≥7.9 KPa, OR = 3.21 (1.96–5.21), p < 0.001. But, neither MTX cumulative dose nor duration of exposure was associated with elevated liver stiffness [OR = 1.02 (0.93–1.12) and 1.00 (0.99–1.0), respectively] and ELF score [OR = 1.06 (1.0–1.12) and 1.00 (0.99–1.0), respectively]. Regular use of non-steroidal anti-inflammatory drugs was associated with ELF score ≥0.8, OR = 1.78 (1.22–2.60), p = 0.003.

Table: Demographic and phenotypic features for cases and controls
Hypertension Center, Shenyang, China; Baoding people’s Hospital, Department of Gastroenterology, Baoding, China; Institute of Liver and Biliary Sciences (ILBS), Department of Hepatology, New Delhi, India; Qingdao Municipal Hospital, Qingdao University, Department of Infectious Disease, Qingdao, China; Ankang Central Hospital, Department of Infectious Diseases, Ankang, China; Guangdong Provincial Hospital of Chinese Medicine, The Second Affiliated Hospital of Guangzhou University of Chinese Medicine, Department of Hepatology, Guangzhou, China; Shanghai Public Health Clinical Center affiliated to Fudan University, Department of Gastroenterology and Hepatology, Shanghai, China; The First Affiliated Hospital of Xi’an Medical University, Department of Gastroenterology, Xi’an, China; Mengzi People’s Hospital, Department of Gastroenterology, Mengzi, China; Dalian Public Health Clinical Center, Dalian, China; Taibe Hospital, Hubei University of Medicine, Department of Infectious Diseases, Shiyan, China; Second Hospital of Nanjing, Nanjing Hospital of Chinese Medicine, Department of Gastroenterology, Nanjing, China; General Hospital of Western Theater Command PLA, Department of Gastroenterology, Chengdu, China

Email: qixiaolong@vip.163.com

Background and aims: Only a few patients with compensated cirrhosis who underwent esophagogastroduodenoscopy (EGD) screening for varices were found to have varices needing treatment (VNT). Our study aimed to identify a novel machine learning-based model (ML EGD) for ruling out VNT and avoiding unnecessary EGD in patients with compensated cirrhosis.

Method: A total of 2794 patients from China, Singapore and India were enrolled. Of them, 1283 patients in a real-world cohort from one university hospital, 966 in a multicenter cohort (test cohort 1) from 14 university hospitals, and 545 in an international cohort (test cohort 2) from Singapore and India were included, respectively. For the real-world cohort, patients were shuffled and sampled randomly into training and validation cohort with a ratio of 9:1. In the training cohort, a light gradient boosting machine algorithm was used to develop the pre-model to detect VNT using clinical data. A shapley value method was used to evaluate the importance of included variables according to pre-model. ML EGD was furthermore developed based on the most related variables to detect VNT using light gradient boosting machine algorithm. Then, we validated it in the validation cohort and tested it in the two external test cohorts.

Results: The main etiology of cirrhosis was hepatitis B infection in the training (68.02%), validation cohort (68.99%) and test cohort 1 (79.19%) and the main etiology in test cohort 2 was hepatitis C infection (47.16%). Liver stiffness, platelet count and total bilirubin were evaluated as the most related variables to detect VNT to develop ML EGD. By receiver operator characteristic curve, the most accurate cut-off to rule out patients with VNT was chosen as a ML EGD below 0.50 with a negative predictive value of 96.4%. In the training cohort, a ML EGD below 0.50 could spare 607 (52.6%) unnecessary EGD with a missed VNT rate of 3.6%. In the validation cohort, test cohort 1 and test cohort 2, a ML EGD score below 0.50 could spare 75 (58.1%), 506 (52.4%), 224 (41.1%) EGD with a missed VNT rate of 1.4%, 2.8%, and 3.1%, respectively. Comparing with Baveno VI criteria, ML EGD improved the proportion of avoided EGD (training cohort: 52.6% vs 29.4%; validation cohort: 58.1% vs 44.2%; test cohort 1, 52.4% vs 26.5%; test cohort 2, 41.1% vs 21.1%).

Conclusion: We developed a robust machine learning-based model, named ML EGD, with excellent performance to exclude VNT in patients with compensated cirrhosis.

OS015
Diagnostic performance of non-invasive liver fibrosis biomarkers: a bayesian individual patient data meta-analysis of hepatitis B cohorts in sub-saharan Africa (HEPSANET)
Alexander Stockdale1,2, Asgeir Johannessen3,4, Marc Henrion2,5, Edith Okeke6, Moussa Seydi7, Gilles Wandeler8, Mark Sonderup9, Wendy Spearman2, Michael Vinikoor2,10,11, Edford Sinkala12, Hailemichael Desalegn13, Fatou Fall13, Nicholas Riches14, Dawwar Pantong Mark14, Mary John Duguri15, Tongai Gibson Maponga16, Jantjie Taljaard16, Philippa Matthews17, Monique Andersson17, Roger Sombie18, Yusuke Shimakawa19, Maud Lemoine20,1 University of Liverpool, Liverpool, United Kingdom; 2Malawi-Liverpool-Wellcome Trust Clinical Research Programme, Blantyre, Malawi; 3Sykehuset i Vestfold, Norway; 4University of Oslo Faculty of Medicine, Norway; 5Liverpool School of Tropical Medicine, United Kingdom; 6Faculty of Medical Sciences, Jos, Nigeria; 7Hepatitis Center University De Fann, Dakar, Senegal; 8Institute of Social and Preventive Medicine (ISPM), Bern, Switzerland; 9UCT Faculty of Health Sciences, Cape Town, South Africa; 10The University of Zambia, Lusaka, Zambia; 11University of Alabama at Birmingham, Birmingham, United States; 12St. Paul’s Hospital Millennium Medical College, Addis Ababa, Ethiopia; 13Hospital Principal de Dakar, Dakar, Senegal; 14University of Jos, Jos, Nigeria; 15University of Jos, Jos, Nigeria; 16Stellenbosch University, Stellenbosch, South Africa; 17University of Oxford, United Kingdom; 18Hospital Center Universitaire Yalgado Ouédraogo, Ouagadougou, Burkina Faso; 19Pasteur Institute, Paris, France; 20Imperial College London, United Kingdom

Email: a.stockdale@liverpool.ac.uk

Background and aims: In sub-Saharan Africa, hepatitis B is the principal cause of liver disease, and associated mortality is rising.
Low-cost non-invasive biomarkers of liver fibrosis are needed to identify patients at risk of HBV-related mortality who therefore require antiviral treatment. We evaluated the performance of the biomarkers APRI (AST to platelet ratio index), FIB-4 and GPR (GGT to platelet ratio) in an individual patient data (IPD) meta-analysis.

**Method:** We included data from HEPSANET, a network comprised of 12 cohorts of HBsAg-positive individuals in 8 sub-Saharan African countries. We used transient elastography as a reference test for cirrhosis (≥12.2 kPa) and significant fibrosis (≥7.9 kPa). We excluded patients who were pregnant, had hepatitis C, D, or HIV co-infection, were on hepatitis B therapy or had acute hepatitis. Upper limits of normal were 40 U/L for AST/AST and 61 U/L for GGT. We fitted a bivariate Bayesian IPD model with patient-level covariates and study-level random effects.

**Results:** We included 3549 patients. Median age was 33 years (IQR 28–41) and 60% were male. The prevalence of significant fibrosis and cirrhosis among included cohorts was 18% and 7%, respectively. APRI and GPR had the best discriminant performance (area under curve (AUC) for cirrhosis of 66.7% and specificity of 80.6% and 64.3%; GPR (0.23) had sensitivity 80.6% and specificity 90.0%; GPR (cut-off 0.47) had sensitivity of 58.6% and specificity 90.9%. At rule-out thresholds for cirrhosis APRI (0.33) had sensitivity and specificity of 80.6% and 64.3%; GPR (0.23) had sensitivity 80.6% and specificity of 66.7% (Figure). The subset of asymptomatic patients who were diagnosed with HBV through routine screening had a mean cirrhosis prevalence of 2.5%, and APRI (cut-off 0.65) had a positive predictive value (PPV) of 13.2% and negative predictive value (NPV) of 98.8%. Among patients diagnosed with HBV due to suspected liver disease, cirrhosis prevalence was 27%; with APRI cut-off 0.65, PPV was 59.6% and NPV 84.5%.

**Conclusion:** APRI at the WHO-recommended threshold of 2.0 has a poor sensitivity for the diagnosis of cirrhosis in sub-Saharan Africa; WHO guidelines should be revised for the WHO African region to reflect these findings. APRI and GPR had equivalent diagnostic performance and performed best at ruling out cirrhosis but were less good at correctly identifying cases. Programs need to be aware of the significant trade-offs between under- and over-diagnosis of liver cirrhosis when implementing low-cost fibrosis markers in hepatitis B programs in sub-Saharan Africa.

**Performance of non-invasive biomarkers for the diagnosis of cirrhosis (≥12.2 kPa).**

### OS016

**Prediction of ten-year risk of severe liver disease in the general population using commonly available biomarkers**

Hannes Hagström1, Jacinth Yan2, Mats Talbäck2, Anna Andreasson3, Göran Walldius3, Matteo Bottai4, Niklas Hammar2, Karolinska Institutet; Karolinska Institutet, Stockholm University, Sweden

**Background and aims:** Estimating risk for severe liver disease, including cirrhosis, in the general population is complicated in part due to the rarity of this outcome. Existing prediction tools are suboptimal and there is a need for improvement. Here, we aimed to identify subgroups of persons in the general population with high risks for development of severe liver disease using commonly available biomarkers.

**Method:** We used laboratory and clinical data on 126,925 individuals aged 35–79, in Stockholm, Sweden, with clinical examinations between 1985 and 1996. No individuals had known chronic liver disease, a drug- or alcohol use disorder at baseline. Nationwide registries were used to ascertain ten-year cumulative incidence of severe liver disease, a composite of diagnoses corresponding to cirrhosis or its complications. Candidate biomarkers were selected based on if they meaningfully improved prediction of severe liver disease in addition to the established FIB-4 score. They were then categorized and combined, creating subgroups with different risk profiles.

**Results:** During a follow-up of average 9.3 years, we ascertained 630 incident cases of severe liver disease (0.5%). On top of the FIB-4 score we identified age, impaired glucose, and gamma-glutamyl transferase (gGT) to meaningfully improve a classification of risk. 24 risk groups were created, with a cumulative incidence of severe liver disease at ten years ranging from 0.2% (age 35–65, low FIB-4, no impaired glucose and normal gGT) to 32.1% (age 35–65, high FIB-4, impaired glucose and high gGT). A heatmap of these risk groups was created (Figure 1).

### Cumulative incidence of severe liver disease at ten years

<table>
<thead>
<tr>
<th>gGT high</th>
<th>Impaired glucose</th>
<th>Non impaired glucose</th>
</tr>
</thead>
<tbody>
<tr>
<td>age ≥ 66</td>
<td>13.0</td>
<td>2.6</td>
</tr>
<tr>
<td>age 35–65</td>
<td>3.8</td>
<td>0.0</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>gGT normal</th>
<th>Impaired glucose</th>
<th>Non impaired glucose</th>
</tr>
</thead>
<tbody>
<tr>
<td>age ≥ 66</td>
<td>13.9</td>
<td>2.8</td>
</tr>
<tr>
<td>age 35–65</td>
<td>0.6</td>
<td>0.0</td>
</tr>
</tbody>
</table>

Figure 1: Heatmap of subgroups with differing risk for severe liver disease at ten years, in percent.

**Conclusion:** Estimates of risk of severe liver disease in the general population using the FIB-4 score can be substantially improved by adding age and biomarkers commonly available in the primary care setting.

**OS017**

Gadoxetic acid-enhanced MRI-derived Functional Liver Imaging Score (FLIS) and spleen diameter provide complementary information for risk stratification in ACLD

Nina Bastati1, Lucian Beer1, Ahmed Ba-Salamah1, Sarah Poetter-Lang1, Raphael Ambros1, Antonia Kristic1, David Lauber1, Lorenz Balcar1, Katharina Pomjej, Teresa Binter2, Benedikt Simbrunner2, Georg Semmle1,2, Yesim Bican1, Jacqueline C. Hodge1, Thomas Weba1, Michael Trauner2, Thomas Reiberger2,3, Mattias Mandorfer2,3,1Department of Biomedical Imaging and Image-Guided Therapy, Medical University of Vienna, Vienna, Austria;2Division of Gastroenterology and Hepatology, Department of Internal Medicine III, Medical University of Vienna, Vienna, Austria;3Vienna Hepatic Hemodynamic Lab, Division of Gastroenterology and Hepatology, Department of Internal Medicine III, Medical University of Vienna, Vienna, Austria;4IT-Systems and Communications, Medical University of Vienna, Vienna, Austria

**Background and aims:** The Functional Liver Imaging Score (FLIS) derived from gadoxetic acid-enhanced MRI (GA-MRI) correlates with hepatic function in chronic liver disease (CLD) patients. Splenic metrics, i.e., volume and craniocaudal diameter (SCCD) are markers of portal hypertension, a key driver of disease progression.
We aimed to investigate the prognostic utility of FLIS and SCCD for hepatic decompensation and transplant-free mortality in CLD.

Method: Three hundred ninety-seven CLD patients undergoing GA-MRI were included. The FLIS was calculated by summing the points (0–2 each) assigned to three hepatobiliary phase features: hepatic enhancement, biliary excretion, and portal vein signal intensity. Patients were stratified into 3 clinical groups according to FIB-4 and presence/history of decompensation: non-advanced CLD (non-ACLD), compensated ACLD (cACLD), and decompensated ACLD (dACLD). The associations between SCCD/FLIS and decompensation/transplant-free mortality were investigated using Cox regression analysis and log-rank test.

Results: We observed a strong correlation between spleen volume and SCCD (Spearman’s rho: 0.887; p < 0.001), and thus, the simple measure SCCD was used for further analyses. The inter-reader (intraclass coefficient, ICC: 0.982; n = 241) and intra-reader (ICC: 0.997; n = 41) agreement for the SCCD were excellent. Median SCCD showed stepwise increases from non-ACLD (11.8 cm), cACLD (13.3 cm), to dACLD (15.2 cm; p < 0.001).

Since non-ACLD patients are at negligible risk of decompensation/liver-related death, we abstained from analysing direct end points in this subgroup. In patients with cACLD, SCCD predicted decompensation (adjusted-hazard-ratio, [aHR]: 1.1, 95% confidence interval [95% CI]: 1.02–1.18; p = 0.014) in an analysis adjusted for MELD and albumin; dichotomizing SCCD resulted in an aHR of 2.51 (95%CI: 1.22–5.21, p = 0.001) for those with a SCCD >13 cm. In patients with ACLD (i.e., cACLD/dACLD combined), FLIS (0–3 vs. 4–6 points) was a risk factor for transplant-free mortality (aHR: 2.64, 95%CI: 1.61–4.01, p < 0.001), even after adjusting for age, MELD, and albumin. Of note, FLIS (0–3 vs. 4–6 points; aHR: 1.74, 95%CI: 1.18–2.58, p = 0.005) and SCCD (>13 vs. ≤13 cm; aHR: 2.16, 95%CI: 1.44–3.24, p < 0.001) were independently predictive of the composite end point of decompensation/transplant-free mortality, even after adjusting for the previously mentioned prognostic indicators. Grouping patients according to FLIS/SCCD accurately stratified the risk of decompensation/transplant-free mortality (Figure).

Conclusion: The FLIS and SCCD are simple GA-MRI-based imaging markers providing complementary information for risk stratification in patients with advanced chronic liver disease.

N.B. and L.B. contributed equally.

ORAL PRESENTATIONS

OS018
ADAPT, a score incorporating PRO-C3, for the early detection of liver fibrosis in a large population-based study
Ann T. Ma1,2,3, Guillem Pera1,4, Martina Perez1,2,3,5, Mette Juul Nielsen6, Morten Karsdal6, Diana Leeming6, Carmen Expósito4, Alba Martínez-Escudé4,7, Isabel Graupera1,2,3,5, Maja Thiele6,9, Aleksander Krat8,9, Núria Fabrellas2,3,5, Llorenc Caballeria3,4, Pere Ginés1,2,3,5, 1Liver Unit, Hospital Clinic de Barcelona, Barcelona, Spain; 2Institut d’Investigacions Biomèdiques August Pi i Sunyer (IDIBAPS), Barcelona, Spain; 3Centro de Investigación Biomédica en Red de Enfermedades Hepática y Digestivas (CIBEREHD), Madrid, Spain; 4Unitat de Suport a la Recerca (USR) Metropolitana Nord, Fundació Institut Universitari d’Investigació en Atenció Primària Jordi Gol i Gurina (IDIP Jordi Gol), Mataró, Spain; 5Facultat de Medicina-Universitat de Barcelona, Barcelona, Spain; 6Nordic Bioscience, Herlev, Denmark; 7Centre d’Atenció Primària La Llagosta, La Llagosta, Spain; 8Department of Gastroenterology and Hepatology, Odense University Hospital, Denmark; 9Department of Clinical Research, Faculty of Health Sciences, University of Southern Denmark, Odense, Denmark
Email: pgines@clinic.cat

Background and aims: Non-invasive screening of liver fibrosis in the general population has become an important target in order to identify liver disease early and avoid its progression. Novel biomarkers of extracellular matrix formation, including PRO-C3, a marker of type III collagen formation, have emerged as accurate predictors of advanced fibrosis in NAFLD and alcohol-related liver disease. A composite score known as ADAPT, that includes PRO-C3, age, platelet count, and diabetes, has recently been validated in both these patient populations, but its effectiveness to screen for liver fibrosis in asymptomatic subjects in the general population is unknown.

Method: This study was performed in a large population-based cohort of randomly selected subjects aged 18–75 in the Barcelona metropolitan area without known liver disease (mean age 54, 43% male, 10% with type 2 diabetes, 28% with metabolic syndrome, 9% with at-risk alcohol consumption). Serum PRO-C3 levels were measured by enzyme-linked immunosorbent assay in 2670 subjects. Liver fibrosis was estimated by measuring liver stiffness with transient elastography (TE). Significant fibrosis was defined as a TE ≥9.2 kPa based on previous data supporting that this cut-off had the best diagnostic accuracy for fibrosis ≥F2 on liver biopsy (Clin. Gastroenterol. Hepatol. 2018 PMID 29452268).

Results: The prevalence of significant fibrosis was 3.1% (83/2670). The median level of PRO-C3 was higher in subjects with significant fibrosis compared to those without (14 vs. 12 ng/ml, p < 0.001). The ADAPT score predicted significant fibrosis with moderate accuracy (AUROC 0.76; 95% CI 0.71–0.82), higher than scores frequently used to identify fibrosis in the general population, such as FIB-4 or APRI, and similar to NAFLD Fibrosis Score (NFS). Fatty liver index (FLI) exhibited the highest discriminative ability (AUROC 0.87; 95% CI 0.84–0.91; Figure 1). Amongst subjects with metabolic/alcohol risk factors and a high FLI≥60, the sequential use of ADAPT using the best cut-off of 6.1 had an excellent negative predictive value for significant fibrosis (Se 51%, Sp 82%, PPV 20%, NPV 95%).
ORAL PRESENTATIONS

Immune-mediated and cholestatic: Experimental and pathophysiology

OS019
Novel anti-cholestatic treatment strategies by combining inhibition of the Apical sodium-dependent bile acid transporter with stimulation of urinary bile salt excretion or lowering bile salt synthesis
Roni Kunst 1,2, Esther Vogels 1, Isabelle Bolt 1, Ronald Ouode-Ellerink 1,2, Stan van de Graaf 1,2. Tytgat Institute for Liver and Intestinal Research, Department of Gastroenterology and Hepatology; 2Amsterdam Gastroenterology Endocrinology Metabolism, Amsterdam, Netherlands

Background and aims: The apical sodium-dependent bile acid transporter (ASBT) is primarily expressed in the small intestine and kidney, where it prevents bile salts from being excreted in respectively feces and urine. Intestine-restricted drugs that inhibit ASBT are currently clinically explored to reduce toxic accumulation of bile acids during cholestasis. Intestine-restricted ASBT inhibitors (ASBTi) may be less effective in severe cholestasis and also yield gastrointestinal side-effects in case of high bile salt load in the colon. Here, we test two ASBT-targeting treatment strategies in pre-clinical models with cholestasis-induced liver injury. First, systemic ASBT inhibition, to increase renal bile acid excretion and second a combination treatment with obeticholic acid (OCA) to limit bile salt synthesis and reduce colonic bile acid load. Method: Systemic ASBT inhibition was tested by performing a bile duct ligation (BDL) in adult ASBT knock-out (KO) mice (129P2/OlaHsd background, Jackson) and wild-type littermates to induce severe cholestasis. In our second strategy, BDL was performed in adult wild-type C57Bl/6 mice after 2 days oral gavage pre-treatment with OCA and ASBTi. In a different model, wild-type C57Bl/6 mice were fed a 0.1% 3, 5-diethoxycarbonyl-1, 4-dihydronicollidine (DDC) diet while receiving daily treatment with either placebo, OCA, ASBTi or both (OCA + ASBTi). After sacrifice, liver injury was determined by plasma liver enzymes, RT-qPCR and liver histology, while HPLC analysis was used to quantify bile salt concentrations in plasma, liver, small intestine and feces.

Results: ASBT KO mice had reduced liver necrosis, reduced bilirubin and alkaline phosphatase (ALP) levels compared to wild-type mice after BDL. ASBT KO mice also showed a trend to reduced bile salt pool size, and increased urinary bile salt excretion. OCA + ASBTi treatment reduced the total bile salt pool size before cholestasis-onset and resulted in reduced bilirubin, ALP and a ∼60% reduction in liver necrosis compared to placebo control in a BDL model. Besides, OCA + ASBTi treatment decreased fecal bile salt excretion compared to monotherapy with ASBTi.

Conclusion: Systemic ASBT inhibition effectively reduces BDL-induced liver damage. Combined OCA + ASBTi treatment lowers the bile salt pool size and improves liver health after BDL-induced cholestasis, while it also shows therapeutic potential by reducing fecal bile salt excretion.

OS020
Low-dose IL-2 alleviates drug-induced primary biliary cholangitis in mice by improving Treg and Th17 balance
Zilong Wang 1, Bo Feng 1, Yandi Xie 1, Rui Jin 1, Zhicheng Liu 1. Peking University Hospitality Institute, Beijing, China

Background and aims: The imbalance of regulatory T (Treg) and T helper 17 (Th17) cells correlates with increased risk of autoimmune diseases. Their imbalance was also reported in primary biliary cholangitis (PBC) patients. Previous studies have suggested that low-dose IL-2 can alleviate disease severity through modulating CD4+ T cell subsets in patients with autoimmune diseases. However, the efficacy of low-dose IL-2 in PBC remains unexplored. Hence, the present study aimed to examine effects of low-dose IL-2 in PBC mouse models.

Method: PBC was induced in female C57BL/6 mice by two immunizations with 2-nonynoic acid (20A-BSA) at two-week intervals. Besides, polynosinic polycytidylic acid (poly I:C) was injected i.p. every three days. The control group was injected with PBS instead of 20A-BSA and poly I:C. PBC mice were divided into the treated and untreated groups, and low-dose IL-2 was injected s.c. every three days after four weeks from modeling in the treated group (Fig. A) and the untreated group was replaced with saline. The serum was isolated from blood sampled by eyeball extirpating for biochemical detection. Th17 and Tregs were analyzed by flow cytometry, and the related cytokines were analyzed by ELISA. Liver histopathology was examined by H&E and immunohistochemical staining. The experimental data were analyzed by SPSS 24.0 software. P < 0.05 indicated statistical significance.

Results: Eight weeks after modeling, the serum AMA was positive and the ALP was significantly increased in PBC mice compared with control group. The pathology showed lymphocyte infiltration in the portal area, and damage and reactive proliferation of small bile duct, and CD4+ and CD8+ T cells were infiltrated around the bile duct. Flow cytometric examination of spleen cells revealed recovery of reduced Tregs and increased Th17 after low-dose IL-2 treatment (Treg/CD4+: 9.26 ± 0.50 vs 6.10 ± 0.14 vs 8.24 ± 0.04; Th17/CD4+: 0.29 ± 0.20 vs 1.00 ± 0.17 vs 0.33 ± 0.09) (∗p < 0.05) (Fig. B). Low-dose IL-2 treatment inhibited IL-17A levels (0 vs 4549 ± 597 vs 1928 ± 387) (∗p < 0.05) and improved serum biochemical index (ALP: 119.1 ± 62.0 vs 82.36 ± 12.6 U/L) (Fig. C). Histopathological examination of liver revealed the improvement of portal area inflammation and reactive bile duct hyperplasia and damage after low-dose IL-2 treatment (Fig. D).
Method: CD100 expression was assessed by spatial transcriptomics and its relevance to the differentiation of pathogenic immune cells. We investigated how CD100 participates in the biliary local inflammation for a familial form of primary sclerosing cholangitis (PSC). Herein, we have recently reported a variant of CD100 to be the causal mutation in the mechanism enabling pathogenic immune cells to adapt and contribute to the disease pathogenesis of most cholangiopathies, but the background and aims:

Email: espen.melum@medisin.uio.no

Centre of Excellence, Institute of Basic Medical Sciences, Faculty of Medicine, University of Oslo, 0317 Oslo, Norway; 3Institute of Clinical Medicine, University Hospital Rikshospitalet, 0424 Oslo, Norway; 4Chemomab Therapeutics Ltd., Tel-Aviv, Israel; 5Chemomab Therapeutics Ltd., Tel-Aviv, Israel; 6Section of Gastroenterology and Hepatology, Karolinska University Hospital Huddinge, Karolinska Institutet, 141 52 Stockholm, Sweden; 7Department of Gastroenterology and Hepatology, Karolinska University Hospital Huddinge, Karolinska Institutet, 171 77 Stockholm, Sweden; 8Section of Gastroenterology, Department of Transplantation Medicine, Division of Surgery, Inflammatory Diseases and Transplantation, Oslo University Hospital Rikshospitalet, 0424 Oslo, Norway; 9Hybrid Technology Hub-Centre of Excellence, Institute of Basic Medical Sciences, Faculty of Medicine, University of Oslo, Oslo, Norway.

Background and aims: Chronic inflammation surrounding bile ducts contributes to the disease pathogenesis of most cholangiopathies, but the mechanism enabling pathogenic immune cells to adapt and survive in the biliary environment remains largely unknown. We have recently reported a variant of CD100 to be the causal mutation for a familial form of primary sclerosing cholangitis (PSC). Herein, we investigate how CD100 participates in the biliary local inflammation and its relevance to the differentiation of pathogenic immune cells.

Method: CD100 expression was assessed by spatial transcriptomics (10x Genomics) and in situ immunohistochemistry (IHC) in explanted livers of patients with PSC (n = 4–6) and other cholangiopathies (Ctrl, n = 4–5). Soluble CD100 (scCD100) was measured by ELISA in paired serum, plasma, and bile samples (n = 11–19). Biliary infiltrating immune cells were collected from endoscopic retrograde cholangiopancreatography brush samples (Ctrl, n = 6; PSC, n = 6) and surface expression of CD100 was evaluated by flow cytometry. To model pathogenic interactions between immune cells and cholangiocytes, splenic cells isolated from C57BL/6 wild-type (WT) and CD100 mutated mice were co-cultured with small or large cholangiocytes. Altered gene expression was assessed with RNA sequencing of purified cell subsets after co-culture.

Results: Spatial transcriptomics revealed SEMA4D/CD100 RNA expression in all examined livers and demonstrated the localization in KRT19 bile duct regions (Ctrl, 7–40%; PSC, 11–94%). In contrast, CD100 protein expression measured by IHC was nearly undetectable in diseased periductal areas of the PSC livers. Moreover, surface expression of CD100 on biliary infiltrating immune cells was reduced and accompanied by increased scCD100 in plasma and bile from PSC patients, suggesting that CD100 is cleaved from the surface of immune cells in regions adjacent to the bile ducts. In co-culture experiments, we observed that activated immune cells adhered to cholangiocytes and correlated with the death of large but not small cholangiocytes. T cells were dominant (49.9–64.4%) in the adherent immune population and lost their surface CD100 expression. RNA sequencing data showed increased Adams4 in co-cultured cholangiocytes which appeared to cleave CD100. Genes involved in anti-apoptosis and T-helper 17 (Th17) differentiation were enriched in adherent T cells and further upregulated in T cells with mutated CD100.

Conclusion: Cholangiocytes induce cleavage of CD100 on biliary infiltrating T cells that facilitates persistent inflammation and local Th17 differentiation. These findings highlight a novel pathway in the liver with cholangiocyte-driven Th17 cell differentiation that is associated with CD100 cytoplasmin signaling. Targeting this pathogenic pathway serves as an attractive target for mitigating bile duct inflammation in PSC.

OS022 Novel approach combining whole liver single-cell RNA sequencing and spatial gene profiling using NanoString GEOMX enables identification of specific cell sub-populations and pathways regulated by CCL24

Michal Segal-Saltco1, Raanan Greenman1, Arnon Aharon5, Ophir Hay3, Amnon Peled2, Adi Mor4, Chemomab Therapeutics Ltd., Tel-Aviv, Israel; 2Chemomab Therapeutics Ltd., Tel-Aviv, Israel.

Background and aims: CCL24 (Eotaxin-2) is a chemokine that regulates profibrotic and proinflammatory activities through the CCR3 receptor. We previously demonstrated that CM-101, a CCL24 blocking antibody, improves liver inflammation, fibrosis and cholangitis in the Mdr2 knockout (Mdr2−/−) mouse model. Characterization of CCL24 expression in relation to the different cell populations in Mdr2−/− mice and its inhibition effect on cholangiocytes and immune response was studied using two gene expression methods.

Method: Identification of cell population, including immune cells and CCL24 expressing cells in livers of Mdr2−/− mice was done by scRNA seq from whole liver. NanoString’s technology was utilized for gene expression studies, focusing on the bile-duct injury sites. In this system segmenting of cholangiocytes (Pan-Ck+) and immune cells (Pan-Ck−) cells was done in liver sections from Mdr2−/− mice treated or treated with CM-101.

Results: Mdr2−/− mice treated with CM-101 resulted in reductions in serum ALP, liver inflammation, liver peribiliary collagen deposition and cholangiocytes proliferation. Using whole liver scRNA seq we demonstrated that CCL24 is expressed in macrophage cells. This analysis identified a few specific disease relevant immune sub-populations, however it is missing crucial information that relates to cell localization. To overcome this, we used NanoString to characterize the alternations in peribiliary transcriptome following CM-101 treatment. Spatial profiling separated cholangiocytes (PanCK+) and non-cholangiocytes (PanCK−) peribiliary cells, distinguishing cholestatic, proinflammatory and profibrotic effects. Gene set enrichment analysis showed reduction in proliferation and senescence pathways in PanCK+ cells, whereas PanCK− cells showed reduction in ECM remodeling pathways and increased metabolic pathways. Cell deconvolution of the heterogeneous PanCK− population revealed alternation in the peribiliary immune cells, marked by reduction in macrophages and monocytes following treatment with CM-101.
**Conclusion:** Augmenting whole liver scRNA seq with spatial transcriptome analysis, is a novel approach to identify cell populations and pathways specific to the damaged peribiliary area. Using this approach we demonstrated that CCL24 regulates cholestatic, inflammatory and fibrotic liver damage, and its underlying mechanisms. Understanding the underlying mechanisms of CCL24 blockade and its ability to prevent liver injury in animal supports its role in PSC and its potential beneficial effect for PSC patients.

### OS023

**T regulatory cells promote bile duct regeneration through modulating ductular reaction in a model of cholestatic liver injury**

Naruhiro Kimura1,2,3, Gareth Hardisty1, Atsunori Tsuchiya3, Shuji Terai1,2, David Withers2, Wei-Yu Lu1,2, 1University of Edinburgh, Centre for Inflammation Research, Edinburgh, United Kingdom; 2University of Birmingham, Institute of Immunology and Immunotherapy, Birmingham, United Kingdom; 3Niigata University, Division of Gastroenterology and Hepatology, Niigata, Japan

**Background and aims:** Reduced regulatory T cells (Tregs) and increased bile duct senescence are observed in primary sclerosing cholangitis (PSC) patients, with the degree of cholangiocyte senescence linking to disease severity and prognosis. Cholangiocytes can act as facultative liver progenitor cells through ductular reaction during extensive liver damage, whether this process is impaired during PSC remains to be investigated. The role of Tregs in modulating tissue resident progenitor cells have been shown in multiple organs, but this remains unclear in the context of liver regeneration. We aim to use transgenic murine models to investigate the cause of reduced Tregs in the liver and whether the lack of Tregs in the liver affect bile duct regeneration and senescence.

**Method:** Foxp3GFPCreERTtdTomloxSTOPlox transgenic mice were used to reduce Tregs number in a dose dependent manner. 50% of Tregs were depleted to avoid triggering systematic autoimmunity whilst cholestatic liver injury was induced by the feeding of 3, 5-diethoxycarbonyl-1, 4-dihydrocollidine (DCC) diet and compared to the control group with intact Tregs population. We generated the Foxp3GFPCreERTtdTomloxSTOPlox mice to investigate Tregs stability. Tamoxifen was injected intraperitoneally to induce tdTom expression in Foxp3 Tregs and cell fate was investigated after DDC diet to determine Tregs stability. CD4 T-cells were isolated and co-cultured with intrahepatic cholangiocytes organoids to confirm the effect of Foxp3 fate mapping experiments showed that the labelled Tregs population reduces Foxp3 expression after DDC diet indicating that the stability of Tregs decreases during liver injury.

**Conclusion:** Our results demonstrated that the role of Tregs in promoting bile duct regeneration by modulating ductular reaction through the Hippo-Yap pathway. Furthermore, the observation that Foxp3 Tregs become unstable in an injured microenvironment in mice may explain the lack of Tregs seen in PSC patients. These show the potential of using Tregs to promote liver regeneration but also highlights the stability of Tregs should be taken into consideration when designing cell based Tregs therapy.

### OS024

**Deep learning for automatic diagnosis and morphologic characterisation of malignant biliary strictures using digital cholangioscopy: a pilot study**

Miguel Mascarenhas1, João Afonso1, Tiago Ribeiro1, Ana Santos1, Heliber Cardoso2, João Pedro Sousa Ferreira2, Filipa Vilas-Boas1, Pedro Pereira1, Guilherme Macedo1, 1Centro Hospitalar Universitário de São João, Department of Gastroenterology, Porto, Portugal; 2Faculdade de Engenharia da Universidade do Porto, Department of Mechanical Engineering, Porto, Portugal

**Background and aims:** Patients with indeterminate biliary strictures (BS) pose a significant diagnostic challenge. Digital cholangioscopy (DC) has enabled morphologic characterization as well as the performance of visually guided biopsies. However, the diagnostic yield of DC remains suboptimal, and the visual characterization of these lesions has significant interobserver variability. Recently, the development of artificial intelligence (AI) algorithms, particularly convolutional neural networks (CNNs) for interpretation of endoscopic images has generated intense interest. We aimed to develop a CNN-based system for simultaneous automatic detection of malignant BS in D-SOC images and identification of three morphologic features: nodules (NN), papillary projections (PP) and tumor vessels (TV).

**Method:** We developed and validated a CNN based on DC images (Spyglass DS II, Boston Scientific, USA). Each frame was labeled as normal/benign finding or as a malignant lesion if definite histologic evidence of biliary malignancy was available. Moreover, we evaluated the performance of the CNN for the detection of morphologic features associated with histology-proved biliary malignancy: NN, PP, and TV. The image dataset was split for construction of training and validation datasets. The performance of the CNN was measured by calculating the accuracy, area under the curve (AUC), sensitivity, specificity, positive and negative predictive values (PPV and NPV, respectively).

**Results:** We included 23 595 images from 125 patients (20719 of malignant BS and 2876 of normal or benign findings). The model had a sensitivity of 98.9%, a specificity of 97.7% and an overall accuracy of 98.7%. The AUC was 1.00. Additionally, the model comprised 2876 images of NN, 1675 images showing PP, and 4153 images of TV. The accuracy for the automatic detection of each of these features was, respectively, 96.9%, 96.1%, and 91.5%.

**Conclusion:** We developed a combined CNN for automatic detection of malignant BS as well as the automatic identification of morphologic features associated with increased probability of malignancy. The application of AI models to DC may increase its diagnostic yield for patients with indeterminate BS. Furthermore, accurate real-time automatic identification of features associated with increased probability of malignancy may help to guide biopsies, thus increasing their rentability.
Table 1: Performance metrics of the combined convolutional neural network

<table>
<thead>
<tr>
<th></th>
<th>Malignant strictures (vs. normal/benign findings)</th>
<th>NN (vs normal/other findings)</th>
<th>PP (vs normal/TV vs normal/other findings)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Sensitivity</strong></td>
<td>98.9%</td>
<td>96.1%</td>
<td>98.2%</td>
</tr>
<tr>
<td><strong>Specificity</strong></td>
<td>97.7%</td>
<td>98.9%</td>
<td>94.8%</td>
</tr>
<tr>
<td><strong>PPV</strong></td>
<td>99.7%</td>
<td>99.5%</td>
<td>91.7%</td>
</tr>
<tr>
<td><strong>NPV</strong></td>
<td>92.8%</td>
<td>91.4%</td>
<td>98.9%</td>
</tr>
<tr>
<td><strong>Accuracy</strong></td>
<td>98.7%</td>
<td>96.9%</td>
<td>96.1%</td>
</tr>
<tr>
<td><strong>AUC</strong></td>
<td>0.987</td>
<td>1.000</td>
<td>1.000</td>
</tr>
</tbody>
</table>

Abbreviations: PPV-positive predictive value; NPV-negative predictive value; AUC-area under the curve.

Non-invasive assessment/treatment and liver related outcomes in NAFLD/ALD

OS025

Non-invasive fibrosis scores as prognostic biomarkers of liver events, cardiovascular events and all-cause mortality in people with obesity and/or type 2 diabetes in the UK: a longitudinal cohort study

Quentin Anstee¹², Tina Landsvig Berentzen³, Louise Nitze³, Maximilian Jara¹, Mette Kjaer¹, Kamal Kant Mangla¹, Jens M. Tarp³, Kamlesh Khunti⁴. ¹Translational and Clinical Research Institute, Faculty of Medical Sciences, Newcastle University, Newcastle Upon Tyne, United Kingdom; ²Newcastle NIHR Biomedical Research Centre, Newcastle Upon Tyne Hospitals NHS Trust, Newcastle Upon Tyne, United Kingdom; ³Novo Nordisk A/S, Søborg, Denmark; ⁴Diabetes Research Centre, University of Leicester, Leicester General Hospital, Leicester, United Kingdom

Email: quentin.anstee@ncl.ac.uk

**Background and aims:** Progression of non-alcoholic steatohepatitis to cirrhosis may lead to life-threatening liver-related complications, increased liver-specific and all-cause mortality and cardiovascular (CV) disease. An important predictor of severe outcomes is biopsy-confirmed liver fibrosis, but biopsies are not scalable outside of specialist practice. This real-world study investigated the prognostic utility of six non-invasive fibrosis scores on clinical outcomes in patients with obesity and/or type 2 diabetes (T2D) seen in routine general practice.

**Method:** In a longitudinal cohort design, patients ≥18 years with obesity and/or T2D, ≥1 fibrosis score calculable from the UK Clinical Practice Research Datalink (CPRD) after 1 January 2001, no alcohol-related disorders and/or other chronic liver diseases in Hospital Episodes Statistics (HES) and/or no prescriptions of drugs inducing liver disease in CPRD were included. Patients were followed from inclusion date until time of first clinical outcome event (liver-related hospitalisation or death [liver event], CV hospitalisation or death [CV event] or all-cause death) recorded in HES or Office for National Statistics Death Registration, database migration, 10 years’ follow-up or 1 January 2020, whichever came first. Fibrosis-4 Index (FIB4), the score of focus, was categorised as low (<130), indeterminate (130–267) or high (>267) risk. Cumulative incidence functions were calculated and hazard ratios (HRs) estimated using Cox proportional hazards models with calendar time as underlying timescale.

**Results:** In total, 44,481 eligible patients (46% male, median age 58.8 years) had measures available for FIB4 calculation. There were 979 liver events, of which ascites (n = 412), cirrhosis (n = 201) and gastro-oesophageal varices (n = 160) were most common. The risk of an incident liver event was highest in the first years after FIB4 measurement in the high FIB4 group and relatively constant over time in the other two groups (Figure). The incidences of a liver event, CV event and death in the high FIB4 group were 15%, 33% and 61%, respectively. Patients in the indeterminate and high FIB4 groups were at greater risk of liver events vs the low-risk group (HR 2.81 [95% confidence interval 2.43, 3.26] and 18.42 [15.67, 21.65], respectively). An increased risk was also seen for CV events and all-cause mortality in these groups. HRs remained higher for the high vs low FIB4 group after adjustment for sex and age. For the other scores, risk of an outcome event was also elevated for patients with a high vs low score.

**Conclusion:** In this real-world population of patients with obesity and/or T2D, and no other clinically recognised liver disease, the risk of a clinical event was significantly higher in patients with high vs low FIB4 score, highlighting the prognostic potential of FIB4 (and other non-invasive fibrosis scores) in this population.
Liver stiffness predicts incident severe liver disease in patients with chronic liver disease

Hannes Hegmar1,2, Axel Wester2, Soo Aleman3, Jens Backman4, Erik Degerman5, Håkan Ekwall6, Katarina Lund7, Åsa Lundgren8, Patrik Näs9,9, Afshin Shahnazav10, Johan Vessby11, Johan Westin12, Kristina Önnerhag13, Hannes Hagström12,14. Division of Hepatology, Department of Upper GI, Karolinska University Hospital, Huddinge, Sweden; 2Karolinska Institutet, Department of Medicine, Huddinge, Stockholm, Sweden; 3Karolinska Institutet/Karolinska University Hospital, Department of Infectious Diseases, Stockholm, Sweden; 4University Hospital of Umeå, Department of Infectious Diseases, Umeå, Sweden; 5Falun Hospital, Department of Infectious Diseases, Falun, Sweden; 6Sundsval-Härnösand Regional Hospital, Department of Infectious Diseases, Sundsvall, Sweden; 7Northern Alvsborg County Hospital, Department of Infectious Diseases, Trollhättan, Sweden; 8Central Hospital Kristianstad, Department of Infectious Diseases, Kristianstad, Sweden; 9Linköping University, Department of Gastroenterology and Hepatology, Department of Health, Medicine and Caring Sciences, Linköping, Sweden; 10Southern Alvsborg Hospital, Department of Infectious Diseases, Borás, Sweden; 11Uppsala University, Department of Medical Sciences, Gastroenterology Research Group, Uppsala, Sweden; 12University of Gothenburg and Sahlgrenska University Hospital, Dept of Infectious Diseases, Gothenburg, Sweden; 13Skåne University Hospital, Department of Gastroenterology and Hepatology, Malmö, Sweden; 14Karolinska Institutet, Clinical Epidemiology Unit, Department of Medicine, Solna, Stockholm, Sweden

Email: hhegmar@gmail.com

Background and aims: Prognosis in chronic liver disease is heterogenous, and fibrosis stage is the best predictor of liver-related events. Liver stiffness measurement (LSM) by Vibration-Controlled Transient Elastography (VCTE) is a non-invasive biomarker of fibrosis. It is uncertain if LSM can predict risk for future liver-related events. The aim was to investigate the prognostic ability of LSM.

Method: This was a Swedish multi-center cohort study including patients (n = 13,170) with chronic liver disease who underwent LSM by VCTE between 2008 and 2019. Exclusion criteria were an unreliable LSM, congestive heart failure, and decompensated cirrhosis at baseline. Liver-related events were ascertained from Swedish national health registers. In patients without baseline cirrhosis, we investigated progression to "severe liver disease," defined as a diagnosis of cirrhosis, decompensated cirrhosis or hepatocellular carcinoma (HCC). In patients with baseline cirrhosis, we investigated progression to decompensation or HCC. Cox regression was used to evaluate the rate of outcomes for categories of LSM values.

Results: Patients (median age 46 years, 59% men) had a median LSM of 5.9 (interquartile range 4.6–8.0) kPa. Etiologies consisted of hepatitis C (n = 6849, 52.0%), hepatitis B (n = 3487, 26.6%), alcohol-related liver disease (n = 211, 1.6%), autoimmune liver disease (n = 624, 4.7%), non-alcoholic fatty liver disease (n = 699, 5.3%) and other or uncertain etiologies (n = 1290, 9.8%). Patients without baseline cirrhosis (n = 11,883) had 333 (2.8%) events of severe liver disease during a median follow-up time of 2.9 years. Patients with cirrhosis at baseline (n = 1287) had 206 (16.0%) events of decompensation or HCC. In patients without cirrhosis, a LSM of 12–15 kPa was associated with a 42-fold higher rate of severe liver disease than a LSM of <6 kPa (Figure A). In patients with cirrhosis, a LSM >30 kPa was associated with a 5.4-fold higher rate of decompensation compared to a LSM of 15–17 kPa (Figure B). Incidence rates per 1000 person-years in severe liver disease ranged from 2.1 (95%CI 1.6–2.8) to 88.9 (95%CI 73.2–107.9) for LSM <6 kPa and 12–15 kPa, respectively. Incidence rates per 1000 person-years in-decompensated cirrhosis ranged from 18.2 (95% CI 10.3–32.0) to 109.6 (95%CI 88.9–135.1) for LSM 15–17 kPa and >30 kPa, respectively. In patients without cirrhosis, the cumulative incidence at two years ranged from 0.4 (0.3–0.6%) to 19.1 (15.1–23.5%), and at five years from 1.1 (0.8–1.6%) to 32.9 (26.9–38.9%), respectively.

Conclusion: Increased LSM by VCTE is associated with higher rates of progression to cirrhosis and decompensation in a dose-response manner. The results can be used to guide follow-up and treatment decisions.

Figure: (abstract: OS026): A. Patients without cirrhosis at baseline. B. Patients with cirrhosis at baseline.
Background and aims: FIB-4 is a clinically relevant marker to track fibrosis in patients with chronic liver disease including NAFLD/NASH. Here, we first defined FIB-4 trajectory by linear slope of serial FIB-4 measurements as a measure of fibrosis progression, then examined its correlation with liver-related complications and genetic associations with a non-invasive ALT-based NAFLD phenotype recently defined among participants in the VA's Million Veteran Program (MVP) with available clinical and genetic data (Serper et al, PLOS ONE 2020).

Method: Individual FIB-4 slopes were estimated via linear regression for MVP participants with greater than 4 outpatient FIB-4 values who met criteria for proxy NAFLD phenotype based on previously validated algorithm for chronic ALT elevation without other known causes of chronic liver disease. Linear models were constructed excluding outliers at >2 Cook's distances from predicted. Patients whose initial FIB-4 values exceeded the 90% percentile (baseline advanced fibrosis) were assigned slopes equivalent to the 99th percentile of the sample. The AUROCs for the coefficient of FIB-4 slope for predicting development of cirrhosis, hepatocellular carcinoma, ascites and death were generated. MFIB4 was then used as a quantitative phenotype in a genome-wide association analysis using REGENIE software. Variants were restricted to MAF >0.01 and INFO >0.30. Three distinct racial/ethnic groups were defined for the cohort (European, African, and Hispanic ancestry) and analyzed separately: a trans-ancestry meta-analysis was performed with METAL software.

Results: FIB-4 slopes were obtained from 61,689 subjects (10,594 African, 46,137 European, and 4,958 Hispanic ancestry subjects). AUROC of FIB-4 slope for prediction of cirrhosis, hepatocellular carcinoma or ascites were 0.75–0.76. Among European ancestry subjects, FIB-4 slope was associated with 6 genome-wide significant loci (p value <5 × 10^-8) including 3 with previously known associations to NAFLD and hepatic fibrosis (GCKR, HSD17B13, and PNPLA3). The GWAS of African and Hispanic ancestry did not return any significant results, however, the trans-ancestry meta-analysis identified an additional signal.

Conclusion: Fibrosis progression based on FIB-4 trajectory correlated with clinically meaningful complications of liver disease progression, as well as known markers of cirrhosis among patients with non-invasive ALT-based NAFLD phenotype. Further work is ongoing to define the use of FIB-4 trajectory and genetic risk factors as predictors for long term outcome of chronic liver disease.

OS028

Machine learned histological fibrosis score empowers characterization of baseline gene signatures associated with fibrosis progression or regression in a NAFLD F3/F4 clinical trial

Michael D. Bereket1, Francesco Paolo Casale1, Lorn Kategaya1, Anna Shcherbina1, Navpreet Ranu1, Alicia Lee1, Kelly Haston1, Rohit Loomba2, Arun Sanayal2, Stephen Harrison4, Zobair Younossi5, Catherine Jia1, David Lopez2, Li Li2, Robert Myers2, David Breckinridge2, Andrew Billin6, Ellen Berg1, Santhosh Satapati1, Eilon Sharon1, Theofanis Karalekos1, Daphne Koller1, Matthew Albert1, 1Insitro, South San Francisco, United States; 2University of California San Diego, La Jolla, United States; 3Virginia Commonwealth University, Richmond, United States; 4University of Oxford, United Kingdom; 5Inova Fairfax Medical Campus, Fairfax, United States; 6Gilead Sciences, Inc., Foster City, United States

Background and aims: We characterized disease severity with a machine learning (ML) analysis of liver biopsy images, and used it to identify baseline gene signatures that are predictive of fibrosis progression or regression in NASH.

Method: Bulk RNA-seq, HandE stained biopsy images, and pathologist Ishak fibrosis scores are curated from screening and week 48 visits in the STELLAR 3 and STELLAR 4 clinical trials (n = 1097 patients with all end points). A continuous score for fibrosis was extracted using convolutional neural networks (CNNs) trained to predict pathologist scores from HandE-stained biopsies (Casale et al, EASL 2020). We identify genes associated with fibrosis state by testing for associations between baseline expression and baseline fibrosis scores, controlling for age and sex. Fibrosis progression/regression genes are identified by testing for associations between baseline expression and the difference between baseline and followup fibrosis scores after controlling for all ML and pathologist baseline fibrosis scores, age, sex, and treatment.

Results: The continuous ML fibrosis scores are highly correlated with pathologist Ishak scores (correlation = 0.88). Variation of the ML fibrosis score within Ishak scores exhibits similar transcriptomic associations as variation in Ishak scores (correlation of z scores = 0.88), suggesting that the ML score identifies intra-score variability consistent with pathologist assessed fibrosis. We identify 12, 862 genes associated with ML fibrosis state (likely driven in part by changes in cell type composition) and 37 genes associated with ML fibrosis progression/regression (A, B). Using the same covariates, analysis of the ML score identifies a superset of the progression/regression genes identified with the pathologist score (37 vs 3 genes). Notably, the progression/regression-associated genes are not the top state-associated genes. Progression associated genes include expected extracellular matrix and cytokskeletal function-related genes. Lipid metabolism genes identified include the progression associated gene AKR1B10 (involved in hepatic carcinogenesis) and the regression associated gene AKR1D1 (involved in resistance to oxidative stress). Other regression associated genes identified include metallothionein genes, involved in the protection against oxidative stress, and CLEC4M, a liver sinusoidal endothelial cell-specific gene.

Conclusion: ML assessment of liver biopsies and the statistical inference framework introduced herein produced insights on baseline gene expression signatures that are predictive of and potential drivers for NASH fibrosis progression or regression.

OS029

Fibroscan-AST (FAST) score predicts liver-related outcomes in 1683 HIV-infected patients at risk for NAFLD

Giada Sebastiani1,2, Jovana Milic2, Dana Kablawi2, Claudia Goe2, Al Shaima Al Hinai2, Bertrand Lebouche2, Amine Bennassaoud2, Marc Deschenes1, Antonio Cascio3, Giovanni Mazzola2, Giovanni Guaraldi2, 1McGill University Health Centre Glen Site (MUHC), Medicine, Montréal, Canada; 2McGill University, Division of Experimental Medicine, Montréal, Canada; 3University of Modena and Reggio Emilia, Modena, Italy

Background and aims: Non-alcoholic fatty liver disease (NAFLD) affects 35% of people living with HIV (PWH) in absence of viral
hepatitis coinfection. About 15% of these PWH have also significant liver fibrosis. Natural history studies employing accurate non-invasive tools are lacking. The FibroScan-AST (FAST) score was developed to identify patients with histologic NASH with advanced fibrosis and elevated NAFLD activity score (NAS) associated with higher risk of end-stage liver disease. We estimated prevalence and evolution of severe NAFLD defined by FAST score in a large multicenter cohort of PWH.

**Method:** FibroScan was performed in consecutive PWH without viral hepatitis coinfection from three prospective cohorts in Canada and Italy (LIVEHIV in Montreal; liver pathologies in HIV in Palermo; Modena HIV metabolic clinic) as part of a routine screening program for NAFLD. We compared prevalence of FAST>0.35 (90% sensitivity and 50% specificity for NASH with ≥F2 fibrosis and NAS≥4) and FAST≥0.67 (50% sensitivity, 90% specificity). Incidence of liver-related outcomes (ascites, encephalopathy, variceal bleeding, hepatocellular carcinoma) and extra-hepatic events (cancer, cardiovascular disease) was evaluated by survival analysis.

**Results:** We included 1683 PWH (mean age 50.1 years, HIV duration 15.5 years, BMI 25.3 Kg/m²; 74.5% male, diabetes prevalence 32%). Prevalence of FAST>0.35 and FAST≥0.67 was 8.1% and 1.5%, respectively. At baseline, on multivariable logistic regression higher BMI (adjusted odds ratio [aOR] 1.15, 95% CI 1.10–1.20), longer duration of HIV infection (aOR 1.05, 95% CI 1.02–1.07), lower CD4 cell count (aOR 0.99, 95% CI 0.99–0.99) and male sex (2.11, 95% CI 1.22–3.65) were associated with FAST >0.35. During a median follow-up period of 3.5 years, incidence of liver-related and extra-hepatic outcomes was 7% and 11.5%, respectively. Incidence of liver-related outcomes significantly increased according to FAST score category (see Figure). There was no difference in extra-hepatic events by FAST score category. On multivariable Cox regression analysis, FAST score >0.35 was an independent predictor of liver-related outcomes (adjusted hazard ratio 4.44, 95% CI 1.66–11.9) after adjusting for sex, BMI, diabetes, duration of HIV infection, protease inhibitors exposure and CD4 cell count.

**Conclusion:** A significant proportion of PWH without viral hepatitis coinfection are at risk for severe NAFLD. FAST score predicts liver-related in this population. Non-invasive testing can help risk stratification and management in this population at risk for NASH and associated liver-fibrosis.

**OS030**

Impact of resmetirom-mediated reductions in liver volume and steatosis compared with placebo on the quantification of fibrosis using second harmonic generation in a serial liver biopsy study

Dean Tai1, Mustafa Bashir2, Rebecca Taub3, Yayun Ren1, Elaine Chng4, Stephen Harrison5.

1Histoindex, Research; 2Duke University, Radiology; 3Madrigal Pharmaceuticals, RandD, Conshohocken, United States; 4Histoindex, 5Pinnacle, Clinical Research

Email: rebeccataub@yahoo.com

**Background and aims:** Resmetirom (MGL-3196) is a liver-directed, orally active selective thyroid hormone receptor-β agonist that reduces steatosis by MRI-PDFF (−43% (80 mg); −53% (100 mg), Phase 3) and liver volume (IV) −20% (Phase 2 serial liver biopsy

**Figure:** Survival curves for incidence of liver-related outcomes by FAST score category.

**Conclusion:** Resmetirom (MGL-3196) is a liver-directed, orally active selective thyroid hormone receptor-β agonist that reduces steatosis by MRI-PDFF (−43% (80 mg); −53% (100 mg), Phase 3) and liver volume (IV) −20% (Phase 2 serial liver biopsy
study) that were elevated at baseline. Assessment of histological features that stage NASH fibrosis may be impacted in the setting of decreased steatosis and LV following therapeutic intervention. Artificial intelligence (AI)-based algorithms such as qFibrosis can incorporate normalization procedures to account for steatosis area and LV reduction, thereby improving the detection of fibrosis changes. The aim of this analysis is to quantify and correct fibrosis changes related to resmetirom-mediated steatosis and LV changes that are not captured by NASH-CRN scoring system.

**Method:** Fibrosis was estimated as a continuous variable using second harmonic generation (SHG) (qFibrosis)/two photon excited fluorescence of 102 paired biopsy samples from MGL-3196-05, a 36-week randomized double-blind, placebo-controlled resmetirom phase 2 serial Liver biopsy study. qFibrosis was then normalized to tissue area was subsequently corrected for steatosis (tissue area-steatosis area), or LV reduction determined by PDDF (volume/average volume raw parameter based on all samples). In the final model, steatosis and LV were both corrected prior to assessment of qFibrosis. Relative changes in 184 fibrosis parameters were determined as (P) progressing (>10%), (R) regressing (<10%) or (N) no change.

**Results:** In normal qFibrosis without correction, resmetirom treatment resulted in a significant reduction in fibrosis (≥1-point reduction) in F3 patients compared to placebo. With LV correction, 45/184 regression parameters demonstrated significant changes after resmetirom treatment (top panel). When steatosis and LV correction factors were combined, 111/184 (p < 0.05) regression parameters were reduced significantly with resmetirom (bottom panel). Fibrosis regression was observed in all regions (portal, per-portal, zone 2, peri-central, central). Progression patterns were different from regression and also significantly impacted by correction.

**Conclusion:** Quantification of changes in NASH fibrosis are impacted by therapeutic interventions that reduce LV. Correcting the AI-based algorithm of qFibrosis for LV and steatosis reveals the significant impact of resmetirom across treated patients in this phase 2 study, regardless of NASH fibrosis stage.

---

**Alcoholic liver disease**

**OS031 Survival and liver recompensation after declined for early liver transplantation for severe alcohol-associated hepatitis**

Christine Hsu,2 Ethan Weinberg,2 Gene Im,3 William Davis,4 Jimin Ko4, Stephanie Rutledge4, Matthew Dukewich4, Mohamed Shoreibah5, Mahmoud Aryan4, Aidan Vosooghi6, Michael R. Lucey7, John Rice7, Stephanie Rutledge3, Matthew Dukewich2, Mohamed Shoreibah5, Mahmoud Aryan4, Aidan Vosooghi6, Michael R. Lucey7, John Rice7, Norah Terrault8, Brian Lee6.

1Medstar Georgetown University Hospital, Medicine, District of Columbia, United States; 2University of Pennsylvania, Medicine, Philadelphia, United States; 3Mount Sinai, Medicine, New York, United States; 4Georgetown University School of Medicine, District of Columbia, United States; 5University of Alabama at Birmingham, Medicine, Birmingham, United States; 6University of Southern California, Medicine, Los Angeles, United States; 7University of Wisconsin, Medicine, Madison, United States; 8University of Southern California, Medicine, Los Angeles, United States

Email: cch87@georgetown.edu

**Background and aims:** Early liver transplantation (LT) for alcohol-associated hepatitis (AH) is controversial in part because some patients may recover, and obviate the need for LT. We aimed to (i) determine factors associated with survival and liver recompensation among patients with severe AH declined for early LT; (ii) delineate the trajectory of recompensation and MELD recovery among survivors.

**Method:** In this retrospective, multi-center study among 5 American Consortium of Early Liver Transplantation for Alcohol-Associated Hepatitis (ACCELERATE-AH) sites, we randomly sampled 134 patients who were evaluated and then declined for early LT for severe AH between 2012 and 2021. All had MELD≥20 and less than 6 months of abstinence at LT evaluation. Recompensation was defined as MELD<15 without evidence of variceal bleeding, or ascites requiring diuretics, or overt hepatic encephalopathy requiring medication. Analyses were adjusted for center clustering.

**Results:** Among 134 patients (median age 49 [IQR 39–57]; 57% male; median abstinent time 36 [IQR 14–70] days; median MELD-Na 33 [IQR 28–38]), the most common reasons for LT decline were: psychosocial (62%), clinical improvement (16%), medical co-morbidities (9%), and financial/insurance (4%). Probability of 3-month, 6-month, and 1-year survival was 58%, 55%, and 48%. Probability of 3-month, 6-month, and 1-year recompensation was 4%, 4%, and 6%. In multivariable analysis, lower MELD-Na (aOR 0.8; p = 0.01) and absence of grade 3 or 4 hepatic encephalopathy (aOR 0.02; p = 0.004) were associated with 3-month survival. In multivariable analysis, lower MELD-Na (aOR 0.9; p < 0.001), married/stable partner (OR 2.0; p = 0.001), and private (aOR 3.4; p = 0.01) or Medicare (aOR 4.7; p = 0.002) vs. Medicaid (reference) insurance were associated with 6-month survival. Among patients declined due to clinical improvement during LT evaluation, 93% were alive at 6 months, but only 15% were recompensated. Among survivors, median MELD at 1-month, 3-months, 6-months, and 1-year were: 28 (IQR 22–38), 26 (IQR 19–33), 15 (IQR 12–23), and 12 (IQR 8–18).

**Conclusion:** Liver recompensation is very rare among patients with severe AH declined for early LT. Lower MELD was predictive of short- and long-term survival, and marital and insurance status emerged as strong predictors of long-term survival. The distinction between survival and liver recompensation after LT evaluation for severe AH would benefit from further analysis.

**OS032 Role of macrophage-derived MLKL in alcohol-associated liver disease**

Xiaoqin Wu1, Xiude Fan1, Megan McMullen1, Tatsunori Miyata1, Adam Kim1, Vai Pathak1, Jianguo Wu1, Nicole Welsh1, Jaividhya Dasarathy2, Srinivasan Dasarathy1, Laura Nagy1, 1Cleveland Clinic; 2Case Western Reserve University, Department of Family Medicine, Metro Health Medical Center

Email: nagyl3@ccf.org

**Background and aims:** Mixed Lineage Kinase Domain like Pseudokinase (MLKL), a key downstream effector of necroptosis, also has non-necroptotic functions in regulating intracellular and extracellular vesicle trafficking that disrupts the balance between cell death and survival, critical for regulating liver injury and inflammation in alcohol-associated liver disease (ALD). Previously, we observed that MLKL−/− mice were partially protected from ethanol-induced injury. Immunohistochemical staining of liver biopsies from patients with alcohol-associated hepatitis (AH) revealed that phospho-MLKL was localized to both hepatocytes and mononuclear immune cells. Moreover, MLKL co-localized with macrophage marker F4/80 in liver of ethanol-fed mice. Given the important contribution of macrophages to the pathogenesis of ALD, we hypothesized that macrophage-derived MLKL has a potential role in ethanol-induced injury.

**Method:** Primary mouse Kupffer cells (mKCs) isolated from MLKL−/− and wild type (WT) mice and peripheral monocytes from healthy controls (HC) and patients with AH, treated or not with an inhibitor of MLKL, were used in phagocytosis assays. Bone marrow transfers between MLKL−/− mice and littersmates were conducted to distinguish the role of myeloid vs non-myeloid MLKL in the Gao-binge murine model of ALD.

**Results:** Challenge of macrophages with lipopolysaccharide (LPS) induced STAT1-mediated expression and phosphorylation of MLKL, as well as translation and oligomerization of MLKL to intracellular compartments including phagosomes and lysosomes, but not the plasma membrane. LPS enhanced uptake and degradation of pHrodo
deficiency in myeloid cells suppressed Gao-binge-triggered F4/80+ cytometry analysis of non-parenchymal cells demonstrated that phagocytes, monocytes and neutrophils in response to ethanol. Flow cytometry analysis of non-parenchymal cells demonstrated that Mlkl deficiency in myeloid cells suppressed Gao-binge-triggered F4/80+ macrophage death via necrosis/necroptosis. Furthermore, Mlkl deficiency in myeloid cells exacerbated ethanol-mediated bacterial burden in livers, likely through inhibiting expression of phagocytic receptors. Pharmacological or genetic inhibition of MLKL restricts ethanol-induced liver inflammation and injury by regulating hepatic innate cell homeostasis and phagocytosis of macrophage.

**OS033**

**Baseline plasma metabolic phenotype of patients with severe alcoholic hepatitis and its association with outcome**

Manisha Yadav1, Gaurav Tripathi1, Nupur Sharma2, Babu Mathew3, Vasundhara Bindal1, Jaswinder Maras1, Shiv Kumar Sarin3. 1Institute of Liver and Biliary Sciences, Molecular and Cellular Medicine, New Delhi, India; 2Institute of Liver and Biliary Sciences, Hepatology, New Delhi, India

Email: jassi2param@gmail.com

**Background and aims:** Severe alcoholic hepatitis (SAH) has a high mortality and corticosteroid therapy is effective in reducing 28-day mortality in only about 60% of patients. There are reliable clinical indicators predicting steroid non-response after 7 days of therapy (Lille score >0.45).

**Method:** Plasma metabolic phenotype was studied using ultra-high-performance liquid chromatography and high-resolution mass spectrometry to identify corticosteroid non-responders at baseline. Altogether, 223 SAH patients were included, 70 in derivative [50 responders (R) and 20 non-responders (NR)] and 153 in validation cohort [136 R, 17 NR]. Temporal change in the metabolic profile and Weighted Metabolome Correlation Network Analysis (WMCNA) were performed and correlated to disease severity.

**Results:** Of the 713 annotated features (metabolomic/biochemical/spectral databases), 8 plasma metabolites significantly discriminated non-responders; most importantly high urobilinogen (13-fold), cholesterol sulfate (6.9-fold), AMP (4.7-fold), N-Formimino-L-glutamate (4.3-fold), tryptophan (4.7 folds), and low 4-imidazoleacetic acid (10 fold), urocanic acid (2.2 fold) and thymine (2.4 fold) levels. Additionally, plasma uric acid, AMP, and cholesterol sulfate discriminated non-survivors (p <0.01). Temporal change in metabolite expression was higher in responders (p <0.05). WMCNA identified metabolite modules and linked pathways specific to NR and mortality with disease severity (r >0.7; P <0.01). In validation cohort, baseline plasma urobilinogen (C05791) showed high reliability [AUC = 0.94, 0.91–0.97] for predicting non-response with hazard-ratio of 1.5 (1.2–1.6) for mortality prediction. C05791 at 10 log (arbitrary units) cut-off reliably segregated non-survivors (p value <0.01, log-rank test) and showed 98% accuracy, 99% sensitivity and 98% specificity using Random Forest-based Machine-Learning model.

**Conclusion:** Plasma metabolome signatures can predict pre-therapy steroid response and disease outcome in patients with SAH. Baseline plasma urobilinogen levels should be used for determining corticosteroid response.

**OS034**

**Il-1beta Signal Inhibition in acute alcoholic hepatitis: a multicentre, randomised, double-blind, placebo-controlled phase 2 trial of canakinumab therapy (ISAIAH)**

Nikhil Vergis1, Vishal C. Patel2,3,4, Karolina Bogdanowicz2, Justyna Czyzewska-Khan2, Rosemary Keshinro5, Francesca Fiorentino6, Emily Day7, Paul Middleton1, Stephen Atkinson1, Mary Cross5, Daphne Babalis8, Neil Foster1, Alberto Quaglia6, Josephine Lloyd1, Robert D. Goldin1, William Rosenberg7, Richard Parker8, Paul Richardson9, Steven Masson10, Gavin Whitehouse11, Cyril Sieberhagen12, David Patch13, Ashwin Dhanda13, Emma Lord1, Ewan Forrest14, Nikolai Naoumov15, Mark Thorsz1. 1Imperial College, Metabolism, Digestion and Reproduction, London, United Kingdom; 2King’s College London, School of Immunology and Microbial Sciences, Faculty of Life Sciences and Medicine, United Kingdom; 3King’s College Hospital NHS Foundation Trust, Institute of Liver Studies, United Kingdom; 4The Roger Williams Foundation for Liver Research, Institute of Hepatology, London, United Kingdom; 5Imperial Clinical Trials Unit, United Kingdom; 6Royal Free Hospital NHS Foundation Trust; 7University College London, United Kingdom; 8Leeds Teaching Hospitals NHS Trust, United Kingdom; 9Liverpool University Hospitals Foundation NHS Trust, United Kingdom; 10The Newcastle Upon Tyne Hospitals Foundation NHS Trust, United Kingdom; 11Chelsea and Westminster Hospitals NHS Foundation Trust; 12Liverpool University Hospitals Foundation NHS Trust; 13University of Plymouth, United Kingdom; 14Glasgow Royal Infirmary, United Kingdom; 15London, United Kingdom

Email: nvergis@imperial.ac.uk

**Background and aims:** Short-term mortality in acute alcohol-related hepatitis (AAH) patients is high and available therapy does not result in durable benefit. A role for IL-1beta has been demonstrated in the pathogenesis of alcohol-induced steatohepatitis in mice. This study explored the safety and potential benefits of canakinumab (CAN), a monoclonal antibody targeting IL-1beta, for patients with AAH in a double-blind placebo (PBO)-controlled randomised trial.

**Method:** Patients with biopsy-confirmed AAH and discriminant function ≥32 but MELD ≤27 were randomly allocated 1:1 to receive either CAN 3 mg/kg or PBO once in 4 weeks. Liver biopsies were taken before and 28 days after treatment. The primary end point was histological improvement at 28 days compared to baseline, adjudicated by 3 independent histopathologists who were blinded to treatment allocation. Key secondary end points were the proportions of Lille responders; changes in MELD; and death within 90 days. Adverse events, including infections, were compared between groups.

**Results:** Fifty-seven patients were randomised: 29 CAN vs 28 PBO. Two patients were withdrawn with negative biopsy results; 1 did not receive allocated intervention due to an adverse event and a further 6 did not attend for second biopsy. Data were therefore available for 48 patients for primary end point analysis. In CAN-treated patients, 14/
24 (58.3%) demonstrated histological improvement compared to 10/24 (41.7%) PBO-treated patients, a difference of 16.7% (p = 0.248).

Regression models did not identify significant improvement of CAN therapy on prognostic scores of liver function such as Lille model or MELD. Four of the 55 AAH patients (7.3%) in the intention-to-treat analysis died within 90 days; 2 in each group. There were 20 vs 29 serious adverse events occurring in 10 vs 10 patients (CAN vs PBO). There were no safety signals: of the 49 serious adverse events, 6 were infectious complications of which 1/20 (5%) occurred in CAN-treated and 5/29 (17%) occurred in PBO-treated patients. In exploratory analyses after adjustment for baseline prognostic factors, CAN therapy was associated with overall histological improvement (p = 0.04), improvement in mononuclear cell infiltrate (p = 0.06), and reduction in serum AST (p = 0.02).

Conclusion: CAN therapy in AAH demonstrated a good safety profile but did not alter biochemical or clinical outcomes compared to PBO. After adjustment for baseline prognostic factors, CAN was associated with histological improvements that did not translate into improved prognostic scores of liver function nor survival.

<table>
<thead>
<tr>
<th>Outcome</th>
<th>Canakinumab</th>
<th>Placebo</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>Histological Improvement (%)</td>
<td>58.3</td>
<td>41.7</td>
<td>0.25</td>
</tr>
<tr>
<td>Lille response (%; Lille score&lt;0.45)</td>
<td>22.2</td>
<td>25.0</td>
<td>0.8</td>
</tr>
<tr>
<td>Day 28 median MELD change</td>
<td>-5.07</td>
<td>-6.50</td>
<td>0.14</td>
</tr>
<tr>
<td>Day 28 median GAHS change</td>
<td>-2</td>
<td>-2</td>
<td>0.69</td>
</tr>
<tr>
<td>SAEs (n)</td>
<td>20</td>
<td>29</td>
<td>-</td>
</tr>
<tr>
<td>Infection SAEs (n)</td>
<td>1</td>
<td>5</td>
<td>0.38</td>
</tr>
</tbody>
</table>

OS036
Probiotic LGG-derived exosome-like nanoparticles inhibit ALD through intestinal FXR activation in mice: role of miR194 and bile acids

Wenke Feng1, Mengwei Jiang1, Fengyuan Li1, Craig J. McClain1, Lihua Zhang1, Jyeon Lee1. 1University of Louisville, Medicine, Louisville, United States
Email: wenke.feng@louisville.edu

Background and aims: Patients with alcohol-associated liver disease (ALD) often exhibit excessive bile acid (BA) accumulation and steatosis. Farnesoid X receptor (FXR)-fibroblast growth factor 15/19 (FGF15/19) signaling plays a critical role in hepatic lipid and BA metabolism. In this study, we aimed to investigate whether alcohol exposure reduced BA-mediated intestinal FXR activation and increased intestinal miR194 expression that suppressed Fx mRNA expression, and whether Lactobacillus rhamnosus GG-derived exosome-like nanoparticles (LDNPs) attenuated ALD through regulation of intestinal miR194-FXR-FGF15 signaling in mice.

Method: C57BL/6, global Fgf15 knockout (Fgf15−/−), and intestinal epithelial cell-specific Fxr knockout (FxrΔEC) mice were administered the NIAAA binge-on-chronic model alcohol exposure protocol. Probiotic strain Lactobacillus rhamnosus GG was cultured and LDNPs were isolated from the culture supernatant.

Results: Alcohol feeding increased intestinal miR194 expression, which suppressed intestine Fxr and subsequently Fgf15 expression, resulting in a reduced circulation FGF15 protein level. Gut microbiota-mediated BA transformation was dysregulated by alcohol leading to the decreased ligand-mediated FXR activation. Reduced FXR-FGF15 signaling resulted in an increase in hepatic BA synthesis and lipogenesis and liver injury. Importantly, three-day oral administration of LDNPs suppressed hepatic BA synthesis and lipogenesis and protected the liver from alcohol-induced injury. We further showed that LDNP treatment decreased intestinal mir194 and increased FXR-FGF15 signaling. mir194 suppressing intestinal Fxr mRNA expression was further confirmed in in Caco-2 cells and mouse enteroïd. mir194 mimicked decreased, and miR194 inhibitor increased, Fxr mRNA expression. Fecal and serum FXR activity was decreased by alcohol and restored by LDNP treatment. Importantly, the beneficial effects of LDNP were eliminated in intestinal FxrΔEC and Fgf15−/− mice.

Conclusion: Our results demonstrate that increased intestinal miR194 suppresses Fxr expression resulting in a defective FXR-FGF15 gut-liver signaling in ALD. LDNP treatment inhibits alcohol-induced liver injury by suppressing intestinal mir194 and improving BA profile that lead to an activated FXR-FGF15 signaling to suppress BA de novo synthesis and lipogenesis during ALD development.

OS035
Probiotic LGG-derived exosome-like nanoparticles inhibit ALD through intestinal FXR activation in mice: role of miR194 and bile acids

Background and aims: Patients with alcohol-associated liver disease (ALD) often exhibit excessive bile acid (BA) accumulation and steatosis. Farnesoid X receptor (FXR)-fibroblast growth factor 15/19 (FGF15/19) signaling plays a critical role in hepatic lipid and BA metabolism. In this study, we aimed to investigate whether alcohol exposure reduced BA-mediated intestinal FXR activation and increased intestinal miR194 expression that suppressed Fxr mRNA expression, and whether Lactobacillus rhamnosus GG-derived exosome-like nanoparticles (LDNPs) attenuated ALD through regulation of intestinal miR194-FXR-FGF15 signaling in mice.

Method: C57BL/6, global Fgf15 knockout (Fgf15−/−), and intestinal epithelial cell-specific Fxr knockout (FxrΔEC) mice were administered the NIAAA binge-on-chronic model alcohol exposure protocol. Probiotic strain Lactobacillus rhamnosus GG was cultured and LDNPs were isolated from the culture supernatant.

Results: Alcohol feeding increased intestinal miR194 expression, which suppressed intestine Fxr and subsequently Fgf15 expression, resulting in a reduced circulation FGF15 protein level. Gut microbiota-mediated BA transformation was dysregulated by alcohol leading to the decreased ligand-mediated FXR activation. Reduced FXR-FGF15 signaling resulted in an increase in hepatic BA synthesis and lipogenesis and liver injury. Importantly, three-day oral administration of LDNPs suppressed hepatic BA synthesis and lipogenesis and protected the liver from alcohol-induced injury. We further showed that LDNP treatment decreased intestinal mir194 and increased FXR-FGF15 signaling. mir194 suppressing intestinal Fxr mRNA expression was further confirmed in in Caco-2 cells and mouse enteroïd. mir194 mimicked decreased, and miR194 inhibitor increased, Fxr mRNA expression. Fecal and serum FXR activity was decreased by alcohol and restored by LDNP treatment. Importantly, the beneficial effects of LDNP were eliminated in intestinal FxrΔEC and Fgf15−/− mice.

Conclusion: Our results demonstrate that increased intestinal miR194 suppresses Fxr expression resulting in a defective FXR-FGF15 gut-liver signaling in ALD. LDNP treatment inhibits alcohol-induced liver injury by suppressing intestinal mir194 and improving BA profile that lead to an activated FXR-FGF15 signaling to suppress BA de novo synthesis and lipogenesis during ALD development.

OS036
Does screening for liver fibrosis change alcohol consumption, diet, and exercise? A prospective cohort study on the consequences of screening in 2, 764 individuals

Maria Kjærgaard1,2, Katrine Prier Lindvig1,2, Johanne Kragh Hansen1, Simon Langkjær Sørensen1, Stine Johansen1,2, Katrine Thorhaug1,2, Peter Andersen1, Isabel Graupera1,2, Pere Gines1,2, Aleksander Krag1,2, Maja Thiele1,2, Odense University Hospital, Department of Gastroenterology and Hepatology, Odense, Denmark; 3University of Southern Denmark, Institute of Clinical Research, Odense, Denmark; 4Hospital Clinic de Barcelona, Institut D’Investigacions Biomèdiques August Pi i Sunyer (IDIBAPS), Barcelona, Spain
Email: maria.kjaergaard@rbsd.dk

Background and aims: There is a growing interest in screening for liver fibrosis, and a belief that early disease detection will lead to lifestyle changes in screening-positive individuals. However, this assumption is not based in evidence. We therefore evaluated self-reported lifestyle changes after screening for liver fibrosis.

Method: Prospective study of participants from the general population at risk of alcohol related (ALD) or non-alcoholic fatty liver disease (NAFLD). All were screened with transient elastography (TE) and all participants, independently on TE, were given information on recommended lifestyle changes. We considered TE ≥8 kPa as screening positive. All participants received an online questionnaire on lifestyle changes one week and six months after the screening visit.

Results: We included 2, 764 participants, 1, 273 at risk of ALD and 1, 491 at risk of NAFLD. Median age was 58 years (52–64), 54% were male, and 268 (10%) had an elevated TE ≥8 kPa. Response rate was high, at 89% after one week and 85% after six months. After one week, half of the ALD group (50%) reported abstinence, or a decrease in alcohol consumption, while only 0.8% reported an increase in alcohol consumption. Screening sustained its effect on alcohol consumption after six months (figure), with a reported median alcohol intake decreasing 8 units/week in the ALD group. Screening-positive subjects disclosed more pronounced reductions in alcohol intake than screening negatives (decreased 13 vs 6 units/week), and a positive screening test predicted alcohol abstinence (odds ratio 2.9, 95% CI 1.8–4.7). We observed the same pattern for diet and exercise: After one week, 26% of all respondents reported that they consumed less food and/or more healthy food, increasing to 34% after six months. This was most pronounced in the at-risk of NAFLD group (Figure), where a positive screening test predicted improved diet (OR 1.8, 1.3–2.4). Both groups reported comparable improvements in exercise (figure). In the NAFLD group, 23% reported a weight loss exceeding 3 kg after six months, and a positive screening test predicted a weight loss above 3 kg (OR 3.5, 1.2–10.5).
Conclusion: After being screened for liver fibrosis, participants report improved lifestyle, with both acute and sustained changes in alcohol consumption, diet, exercise, and weight loss. The changes are most pronounced in participants with elevated liver stiffness, but not limited to this.

Fibrosis

OS037
Peroxidasin deficiency reprograms macrophages toward pro-fibrolysis function and promotes collagen resolution in liver
Mozhdeh Sojoodi1, Derek J. Erstad1, Stephen Barrett1, Shadi Salloum2, Shijia Zhu1, Tongqi Qian2, Eric Gale3, Veronica Clavijo Jordan4, Yongtao Wang1, Shen Li1, Michael Lanuti1, Peter Caravan4, Yujin Hoshida1, Raymond Chung2, Gautam Bhave4, Georg Lauer2, Bryan C. Fuchs1, Kenneth K. Tanabe1, 1Massachusetts General Hospital, Surgery, Boston, United States; 2Massachusetts General Hospital, Gastroenterology, Boston, United States; 3University of Texas Southwestern Medical Center, Internal Medicine, United States; 4Massachusetts General Hospital, Radiology, Boston, United States; 5Vanderbilt University Medical Center, Division of Nephrology and Hypertension, United States
Email: msojoodi@mgh.harvard.edu

Background and aims: Non-alcoholic liver disease (NAFLD) is stimulated by excessive fat deposition in hepatocytes. During NAFLD, inflammation and activation of tissue repair mechanisms replaces necrotic tissue with extracellular matrix (ECM), which are stabilized into a complex fibrotic scar and creates fibrosis. Peroxidasin (PXDN) is a peroxidase enzyme that is known to stabilize ECM proteins through cross-linking of collagen molecules. In this project, we aim to investigate the expression and function of PXDN during the development of liver fibrosis.

Method: Pxdn−/− and Pxdn+/− mice were fed with a choline-deficient L-amino acid-defined high-fat diet (CDAHFD) for 16 weeks to create a NAFLD-HCC preclinical model. Liver histology, collagen content, flow cytometry, immunostaining of immune cells, RNA-seq, and liver function tests were analyzed. In vivo imaging of liver reactive oxygen species (ROS) was performed using a redox-active iron complex, Fe-PyC3A.

Results: Genome-wide expression analysis of liver tissue and differential gene expression (DGE) combined with Gene Ontology (GO) analysis identified significant upregulation of genes associated with hypoxia and TGFβ signaling pathways already in Pxdn−/− sham livers (without injury). Using Fe-PyC3A as an MRI contrast agent, we detected a higher content of ROS in Pxdn−/− mice (healthy) that could activate hypoxia-related molecular pathways. In addition, we observed an upregulation of genes involved in the innate immune response, leukocyte activation, and chemotaxis. After 16 weeks of CDAHFD, gross analysis of collected liver showed no HCC nodules in Pxdn−/− mice while 60% of the WT mice had HCC tumors. Collagen staining showed less collagen accumulation in Pxdn−/− mice. Flow cytometry of macrophages showed Pxdn−/− mice had increased pro-healing M2 macrophages recruitment in early- and mid-stage NAFLD (4 weeks and 8 weeks on CDAHFD) compared to WT controls. In addition, we observed a significant decrease in the number of CD3+ T cells and CD8+ cytotoxic T cells in the late-stage of NAFLD in Pxdn KO mice. DGE analysis revealed that IL-12 is highly expressed in Pxdn−/− injured livers. Additionally, multiple other T cell-related molecules such as IL-10, IL-6, CCL2, IL-7, and CD4 were elevated in Pxdn−/− injured liver. Elevation of these cytokines is an indicator for higher recruitment of pro-healing and anti-HCC macrophage to the site of injury.

Conclusion: Our findings demonstrate that PXDN deficiency is associated with the induction of the hypoxia and TNFα signaling pathways and the recruitment of pro-healing and anti-HCC macrophages to the liver. This results in significantly decreased collagen stabilization during liver fibrosis and accelerates fibrosis reversal. In addition, recruited macrophages-controlled T cell response and inhibited HCC formation in Pxdn−/− mice.

OS038
Targeting the liver circadian clock by REV-ERB-alpha activation improves liver fibrosis by circardian gating of TGF-beta signaling
Mayssa Dachaour1, Frank Jühring2, Natascha Roehlen1, Emilie Crouchet1, Romain Martin1, Nicolas Brignon1, Laurent Mailly1, Antonio Saviano1, Sarah Durand1, Catherine Schuster1, Emanuele Felli2, Patrick Pessaux2, Joachim Lüpberger1, Atish Mukherji1, Thomas Baumert3, 1Université de Strasbourg, Institut de Recherche sur les Maladies Virales et Hépatiques Inserm, UMR_S110, Strasbourg, France; 2Université de Strasbourg, Institut de Recherche sur les Maladies Virales et Hépatiques Inserm, UMR_S110, Institut Hospitalo-Universitaire, Pôle Hépato-digestif, Nouvel Hôpital Civil, Strasbourg, Strasbourg, France; 3Université de Strasbourg, Institut, Institut de Recherche sur les Maladies Virales et Hépatiques Inserm, UMR_S110, Institut Hospitalo-Universitaire, Pôle Hépato-digestif, Nouvel Hôpital Civil, Strasbourg, and Institut Universitaire de France, Paris, Strasbourg, France
Email: mukherji@unistra.fr

Background and aims: Liver fibrosis is the key risk factor for hepatocellular carcinoma, a leading cause of cancer death worldwide. Approved anti-fibrotic therapies are absent and most compounds in clinical development have limited anti-fibrotic efficacy. The circadian clock (CC) is a major regulator of liver metabolism, but its role in the pathogenesis of liver fibrosis and as a potential therapeutic target is unknown.

Method: We utilized liver specific CC-mutant mice to establish the molecular relationship between the CC-oscillator and TGF-beta signaling under physiological conditions. Moreover, we profiled the circadian gene expression pattern in patient-derived models for NASH and fibrotic liver disease including primary human hepatocytes, human myofibroblasts, spheroids and a human liver chimeric mouse model for diet-induced fibrotic liver disease. Furthermore, we performed functional studies using small molecules targeting CC components.

Results: Here we show that the physiological liver CC-oscillator is temporally restricting (gating) TGF-beta signaling and that this regulation is lost in metabolic liver disease progressing to fibrosis. The loss of TGF-beta signaling regulation leads to constitutive expression of genes driving fibrosis in patients. Mechanistic studies in primary human hepatocytes and myofibroblasts revealed a reciprocal relationship between increased TGF-beta-driven fibrotic-signaling and the CC, which we confirmed in patient-derived liver spheroids and in two mouse models for NASH-driven fibrosis. Remarkably, a pharmacological restoration of REV-ERB-alpha activity markedly inhibited fibrosis in a human liver chimeric NASH mouse model in vivo and spheroids generated from patients with liver fibrosis.

Conclusion: We discovered that the perturbation of the liver CC plays a key role in the pathogenesis of liver fibrosis. Furthermore, our in vivo and ex vivo studies in patient-derived models suggest that targeting REV-ERB-alpha is an effective approach for treatment of liver fibrosis—an important and rising global unmet medical need.
OS039
The proteomic analysis of hepatic stellate cell differentiation from iPSCs identifies RORalpha as an antifibrogenic target
Ricardo A. Martinez García de la Torre1, Julia Valverdá1, Silvia Artero Mons1, Beatriz Aguilar-Bravo1, Mikel Azkargorta2, Felix Elortza2, Laura Zanatto2, Paula Cantallops Vilà1, Juanjo Lozano3, Benedicte Antoine4, Isabel Graupera5,6,7, Pere Giné5,6,7, Pau Sancho-Bru1,3,7. 1Institut d’Investigacions Biomèdiques August Pi i Sunyer (IDIBAPS), Liver Cell Plasticity and Tissue Repair Group, Barcelona, Spain; 2CIC bioGUNE-Centro de Investigación Cooperativa en Biociencias, Proteomics Platform, Derio, Spain; 3Centro de Investigación Biomédica en Red de Enfermedades Hepáticas y Digestivas (CIBERehd), Barcelona, Spain; 4Sorbonne Université, INSERM, Paris, France; 5Hospital Clinic de Barcelona, Chronic Liver Diseases Group, Barcelona, Spain; 6Institut d’Investigacions Biomèdiques August Pi i Sunyer (IDIBAPS), Barcelona, Spain; 7Universitat de Barcelona, Barcelona, Spain. Email: rmartinezg@clinic.cat

Background and aims: Understanding the embryonic development of Hepatic stellate cells (HSCs) and their activation is fundamental to develop new therapeutic strategies. We developed a protocol to differentiate iPSCs to HSCs by sequential addition of growth factors. We hypothesized that the differentiation protocol may be an excellent tool for drug discovery. By performing a time course proteomic characterization, we envision to understand the protein dynamics across differentiation and identify transcription factors involved in the maintenance HSC phenotype and cell activation.

Method: MS proteomics was performed in 4 independent differentiations of iPSC to HSCs and primary human HSCs. Seven staggerer mice (RORA−/−) and their wildtype littermates were treated with CCl4 during 4 weeks. Fourteen mice were treated with CCl4 and 7 were treated with the RORA agonist SR1078. qPCR, immunofluorescence and immunohistochemistry assays were used as validation. RORA expression was evaluated in a cohort of 25 patients with alcohol and metabolic associated chronic liver disease.

Results: Proteomic results indicated that iPSC-HSC differentiation occurred in three stages: undifferentiated phase (Day 0 to 4), intermediate fetal stage (Day 6 to 8) and final maturation stage (Day 10 to 12). Developmental markers of fetal HSC, such as VIM, ALCAM, FBLN1 and DCN were sequentially expressed and followed by mature HSC markers, indicating the recapitulation of the embryonic development in vitro. Pathway enrichment of iPSC-HSCs and primary HSCs revealed RORA as an important transcription factor in HSC phenotype and commitment. Experimentally, we first evaluated the effect of RORA on HSC development. iPSC-HSC across differentiation were treated with SR1078, which increased the expression of HSC phenotype and quiescence markers such as RELN, PDCD7, LRTAT and LHX2. Next, we evaluated the role of RORA on HSC activation by treating iPSC-HSCs, which decreased the expression of ACTA2 and increased the expression of quiescent markers (LRTAT and LHX2). In vivo studies with the staggerer mice, showed an increased fibrotic content by Sirius Red staining and an increased gene expression of fibrogenic markers such as ACTA2, collagens and MMPs in the mutant group. In addition, SR1078 treatment of CCl4 mice showed a reduction of collagen deposition and aSMA staining, together with a reduced expression of fibrogenic markers. In patients, expression of RORA correlated negatively with fibrogenic markers and MELD Score. These results suggest that RORA plays a role in the progression of liver fibrosis.

Conclusion: The present study demonstrates that the differentiation protocol is a new and reliable tool for the study of HSC biology and the discovery of new antifibrogenic targets. Moreover, we identify RORA as a targetable transcription factor to mitigate liver fibrosis.

OS040
Stellate cell dynamics in progression and regression of hepatic fibrosis
Laura Almale del Barrio1, Emma A.H. Scott1, Frederik Adam Bjørner1, Mike Tørkelsen2, Kim Ravnskjaer1,2, 1University of Southern Denmark, Department of Biochemistry and Molecular Biology, Odense, Denmark; 2University of Southern Denmark, Center for Functional Genomics and Tissue Plasticity (ATLAS), Odense, Denmark. Email: ravnskjaer@bmb.sdu.dk

Background and aims: Non-alcoholic steatohepatitis (NASH) is a metabolic liver disease characterized by hepatic lipid accumulation, chronic inflammation and fibrosis, in which fibrogenic myofibroblasts are central players. These scar-forming cells are derived mainly from activated hepatic stellate cells (HSCs). NASH and cirrhosis were traditionally considered irreversible conditions, but clinical studies have demonstrated that they can be reversed. HSC inactivation seems to be a key mechanism, but the inactivation process is poorly understood. This prompted us to characterize HSC dynamics at single-cell resolution during the induction and regression of NASH-associated fibrosis in vivo.

Method: Lrat−/−mCherry knock-in mice were fed a western diet (WD) combined with carbon tetrachloride (CCL4) for eight weeks (treated) or Chow diet (untreated). Regression of liver disease was studied four weeks after WD/CCL4 cessation (reversal). RNA-sequencing, single-cell RNA-sequencing and immunohistochemistry/immunofluorescence were performed to investigate HSC activation and inactivation.

Results: NASH regression led to profound changes at histological, whole-liver transcriptional, and single-cell levels. We annotated 14 discrete hepatic populations including activated and quiescent HSCs in our single-cell data set obtained from treated, reversal, and untreated mice. We next performed gene expression distribution analyses of cells within and across treatment groups to stratify the HSC population. We here identified HSC subpopulations relating to NASH regression; potentially inactivated HSCs and HSCs that had reverted towards a more quiescent state. Additionally, using single-cell gene regulatory network analysis we determined specific gene regulatory networks for the aforementioned HSC subpopulations.

Conclusion: Our results broaden our understanding of HSC transitions in the liver during induction and regression of NASH, and suggest new molecular mechanisms that could mediate the HSC inactivation and reversion during NASH resolution.

OS041
Machine learning methods for detailed characterization of TGF-beta-induced signatures in a large iPSC-derived hepatic stellate cell cohort
Panagiotis Stanitsas1, Kara Marie Liu1, Lorn Kategaya1, Kelly Haston1, Alicia Lee1, Shahin Mohammadi1, Haoyang Zheng1, Francesco Paolo Casale1, Navpreet Ranu1, Ahmed Sandakli1, Pooja Prasad1, Owen Chen1, Anne Baldwin1, Albert Kim1, Elion Sharon1, Ajamete Kaykas1, Daphne Koller1, Matthew Albert1. 1Insitro, South San Francisco, United States. Email: research_operations@insitro.com

Background and aims: Activation of hepatic stellate cells (HSCs) by TGF-beta plays a central role in fibrotic changes related to Non-Alcoholic Steatohepatitis (NASH). We aimed to establish a screenable in vitro system for identification of anti-fibrotic targets in activated HSCs. This required the development of a novel machine learning (ML) framework which was used to characterize a large cohort of control and NASH induced pluripotent stem cell-derived HSCs (iHSCs).

Method: We differentiated iHSCs from 56 iPSC lines and characterized them using high content imaging and single cell (sc) RNA-seq analysis. For ML image analysis, we derived a novel deep learning method that was tasked with producing informative faturizations of segmented cell images, followed by covariate correction.
Transcriptomic datasets were featured using a state-of-the-art archetypal analysis based framework. Using each of our transcriptomic and imaging datasets separately, and viewing pHSCs as ground truth, we quantified three quality metrics for iHSCs: (i) predictiveness of TGF-beta response in an ML classifier trained on pHSCs; (ii) separation between TGF-beta and DMSO in an unsupervised ML model; (iii) similarity of the overall cell state distribution between iHSCs and pHSCs.

Results: The established ML framework provided informative features of our cellular assays and allowed for the correction of experimental artifacts. We showed robustness of TGF-beta-induced ML phenotype in pHSCs both in imaging and transcriptomics (mean AUC 0.96 for out-of-line assessment in imaging, Figure 1A; mean AUC 0.98 in transcriptomics, data not shown). Interpretation of learned ML phenotypes revealed insights into the TGF-beta responsiveness of pHSCs. This allowed us to utilize multi-parametric criteria to evaluate the cohort of iHSCs. We observed a strong correlation between transcriptomic and imaging characterizations used for the ranking of iHSC lines (spearman = 0.66, p = 8.7 \times 10^{-5}, Figure 1B).

Conclusion: We developed a state-of-the-art approach for the characterisation of HSC morphological and transcriptional phenotypes. Using the developed framework, we successfully modeled TGF-beta-induced activation signatures in HSCs. These image-based phenotypic assays paired with high-performance ML models present unique opportunities for genetic and chemical screens and the discovery of novel fibrosis targets.

OS042
Enter epithelial cell-specific RAGE controls ductular reaction-mediated fibrosis during cholestasis

Wai Ling Macrina Lam1,2, Amruta Damle-Vartak1, Gisela Gabernet3, Doris Schneller1, Tanja Poth1, Simone Jörs2, Melanie Sator-Schmitt1, Aurora De Pont2, Lena Weiβ1, Mathias Heikenwälder4, Nachiket Vartak2, Jan G. Hengstler1, Fabian Geisler5, Sven Nahnsen3, Peter Angel1. 1German Cancer Research Center, Division of Signal Transduction and Growth Control, Heidelberg, Germany; 2Ruprecht Karl University of Heidelberg, Faculty of Biosciences, Heidelberg, Germany; 3Eberhard Karls University of Tübingen, Quantitative Biology Center, Tübingen, Germany; 4University Hospital Heidelberg, Center for Model System and Comparative Pathology, Heidelberg, Germany; 5Technical University of Munich, Clinic and Polyclinic for Internal Medicine II, Germany; 6German Cancer Research Center, Division of Chronic Inflammation and Cancer, Heidelberg, Germany; 7Leibniz Research Centre for Working Environment and Human Factors at the Technical University Dortmund (IfADo), Systems Toxicology, Germany

Email: m.lam@dkfz-heidelberg.de

Background and aims: Ductular reaction (DR) is the hallmark of cholestatic diseases characterized by the proliferation of bile ductules lined by biliary epithelial cells (BECs). DR is thought to serve as a reparative and regenerative mechanism in the damaged liver to compensate for the anatomical or functional loss of the biliary system. Surprisingly, it is also commonly associated with increased risk of fibrosis, cirrhosis and liver cancer. The Receptor for Advanced Glycation End Products (RAGE, encoded by Ager) was identified as a critical mediator of DR during chronic injury and carcinogenesis (Pusterla et al. Hepatology. 2013.). Nevertheless, whether DR is reparative or detrimental to the liver during cholestasis remains elusive. Thus, we aimed to delineate the specific function of RAGE on DR and its potential association with fibrosis in the context of cholestasis.

Method: We utilized a biliary tracing reporter murine model (R26<sup>lox/lox</sup>Hnf1βCreER) and deleted Ager conditionally in BECs. Choline-deficient ethionine-supplemented (CDE) diet was fed to the mice for three weeks to induce cholestasis. RNA-seq analysis of FACS-sorted primary BECs from CDE-challenged mice, immunofluorescence (IF) staining and multi-modal 3D architectural staining were employed to investigate the role of BEC-specific RAGE activity in DR and fibrosis. In vitro co-culture assays of BECs and hepatic stellate cells (HSCs) combined with flow cytometry and mass spectrometry analysis were utilized to delineate the newly identified RAGE-dependent paracrine crosstalk between BECs and HSCs.

Results: BEC-specific deletion of Ager strongly impairs ductular reaction. Remarkably, the number of stellate cell is substantially diminished concomitantly with an attenuation of bridging fibrosis. RNA-seq data revealed a RAGE-dependent mechanistic role of BECs in the modulation of cholestasis-induced fibrosis. Classical fibrogenic mediators and ECM genes were differentially expressed between Ager wildtype and knockout BECs. Flow cytometry of direct co-culture assay demonstrated that HSCs were activated by BECs in RAGE-dependent manner. Mass spectrometry and indirect co-culture analysis, combined with immunohistochemistry analyses of livers from CDE-treated mice showed that BEC-derived secretory JAG protein activates Notch signalling in HSC in trans.

Conclusion: This present study provides a novel insight into the adverse consequence of DR in cholestasis-associated fibrosis. Although hypothesized to provide a regenerative mechanism during cholestasis, it is evident that BEC-specific RAGE activity enhances DR-associated fibrosis via a trans-regulatory mechanism in the current CDE diet model. We demonstrate that Notch signaling in HSCs is activated by BEC in RAGE-dependent manner via paracrine JAG protein, thereby turning HSCs into a myofibroblastic phenotype to establish a profibrotic milieu.
**Background and aims:** The prevalence of type 2 diabetes (T2D) in young people is increasing, but little is known regarding the association between age of onset of T2D and risk of liver-related events. This study aimed to determine the incidence of liver-related events of patients of different ages of onset of T2D.

**Method:** We conducted a retrospective territory-wide cohort study of adult patients with non-alcoholic fatty liver disease (NAFLD) diagnosed between January 1, 2000 and June 30, 2021. T2D was defined by exposure to any antidiabetic agents, haemoglobin A1c ≥6.5%, fasting plasma glucose ≥7.0 mmol/L in two measurements at least one month apart, and/or ICD-9-CM diagnosis codes. The primary end point was liver-related events, defined as a composite end point of HCC and cirrhotic complications. Fine-Gray model was used to adjust for competing risk of death.

**Results:** We analysed data from 30, 360 NAFLD patients (mean age, 56.4 ± 13.4 years; 46.0% men); a total of 15, 430 cases of T2D and 456 events of patients of different ages of onset of T2D.

**Conclusion:** Younger-onset T2D increases the risk of liver-related events. Further studies should determine the role of fibrosis assessment and more aggressive treatment of steatohepatitis in this high-risk group.

**Figure:** Association between age of onset of T2D and risk of liver-related events (reference group was patients who did not have T2D at the corresponding ages).

---

**OS044**

**Non-alcoholic fatty liver disease patients have worse health-related quality of life compared to the general population irrespective of their fibrosis stage: results from a prospective multicenter UK study**

Margarita Papatheodoridi1, Giada Pallini1, Guruprasad Aithal2, Hong Kai Lim3, Jeremy Cobbold4, Maria Corina Plaz Torres1, Marta Guerrero Misas1, John Ryan1, Jeremy Tomlinson4, Michael Allison3, Louise Longworth5, Emmanuel Tsochatzis3

1University College of London, Royal Free Hospital, Institute for Liver and Digestive Health, United Kingdom; 2Nottingham University, Digestive Diseases Centre, United Kingdom; 3Cambridge University Hospital NHS Foundation Trust, Liver Unit, Department of Medicine, NIHR Cambridge Biomedical Research Centre, Cambridge, United Kingdom; 4Oxford University Hospitals NHS Foundation Trust, Oxford Liver Unit, Department of Gastroenterology and Hepatology, Oxford, United Kingdom; 5PHMRLimited, United Kingdom

Email: margarita.gpap@gmail.com

**Background and aims:** Health-related quality of life (HRQL) is impaired in patients with chronic liver disease, including those with non-alcoholic fatty liver disease (NAFLD). The primary aim of the study was to assess the HRQL of patients with NAFLD and compare this to the general population. Secondary aims were to examine the associations of fibrosis severity and metabolic comorbidities with impairments in HRQL.

**Method:** We included 561 consecutive patients with NAFLD prospectively evaluated in 4 UK secondary care centres between 2016 and 2019. Patients completed two HRQL questionnaires: the EQ-5D-5L and the Chronic Liver Disease Questionnaire (CLDQ). Demographic and clinical information, liver stiffness by transient elastography and/or liver biopsy results and history of cirrhosis were recorded. A general population sub-cohort of the Health Survey of England 2018 without alcohol misuse who had completed the EQ-5D-5L was used as a comparator. For the comparison of HRQL in NAFLD patients and the general population, propensity-score (PS) matching was performed, according to age, sex and body mass index (BMI).

**Results:** The EQ-5D-5L index was significantly lower in 514 NAFLD patients compared to the 514 PS-matched healthy controls (0.762 ± 0.276 vs 0.844 ± 0.200, p < 0.001). The difference was also significant in a subgroup of NAFLD patients without advanced fibrosis (F < 3 or LS < 8 kPa) compared to the general population (0.781 ± 0.276 vs 0.845 ± 0.200, p < 0.001). Among NAFLD patients, the EQ-5D-5L index, EQ-visual analogue scale (VAS) and CLDQ scores were significantly lower in patients with cirrhosis compared to patients without cirrhosis (p = 0.021, p = 0.011 and p = 0.001 respectively). However, in patients with NASH, there was no difference between patients with and without advanced fibrosis on any of the HRQL measures.

Liver stiffness was the only factor significantly associated with lower scores in all HRQL measures, both in the whole patient population and in non-cirrhotic patients.

In multivariate analysis, the EQ-5D-5L index was negatively associated with type II diabetes, depression and osteoarthritis both in the whole patient population and in patients without cirrhosis. EQ-VAS was associated with age, sex, BMI, depression and osteoarthritis in all patients and non-cirrhotic patients. Lower CLDQ scores were associated with lower age, male sex, presence of type II diabetes, ischemic heart disease, depression and osteoarthritis in all patients; in the sub-group of non-cirrhotic patients, lower CLDQ was associated with male sex, type II diabetes and depression.

**Conclusion:** HRQL is similar for NASH patients with or without advanced fibrosis. However, even those without advanced fibrosis (LS < 8 kPa or F < 3) have worse HRQL compared to the general population, implying that a multi-disciplinary management is required for NAFLD patients, irrespectively of their disease severity.
OS045
Genetics of liver fat and volume associate with altered metabolism and whole body magnetic resonance imaging
Shafqat Ahmad, Germán Carrasquilla, Taro Langner, Uwe Menzel, Filip Malmberg, Ulf Hammar, Jenny C. Censin, Sergi Sayols, Diem Nguyen, Andrés Martínez Mora, Jan W. Eriksson, Robin Strand, Joel Kulbberg, Håkan Ahlström, Tove Fall. 1Uppsala University, Medical Sciences, Uppsala, Sweden; 2The University of Copenhagen, Faculty of Health and Medical Sciences, København, Denmark; 3Uppsala University, Uppsala, Sweden; 4University of Oxford, United Kingdom
Email: shafqat.ahmad@medsci.uu.se

Background and aims: An improved understanding of the underlying biological mechanisms of genetic variation linked to liver fat and volume is pivotal for translational and prevention efforts to tackle liver disease. Here we aim to gain biological insight of liver fat and volume loci using a novel image analysis approach allowing whole-body voxel-wise associations to tissue volume and fat content as well as a large set of other phenotypes.

Method: Liver volume was measured from neck-to-knee water-fat MRI images collected in UK Biobank cohort using a deep learning-based segmentation approach. Liver proton density fat fraction (PDFF) were readily available for 4,613 subjects. Using deep regression on the above mentioned neck-to-knee MRI images, liver PDFF was inferred for remaining subjects. We conducted a genome-wide association analysis (GWAS) of liver fat (n = 27,243) and liver volume (n = 24,752) on non-related European participants of the UK Biobank cohort. We further investigated the associated genetic loci in association with whole body composition in high-resolution anatomical correlation voxel-based maps (“Imiomics”). We also analyzed these loci with various biomarkers and liver disease using independent UK Biobank participants (n = 310,239).

Results: We confirmed four previously identified liver fat variants TM6SF2 rs8107974, TM6SF2 rs188247550, APOE rs429358 and PNPLA3 rs738408. A positive and highly specific relationship was observed between liver fat-associated variants and fat fraction in liver area (PNPLA3 rs738408 Figure 1). The liver fat-increasing allele of all four genetic variants were positively associated with alanine aminotransferase, conjugated bilirubin while negatively associated with total cholesterol, triglycerides and low-density lipoprotein cholesterol biomarkers. For liver volume, we identified two novel independent variants CENPW rs1490384, ADH4 rs6858148 and confirm eight previously identified variants SFN rs75460349, GCKR rs1260326, TNFSF10 rs79287178, PPP1R3B rs4240624, REMP3 rs7896518, TNKS2 rs10881959, and PDIA3 rs139974673. We observed a heterogeneous pattern for association with body composition and biomarkers, as for CENPW rs1490384, with strong positive association with muscle tissue volume in neck, abdomen, thigh and hip as well as heart and liver volume among both males and females (Figure 1). Two liver fat and three liver volume-associated genetic variants were positively associated with non-alcoholic fatty liver disease and chronic liver disease.

Conclusion: We report two novel liver volume loci and provide specific association with voxel-based maps body composition architecture while confirming previously reported liver fat and volume genetic variants. Liver fat-associated variants were positively associated with liver injury markers and negatively associated with dyslipidemia biomarkers.

Figure: (abstract: OS045)
Hepatic steatosis is not associated with increased mortality in the elderly-time for a paradigm shift?
Laurens van Kleeft1, Milan Sonneveld1, Maryam Kavousi2, Arfan Ikram2, Robert De Man1, Robert De Knegt1. 1Erasmus MC, University Medical Center, Gastroenterology and Hepatology, Rotterdam, Netherlands; 2Erasmus MC, University Medical Center, Cardiology, Rotterdam, Netherlands; 3Erasmus MC, University Medical Center, Epidemiology, Rotterdam, Netherlands

Background and aims: Fatty liver disease has been associated with excess mortality. Screening for hepatic steatosis in patients with metabolic dysfunction is therefore widely advocated. However, the association between hepatic steatosis and mortality amongst community-dwelling elderly individuals is unclear.

Method: We studied participants of an ongoing prospective cohort: the Rotterdam Study. Individuals aged ≥65 years were enrolled from 2009 to 2014 and were followed through 2018. Steatosis was assessed by ultrasound, and liver stiffness by transient elastography. Subsequently, NAFLD was defined as steatosis in the absence of diabetes, or at least two minor metabolic dysfunction criteria. The presence of fatty liver disease was not associated with impaired survival in multivariable analysis (aHR:0.87, 95%CI:0.73–1.03), similar results were obtained for MAFLD and NAFLD. Furthermore, findings were consistent across a range of clinically relevant subgroups, including age categories, sex, and in participants with metabolic syndrome, elevated liver enzymes, or cardiac disease, as shown in Figure 1.

Figure 1: Mortality risk among the elderly with steatosis

<table>
<thead>
<tr>
<th>Entire population</th>
<th>HR</th>
<th>HR-Plot</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age</td>
<td></td>
<td></td>
</tr>
<tr>
<td>65-70</td>
<td>0.98</td>
<td></td>
</tr>
<tr>
<td>70-75</td>
<td>0.86</td>
<td></td>
</tr>
<tr>
<td>75+</td>
<td>0.85</td>
<td></td>
</tr>
<tr>
<td>Sex</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Male</td>
<td>0.91</td>
<td></td>
</tr>
<tr>
<td>Female</td>
<td>0.81</td>
<td></td>
</tr>
<tr>
<td>Metabolic syndrome</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Hypertension</td>
<td>0.74</td>
<td></td>
</tr>
<tr>
<td>(pre)diabetes</td>
<td>0.81</td>
<td></td>
</tr>
<tr>
<td>Hypo-HDL</td>
<td>0.80</td>
<td></td>
</tr>
<tr>
<td>Hypertriglyceridemia</td>
<td>0.82</td>
<td></td>
</tr>
<tr>
<td>High waist circumference</td>
<td>0.88</td>
<td></td>
</tr>
<tr>
<td>Elevated liver enzymes</td>
<td>0.94</td>
<td></td>
</tr>
<tr>
<td>Cardiovascular disease</td>
<td>0.91</td>
<td></td>
</tr>
</tbody>
</table>

Results: We included 4,093 elderly participants (aged 74.4 ± 6.6; 42.7% male, BMI 27.6 ± 4.2 kg/m², 44.5% metabolic syndrome, 36.8% had ultrasound-based steatosis and 7.1% had liver stiffness ≥8.0 kPa. During the median follow-up of 6.9 years, 793 participants died, resulting in a mortality rate of 29.6 per 1,000 person-years. Among the elderly, steatosis was not associated with impaired survival in multivariable analysis (aHR:0.87, 95%CI:0.73–1.03), similar results were obtained for MAFLD and NAFLD. Furthermore, findings were consistent across a range of clinically relevant subgroups, including age categories, sex, and in participants with metabolic syndrome, elevated liver enzymes, or cardiac disease, as shown in Figure 1. Sensitivity analyses showed similar results for mortality beyond five years of follow-up and for both cancer-related and cerebro-cardiovascular mortality. Furthermore, among participants with steatosis, higher liver stiffness (aHR:1.02 per kPa, 95%CI:0.93–1.12) was not associated with mortality.

Conclusion: The presence of fatty liver disease was not associated with increased mortality risk in this cohort of community-dwelling elderly subjects. Findings were consistent across a range of clinically relevant subgroups. This indicates that screening for fatty liver disease is unlikely to improve outcomes in the elderly.

OS047

Burden of hepatocellular cancer in patients with type-2 diabetes mellitus: a 2011–2020, french, longitudinal, retrospective, national, cohort study
Lucia Parlati1, Samir Bouam2, Michael Schwarzerling3, Emmanuel Tschatzis4, Philippe Sogni5, Stanislas Poit5, Vincent Mallet5,6. 1Institut Cochin, Paris, France; 2Assistance Publique Hôpitaux de Paris, Paris, France; 3Inserm UMR 1219, Bordeaux, France; 4UCL Institute for Liver and Digestive Health, Royal Free Hospital and UCL, London, United Kingdom; 5Université de Paris, France, France

Background and aims: There are uncertainties on the burden of hepatocellular cancer (HCC) in patients with type-2 diabetes (T2D) in France. We therefore measured national incidences and risks of in-hospital HCC.

Method: The data source was the 2011–2020 National Hospital Discharge database. We selected all T2D patients. HCC and competing death incidences were measured overall and without well-identified risk factors of liver disease progression, HCC death. Risks were computed with multinomial logistic regression models.

Results: The sample comprised 2,883,684 adults. Mean (IQR) age was 67 (58, 77) years and 54% were men. HCC incidence (95% CI) was 1.19 (1.17–1.21) per 1000 person-years at risk, totaling 26,136 (0.9%) cases over 12,504,690 patient-years. A history of alcohol use disorders and non-metabolic liver-related risk factors were recorded among 55% and 21% of incident cases, respectively. In patients without well-identified risk factors of liver disease progression, HCC incidence was 0.57 (0.55–0.58) per 1000 person-years at risk. Male sex, age in the 40–70 years category, alcohol use disorders [aOR 20.8 (20.0–21.5)], and obesity [aOR 1.24 (1.2–1.28)] were independently associated with a higher risk of HCC than of competing mortality.

Conclusion: A history of alcohol use disorders was the main driver of liver disease progression to HCC in French patients with T2D. Obesity increased the risk of HCC by ~25%. Patients with T2D should be advised to abstain from alcohol.

Journal of Hepatology 2022 vol. 77(S1) | S1–S118 541
Table: Multivariate risks for HCC and competing mortality in 2011–2020 French residents with T2D

<table>
<thead>
<tr>
<th>Predictors</th>
<th>Hepatocellular carcinoma</th>
<th>Competing mortality</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age categories at cohort inception¹</td>
<td>aOR²</td>
<td>P Value</td>
</tr>
<tr>
<td>(30, 40]</td>
<td>2.34 (1.25–4.38)</td>
<td>0.008</td>
</tr>
<tr>
<td>(40, 50)</td>
<td>6.29 (3.49–11.37)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>(50, 60]</td>
<td>12.69 (7.06–22.83)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>(60, 70]</td>
<td>20.02 (11.44–36.00)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>(70, 80]</td>
<td>23.47 (13.05–42.20)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>(80, Inf)</td>
<td>17.41 (9.66–31.39)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Male sex</td>
<td>3.22 (2.07–5.37)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Alcohol use disorders</td>
<td>20.76 (20.02–21.54)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Obesity</td>
<td>1.24 (1.20–1.28)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Non-liver-related risk factors³</td>
<td>1.05 (1.01–1.10)</td>
<td>0.004</td>
</tr>
<tr>
<td>Smoking</td>
<td>0.71 (0.68–0.74)</td>
<td>&lt;0.001</td>
</tr>
</tbody>
</table>

¹T2D patients with alcoholic liver disease or non-metabolic liver-related risk factors were excluded from the analysis. HCC cases were recorded after a 2011–2013 (3-year) washout period to reduce the risk of non-incident cases.
²Risks were computed with multinomial logistic regression models.
³Reference was the [18, 30] age category.
⁴Non-liver risk factors were extraplastic cancer; AIDS; connective tissue disorders; ischemic heart disease; and stage 3–5 chronic kidney disease.

OS049 Randomized controlled trial of home-based hepatitis C self-testing for key populations in Malaysia

Xiaohui Sem¹, Sonjelle Shilton¹, Huan-Keat Chan², Han Yang Chung³, Anu Karunanithy³, Jessica Markby³, Po-Lin Chan⁴, Niklas Luhmann⁴, Cheryl Johnson⁴, Pamela Nabet⁵, Naziril Hairizan Binti Nasis⁵, Stefano Ongarello⁶, Elena Ivanova⁵, Muhammad Radzi Abu Hassan⁵.

FIND; ²Clinical Research Centre, Hospital Sultanah Bahiyah; ³Drugs for Neglected Diseases Initiative South-East Asia Regional Office; ⁴Malaysian AIDS Council; ⁵World Health Organization Regional Office for Western Pacific; ⁶World Health Organization, Global HIV, Hepatitis and STI Programmes; ⁷Ministry of Health

Email: xiaohui.semin@findd.org

Background and aims: Malaysia is an upper middle-income country and has been expanding and decentralizing HCV care to the community. HCV self-testing (HCVST), recommended by the World Health Organization, provides an additional way to increase access and uptake of HCV testing among key populations who are disproportionately affected by HCV. We integrated HCVST with an existing online HIV self-testing platform to assess the impact of home-based HCVST on the uptake of HCV testing among key populations nationwide.

Method: This is a randomized controlled trial comparing HCVST sent via post (intervention arm, n = 500) with standard of care testing at a facility (control arm, n = 250). In the intervention arm, participants received either an oral fluid- or blood-based HCVST; in the control arm, participants were provided information about the nearest HCV testing center. All participants also received HCV information and support resources (e.g. access to a call center). We describe preliminary findings for this study reporting on the primary outcome—the uptake of HCV testing. Acceptability, feasibility and attitudes around HCVST were also evaluated via a series of surveys.

Results: To date, 258 individuals, with a median (IQR) age of 26 (22–30.75) years, were recruited, of whom 88.8% were MSM. Most participants were male (97.6%), completed university (46.9%), and were employed (61.4%). Prior to this study, 60.6% of the participants were not tested for HCV; of these, the top reason why they did not get tested was they did not know how (57.1%). Additionally, acceptability of HCVST was high—71.7% of the participants stated that they preferred to test for HCV by themselves at home; 98.4% were willing to test themselves at home if they had a test kit and instructions on how to do it. After either receiving a HCVST or information about the nearest testing center, 99.0% (119/120) in the intervention arm and 30.9% (13/42) in the control arm reported completing HCV testing (p < 0.01) (see Figure).
Conclusion: Preliminary results show that HCVST via an online distribution model, compared with standard testing services, significantly increased the uptake of HCV testing among key populations. The outcomes of this study can further provide critical evidence about testing uptake, linkage to care, acceptability and any social harm due to HCVST. Updated data will be presented at the conference.

OS050
The disease burden of hepatitis B and hepatitis C from 2015 to 2030: the long and winding road
Devin Razavi-Shearer1, Sarah Blach1, Ivane Gamkrelidze1, Chris Estes1, Ellen Mooneyhan1, Kathryn Razavi-Shearer1, Homie Razavi1.1Center for Disease Analysis Foundation, Lafayette, United States Email: drazavishearer@cdafound.org

Background and aims: This study aims to estimate the future disease burden of HBV and HCV at the global and continental level through 2030. 2015 was used as a baseline in line with the WHO targets to show what progress has been made to date.

Method: The results of a literature review and Delphi expert interviews were integrated into country-specific PRoGReSs and Bright Models for the HBV and HCV analyses respectively. Both are Markov models that utilize country specific inputs to estimate the natural history of the disease and future burden. Where data were unavailable, regional averages were applied to the total population of the country.

Results: 166 country level HBV and 110 HCV models were available. At the current trends, the prevalence of HBV is expected to decrease from 282 million in 2015 to 247 million in 2030, representing an 11% decrease globally with Africa’s prevalence to remain relatively constant. The incidence of chronic HBV is expected to decline by 43% from 1, 459, 000 to 827, 000 new cases per year with all continents seeing a decline. Globally, the mortality of HBV is expected to increase by 39% between 2015 and 2030 from 850, 300 to 1, 019, 000 deaths annually. Similarly, the incidence of HCC is expected to increase by 34% from 682, 000 to 912, 000 cases per year. For both indicators all continents are expected to increase in this time frame. The prevalence of HCV is expected to decrease from 64 million in 2015 to 54 million in 2030, representing a 15% decrease globally. The incidence of chronic HCV is expected to decline by 7% by 1, 521, 000 to 1, 409, 000 new cases per year with Asia and North America increasing. Globally the mortality of HCV is expected to increase by 3% between 2015 and 2030 from 284, 000 to 293, 000 deaths annually. The incidence of HCC is expected to increase by 9% from 202, 000 to 220, 000 cases per year. Increases are expected in Asia, Oceania, and South America for both indicators.

Conclusion: Progress has been made particularly in regard to prevalence and incidence. However, without additional interventions almost 12 million individuals will die early from preventable deaths. Early gains made by Egypt, high income countries, and other early adopters, for HCV elimination, are offset by raising disease burden in the rest of the world. Innovative guidelines and funding mechanisms are necessary to meet countries where they are to live up to international commitments to elimination.

OS051
The HCV care cascade for children and young people in British Columbia, Canada: a large, linked administrative population-based cohort study
Dahn Jeong1, Margo Pearce2, Amanda Yu2, Laura Sauve3,4, Richard A. Schreiber1,4, Sofia Bartlett2,5, Muhammad Furqan Waleed6,7, Makuza Jean Damascene1, Prince Adu1,2, Jane Buxton3,4, Hector Velasquez1,2, Mawuena Binka2, Chelsea Elwood8,9, David GoldFarb3,5, Hasina Samji2,10, Stanley Wong2, Maria Alvarez2, Neora Pick8,11, Naveed Janjua1,2,7.1The University of British Columbia, School of Population and Public Health, Vancouver, Canada; 2BC Centre for Disease Control, Vancouver, Canada; 3BC Children’s Hospital, Vancouver, Canada; 4The University of British Columbia, Department of Pediatrics, Vancouver, Canada; 5The University of British Columbia, Department of Pathology and Laboratory Medicine, Vancouver, Canada; 6Youthco HIVand Hep C Society, Vancouver, Canada; 7The University of British Columbia, Department of Pathology and Laboratory Medicine, Vancouver, Canada; 8Youthco HIVand Hep C Society, Vancouver, Canada; 9Youthco HIVand Hep C Society, Vancouver, Canada; 10Youthco HIVand Hep C Society, Vancouver, Canada; 11Youthco HIVand Hep C Society, Vancouver, Canada;

Figure: (abstract: OS050)
Background and aims: In high income countries, new hepatitis C virus (HCV) infections have been occurring at the highest rate among people under 30 years of age, driven by the ongoing opioid crisis and other co-occurring socioeconomic conditions. The clinical experiences of young people living with HCV are underrepresented in research. We aimed to build the HCV care cascade for children and young people under age 30 living with HCV in British Columbia (BC), Canada.

Method: We used data from the BC Hepatitis Testers Cohort, a large population-based administrative dataset linked with data on primary care visits, hospitalizations, and medication dispensations. This study includes all BC residents under age 30 who have been diagnosed with HCV by the end of 2019. The HCV care cascade was defined as: 1) HCV antibody (Ab) diagnosed 2) ribonucleic acid (RNA) tested 3) RNA positive 4) genotyped 5) initiated treatment and 6) achieved sustained virologic response (SVR). We estimated the number and proportion of people in each stage.

Results: There were 1,350 children and young people (aged 4 to 29) diagnosed as HCV Ab positive living in BC at the end of 2019. Of these, 82.2% (1,110) had received an RNA test, and 60.6% (673) were RNA positive. Among those who were RNA positive, 79.9% (538/673) had their HCV genotyped; however, only 40.3% (217/538) initiated treatment. SVR was achieved by 87.7% (121/138) of individuals for whom data on SVR assessment was available. In 2019, the proportion of HCV RNA positive persons receiving treatment varied by age group: 17.1% (6/35) in 14–19 years, 34.4% (45/131) in 20–24 years, and 34.1% (164/481) in 25–29 years. Treatment initiation increased over time, with the majority of treatments started between 2018 and 2019: 3.7% (8/217) treated between 2009–2011, 7.8% (17/217) between 2012–2014, 25.8% (56/217) between 2015–2017, and 62.7% (136/217) between 2018–2019. Many young people living with HCV were socioeconomically marginalized, had other comorbidities, particularly mood and anxiety disorders, and were accessing harm reduction services such as opioid agonist therapy.

Conclusion: By the end of 2019, more than two-thirds of people under age 30 in BC with chronic HCV remained untreated. The approval of highly effective pangenotypic direct-acting antiviral regimens provides the opportunity for early treatment for young people. Identifying and addressing the barriers that young people experience would be crucial to optimizing access to HCV care and services in this population.
**OS054**

Hepatitis C elimination in diabetic population from a shared care cascade cohort- under Changhua-Integrated Program to Stop hepatitis C infection (CHIPS-C)

Tsung-Hui Hu, Yo-Yu Tsao, Wei-Wen Su, Chi-Chao Yang,
Chi-Chieh Yang, Sam Li-Sheng Chen, Yen-Po Yeh, Hsiu-Hsi Chen.
1Kaohsiung Chang Gung Memorial Hospital, and Chang Gung University College of Medicine, Kaohsiung, Taiwan; Kaohsiung, Taiwan; 2Changhua County Public Health Bureau, Changhua, Taiwan; 3Changhua Christian Hospital, Changhua, Taiwan, 4Changhua Hospital, Ministry of Health and Welfare, Changhua, Taiwan; 5Show Chwan Memorial Hospital, Changhua, Taiwan, 6School of Oral Hygiene College of Oral Medicine, Taipei Medical University, Taipei, Taiwan; 7Changhua County Public Health Bureau, Changhua, Taiwan; 8Graduate Institute of Epidemiology and Preventive Medicine, College of Public Health, National Taiwan University, Taipei, Taiwan; 9Taiwan Diabetes Society.

**Background and aims:** Several clinical studies have suggested an association between chronic HCV infection and diabetes mellitus (DM). HCV micro-elimination approach, which focuses treatment on DM population was rarely reported. We aim to conduct HCV elimination for population with diabetes mellitus in a county of Taiwan via 27 local health centers under Changhua-Integrated Program to Stop Hepatitis C Infection (CHIPS-C).

**Method:** Changhua County, has 26 towns and a total of 1, 289,000 residents. In addition to hospitals and local clinics in the county, there are 27 local health centers handled by the Changhua County Public Health Bureau of government. Taking the diabetic cases in the clinics of various township health centers from 2018 to 2020 as the tracking generation, combined with the Changhua County Diabetes Common Care Network since 1996, HCV screening and treatment were implemented and evaluated. The achievement rate of HCV care chain-related indicators, and the difference in HCV positive rate and treatment rate under different influencing factors were analysed.

**Results:** By excluding those who were unable to enter the program such as deaths, aging, and mobility, the screening targets total 10,684 people. The HCV antibody screening rate reached 93.4% (9,978 people), with HCV antibody positive rate of 6.1% (608 people), HCV RNA referral rate of 93.4% (568 people), HCV RNA virus checking rate of 92.1% (523 people), detectable HCV RNA rate of 69.6% (364 people), eligible treatment rate was 97.5% (355 people), and final treatment rate was 92.1% (327 people). When compared with the situation before intervention of program, the screening rate and treatment rate have been significantly improved which achieve the goal of HCV elimination. The risk of HCV infection is 1.27 (95%CI: 0.793–2.035), 1.64 (95%CI: 1.057–2.536), 1.90 (95%CI: 1.232–2.937), for patients of 50–59 years, 60–69 years, and over 70 years respectively when compared with patients less than 50 years. Furthermore, the risk of HCV infection is 0.43 (95%CI: 0.253–0.712; p = 0.0012) in patients of senior high school, and 0.26 (95%CI: 0.108–0.524, p = 0.0026) in patients of university compared with patients of illiterate. HCV risk is not associated with other factors such as gender, the duration of diabetes, cigarette smoking, presence of chronic kidney, retinopathy, and foot disease at all. We further evaluated the heterogeneity among towns by using the random effect model, and found that the antibody positive rate was significantly different among towns, but not different on the RNA positive rate and treatment rate.

**Conclusion:** A novel model was successfully implemented for HCV elimination in diabetic population in the community of Changhua county in Taiwan, by using a series of indicators for caring cascade. This population-based service was provided to the 26 towns with a homogenous quality.

---

**Primary Liver Cancer: Experimental and pathophysiology**

**OS055**

PMEPA1: an oncopogene in hepatocellular carcinoma linked to TGF-beta signaling

Carmen Andreu-Oller, Marta Piquè-Gil, Marina Barcena-Varela, Roser Pinyol, Roger Esteban-Fabrò, Judit Peix, Kelly Sahin, Miguel Torres-Martín, Daniela Siala, Anna Lujambio, Josep M. Llovet, Icahn School of Medicine at Mount Sinai, Division of Liver Diseases, New York, United States; Institut d’Investigacions Biomèdiques August Pi i Sunyer (IDIBAPS), Translational Research in Hepatic Oncology, Liver Unit, Barcelona, Spain; Universitat de Barcelona, Barcelona, Spain; Institut Catalana de Recerca i Estudis Avancats (ICREA), Barcelona, Spain.

**Background and aims:** Transforming growth factor beta (TGF-beta) has a dual role in cancer, including hepatocellular carcinoma (HCC). It acts as a tumor suppressor in early stages of hepatocarcinogenesis, but promotes epithelial-to-mesenchymal transition, angiogenesis and immunosuppression in advanced stages. PMEPA1 (prostate transmembrane protein androgen induced 1), a direct target gene of the TGF-beta pathway that negatively regulates TGF-beta signaling by interacting with SMAD proteins, has been shown to promote TGF-beta oncogenic effects in other cancers. Here, we explored its role in HCC pathogenesis.

**Method:** We analyzed transcriptomic, genomic, epigenomic and clinicopathological data of a discovery cohort of 228 HCCs and a validation cohort of 361 HCCs. PMEPA1 levels were quantified by qPCR and IHC in the discovery cohort. PMEPA1 overexpression was validated in 6 independent cohorts (n = 916) using microarray and RNAseq data. We evaluated PMEPA1 expression at the single-cell level using a publicly available scRNAseq dataset from 25 HCCs. Genetically engineered mouse models were generated through hydrodynamic
tail-vein injection. Equal amounts of plasmids overexpressing PMEP1, TGFB1 and MYC were injected in mice to evaluate survival. Molecular and histopathological analyses of the murine tumours are currently ongoing.

**Results:** PMEP1 was overexpressed in 18% of human HCCs [FC > 2; n = 203/1144], a feature associated with TGF-beta signaling (p < 0.0001). PMEP1 was expressed by both malignant and tumor microenvironment (TME) cells including endothelial cells, cancer associated fibroblasts, T cells and B cells. Overexpression of PMEP1 was associated with gene body hypermethylation (p < 0.0001). HCCs displaying both TGF-beta signaling and high PMEP1 levels (11% of cases) were significantly enriched in signatures of immune exhaustion, late TGF-beta activation, TME response to TGF-beta and active TME cells including endothelial cells, cancer associated fibroblasts, T cells and B cells. Overexpression of PMEP1 led to HCC development in 9/16 mice and showed a lower survival when compared to the control arm, overexpression of MYC alone (p = 0.014) (Figure). On the contrary, only 1/12 mice in the MYC+PMEP1+TGFB1 condition developed HCC and none of the MYC+TGFB1 mice.

**Conclusion:** PMEP1 upregulation is linked to TGF-beta activation and an aggressive phenotype in human HCC. Overexpression of PMEP1 in combination with MYC in vivo led to HCC development, showing for the first time the oncogenic role of PMEP1 in this cancer.

**OS056**

**Targeting NAE1-mediated protein hyper-NEDDylation halts cholangiocarcinogenesis and impacts on tumour-stroma crosstalk in experimental models**

Paula Olaizola1, Pui-Yuen Lee-Law1,2, Maite G. Fernandez-Barrena2,3,4,5, Laura Alvarez1, Massimiliano Cadamuro3,6, Mikel Azkargorta7, Colm O. Rourke8, Francisco J. Caballero1, Rocio IR Macias3,5, Jose Marin5,6, Marina Serrano-Macia3,6, Maria Luz Martinez-Chantar3,4,5, Matias A. Avila3,4,5, Jose Marin5,6, Marina Serrano-Macia3,6, Laura Alvarez3, Massimiliano Cadamuro3,6, Mikel Azkargorta7, Felix Elortza5,7, Jesper Andersen8, Luis Bujanda1,5, Laura Alvarez3, Massimiliano Cadamuro6, Mikel Azkargorta7, Jesper Andersen8, Luis Bujanda1,5, Pedro Miguel Rodrigues1,5,15,17, Jesus Maria Bañales1,5,15,17, Department of Liver and Gastrointestinal Diseases, Biodonostia Health Research Institute-Donostia University Hospital-, University of the Basque Country (UPV/EHU), San Sebastian, Spain; 2Department of Gastroenterology and Hepatology, Radboud University Nijmegen Medical Center, Nijmegen, Netherlands; 3Hepatology Program, CIMA, University of Navarra, Pamplona, Spain; 4Instituto de Investigaciones Sanitarias de Navarra (IdiSNA), Pamplona, Spain; 5National Institute for the Study of the Liver and Gastrointestinal Diseases (CIBERehd, “Instituto de Salud Carlos III”), Spain; 6Department of Molecular Medicine (DMM), University of Padua, Padua, Italy; 7Proteomics Platform, CIC bioGUNE, CIBERehd, ProteoRed-ISCIII, Bzikaià Science and Technology Park, Derio, Spain; 8Department of Health and Medical Sciences, Biotech Research and Innovation Centre (BRIC), University of Copenhagen, Copenhagen, Denmark; 9Experimental Hepatology and Drug Testing (HEVEPHARM) Group, Institute of Biomedical Research of Salamanca (IBSAL), University of Salamanca, Salamanca, Spain; 10Liver Disease Laboratory, CIC bioGUNE, Basque Research and Technology Alliance (BRTA), Spain; 11Department of Physiology, Faculty of Medicine and Nursing, University of the Basque Country (UPV/EHU), Leioa, Spain; 12Biocrues Bizkaia Health Research Institute, Cruces University Hospital, Barakaldo, Spain; 13Institute of Pathology, University of Regensburg, Regensburg, Germany; 14Department of Internal Medicine, Yale Liver Center (YLC), School of Medicine, Yale University, New Haven, CT, United States; 15IKERBASQUE, Basque Foundation for Science, Bilbao, Spain; 16Faculty of Medicine and Nursing, University of the Basque Country (UPV/EHU), Leioa, Spain; 17Department of Biochemistry and Genetics, School of Sciences, University of Navarra, Pamplona, Spain

**Email:** jesus.banales@biodonostia.org

**Background and aims:** Cholangiocarcinoma (CCA) comprises a heterogeneous group of malignant tumors with dismal prognosis. Alterations in post-translational modifications (PTMs), including NEDDylation, result in abnormal protein dynamics, cell disturbances and disease. Here, we investigate the role of NEDDylation in CCA development and progression.

**Method:** Levels and function of NEDDylation, together with response to Pevonedistat (NEDDylation inhibitor) or CRISPR/Cas9 against NAE1 were evaluated in vitro, in vivo and/or in patients with CCA. Development of preneoplastic lesions in Nae1−/− mice was investigated using an oncogene-driven CCA model. The impact of NEDDylation in CCA cells on tumor-stroma crosstalk was assessed using CCA-derived cancer-associated fibroblasts (CAF). Proteomic analyses were carried out by mass spectrometry.

**Results:** NEDDylation machinery was found overexpressed and overactivated in human CCA cells and tumors, correlating with poor prognosis. Most NEDDylated proteins found upregulated in CCA cells, after NEDD8-immunoprecipitation and further proteomics, participate in cell cycle, proliferation or survival. Genetic (CRISPR/Cas9/NAE1) and pharmacological (pevonedistat) inhibition of NEDDylation reduced CCA cell proliferation and impeded colony formation in vitro. NEDDylation depletion (pevonedistat or Nae1−/− mice) halted tumorigenesis in subcutaneous, orthotopic, and oncogene-driven models of CCA in vivo. Moreover, pevonedistat potentiated chemotherapy-induced cell death in CCA cells in vitro. Mechanistically, impaired NEDDylation triggered the accumulation of cullin RING ligase or NEDD8 substrates, inducing DNA damage and cell cycle arrest. Furthermore, NEDDylation impairment in CCA cells reduced the secretion of proteins involved in fibroblast activation, angiogenesis, and oncogenic pathways, ultimately hampering CAF proliferation and migration.

**Conclusion:** aberrant protein NEDDylation contributes to cholangiocarcinogenesis by promoting cell survival and proliferation. Moreover, NEDDylation impairment reduces the CCA-stroma crosstalk. Inhibition of NEDDylation with pevonedistat may represent a potential therapeutic strategy for patients with CCA.

**OS057**

**Induction of branching morphogenesis in cholangiocarcinoma organoids in vitro improves similarity with the original tumour**

Gilles van Tienderen1,2, Katharyn Monfilis2, Floris Roos3, Luc J.W. van der Laan3, Monique M.A. Verstegen1,1 ErasmusMC Transplant Institute, Department of Surgery, Rotterdam, Netherlands

**Email:** g.vantienderen@erasmusmc.nl

**Background and aims:** Cholangiocarcinoma (CCA) is an aggressive, heterogeneous cancer with low survival rates. Patient-derived cholangiocarcinoma organoids (CCAOs) hold potential for understanding disease progression and developing novel treatment options, based on their ability to mimic the original tumor. Currently, most organoid expansion protocols focus on stimulation of the canonical WNT/-catenin pathway, however there is growing evidence showing that non-canonical WNT pathways also play a crucial role in cancer progression. This project aims to establish a novel in vitro model for CCA, better recapitulating the in vivo tumor, by stimulating both canonical and non-canonical WNT pathways.

**Method:** Branching cholangiocarcinoma organoids (BRCCAOs) (n = 3 patients) were established with a two-step protocol. First, CCAOs were initiated and cultured under standard conditions in canonical
WNT stimulating expansion medium. Next, expansion medium was replaced by medium that stimulates canonical WNT-signaling (through R-spondin) and non-canonical WNT-signaling (with Dickkopf-related protein 1) simultaneously, after which a branching-like morphology could be observed. Tumor cell behavior in BRCCAOs and CCAOs was assessed and compared through immunohistochemical stainings, bulk RNA-sequencing, and drug response studies.

Results: BRCCAOs presented a distinct branching morphology, displaying a morphological architecture similar to in vivo tumors, while maintaining tumorigenic potential and expression of cytokeratin-7, with an accompanying lack of defined cellular polarity. Bulk RNA-sequencing of BRCCAOs showed significant upregulation of cancer-associated molecular pathways, including hypoxia, compared to CCAOs and a close correlation (coefficient 0.80 ± 0.05) to the transcriptome of the original tumor tissue. BRCCAOs also exhibited a strong resistant phenotype to a large panel of 166 anti-cancer drugs, including multiple drugs that have previously failed in clinical trials for CCA patients (e.g. docetaxel, palbociclib, and irinotecan). Specifically, compared to CCAOs, BRCCAOs showed an approximately 10,000-fold (p < 0.0001) increase in chemo resistance against gemcitabine and cisplatin, first-line chemotherapy drugs for CCA, independent of patient variance.

Conclusion: These results demonstrate that BRCCAOs better resemble in vivo CCA tumor tissue compared to conventional CCAOs, particularly with regards to morphology, transcriptome, and drug responses.Gemcitabine and cisplatin combinational therapy only provides CCA patients with a modest benefit in overall survival, and BRCCAOs appear to mimic this response more closely, thus providing possibilities for personalized medicine applications.

OS058
Cross-talk between MerTK-expressing stromal cells and cholangiocarcinoma
Mirrella Pastore1, Öykü Gönül Geyik1,2, Jesper Andersen3, Monika Lewinska3, Ana Lleo4, Paolo Kunderfranco4, Chiara Ragggi1, Fabio Marra1. 1University of Florence, Firenze, Italy; 2Istinye University, Turkey; 3Copenhagen University, København, Denmark; 4Humanitas University, Italy

Background and aims: A typical feature of cholangiocarcinoma (CCA) is a dense stromal reaction populated by fibrogenic myofibroblasts and immune cells, creating a complex tumor microenvironment where malignant cells survive and proliferate. Cancer stem cells (CSCs) have been proposed as a driving force of tumor initiation, dissemination and drug-resistance in many solid tumors, including cholangiocarcinoma (CCA). Increasing evidence indicates that myeloid-epithelial-reproductive tyrosine kinase (MerTK) is highly expressed by a macrophage subset defined as M2c. The present study aims to investigate whether signals generated by MerTK-expressing macrophages modulate the biology of CCA.

Method: 3D-tumor sphere cultures enriched in CSC were generated from intrahepatic CCA cell lines (HuCCT-1 and CCLP-1). Circulating monocytes were differentiated into M2c macrophages in vitro. Recombinant Gas-6, a MerTK ligand, was used to activate this receptor. MerTK mRNA expression in human CCA tissues was also analyzed.

Results: In CCA cell lines cultured with conditioned medium from Gas-6-stimulated M2c macrophages, cell survival, invasion, sphere-forming efficiency and drug resistance were significantly increased. These effects were reduced following macrophage pre-treatment with the MerTK inhibitor, UNC2025. Analysis of the transcriptome of laser-captured, micro-dissected epithelium and stroma from 23 CCA patients showed that MerTK mRNA expression is significantly higher in intratumoral stroma. Single-cell RNA sequencing of CD45+ sorted cells from paired non-tumoral and tumoral specimens from iCCA patients (n = 6) defined eleven clusters characterized by their gene expression profiles. A further re-clustering of myeloid cells showed MerTK expression in Kupffer cells, lipid macrophages, TREM2+ macrophages, and non-classical monocytes.

Conclusion: These data suggest a cross-talk between MerTK-expressing cells in the stroma and CCA cells, to induce increased malignant features.

OS059
Mixed HCC-CCA originates from hepatic progenitor cells, is dependent on IL6 singling and is ablated by senolytic agents
Nofar Rosenberg1, Matthias Van Hael2, Maria Garcia Beccaria2, Mirian Fernández-Vaquero3, Danijela Heide3, Neta Barashi1, Amnon Peled1, Yuval Nevo5, Shrona Elgavish5, Dirk Schmist-Arras5, Hanan Edler1, Alina Simerzin1, Michal Shoshkes-Carmel5, Klaus Kaestner5, Hilla Giladi1, Stefan Rose-John2, Tania Roskams2, Mathias Heikenvälder2, Eithan Galun1. 1The Goldyne Savv Institute of Gene and Cell Therapy, Hadassah Hebrew University, Jerusalem, Israel; 2University of Leuven, Department of Translational Cell and Tissue Research, Leuven, Belgium; 3DKFZ, Department of Translational Cell and Tissue Research, Germany; 4Hebrew University of Jerusalem, Hadassah Medical School, Bioinformatics Unit, Israel; 5Christian-Albrechts-Universität zu Kiel, Institut für Biochemie, kiel, Germany; 6University of Pennsylvania Perelman School of Medicine, Penn Center for Molecular Studies in Digestive and Liver Diseases, Philadelphia, United States

Email: nofar.ros@gmail.com

Background and aims: Primary liver cancer is the 3rd leading cause of cancer-related death worldwide. Primary liver cancers include: Hepatocellular carcinoma (HCC), intrahepatic cholangiocarcinocarcinoma (CCA) and Mixed HCC-CCA tumors. Chronic liver inflammation, which develops to cirrhosis, is a risk for the development of primary liver cancer. It has been suggested that hepatic progenitor cells (HPCs) could contribute to hepatocarcinogenesis. However, this has not yet been proven. HPCs proliferate in response to injury and chronic inflammation. In this study, we aimed to determine whether HPCs contribute to HCC, Mixed HCC-CCA or both types of tumors, in the MDR2 KO mouse model of inflammation-induced cancer.

Method: In order to enable tracing of progenitor cells, we generated a transgenic mouse based on the MDR2 KO that harbours a YFP reporter gene driven by the Fox11 promoter. Fox11 is expressed specifically in adult HPCs. These mice (MDR2 KOFox11CRE; RosaYFP) develop chronic inflammation by the age of 1 month and develop HCCs by the age of 14–16 months, followed by mixed HCC-CCA tumors at the age of 18 months, as we have first observed, suggesting that the aged mice are a suitable model for mixed HCC-CCA tumors.

Results: In this model, we show that liver progenitor cells are the source of mixed HCC-CCA tumors, but they are not the source of HCC in the chronically inflamed liver. By generating mice with a Diphtheria toxin (DT) receptor in HPCs and administering DT, we ablated the progenitors, and we observed a significant reduction in the development of mixed HCC-CCA tumors but no change in HCCs. RNA-seq analysis revealed enrichment of the IL6 signaling pathway in mixed HCC-CCA tumors in comparison to HCC tumors. A single cell RNA-seq analysis revealed that in the liver, IL6 is expressed from both, immune cells and parenchymal cells which are in senescence, and that IL6 is part of the senescence-associated secretory phenotype (SASP). Upon administration of anti-IL6 antibodies to the MDR2 KOFox11CRE; RosaYFP mice, we inhibited the development of the mixed HCC-CCA tumors. Furthermore, by blocking IL6 transsignaling with sgp130, we also decreased mixed HCC-CCA tumors, indicating that blockade of IL6 signaling pathway at least in part, derives from SASP of cells in senescence. These findings could enhance the development of new therapeutic approaches for mixed HCC-CCA liver cancer.
OS060
MAP17 promotes metastasis in hepatocellular carcinoma by modulating the epithelial-mesenchymal-amoeboid transition
Claudia Gil-Pitarch1,2,3, Esther Bertran4,5, Ilker Uyari6,7, Natalia Herman-Sanchez8, Jose Manuel Garcia-Heredia8,9,10, Nana Goikoetxea1,2,3, Marina Serrano-Macia1,2,3, Rubén Rodríguez Agudo1,2,3, Sofia Lachiondo-Ortega1,2,3, Maria Mercado-Gómez1,2,3, Miriam Rábano2,3, Teresa Cardoso Delgado1,2,3, Jorge Simón Espinosa1,2,3, Luis Alfonso Martinez-Cruz1,2, Cesar Augusto Martín1,2, Maria Vivanco2,3, Matías A. Avila4,7,13, Manuel Gañete Ortiz8,14,15,16, Isabel Fabregat4,17,18, Amancio Carnero10,19, María Luz Martinez-Chantar1,2,17, 1CIC bioGUNE, Liver disease lab, Derio, Spain; 2Basque Research and Technology Alliance (BRTA), Mendaro, Spain; 3Centro de Investigación Biomédica en Red de Enfermedades Hepáticas y Digestivas (CIBERehd), Derio, Spain; 4Belvitge Biomedical Research Institute (IDIBELL), CIBER Enfermedades hepáticas y digestivas (CIBERehd), Hospitalet de Llobregat, Spain; 5Instituto de Biomedicina de Sevilla (IBIS), Sevilla, Spain; 6CIMA, University of Navarra, Pamplona, Spain; 7CIBERehd, Instituto de Salud Carlos III, Madrid, Spain; 8Maimonides Institute for Biomedical Research of Cordoba (IMIBIC), Córdoba, Spain; 9Universidad de Sevilla, Departamento de bioquímica vegetal y biología molecular, facultad de biología, Sevilla, Spain; 10Grupo CIBER de Cáncer, Sevilla, Spain; 11CIC bioGUNE, Basque Research and Technology Alliance, Cancer Heterogeneity Lab, Derio, Spain; 12UPV/EHU, CSIC, Department of Molecular Biophysics, Biofísica Institute and Department of Biochemistry and Molecular Biology, Leioa, Spain; 13IdiSA, Navarra Institute for Health Research, Pamplona, Spain; 14University of Córdoba, Department of Cell Biology, Physiology and Immunology, Córdoba, Spain; 15Reina Sofia University Hospital, Córdoba, Spain; 16CIBER Pathophysiology of Obesity and Nutrition (CIBERobn), Córdoba, Spain; 17CIBER Enfermedades hepáticas y digestivas (CIBERehd); Spain; 18University of Barcelona, Department of Physiological Sciences II, Barcelona, Spain; 19Instituto de Biomedicina de Sevilla (IBIS), Hospital Universitario Virgen del Rocío, Universidad de Sevilla, Consejo Superior de Investigaciones Científicas, Sevilla, Spain
Email: mlmartinez@cicbiogune.es

Background and aims: Epithelial-mesenchymal transition (EMT), a key process during embryonic development, promotes cell migration and resistance to apoptosis during tumour invasion and metastasis. In hepatocellular carcinoma (HCC) an amoeboid behaviour tends to increase the aggressiveness and metastatic capacity of epithelial tumours.

MAP17 is a 17 kDa membrane protein expressed during embryogenesis, absent in most adult organs. The presence of MAP17 correlates with an inflammatory environment, hypoxia and increased reactive oxygen species (ROS). MAP17 has been identified in several types of cancer, including HCC. Modulation of EMT and amoeboid behaviour via MAP17 offers an attractive approach to prevent metastasis.

Method: Two separated HCC patient cohorts were used to characterise MAP17 levels. In vitro, expression of MAP17 was measured in mesenchymal and epithelial hepatoma cells, and its levels were modulated to study its implication in cell proliferation, drug resistance, mitochondrial dynamics, metabolic rewiring, and proteome homeostasis. In vivo, the role of MAP17 in the metastatic capacity was evaluated using orthotopic HCC mice models.

Results: A positive correlation of MAP17 and mesenchymal markers was established in 751 HCC patients in silico study and by mRNA expression in 246 HCC patients. Additionally, MAP17 appeared statistically associated with RAC/RHO family genes, markers of amoeboid movement, in the same patient cohort. MAP17 overexpression in 3D epithelial cell experiments let to the formation of rosette invadopodia, proinvasive structures with high metastatic capacity. MAP17 overexpression in vitro produced a reprogramming of energy metabolism in hepatoma cells with epithelial phenotype, increasing mitochondrial dynamics and Warburg effect-mediated lactic acidosis, which support a tumour microenvironment conducive to cancer cell proliferation. ROS generation was increased as a protective mechanism to avoid apoptotic and senescence processes. Rewiring of the one-carbon metabolic pathway was also identified, proving an accelerated metabolism of the cell. Accordingly, overexpression of MAP17 in PLC/PFK/S cells in the orthotopic model led to the formation of multiple tumour foci in the liver.

Conclusion: Modulation of MAP17 in epithelial and mesenchymal hepatoma cells leads to the reprogramming of the transitional genes that define each phenotype. Our findings have identified the metastatic potential of MAP17 in liver cancer, as it triggers the mesenchymal phenotype and amoeboid behaviour in HCC.

Cirrhosis and its complications: ACLF and Critical illness

OS061
Liver transplantation within 7-days of listing improves survival in ACLF-3
Joseph Alukal1, Feng Li1, Paul J. Thuluvath1, 1Institute of Digestive Health and Liver Disease, Gastroenterology, Baltimore, United States
Email: jjalukal@gmail.com

Background and aims: ACLF-3 is associated with a very high short-term mortality without liver transplantation (LT). The timing of LT, therefore, may be critical for optimal outcomes. The objective of our study was to determine if early LT (<7 days from listing), stratified by the number of organ failures (OF), had an impact on 90-day and 1-year survival in ACLF-3 patients.

Method: United network for organ sharing (UNOS) database was queried to identify adults (>18 years) with ACLF-3 who underwent LT between 2005–2021. We excluded those listed with status 1, 1A, or 1B, multi-organ transplant, living donor transplant and HCC. ACLF patients were identified using EASL-CLIF criteria. Unadjusted Kaplan-Meier (KM) survival curves were used to evaluate patient survival. The Cox proportional hazards (PH) regression model was used to evaluate the risk factors for survival.

Results: We identified 3, 498 patients with ACLF-3 who underwent early LT while 1, 485 had transplant >7 days from listing. 90-day and 1-year survival in ACLF-3 patients who underwent early LT were 92% and 87% respectively. KM survival analysis showed that those who were transplanted early (<7 days) had significantly better 90-day and 1-year survival than who underwent late LT (>7 days) (Figure A and Figure B). This survival benefit was seen across all sub-groups of ACLF-3 including those with 5 and 6 OF (Figure C and Figure D). On multivariable analysis, age (Hazard Ratio [HR]1.02), body mass index (HR 1.01), donor risk index >1.7 (HR 1.3), respiratory failure (HR 1.9), and etiology of cirrhosis were independent predictors of higher 90-day post-transplant mortality. Similarly, age (HR 1.01), donor risk index >1.7 (HR 1.3), diabetes (HR 1.3), respiratory failure (HR 1.7) and etiology of cirrhosis were independent predictors of higher 1-year mortality while higher albumin (HR 0.87) was associated with a reduced mortality.
Conclusion: Early LT (<7 days from listing) in ACLF-3 after listing is associated with a better 90-day and 1-year survival than those who were transplanted late (>7 days). This survival benefit was seen even in those with 5 and 6 OF.

OS062

Neutrophil gelatinase-associated lipocalin predicts response to terlipressin and albumin in patients with hepatorenal syndrome

Carmine Gabriele Gambino1, Matteo Stenico1, Marta Tonon1, Alessandra Brocca1, Valeria Calvino1, Simone Incicco1, Chiara Cosma2, Paolo Angelil1, Salvatore Piano1. 1Unit of Internal Medicine and Hepatology, Department of Medicine, University of Padova, Padova, Italy; 2Laboratory Medicine Unit, Department of Medicine, Hepatology, Department of Medicine, University of Padova, Padova, Italy; 3Multivisceral Transplant Unit, Padova, Padova, Italy; 4Hepatobiliary Surgery and Liver Transplantation, Department of Surgery, Oncology and Gastroenterology, University of Padova, Padova, Italy.

Background and aims: Acute Kidney Injury (AKI) commonly occurs in patients with decompensated cirrhosis. Neutrophil Gelatinase-associated Lipocalin (NGAL) is a novel urinary biomarker that could help in discriminating between different etiologies of AKI. The aim of this study was to investigate the ability of urinary NGAL (uNGAL) in: (1) the differential diagnosis of AKI, (2) predicting the response to treatment with terlipressin and albumin in patients with Hepatorenal Syndrome (HRS)-AKI and (3) predicting in-hospital and 90-day mortality.

Method: We included cirrhotic patients with AKI not solved within 48 hours, who were consecutively admitted from 2015 to 2020 at the University Hospital of Padova. uNGAL and standard urinary biomarkers were measured. Data on the type of AKI, AKI treatment, duration of hospitalization and patients were followed up until transplant, death or 90 days.

Results: We enrolled 162 patients (mean age: 62 ± 10 years, male: 77%; alcoholic etiology: 48%; mean MELD: 25 ± 8). Thirty-five patients (22%) had hypovolemic AKI, 64 (39%) HRS-AKI, 27 (17%) acute tubular necrosis (ATN)-AKI and 36 (22%) a mixed form. uNGAL values were significantly higher in patients with ATN-AKI than in patients with other types of AKI (1162 [423–2105] vs 109 [52–192] ng/ml; p < 0.001; Fig. A). uNGAL showed a high discrimination ability in predicting ATN-AKI (AUROC = 0.854; [95% CI = 0.767–0.941]; p < 0.001; Fig. B) and the best threshold was 220 ng/ml (sensitivity 89%; specificity 78%).

Sixty-two patients with HRS-AKI were treated with terlipressin and albumin. Among them, patients with uNGAL ≥220 ng/ml had a significantly lower rate of response to terlipressin and albumin (33 vs 70%; p = 0.015; Fig. C). After adjusting for serum creatinine, uNGAL ≥220 ng/ml was independently associated with a higher risk of non-response (aOR = 4.55, 95% CI = 1.28–16.67; p = 0.02).

In multivariable analysis (adjusted for age, MELD, ACLF, leukocytes and type of AKI) uNGAL was an independent predictor of in-hospital mortality (aOR = 1.74 [95% CI = 1.26–2.38]; p = 0.001) and 90-day mortality (aHR = 1.32 [95% CI = 1.13–1.55]; p = 0.001). Probability of survival was significantly lower in patients with uNGAL ≥220 ng/ml (57% vs 30%; p < 0.001; Fig. D).

Conclusion: uNGAL is an excellent biomarker for the differential diagnosis of AKI in cirrhosis, it predicts response to treatment with terlipressin and albumin in patients with HRS-AKI and is an independent predictor of mortality.

OS063

CLEARED Global consortium results highlight regional variation and need for equity in inpatient outcomes in hospitalized patients with Chronic Liver Disease


Journal of Hepatology 2022 vol. 77(S1) | S1–S108

S49
Background and aims: A global study with equitable participation in cirrhosis and chronic liver disease (CLD) outcomes is needed. We prospectively enrolled pts with CLD/Cirrhosis >18 years without organ transplant or COVID-19 who were admitted non-electively. To maintain equity in outcome analysis, a maximum of 50 pts/site were allowed. Data for admission variables, hospital course, and inpatient outcomes (ICU, death, organ dysfunction [OD]) were recorded. This was analyzed for death and ODF using significant variables on admission and including World Bank classification of low/middle-income countries (LMIC). A model for in-hospital mortality for all variables during the hospital course, including ODFs, was analyzed.

Results: 1383 pts (55 ± 13 yrs, 64% men, 39% White, 30% Asian, 10% Hispanic, 9% Black, 12% other) were enrolled from 49 centers (Fig A). 39% were from high-income while the rest were from LMICs. Admission MELDNa 23 (6–40) with history in past 6 months of hospitalizations 51%, infections 25%, HE 32%, AKI 23%, prior LVP 15%, hydrothorax 8% and HCC 4%. Leading etiologies were Alcohol 46% then NASH 23%, HCV 11% and HBV 13%. Most were on lactulose 52%, diuretics 53%, PPI 49% and statins 11%, SBP prophylaxis 16%, beta-blockers 35% and rifaximin 31%, 90% were admitted for liver-related reasons; GI bleed 30%, HE 34%, AKI 33%, electrolyte issues 30%, anasarcara 24% and 25% admission infections. In-hospital course: Median LOS was 7 (1–140) days with 25% needing ICU. 15% died in hospital, 3% were transplanted, 46% developed AKI, 15% grade 3–4 HE, 14% shock, 13% nosocomial infections and 13% needed ventilation.

Conclusion: In this worldwide equitable experience, admission cirrhosis severity and infections are associated with inpatient outcomes, which are greater in low-income settings. Liver-related and unrelated factors and regional variations are important in defining critical care goals and outcome models in inpatients with cirrhosis.
OS064 Maladaptive tubular repair is a harbinger of chronic kidney disease development in critically-ill cirrhosis patients admitted to intensive care unit—a prospective cohort study

Rakhi Maiwall1, Sama Siva Rao Pasulapeti2, Archana Rastogi3, Ashini Hidam3, Guresh Kumar2, Sherin Thomas3, Anupam Kumar4, Shiv Kumar Sarin1. 1ILBS, Hepatology, India; 2Pachhunga University College, Statistics, Mizoram, India; 3ILBS, Pathology, New Delhi, India; 4ILBS, Clinical and Molecular Medicine, New Delhi, India; 5ILBS, Statistics, New Delhi, India

Email: shivsarin@gmail.com

Background and aims: Critically ill cirrhosis (CIC) patients with acute kidney injury (AKI), are predisposed to increased CKD risk. Renal tubular epithelial cells (RTECs) initiate repair mechanisms following tubular injury and failure of repair causes renal fibrosis. We evaluated serum Cystatin C (CysC), urinary neutrophil gelatinase-associated lipocalin (u-NGAL) and RTECs as risk factors of progressive AKI (AKI-Pro) and CKD in CIC.

Method: At enrolment we performed CysC, u-NGAL and urine microscopy (repeated at day 7) in all included patients. In a subset of patients (n = 30, 15-AKI-Prog and 15-AKI resolution), a panel of 17 renal biomarkers (in urine), endothelial injury and repair markers and monocyte-chemoattractant-protein-1 (MCP-1) (in plasma), mitochondrial biogenesis markers by QRT-PCR in RTECs was performed. Immunohistochemistry (IHC) for alpha-smooth muscle actin (α-SMA) and collagen (col) 1 and 3 was performed on post-mortem renal biopsies.

Results: Altogether, 369 CIC patients, aged 47.9 ± 11.4 years, 87% males, 84% with AKI at enrolment, sepsis-related AKI in 47%, hepatorenal syndrome in 42%, acute tubular necrosis in 27% were enrolled from August 2016 to September 2020. Of these, 24.9% patients had coarse granular casts, 34.4% had RTECs and 5.7% had albuminuria (>300 mg) at enrolment. At day seven, 58% had AKI-Prog. On median follow-up of 204 days [range 43–365]; 46% developed CKD and 30% died or underwent liver transplant. uNGAL and CysC correlated significantly with AKI cause, severity, presence of sepsis and progression at day 7 (p < 0.001). Presence and persistence of granular casts and RTECs, uNGAL, serum CysC, SOFA scores and AKI-Prog at day seven were independent predictors CKD development in different multivariate competing risk models. Patients with AKI-Prog showed higher MCP-1, increase in renal endothelial injury and markers of fibrosis, a decrease in repair markers of tubular injury [significantly lower osteopontin, calbindin and epidermal growth factor] and failure of mitochondrial biogenesis [figure]. Post-mortem renal biopsies showed a predominance of chronic inflammatory infiltrate comprising of monocyte-macrophages and tubulointerstitial fibrosis, which correlated with uNGAL, CysC, AKI duration and IHC staining for α-SMA, col-1 and 3 [p < 0.05].

Conclusion: Almost two-thirds of CICs have AKI, which is often progressive, and associated with sepsis. NGAL and CysC can accurately predict AKI progression and CKD development. Persistence of RTECs in urinalysis at day-7 correlates with AKI progression and CKD development. The RTECs of patients with progressive AKI show loss of renal repair markers and failure of mitochondrial biogenesis. Infiltration with monocyte-macrophages plays a dominant role in renal fibrogenesis in CICs.

OS065 Hyperammonaemia defines the risk of acute-on-chronic liver failure in clinically stable outpatients with cirrhosis

María Pilar Ballester1,2, Thomas H. Tranah3, Juan Antonio Carbonell-Asins3, Anareena Kerbert4, Gonçalo Alexandrino5, Paloma Poyatos-Garcia1, Andra Caracoste3, Jose Sanchez-Serrano1, Carmina Montoliu2, Karen L. Thomsen6, Rajiv Jalan4,2, Debbie L. Shawcross3, 1Hospital Clinico Universitario de Valencia, Digestive Disease Department, Valencia, Spain; 2Institute of Liver Studies, School of Immunology and Microbial Sciences, King’s College London, London, United Kingdom; 3Liver Failure Group, Institute for Liver and Digestive Health, University College London, Royal Free Campus, London, United Kingdom; 4Gastroenterology and Hepatology Department, Hospital Prof. Doutor Fernando Fonseca, Amadora, Portugal; 5Department of Hepatology and Gastroenterology, Aarhus University Hospital, Denmark; 6European Foundation for the Study of Chronic Liver Failure (EF Clif) and the European Association for the Study of the Liver-Chronic Liver Failure (EASL-CLIF) Consortium

Email: t.tranah@nhs.net

Background and aims: Ammonia level correlates with the severity of hepatic encephalopathy and organ failure and is an independent predictor of mortality in patients with acute decompensation or acute-on-chronic liver failure (ACLF). However, its utility as a prognostic biomarker in patients with cirrhosis remains unclear. We hypothesized that hyperammonaemia predisposes to ACLF in outpatients with cirrhosis. We aimed to determine (i) whether hyperammonaemia is an independent risk factor for ACLF in clinically stable outpatients with cirrhosis, (ii) a threshold value of ammonia that defines this risk of ACLF, and (iii) its association with mortality.

Method: A prospective observational study of clinically stable cirrhotic outpatients followed-up in two tertiary hospitals was performed. Main outcomes were development of ACLF and mortality. Ammonia levels were normalized according to the upper limit of normality (A_ULN). Multivariable frailty competing risk modelling was performed with ACLF as event of interest and liver transplantation as a competing risk. Cut-off for A_ULN was calculated using maximally selected rank statistics and Kaplan-Meier curves with log-rank test were used to compare ACLF in the high and low risk groups and ACLF as risk factor for mortality.

Results: 603 patients were included (69% males; mean 56 years) with median follow-up of 215 days (range: 2–2453). A total of 68 (11%) patients developed ACLF. A_ULN was an independent predictor of ACLF (HR = 2.62; 95CI = 2.34–3.51; p < 0.001). Other risk factors were diabetes (HR = 2.6; 95CI = 1.57–4.37; p < 0.001), MELD score (HR = 1.1; 95CI = 1.03–1.10; p < 0.001) and albumin (HR = 0.5; 95CI = 0.30–0.85; p = 0.001). Using 1.48 as cut-off from the training set, statistically differences were found between high and low levels of A_ULN for ACLF (p < 0.001) in the test set (Figure 1). Overall survival was significantly lower in patients with ACLF (log-rank = 162; p < 0.001) and in patients with A_ULN > 1.48 (log-rank = 19; p < 0.001).
**Figure**: (abstract: OS064)

**C** Renal injury markers

**D** Renal repair markers

---

**E**

**F**

**G**

Fold elevation in expression of various genes related to mitochondrial biogenesis [peroxisome proliferator-activated receptor-gamma coactivator (PGC1), cyclooxygenase-1(Cox1), nicotinamide riboside (NR), succinate dehydrogenase (SDHA), transcription factor A mitochondrial (TFAM)] in exfoliated urine epithelial cells in AKI-R vs. AKI-P.

**Monocyte chemoattractant protein-1**  Genes of mitochondrial biogenesis
Conclusion: Ammonia is an independent predictor of ACLF and its associated mortality in clinically stable outpatients with cirrhosis. An ammonia level over 1.48 times the ULN defines the high-risk group for ACLF.

OS066
Predicting prognosis in large cohort of decompensated cirrhosis of liver (DCLD)- a machine learning (ML) approach
Ashok Choudhury1, Vinod Arora1, Kajali Mishra2, Harshvardhan Tevethia1, Vishal Kaushik1, Babita Prasad1, Manoj Kumar1, Shiv Kumar Sarin1. 1Institute of Liver and Biliary Sciences, New Delhi, India; 2Henry Ford Hospital, Detroit, United States
Email: doctor.ashokchoudhury@gmail.com

Background and aims: Onset of decompensation in cirrhosis is associated with poor outcome. The current clinico-biochemical tools have limited accuracy in predicting outcomes reliably. Identifying the predictors with precision model on the big data using artificial intelligence may improve predictability. We aimed to develop a machine learning (ML) based prognostic model for predicting 90 day survival in patients of cirrhosis presenting with decompensation.

Method: We analysed electronic medical records retrospectively of hospitalised cirrhosis patients at the ILBS, with a complete 90-day follow-up. Clinical data, laboratory parameters and organ involvement were serially noted. AI-modelling was done after appropriate mining, feature engineering, splitted randomly into train and test-sets (20:80). The class imbalance problem was handled by random over-sampling technique, to make balanced 50:50 ratios. After 10-fold cross validation, 3 repetitions and grid search for optimal hyper parameters, the XGB-CV model was chosen. AUC was the primary selection criteria and confusion matrix was used to compare AUCs between AI-models and existing indices; CTP and MELD-score.

Results: Total of 6326 patients [mean age 48.2 ± 11.5 years, 84% male, Mean CTP 10.4 ± 2.2 and MELD Na-30.4 ± 11.9, alcohol 49.4%] were included. Ninety day mortality was 29.2%. Acute insult was identified in 80% cases; of which extra-hepatic 49%, hepatic 46% and unknown 5% cases respectively. The XGB-CV model had the best accuracy for prediction of 90 days event in the train set 0.90 (0.90–0.93), validation set 0.80 (0.79–0.81) and for overall dataset 0.80 (0.79–0.81). The AUC of the XGB-CV model was better than CTP and MELD Na-score by 16% and 15% respectively. The prediction model considered 43 variables; 18 of which predicted the outcome, and 10 maximum contributors are shown in concordance classifier. The most contributors to poor outcome included, index presentation as HE, diagnosis of AD/ACLF/ESLD, PT-INR, serum creatinine, total bilirubin, acute insult etiology, prior decompensation, acute hepatic or extrahepatic insult, leukocyte count and present duration of illness. In the Decision Tree Model, the presence of HE, PT-INR and syndromeic diagnosis of AD or ACLF/ESLD was able to stratify the patients into low (22%), intermediate (23–46%) and high risk (>75%) of mortality at 90 days.

Conclusion: The AI based current model developed using a large data base of CLD patients presenting with decompensation immensely adds to the current indices of liver disease severity and can stratify patients at admission. Simple ML algorithms using HE and INR besides syndromic presentation, could help treatment decisions and prognostication.

Liver Immunology

OS067
Differential changes in global and antigen-specific B cell frequencies and function associate with the outcome of HBV nucleos (t)ide analog treatment withdrawal
Sabela Lens1,2, Alice Burton1, Jessica Davies1, Mireia García-López2, Anna Jeffery-Smith1, Nikolai Novikov2, Simon Fletcher3, Sofía Pérez-del-Pulgar4, Xavier Forns2, Mala Maini1. 1University College of London, Division of Infection and Immunity, United Kingdom; 2Hospital Clinic, Liver Unit, Barcelona, Spain; 3Gilead Sciences, United States; 4Liver Unit, Hospital Clinic, University of Barcelona, IDIBAPS, CIBERehd, Barcelona, Spain
Email: slens@clinic.cat

Background and aims: Despite HBsAg loss and the development of anti-HBs being the hallmark of natural resolution of HBV or achievement of ‘functional cure’, humoral immunity has not yet been examined in the setting of nucleos (t)ide analog (NA) discontinuation. We analysed HBeAg and HBsAg-specific frequencies and functional potential longitudinally in HBsAg-negative chronic Hepatitis B (CHB) patients stopping NA therapy to assess whether HBsAg loss ± off-treatment viral control associated with a recovery of the defective B cell response characteristic of CHB.

Method: Twenty-one HBeAg- CHB patients with complete viral suppression (>3 years) and without cirrhosis were studied prospectively. 16-colour flow cytometry was used to quantitate and phenotype circulating HBsAg- and HBeAg-specific B cells (dual fluorochrome-labelled antigen baits), global B cells, plasmablasts and Tfh at baseline, 12 and 48 weeks after stopping NA (W12 and W48). Cultured ELISPOTs were used to longitudinally evaluate antibody-secreting cells against HBsAg and HBeAg.

Results: After a median follow-up of 34 months (IQR 26–37), 16 (76%) patients remained off-therapy, with 5 (24%) of the total cohort losing HBsAg, whilst 5 (24%) required NA reintroduction. Frequencies of HBsAg and HBeAg-specific B cells were comparable between groups at baseline and did not correlate with levels of qHBsAg or HBeAg respectively, but did show differential temporal dynamics according to clinical outcome. HBeAg-specific B cells increased at W12 in all groups in association with viral rebound, but decreased to baseline values by W48 only among those achieving HBsAg loss or being re-treated. By contrast, patients remaining off-therapy had a significant increase in HBsAg-specific B cells by W48 compared to re-treated patients. Compared to patients remaining HBsAg+ after NA discontinuation, B cells in patients with HBsAg loss were enriched for the
activated memory phenotype and had a marked expansion of plasmablasts by W48. In parallel, ELISPOT data showed an increase in SFU against HBsAg in the 3 patients with HBsAg loss and anti-HBs+ by W48, confirming the recovery of antibody-producing functionality.

**Conclusion:** Functional cure (HBsAg loss) and viral control following NA withdrawal associate with recovery of the low frequencies and poor functionality of HBV-specific B cells in CHB. These findings support larger studies to explore the use of B cells as biomarkers of clinical outcome and as targets for further immunotherapeutic boosting.

**OS068**

**Enforced cytotoxic signature of HBV pol455-specific CD8+ T cells in chronic HBV infection**

Kathrin Heim1,2, Sagar Sagar3, Maike Hofmann1, Robert Thimme1, 2University of Freiburg Faculty of Biology, Freiburg im Breisgau, Germany; 1University Hospital Freiburg, Freiburg im Breisgau, Germany; Kathrin Heim1, 2, Sagar Sagar1, Maike Hofmann1, Robert Thimme1.  

**Background and aims:** T-cell exhaustion represents a distinct T-cell differentiation program associated with chronic viral infections. Several studies have shown that exhausted CD8+ T cells are heterogeneous. In chronic HBV infection, we and others observed major differences in the phenotype and function as well as in the degree of dysfunction of HBV-specific CD8+ T cells targeting different antigens. The aim of this study was to investigate the molecular heterogeneity of HBV-specific CD8+ T cells targeting different antigens.

**Method:** To determine the subset diversification of HBV-specific CD8+ T cells targeting different antigens, we performed high-throughput single-cell RNA sequencing using CEL-Seq2 technology. We obtained HBVcore18- and HBVpol455-specific CD8+ T cells from HBeAg-negative chronically HBV-infected patients who endogenously control the viral infection as well as under NUC treatment. Phenotypic and functional analyses were performed after pMHC tetramer-based enrichment and peptide-specific expansion.

**Results:** Cluster analysis of single-cell transcriptomes revealed a different subset diversification of HBVcore18- versus HBVpol455-specific CD8+ T cells. In particular, HBVcore18-specific CD8+ T cells were mostly comprised of precursor/memory-like exhausted T-cell subsets. Within HBVpol455-specific CD8+ T cells, we could identify a cluster of cells that highly expressed cytotoxic genes including GZMB, PRF1. Moreover, the cytotoxic regulator NKG7 was also elevated in this subset. Interestingly, we further observed that the cytotoxic subset is restricted to HBVpol455-specific CD8+ T cells obtained from patients who endogenously control the viral infection indicating that the enforced cytotoxic signature may be linked to virological HBV control in these patients. The differential transcriptional profile of HBVpol455-specific CD8+ T cells was further confirmed ex vivo after pMHC tetramer-based enrichment. Indeed, at the protein level, we detected a terminal effector differentiation and higher cytotoxic effector capacity of HBVpol455-specific CD8 T cells obtained from treatment-naive patients in comparison to patients requiring antiviral therapy.

**Conclusion:** In sum, our data highlight an enforced cytotoxic signature in HBVpol455-specific CD8+ T cells of treatment-naive patients which may be related to virological control in these patients. This observation might have potential implications for the design of immunotherapeutic approaches in HBV cure.

**OS069**

**Humoral and cellular immune responses to SARS-CoV-2 vaccination across multiple vaccine platforms and liver disease types: an EASL registry multicentre prospective cohort study**

Thomas Marjot1,2,3, Sam Murray4, Elisa Pose5,6, Zixiang Lim7, Maria Carlota Londoño8,9, Melanie Wittner9,9, Marc Luettegheon8,10, Virginia Hernandez-Geo8,11,12,13, Juan Carlos Garcia Pagan11,12, Colda Schaub14, Paul Duengelhoeft15, Martina Sterneck14, Angsar W. Lohe13,14,16, Palak Trivedi17, Khushpree Bhandal18, Benjamin H. Mullish13, Pinelopi Manousou19, Patrizia Burra20, Floriana Facchetti23, Susan L. Dobson22, Alexandra S. Deeke21, Lance Turtle22, Paul Klerenman8,24, Susanna Dunachie4, Pere Gines5,6, Massimo Iavarone25, Julian Schulze zur Wiesch14, Francesco Paolo Russo20, Eleanor Barnes4 and On behalf of the EASL Covid-HeP network, OCTAVE study, and PITCH consortium25. 1Oxford Liver Unit, Oxford University Hospitals NHS Foundation Trust, Oxford, UK; 2Nuffield Department of Clinical Medicine, University of Oxford, Oxford, UK; 3Oxford Centre for Diabetes, Endocrinology and Metabolism (OCDEM), NIHR Oxford Biomedical Research Centre, Churchill Hospital, University of Oxford, Oxford, UK; 4University of Oxford, Nuffield Department of Clinical Medicine, Oxford, United Kingdom; 5Centro de Investigación Biomédica en Red de Enfermedades Hepáticas y Digestivas (CIBERehd), Barcelona, Spain; 6University of Barcelona, Institut de Recerca Biomédica August Pi-Sunyer (IDIBAPS), Liver Unit, Hospital Clinic de Barcelona, Barcelona, Spain; 7Oxford University Hospitals NHS Foundation Trust, Oxford, UK; 8German Center for Infection Research (DZIF), Partner Site Hamburg-Lübeck-Borstel-Riems, Germany; 9Department of Internal Medicine, University Medical Center Hamburg-Eppendorf, Hamburg, Germany; 10Institute of Medical Microbiology, Virology and Hygiene, University Medical Center Hamburg-Eppendorf, Hamburg, Germany; 11Institut d’Investigacions Biomèdiques August Pi i Sunyer (IDIBAPS), University of Barcelona, Barcelona Hepatic Hemodynamic Laboratory, Liver Unit, Hospital Clinic, Barcelona, Spain; 12Centro de Investigación Biomédica en Red de Enfermedades Hepáticas y Digestivas (CIBERehd), Barcelona, Spain; 13European Reference Network on Hepatological Diseases (ERN RARE-LIVER); 14University Medical Center Hamburg-Eppendorf, Department of Internal Medicine, Hamburg, Germany; 15Department of Immunology, University Medical Center Hamburg-Eppendorf, Martinistraße 52, 20249 Hamburg, Germany; 16Hamburg Center for Translational Immunology (HTI); 17National Institute for Health Research Birmingham Biomedical Research Centre, Centre for Liver and Gastroenterology Research, Birmingham, Birmingham, United Kingdom; 18University Hospitals Birmingham NHS Foundation Trust, Birmingham, United Kingdom; 19Imperial College London, Department of Metabolism, Digestion and Reproduction, London, United Kingdom; 20University of Padova, Department of Surgery, Oncology and Gastroenterology, Italy; 21Division of Gastroenterology and Hepatology, Fondazione IRCCS Ca’ Granda Ospedale Maggiore Policlinico, Milan, Italy; 22NIHR Health Protection Research Unit in Emerging and Zoonotic Infections, Institute of Infection, Veterinary and Ecological Sciences, University of Liverpool, UK; 23Peter Medawar Building for Pathogen Research, Nuffield Dept. of Clinical Medicine, University of Oxford, UK; 24Translational Gastroenterology Unit, University of Oxford; 25Fondazione IRCCS Ca’ Granda Ospedale Maggiore Policlinico, Division of Gastroenterology and Hepatology, Milan, Italy; 26Nuffield Department of Medicine, University of Oxford, Oxford, UK. Email: ellie.barnes@ndm.ox.ac.uk

Abstract OS069 is under embargo until Friday 24 June 2022, 13:40 BST. It will be made publicly available on the congress website once the embargo has lifted. Journalists, industry, investigators and/or study sponsors must abide by the embargo times set by EASL. Violation of the embargo will be taken seriously. Individuals and/or sponsors who violate EASL’s embargo policy may face sanctions relating to current and future abstract submissions, presentations and
CD8+ T cell acquisition of the LPS receptor within the hepatic stroma shapes anti-viral/anti-tumour potential

Laura J. Pallett1, Mariana Diniz2, Leo Swadling1, Jessica Skelton2, Alexander Maini3, Jessica Davies1, Stephanie Kucykowicz1, Nathalie Schmidt1, Oliver E. Amin1, Upkar Gill4, Alice Burton1, Jenifer Sanchez5, Giuseppe Fusai6, Sabela Lens7, Sofia Pérez-del-Pulgar8, Patrick Kennedy4, Brian R. Davidson6, Muzlifah Haniffa9, Marcus Dorner2, Anna Schurich5, Mala Maini1. 
1University College London, Division of Infection and Immunity, London, United Kingdom; 2Imperial College London, Department of Medicine, London, United Kingdom; 3University College London, Division of Medicine, London, United Kingdom; 4QMUL, Barts and The London School of Medicine and Dentistry, London, United Kingdom; 5Kings College London, School of Immunology and Microbial Sciences, London, London, United Kingdom; 6University College London, Division of Surgery, London, United Kingdom; 7University of Barcelona, Hospital Clinic, August Pi i Sunyer Biomedical Research Institute, Barcelona, Spain; 8Liver Unit, Hospital Clinic, University of Barcelona, IDIBAPS, CIBERehd, Barcelona, Spain; 9Newcastle University, Faculty of Medical Sciences
Email: laura.pallett@ucl.ac.uk

**Background and aims:** Despite being bathed in bacterial products, the liver maintains a state of tolerance, exploited by HBV and tumours. The cellular basis mediating immune tolerance, yet allowing a rapid switch to immunity, needs to be better defined to deliver successful immunotherapy for the treatment of chronic HBV infection.

**Method:** We analysed the phenotype and function of CD14-expressing CD8 T cells directly ex vivo from resected/explanted human liver and explored their derivation, functionality, expansion and LPS-responsiveness in multiple in vitro and in vivo models.

**Results:** CD8 T cells expressing CD14 (and other LPS receptor components) were found to be compartmentalised in human liver and to preferentially accumulate amongst donor lymphocytes surviving in liver allografts, within HCC-infiltrating lymphocytes, and in cirrhotic ascites. Moreover, HBV-specific CD8 T cells were significantly enriched for the expression of CD14 compared to the residual, global CD8 T cell pool. CD14+CD8 T cells were highly activated and proliferative, with constitutive immunomodulatory features at rest (IL-10, IL-2 production) compared to CD14-CD8 T cells. They selectively expressed receptors (CXCR4/CD49a/CD49b) supporting retention with the stromal cell network to acquire CD14 from neighbouring macrophages. Human CD8 T cells acquire CD14, TLR4 and MD-2 from mononuclear phagocytes by actin cytoskeleton-dependent trogocytosis, promoted by E.coli, stromal cells and CXCL12. CD14 acquisition conferred the capacity to bind LPS and respond with a unique functional profile of chemotactic cytokines. Instead, upon TCR engagement, ex vivo and in vitro-derived CD14+CD8 T cells were poised to mount rapid, potent anti-viral effector function (IFNγ/TNF/MIPI1b). Importantly, CD14 acquisition by HBV-directed CD8 T cells (HLA-A0201/HBs183-91) could be exploited to induce superior immunotherapeutic efficacy, with enhanced lysis of hepatoma cells expressing HBsAg (HepG2-PreS1–GFPI).

**Conclusion:** A proportion of CD8 T cells compartmentalised in the liver express CD14/TLR4/MD2, recapitulated in vitro by trogocytosis from mononuclear phagocytes. CD14+CD8 T cells have enhanced TCR-directed effector function and can be induced to target HBV infection. Thus bacterial products in the gut-liver axis can therefore
A novel immunophenotyping of hepatocellular carcinoma based on amplified and mutated neoantigens for mRNA vaccine development

He Jing, Boqiang Liu, Liang Shi, Xiujun Cai. Zhejiang University, China
Email: srrsh_cxj@zju.edu.cn

Background and aims: Hepatocellular carcinoma (HCC) is the most common malignancy with poor prognosis. Genetic and phenotypic heterogeneity is a hallmark of HCC and also poses a daunting challenge for treatment. Recently, accumulating evidence suggests that immunotyping can indicate the comprehensive immune microenvironment, which is closely associated with therapeutic response and vaccination potential. In this study, we try to identify potent neoantigens in HCC for tumor immunotherapy, and further distinguish immune subtypes of HCC to construct an immune landscape for predicting the prognosis.

Method: Gene expression profiles, clinical information and simple nucleotide variation data of 328 HCC samples were obtained from TCGA. GEPIA was used to calculate differential expression levels, prognostic indices, and compare genetic alterations. TIMER was used to explore correlation between genes and immune infiltrating cells. Consensus cluster was used for consistency matrix construction and data clustering.

Results: Nineteen novel tumor neoantigens associated with poor prognosis and infiltration of antigen presenting cells were identified in HCC, including CDK1, CCNB1, CDC25C, PTTG1, CHEK1, KPNA2, MKI67, KIF2C, MCM3, EZH2, CDT1, PES1, PRC1, PPM1G, NEK2, TRIP13, TUBG1, AURKA, G6PD (Fig. A–C). Based on these neoantigens, we construct six immune subtypes (IS1-IS6, Fig. D). The immune subtypes showed distinct molecular, cellular and clinical characteristics. Patients with IS1 and IS3 tumors had a superior survival than those with the other subtypes (Fig. E). IS4 and IS6 tumors had immunosuppressive phenotype, and were also associated with higher tumor mutation burden and tumor stage (Fig. F–H). Furthermore, distinct expression of immune checkpoints and immunogenic cell death modulators was observed between different immune subtype tumors (Fig. I).

Conclusion: This study constructed a novel immunophenotyping of HCC for predicting the prognosis of patients. Meanwhile, CDK1, CCNB1, CDC25C, PTTG1, CHEK1, KPNA2, MKI67, KIF2C, MCM3, EZH2, CDT1, PES1, PRC1, PPM1G, NEK2, TRIP13, TUBG1, AURKA, G6PD are potent neoantigens for HCC-mRNA vaccine development, specifically for patients with IS4 and IS6 type.

Figure: (abstract: OS071)
OS072A
T cell and humoral immune response to multiple SARS-CoV-2 variants including omicron (B.1.1.529) after two doses of COVID-19 vaccine in patients with cirrhosis and liver diseases requiring immunosuppression: data from the EASL COVID-Hep network
Sam Murray1, Stephanie Longet2, Tom Tipton2, Maria Carolina Londoño2, Elisa Pose3, Stephen Laidlaw2, Dung Nguyen2, Georgina Meacham1, Zixiang Lim4, Stavros Dimitriadis5, Sophie Irwin1, Jonathan Cook5, Massimo Lavarone6, Pietro Lampertico6, Virginia Hernandez-Gea7,8,9, Juan Carlos Garcia Pagan7,8,9, Julian Schulze zur Wiesch10,11, Martina Sterneck10, Francesco Paolo Russo12, Jack Satsangi13, Susanna Dunachie1,14, Paul Klererman1,13, Carl Goodyear15, Iain B. McInnes15, Pere Ginés7,8,9, Miles Carroll2, Thomas Mar jot1,16, Eleanor Barnes1,16. 1University of Oxford, Nuffield Department of Medicine, United Kingdom; 2University of Oxford, Wellcome Centre for Human Genetics; 3University of Barcelona, Liver Unit, Hospital Clinic de Barcelona; 4Oxford University Hospitals NHS Foundation Trust, Department of Gastroenterology; 5University of Oxford, Centre for Statistics in Medicine and Surgical Interventions Trials Unit, Nuffield Department of Orthopaedics, Rheumatology and Musculoskeletal Sciences; 6Foundation IRCCS Ca’ Granda Ospedale Maggiore Policlinico; 7University of Barcelona, Liver Unit, Hospital Clinic, Institut d’Investigacions Biomèdiques August Pi i Sunyer (IDIBAPS); 8Centro de Investigación Biomédica en Red de Enfermedades Hepáticas y Digestivas (CIBERehd); 9Health Care Provider of the European Reference Network on Rare Liver Disorders (ERN-Liver); 10University Medical Center Hamburg-Eppendorf, Department of Internal Medicine; 11German Center for Infection Research (DFZ), Partner Site Hamburg-Lübeck-Borstel-Riems; 12University of Padova, Department of Surgery, Oncology and Gastroenterology DISCOG; 13University of Oxford, Translational Gastroenterology Unit, Nuffield Department of Experimental Medicine; 14University of Oxford, Oxford Centre for Global Health Research, Nuffield Department of Medicine; 15University of Glasgow, Institute of Infection, Immunity and Inflammation; 16Oxford University Hospitals NHS Foundation Trust, Oxford Liver Unit
Email: ellie.barnes@ndm.ox.ac.uk

Abstract OS072A is under embargo until Friday 24 June 2022, 13:40 BST. It will be made publicly available on the congress website once the embargo has lifted. Journalists, industry, investigators and/or study sponsors must abide by the embargo times set by EASL. Violation of the embargo will be taken seriously. Individuals and/or sponsors who violate EASL’s embargo policy may face sanctions relating to current and future abstract submissions, presentations and visibility at EASL Congresses. The EASL Governing Board is at liberty to ban attendance and/or retract data.

Copyright for abstracts (both oral and poster) on the website and as made available during The International Liver Congress™ 2022 resides with the respective authors. No reproduction, re-use or transcription for any commercial purpose or use of the content is permitted without the written permission of the authors. Permission for re-use must be obtained directly from the authors.
OS072B
Humoral and cellular immune responses to wild-type and omicron (B.1.1.529) SARS-CoV-2 variants following a fourth COVID-19 vaccination in liver transplant recipients and patients with autoimmune hepatitis
Stavros Dimitriadis1, Georgina Meacham1, Sophie Irwin1, Victoria Walker1, Sam Murray2, Zixiang Lim3, Thomas Marjot1,4, Jack Satsangi3, Eleanor Barnes2. 1University of Oxford, Nuffield Department of Medicine, United Kingdom; 2Peter Medawar Building for Pathogen Research, Nuffield Department of Clinical Medicine, United Kingdom; 3Oxford University Hospitals NHS Foundation Trust, Department of Gastroenterology, United Kingdom; 4Oxford University Hospitals NHS Foundation Trust, Oxford Liver Unit, Oxford, United Kingdom; 5University of Oxford, Translational Gastroenterology Unit, United Kingdom
Email: ellie.barnes@ndm.ox.ac.uk

Abstract OS072B is under embargo until Friday 24 June 2022, 13:40 BST. It will be made publicly available on the congress website once the embargo has lifted.
Journalists, industry, investigators and/or study sponsors must abide by the embargo times set by EASL. Violation of the embargo will be taken seriously. Individuals and/or sponsors who violate EASL’s embargo policy may face sanctions relating to current and future abstract submissions, presentations and visibility at EASL Congresses. The EASL Governing Board is at liberty to ban attendance and/or retract data.
Copyright for abstracts (both oral and poster) on the website and as made available during The International Liver Congress™ 2022 resides with the respective authors. No reproduction, re-use or transcription for any commercial purpose or use of the content is permitted without the written permission of the authors. Permission for re-use must be obtained directly from the authors.

OS073
In vivo CRISPR/Cas9 editing of the TTR gene with NTLA-2001 in patients with transthyretin amyloidosis- dose selection considerations
Edward J. Gane1, Jörg Täubel2, Björn Pilebro3, Marianna Fontana4, Justin Kao5, Michael Maitland6, Mark Stroh6, Jessica Seitzer6, Jonathan Phillips6, Kristy Wood6, Yuanxin Xu6, Carri Boiselle6, Adam Amaral6, Adam Boyd6, Jeffrey Cehelsky6, David Gustein7, Odelya Pagovich7, Laura Sepp-Lorenzino6, Liron Walsh6, David Lebwohl8, Gillmore Julian8. 1The University of Auckland, New Zealand Liver Transplant Unit, Auckland, New Zealand; 2Richmond Pharmacology Limited, London, United Kingdom; 3Umeå University, Department of Public Health and Clinical Medicine, Sweden; 4University College London, National Amyloidosis Centre, Division of Medicine, United Kingdom; 5Auckland City Hospital, Department of Neurology, New Zealand; 6Intellia Therapeutics, Inc., Cambridge, United States; 7Regeneron Pharmaceuticals, Inc., Tarrytown, United States; 8University College London, United Kingdom
Email: edgane@adhb.govt.nz

Background and aims: The liver produces the toxic precursor protein transthyretin (TTR) in ATTR amyloidosis, a fatal disease of misfolded protein accumulation. Until recently, the only therapeutic
intervention for variant ATTR amyloidosis (ATTRv) was liver transplantation. Gene-silencing agents targeting TTR mRNA prevent disease progression but require lifelong administration. In contrast, gene editing is designed as a single-dose treatment. NTLA-2001 comprises a lipid nanoparticle (LNP) encapsulating mRNA for SpCas9 protein and single guide RNA targeting the transthyretin (TTR) gene. After infusion, LNP uptake into hepatocytes results in precise TTR knockout regardless of disease-causing mutation. This is the first report of the dose, exposure and pharmacodynamic (PD) response relationship in humans for systemically administered liver-directed gene-editing therapy.

Method: The first-in-human phase 1 trial (NCT04601051) enrolls adults with confirmed ATTRv amyloidosis and peripheral neuropathy. Safety, pharmacokinetics (PK), and PD of NTLA-2001 are assessed in 3 + 3 dose escalation, with a subsequent expansion cohort. Circulating serum TTR was measured in samples collected at baseline, Days 7, 14, and 28, and every 2 months thereafter. Dose selection for the expansion cohort is based on review of safety, PK and PD in the escalation phase.

Results: As of this submission, 14 subjects received NTLA-2001 as single-ascending doses [3 subjects each at 0.1, 0.3, and 0.7 mg/kg, and 5 subjects at 1 mg/kg]. Mild and transient infusion reactions were the most common adverse event with NTLA-2001. Interim pharmacokinetic data suggest that following intravenous (IV) infusion NTLA-2001 ionizable lipid exhibited a rapid decline from peak levels followed by a secondary peak and then a log-linear phase. Serum TTR levels were significantly reduced from baseline in a dose-dependent manner; patients receiving 0.3 mg/kg achieved durable reductions with mean Day 28 TTR reduction of 87% (n = 3) and greater reductions at higher doses (Figure 1, interim data to Day 28 from 10 subjects as of September 13, 2021). Additional data will be available for presentation.

Conclusion: A single IV infusion of the gene editing therapeutic NTLA-2001 resulted in dose-dependent reductions in serum TTR protein with predominately mild adverse events reported. NTLA-2001 represents a potential paradigm shift in the treatment of ATTR amyloidosis.

OS074
AOCX2 deficiency-induced liver fragility (ADILF), a not-so-rare inborn error in bile acid metabolism that responds to ursodeoxycholic acid treatment

Background and aims: A variant (p.Arg225Trp) in peroxisomal acyl-CoA oxidase 2 (AOCX2), involved in bile acid (BA) side-chain shortening, has recently been associated with persistent unexplained hypertransaminasemia and accumulation of C27-BAs, mainly trihydroxycholestanolic acid (THCA). Our aim was to investigate the prevalence of AOCX2 deficiency-induced liver fragility (ADILF) among patients with hypertransaminasemia of unknown origin and their response to ursodeoxycholic acid (UDCA), to identify other inborn errors that could cause this alteration and to elucidate its pathophysiological mechanisms.

Method: Serum BA profile was determined by HPLC-MS/MS. Genetic analysis of AOCX2 was performed by exon sequencing. In HuH-7 cells exposed to THCA, viability was determined by MTT, reactive oxygen species (ROS) production by flow cytometry and endoplasmic reticulum (ER) stress by analyzing GRP78 and CHOP levels (RT-qPCR and Western Blot), and XBP1-S/XBP1-U ratio (RT-qPCR). The 1000-Genomes database and SIFT and Polyphen scores were used to select AOCX2 variants that were expressed in HuH-7 cells to determine by HPLC-MS/MS its ability to metabolize THCA.

Results: Among 33 patients with suspected ADILF from 11 hospitals and 13 relatives, 7 individuals with abnormally high C27-BA levels (>50% of total BAs) were identified. The p.Arg225Trp variant was found in homozygosity in 2 patients and 3 relatives. Moreover, other 2 non-related patients were heterozygous carriers of different alleles, for c.673C>T (p.Arg225Trp) and c.456_459del (p.Thr154del). Impaired expression of AOCX2, but not AOX3 in the liver of these patients was found (immunohistochemistry). Treatment with UDCA normalized
transaminases levels. Culture of HuH-7 liver cells with THCA increased ROS production and the ER stress biomarkers GRP78, CHOP and XBP1-S/XBP1-U ratio, whereas decreased cell viability. THCA-induced toxicity was higher than that of major BAs. Among 14 in silico selected genetic variants, in vitro functional tests identified 6 ACOX2 variants as a potential cause of ADILF.

**Conclusion:** Dysfunctional ACOX2 is found in a substantial proportion of patients with unexplained hypertransaminasemia, suggesting that this disorder of BA metabolism causes enhanced liver fragility, which can be attenuated by UDCA treatment.

**OS075**

**Efficacy and safety of givosiran in patients with acute hepatic porphyria: 36-month results of the phase 3 ENVISION randomised clinical trial**

Manish Thapar1, Herbert L. Bonkovsky2, Susana Monroy1, Gayle Ross4, Encarna Guillén-Navarro5, Maria Domenica Cappellini7, Anna-Elisabeth Minder8, Shangbin Liu9, Marianne T. Sweetser9, David Kuter10, 1Thomas Jefferson University, Philadelphia, United States; 2Wake Forest University/North Carolina Baptist Medical Center, Winston-Salem, United States; 3Instituto Nacional de Pediatría, Mexico City, Mexico; 4Royal Melbourne Hospital, Melbourne, Victoria, Australia; 5Medical Genetics Section, Virgen de la Arrixaca University Hospital, IMIB-Arrixaca, Universidad de Murcia, Murcia, Spain; 6CIBERER-ISCIII, Madrid, Spain; 7University of Milan, Milan, Italy; 8Division of Endocrinology, Diabetes and Porphyria, Stadspital Zürich, Zürich, Switzerland; 9Alnylam Pharmaceuticals, Cambridge, United States; 10Massachusetts General Hospital, Boston, United States

Email: manish.thapar@jefferson.edu

This abstract is under embargo until Thursday 23 June 2022, 13:30 BST. It will be made publicly available on the congress website once the embargo has lifted.

Journalists, industry, investigators and/or study sponsors must abide by the embargo times set by EASL. Violation of the embargo will be taken seriously. Individuals and/or sponsors who violate EASL’s embargo policy may face sanctions relating to current and future abstract submissions, presentations and visibility at EASL Congresses. The EASL Governing Board is at liberty to ban attendance and/or retract data.

Copyright for abstracts (both oral and poster) on the website and as made available during The International Liver Congress™ 2022 resides with the respective authors. No reproduction, re-use or transcription for any commercial purpose or use of the content is permitted without the written permission of the authors. Permission for re-use must be obtained directly from the authors.
OS076
High-risk Thrombophilia predict early thrombosis recurrence in acute non-cirrhotic portal vein thrombosis related to local factors: LOCAPORT
Louise Lebedel1, Aurélie Plessier2, Odile Goria3, Christophe Bureau4, Alexandra Heurgue-Berlot5, Pierre-Emmanuel Rautou2, Audrey Payance2, Kamal Zekrini2, Thi Thu Nga Nguyen1, Thong Dao1, Rémi Morello1, Isabelle Ollivier-Hourmand1,1 University of Caen Normandie Hospital Center, Caen, France; 2Beaujon Hospital, Clichy, France; 3Hospital Center University De Rouen, Rouen, France; 4Hospital Center University De Toulouse, Toulouse, France; 5CHU Reims, Department of Hepato-Gastroenterology, Reims, France
Email: louise.lebedel@gmail.com

Background and aims: A local factor is identified in 21% of acute non-cirrhotic portal vein thrombosis (PVT). We aim to determine the risk of thrombosis recurrence in this situation, and risk factors associated with recurrence.

Method: This is a retrospective multicenter study from the French Vascular Liver Diseases cohort between 1992 and 2021. We included acute non-cirrhotic portal vein thrombosis (right or left branch or portal vein extending or not to mesenteric and splenic veins), with at least one local factor (infectious, inflammatory, traumatic, surgical or neoplastic) identified, either concomitantly or in the last 3 months. We screened for prothrombotic factors such as 1st degree unprovoked personal or family history of deep vein thrombosis, High-risk Thrombophilia (myeloproliferative neoplasm, homozygous or composite heterozygous mutation of factor V Leiden and G20210 prothrombin gene, antiphospholipid syndrome, familial antithrombin deficiency), Low-risk Thrombophilia (heterozygous factor V Leiden or prothrombin gene G20210 mutation, hyperhomocysteinemia, protein C or S deficiency, homozygous MTHFR mutation), ongoing oestroprogestative or pregnancy up to 6 weeks postpartum, paroxysmal nocturnal haemoglobinuria and Behçet’s disease.

Results: A thrombophilia was identified in 34/118 (29%) patients, of which 18/118 (15%) were a High-risk Thrombophilia. Thrombosis recurrence incidence rate was 2.94, 95CI = [0.00–6.22] per 100 patient-years (PY) at one year and 4.75, 95CI = [2.46–7.04] per 100 PY after a median follow-up of 19.5 months. The prevalence of thrombophilia did not differ significantly between groups with or without thrombosis recurrence (p = 0.775). However, presence of at least a High-risk Thrombophilia was significantly associated with thrombosis recurrence (RR = 4.2, 95CI = [1.18–14.91], p = 0.026) (Figure 1). Absence of portal recanalisation was significantly associated with thrombosis recurrence as compared to partial recanalisation (66.7% vs 32.4%, p = 0.019). Anticoagulation duration did not appear to be significantly associated with the risk of thrombosis recurrence. However, 91/115 (79%) received long-term anticoagulation (>6 months) while short-term anticoagulation (<6 months) was administered in 24/115 (21%) patients. Thrombosis incidence rate was 5.48, 95CI = [0.00–11.50] per 100 PY in short-term anticoagulation group as compared to 4.83, 95CI = [2.16–7.50] per 100 PY in long-term anticoagulation group (p = 0.47).

Conclusion: In acute non-cirrhotic PVT secondary to local factors, a High-risk Thrombophilia is frequently identified, and increase the risk of thrombosis recurrence. The high number of patients treated by long term anticoagulation in our cohort, does not allow us to draw any conclusion about the potential protective role of anticoagulant.

OS077
Clinical utility of non-ceruloplasmin copper determined by copper speciation for monitoring Wilson disease therapy: comparative data analysis with 24-hour urinary copper excretion from the CHELATE trial
Michael Schilsky1, Aurelia Poujois2, Massimo Giovanni Zuin3, Peter Ort4, Karl Heinz Weiss5, David Cassiman6, Aftab Ala7, Anna Czlonkowska8, Nicolas Dubois9, Naseem Amin10, C. Omar Kamlin11,1 Yale University, Departments of Medicine and Surgery, Divisions of Digestive Diseases and Transplant and Immunology, Connecticut, United States; 2Fondation Hospital Rothschild, Paris, France; 3University of Milan, Milan, Italy; 4Aarhus University Hospital, Denmark; 5Salem Medical Center, Heidelberg, Germany; 6University of Leuven, Belgium; 7Kings College University Hospital, Institute of Liver Studies, London, United Kingdom; 8Institute of Psychiatry and Neurology, Warsaw, Poland; 9International Drug Development Institute (IDDI), Belgium; 10Orphalan SA France, Paris, France; 11Orphalan SA France, France
Email: omarkamlin@doctors.org.uk

Background and aims: Monitoring efficacy of therapy in Wilson disease (WD) is challenging; 24-hour urinary copper excretion from the CHELATE trial

Results: A thrombophilia was identified in 34/118 (29%) patients, of which 18/118 (15%) were a High-risk Thrombophilia. Thrombosis recurrence incidence rate was 2.94, 95CI = [0.00–6.22] per 100 patient-years (PY) at one year and 4.75, 95CI = [2.46–7.04] per 100 PY after a median follow-up of 19.5 months. The prevalence of thrombophilia did not differ significantly between groups with or without thrombosis recurrence (p = 0.775). However, presence of at least a High-risk Thrombophilia was significantly associated with thrombosis recurrence (RR = 4.2, 95CI = [1.18–14.91], p = 0.026) (Figure 1). Absence of portal recanalisation was significantly associated with thrombosis recurrence as compared to partial recanalisation (66.7% vs 32.4%, p = 0.019). Anticoagulation duration did not appear to be significantly associated with the risk of thrombosis recurrence. However, 91/115 (79%) received long-term anticoagulation (>6 months) while short-term anticoagulation (<6 months) was administered in 24/115 (21%) patients. Thrombosis incidence rate was 5.48, 95CI = [0.00–11.50] per 100 PY in short-term anticoagulation group as compared to 4.83, 95CI = [2.16–7.50] per 100 PY in long-term anticoagulation group (p = 0.47).

Conclusion: In acute non-cirrhotic PVT secondary to local factors, a High-risk Thrombophilia is frequently identified, and increase the risk of thrombosis recurrence. The high number of patients treated by long term anticoagulation in our cohort, does not allow us to draw any conclusion about the potential protective role of anticoagulant.
ORAL PRESENTATIONS

UCE) is cumbersome, and results show large intra-subject variability. A new non-ceruloplasmin copper assay using liquid chromatography and ICP mass spectroscopy (NCC-Sp) was developed for the CHELATE Trial [trientine tetrahydrochloride (TETA4) vs. d-Penicillamine (DPA)]. We aim to describe the intra-patient variability and compare the clinical utility of UCE and NCC-Sp in monitoring WD therapy.

Method: A multicentre, open label, non-inferiority randomised controlled trial was conducted in which 53 stable adult WD subjects were randomly allocated after a 12-week baseline observation period to either DPA or TETA4 for 24 w with a primary end point (NCC-Sp). An independent adjudication committee blinded to site and treatment allocation assessed clinical stability at randomisation and end of study. Paired samples for NCC-Sp and 24 hr UCE were compared pre- and 24 post-randomisation. Validation studies for NCC-Sp included 50 healthy adults, identifying a range (2.5% to 97.5%) of 40–150 mcg/L. This was used as reference target range for the study population and compared to UCE (recommended therapeutic range of 200–500 mcg/24 hr). Intra-patient (SD) variability was computed for NCC-Sp and UCE measurements during baseline and post-randomisation periods.

Results: The independent adjudication committee unanimously assessed all subjects as clinically stable at randomisation and study end point. NCC-Sp was in the reference range at randomization versus study end in 86% vs. 84% of subjects respectively, while UCE was in the recommended therapeutic range in only 41% vs. 37% respectively (Table). Agreement when both NCC-Sp and UCE were in range at randomization/study end was 17/49 (35%) and 17/51 (33%) respectively. Mean (SD) NCC-Sp and UCE intra-patient variability during baseline (all receiving DPA) was 15.5 (7.8) mcg/L and 196 (125) mcg/24 hr respectively. Mean (SD) NCC-Sp intra-patient variability for DPA and TETA4 post randomisation was 17.9 (11.6) and 14.9 (12.1) mcg/L respectively (p < 0.0001). Mean (SD) NCC-Sp intra-patient variability for DPA and TETA4 post randomisation was 148.9 (127) and 107 (101) mcg/24 hr respectively (p = 0.74).

Conclusion: UCE is a test with significant intra-patient variability for WD patients on chelation therapy with either DPA or TETA4. That NCC-Sp had less intra-patient variability than UCE suggests NCC-Sp is a more reliable biomarker for monitoring chelation therapy in WD.

Table: Comparative analysis of “in range” data for NCC-Sp and UCE at randomization and study end point.

<table>
<thead>
<tr>
<th>At Randomisation</th>
<th>Primary End point (wk 24 post randomisation)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>UCE in range**</td>
</tr>
<tr>
<td>NCC-Sp in range</td>
<td>17</td>
</tr>
<tr>
<td>NCC-Sp not in range</td>
<td>3</td>
</tr>
</tbody>
</table>

*range for NCC-Sp = 40–150 mcg/L; **range for UCE = 200–500 mcg/24 hr.

OS078
North American evaluation of 2519 patients with primary sclerosing cholangitis: longitudinal patterns of disease activity identify and validate stable and progressive phenotypes
Marwa Ismail1, John Eaton2, Ailiya Gulamhusein1, Morven Cunningham2, Christina Plagiannakos2, Bettina Hansen1, Gideon Hirschfield1.1 Insetute of Health Policy Management and Evaluation, Health Services Research, Toronto, Canada; 2 Mayo Clinic, Rochester, United States; 3 UHN, Toronto Centre for Liver Disease, Toronto, Canada

Email: marwa.ismail@uhn.ca

Background and aims: Markers of outcome in patients with primary sclerosing cholangitis fluctuate, reducing utility at single time points. Longitudinal assessment offers an opportunity to improve surrogate marker utility.

Method: Using retrospectively collected data on 2519 North American patients diagnosed as per AASLD criteria with PSC, a derivation (Toronto: Jan. 2000 to Dec. 2020) and validation cohort (Mayo: Apr. 1978 to Dec. 2017) were evaluated to define progressive and stable disease states (PDS/SDS). Progressive disease was defined as death or transplant. Linear mixed-effects regression with random intercept and random slope was used to study biochemical and transient elastography (fibroscan) trajectories longitudinally over time. Piecewise linear splines and polynomial terms were employed. Time was calculated backwards from death, transplant, or last follow-up (time zero).

Results: Across combined cohorts median follow-up (IQR) was 8.3 (3.6–15) yrs, 63% were male, and mean age at diagnosis 39.5 (SD:16.1) yrs. 88.3% had large duct disease and 78% had IBD at last follow-up. Throughout the 10 yrs prior to death or transplant, patients with PDS in the derivation cohort had estimated ALP means ranging from 1.87–2.64 the upper limit of normal (ULN) with major fluctuations (p < 0.01); patients with SDS had lower and stable ALP courses (ALP 1.27–1.37 × ULN). A similar pattern existed for the validation cohort, where patients with progressive disease had ALP 2.25–3.12 × ULN, while patients with stable disease had ALP around 1.44–1.57 × ULN (p < 0.0001). The derivation cohort experienced bilirubin (TB) elevation 6 yrs before experiencing death or transplant; similarly for the validation cohort bilirubin elevation was 8 yrs before event. Patients with SDS maintained normal bilirubin values. Both cohorts experienced increases in the 2 yrs prior to death or transplant to reach an estimated mean TB of ~5 × ULN (p < 0.0001). Alb and PLT estimated means were lower for patients with progressive disease than those with stable disease in both cohorts; estimated AST and ALT means were notably higher for patients with PDS vs those with SDS (derivation cohort: AST: 1.64–3.34 × ULN vs 1.21–1.28 × ULN; ALT: 2.83 × ULN vs 1.56–1.7 × ULN; validation cohort AST: 1.66–2.88 × ULN vs 1.09–1.32 × ULN; ALT 1.65–2.06 × ULN vs 1.15–1.56 × ULN) in both derivation and validation cohorts. In the Toronto derivation cohort patients with PDS had progressively increasing estimated transient elastography measurements from 10.8–31.3 kPa between yr 6 and time of death or transplant. Patients with SDS had transient elastography measurements over 6 yrs of study ranging from 7.7–9 kPa.

Conclusion: We evaluate progressive and stable disease phenotypes in >2500 PSC patients. A stable disease course was validated for patients with sustained ALP <1.5 × ULN, as well as those with longitudinal transient elastography values <10 kPa.
Nurses and AHP

OS079
Nurse-led inpatient fibrosis assessment for patients with suspected alcohol related liver disease and previous poor engagement with services
Rebecca Fennell¹, Dianne Backhouse¹, George Abouda¹, Lynsey Corless².¹Hull University Teaching Hospitals NHS Trust, Kingston upon Hull, United Kingdom
Email: lynsey.corless@nhs.net

Background and aims: Identification and staging of fibrosis is a critical part of assessment for people with alcohol related liver disease. For those presenting acutely in hospital, staging tests are frequently deferred until out-patient review. However, engagement with elective services is often poor in those with ongoing alcohol use, leaving investigation incomplete and the need for hepatology follow-up uncertain. To mitigate this, we instituted an in-patient fibrosis assessment service within our Alcohol Care Team (ACT) and evaluated the results.

Method: From February 2020-October 2021, we sought out acutely admitted patients who had been identified as drinking excessively (more than the United Kingdom guidance of 14 units/week) and who had previously not engaged with the ACT for staging of suspected liver disease. All patients were staged by Fibroscan (Echosens). Enhanced Liver Fibrosis (ELF) test was also performed when it became available at our facility. Implementation of the pilot was delayed and disrupted due to the impact of Covid-19 on service delivery, with most patients identified from March 2021 onwards.

Results: 70 patients were identified—45 (64%) male, 25 (36%) female, with median age 53 years (range 25–80 yr). Fibroscan results ranged from 3.4 kPa–75 kPa. 40 (57%) were normal (<7.0 kPa), 13 (19%) F1–F3 (7.1 kPa–18.5 kPa) and 17 (24%) F4 (>18.5 kPa). ELF was performed in 32 (46%) patients; 19 (59%) showed severe fibrosis (score 9.8–14.3) and 13 (41%) moderate fibrosis (score 7.9–9.6). ELF and Fibroscan were well matched for identification of cirrhosis, with cirrhotic range Fibroscan results only found in those with severe fibrosis on ELF, suggesting either test could be used to rule out cirrhosis in this group. Following Fibroscan assessment, annual ACT follow-up was arranged for all patients in F1–F3 range, and the 25 patients with a normal Fibroscan who continued to drink excessively. Patients with any results in the cirrhotic range were referred to hepatology for ongoing management.

Conclusion: By performing fibrosis assessment during an inpatient stay, we were able to exclude significant liver disease in many people we had previously been unable to stage, providing important information to the patient and avoiding unnecessary hepatology follow-up. Provision of in-patient non-invasive fibrosis assessment may therefore be a valuable addition to hospital ACT services for capturing patients who poorly engage.
OS081 The effort for HCV elimination: dedicated nurse based protocol, single center experience

Assaf Issachar1,2, Evelyn Oxtrud3, Yael Harifi3, Orly Sneh Arbib1,2, Amir Shalom3,2, Ran Tur-Kaspa1,2, Marius Brown1,2, Michal Cohen-Naftaly1,2, Rabin Medical Center, Beilinson Hospital, Liver Institute, Petah Tikva, Israel; 2Tel Aviv University, Sackler Medical School, Tel Aviv, Israel
Email: assafissa@gmail.com

Background and aims: As part of the global effort for elimination of HCV, Israel, as other countries, adopted a simplified guidelines for HCV treatment. Our center is a referral center for liver diseases, since the introduction of the first generation of DAA (INF based protocols) we adopted a protocol based on open access for HCV patient, dedicated nurse that communicate with the patients and primary physician before and during treatment, same day fibrosan test for every patient followed by physician recommendation for HCV treatment. Following very good SVR results after this treatment (higher from SVR reported in literature), we implement the dedicated nurse protocol for the INF free protocols.

The aim of our study is to present the result of our experience.

Method: Using our prospective collected database of HCV patients who was treated with DAA in our center, we analyzed SVR rate and some of the patients were asked to complete a questionnaire about the added value of nurse intervention.

Results: During 2011–2013 we treated 105 patients with first generation Peginterferon based DAA with SVR rate of 81%. In the end of 2014, we started to treat with INF free DAA regimens DAA. 831 patients were treated with SVR rate of 98.9%. 33 of the patients were organ transplant patient. 426 patients were diagnosed to have F3–4 fibrosis based on their fibroscan results and these patients continue surveillance post SVR. 74 patients completed the questionnaire about the value of the dedicated nurse intervention. All patients were satisfied with the professionalism of the team. 85% of the patients felt that the explanation provided by the nurse during the appointment contributed to their understanding of their medical situation and the importance of the treatment.

Conclusion: SVR rate of DAA based HCV treatment in our center is very high. The patients pointed the added value of nurse explanation, instruction and follow-up for better understanding of the disease and the importance of treatment and follow-up. Intervention by dedicated nurses improves the communication and compliance.

OS082 Advanced liver disease: master’s students’ perception. An exercise of introspection

Eva Roman1,2, Montserrat Guillaumet1, German Soriano2, Maria Poca2, Edilmar Alvarado-Tapias2, Ángels Escorsell2, 1School of Nursing, Universitat Autònoma de Barcelona, Spain; 2CIBERehd. Instituto de Salud Carlos III, Madrid
Email: eroman@santpau.cat

Background and aims: Advanced liver disease (ALD) produces physical and mental changes that drastically affect the lived experience of people who suffer from it, affects self-image and self-perception, social and affective relationships, activities and the idea of the future. Empathy allows us to understand each other’s experiences, concerns, and perspectives, as well as communicate this understanding (Moser, Intensive Crit Care Nurs 2003). To analyze the understanding of the losses and changes experienced by persons with ALD, their experience and transformation, through the narrative based on an exercise of introspection centered on reflection by resident physicians studying a master on digestive diseases.

Method: 3rd year resident doctors of the gastroenterology speciality, students of the master’s degree of the Catalan Society of Gastroenterology during the 2019–2020 academic year. Students had to do an introspection exercise and tell in the first person how they would feel if they were diagnosed with liver cirrhosis: what would change in their life and what would not? Family role, work and social life, economic situation, leisure activities, priorities, future perspective, image (physical and sexual appearance). The writings were analyzed following a semantic interpretative approach (van Manen 1977), and compared with the literature on patients’ point of view and perception.

Results: Thirty-three stories were collected of which 30 were written in the first person. Four emerging issues were identified: family, friends and social circles, work situation and self-esteem. The expressed emotions showed higher coincidence with those previously described by patients with ALD. The most recurrent unit of meaning was: “Being diagnosed with cirrhosis would mean a radical change in my life”

Conclusion: The narrative is a useful pedagogical tool in training and provides elements of learning to understand responses to complex situations. In the narratives, issues and emotions coincided with those described by patients with ALD were identified. Observing and analyzing oneself by interpreting the cognitive and emotional processes generated by a disease allows one to identify aspects that contribute to becoming aware of the other’s reality and thus fostering empathy.

OS083 Nurse-driven post-discharge intervention reduces risk of readmission and non-attendance in patients with decompensated liver cirrhosis: a randomized controlled study

Malene Barford O’Connell1, Lise Hobolth1, Anne Broedsgaard Madsen1, Flemming Bentsen1,2, Nina Kimer1, 1Copenhagen University Hospital, Amager Hvidovre, Gastro Unit, Medical Division, Hvidovre, Denmark; 2Copenhagen University Hospital, Amager Hvidovre, Department of Paediatrics and Adolescent Medicine, Hvidovre, Denmark; 3Aarhus University, Department of Public Health, Research Unit for Nursing and Health Care, Aarhus C, Denmark; 4Copenhagen University Hospital, Amager Hvidovre, Department of Clinical Medicine, Hvidovre, Denmark
Email: malene.barford.oconnell@region.dk

Background and aims: Patients with decompensated liver cirrhosis are on average admitted 3 times per year and 20–37% of the patients are readmitted within 30 days from discharge. Repeated admissions have great personal and societal consequences and non-attendance at outpatient visits may impact clinical outcome. In this study we investigated how a post-discharge nurse-driven intervention affected readmissions and outpatient attendance for patients with decompensated liver cirrhosis.

Method: This randomized controlled intervention was conducted in the Gastro Unit of a university hospital in the Capital region of Denmark. Patients admitted with decompensated liver cirrhosis were eligible for inclusion. The control group received standard post-discharge care. The intervention group participated in a nurse-driven post-discharge intervention based on concepts from Family Nursing. Before discharge the patient and family received a pamphlet with information on preventive measures. After discharge the participants received three monthly home visits by a nurse specialist in liver diseases comprising: therapeutic conversations; evidence-based information and help to initialize contact to municipal offers. After three months the patients received three monthly follow-up telephone calls, to a total of six months follow-up.

Results: Between December 2019 and October 2021, 111 participants were included. Twenty-four participants were excluded due to cancer, death before intervention or withdrawal of consent, leaving 42 participants in the intervention group and 44 participants in the control group. Fifty-three (62%) were male, mean age was 60.7 years, 81 (94%) had alcohol related cirrhosis, and 43 was classified as Child-Pugh C (Child score ≥10), without significant difference between the two groups. Nineteen (45%) participants in the intervention group were readmitted within six months compared to 27 (61%) in the
control group; (HR 0.42; 95% CI: 0.253 to 0.692; stratified log-rank p = 0.002). Therefore, the intervention was associated with a 58% reduction in the risk of readmission compared to the control group. Median time to readmission was 42 days in the intervention group as compared to 21 days in the control group (p = 0.0596). Five participants in the intervention group did not appear for a total of six outpatient visits during the follow-up period, compared to 17 participants in the control group who did not appear for 29 visits (HR 0.21; 95% CI 0.07 to 0.65; stratified log-rank p = 0.007).

Conclusion: In a randomized controlled study, a nurse-driven post-discharge intervention for patients with liver cirrhosis proved a significant reduction in readmissions and in non-attendance for outpatient visits in the intervention group. The period from discharge to first readmission was longer in the intervention group but not statistically significant from the control group.

Gut microbiota in liver disease and liver regeneration

OS084 Monoacylglycerol lipase inhibition specifically in macrophages compromises liver regeneration by inducing interferon type 1 that negatively impacts on hepatocyte proliferation

Manon Allaire1, Rola Al-Sayegh1, Morgane Maibire1, Matthieu Siebert1, Mathilde Cadoux1, JingHong Wan1, Maude Le Gall1, Catherine Postic2, Hervé Guillou3, Pierre de la Grange4, Sophie Lotersztajn1, Hélène Gilgenkrantz1, 1Université de Paris, Centre de Recherche sur l’Inflammation (CRI), Paris, France; 2Université de Paris, Institut Cochin, INSERM U1016, CNRS, Paris, France; 3Toulouse University Hospital, Digestive Oncology, Toulouse; 4GenoSplice, Paris, France

Background and aims: Monoacylglycerol lipase (MAGL) is a proinflammatory enzyme that reprograms lipid metabolism by converting monoacylglycerols into free fatty acids, in particular arachidonic acid. We have previously shown that MAGL displays pro-regenerative properties in the liver by demonstrating the direct contribution of MAGL from hepatocytes and the indirect effects of MAGL from liver macrophages in this impact (Allaire et al, EASL 2021). The aim of this study is to uncover the mechanisms by which MAGL from macrophages modulates liver regeneration.

Method: Mice with genetic invalidation in myeloid cells (MAGLMye−/−) were submitted to a liver regeneration stimulus induced by an acute intraperitoneal injection of carbon tetrachloride (CCl4). Gene expression profiling of liver MAGLMye−/− macrophages was assessed by RNA sequencing analysis. The role of identified pathways was confirmed in vitro in primary hepatocyte cell culture and in vivo by injecting neutralizing antibodies.

Results: Mice with a specific MAGL deletion in myeloid cells showed a regeneration defect compared to their wild type counterparts. RNAseq analysis demonstrated an induction of interferon-stimulated genes in MAGL depleted liver macrophages, suggesting that interferon type 1 (IFN-1) pathway plays a major role in the delayed regeneration. The induction of IFN-1 was also confirmed in the liver of MAGLMye−/− mice 24 h after the injury and in bone marrow derived macrophages (BMDM) exposed to the MAGL pharmacological inhibitor MJN110. We cultured primary hepatocytes with IFN-α and/or-β and found that both reduce hepatocyte proliferation in vitro with a cumulative effect of IFN-α and IFN-β. The link between IFN pathway and liver regeneration defect was finally demonstrated in an in vivo rescue experiment since the injection of IFN type 1 receptor neutralizing antibodies in MAGLMye−/− mice before and during the regeneration process restored hepatocyte proliferation to the level of control mice.

Conclusion: Inhibition of MAGL macrophages compromises liver regeneration by inducing IFN-1 pathway that negatively impacts on hepatocyte proliferation.

OS085 Complete vascular tree reconstruction in rat decellularized liver scaffolds using differential recellularization pressures

Sandra Melitón Barbancho1,2, Pedro Baptista1,3,4,5, Aliza Pueyo Moliner6, 7, 8, Aragón Health Research Institute (IIS Aragón), CIBA, Zaragoza, Spain; 2University of Zaragoza, Zaragoza, Spain; 3Centro de investigación biomédica en red, Hepatic Diseases, Madrid, Spain; 4Universidad Carlos III de Madrid, Department of Biomedical and Aerospace Engineering, Madrid, Spain; 5Fundación ARAID, Zaragoza, Spain

Background and aims: There are still several challenges slowing the translation of bioengineered livers to the clinic in order to reduce the shortage of organs. One of the most important is to provide the whole organ with a robust vascular network that allows its perfusion and maintenance in vivo. Effective revascularization of decellularized liver scaffolds (DLS) is still elusive, so this work focused on the revascularization of DLS, presenting an effective approach for generating functional vasculature that allows us to be closer to the bioengineered liver.

Method: Within a bioreactor setup, endothelial cells [unlabelled for vena cava and labelled with GFP and tdTomato, for portal vein (PV) and hepatic artery (HA), respectively] (pUVECs), smooth muscle cells (pA-SMCs) and mesenchymal stem cells (pBM-MSCs) were injected through HA, PV, and vena cava respectively (pUVECs), smooth muscle cells (pA-SMCs) and mesenchymal stem cells (pBM-MSCs) were injected through HA, PV, and vena cava using distinct seeding pressures to target the different vessel diameters. Next, maturation was enhanced by providing growth factors for vasculogenesis and angiogenesis process keeping constant mechanical-stimulation for 14 days. Microscopic analysis was performed by hematoxylin-eosin (H&E) and immunofluorescence (IF) staining. Finally, pUVECs function was evaluated by nitric oxide (NO) and prostacyclin (PGI2) secretion and the contraction of pA-SMC after carbachol inoculation was observed.

Results: H&E analysis confirmed the lining growth of the different kind of cells inside of the decellularized vascular tree. Moreover, IF confirmed the accurate arrangement of pUVECs into vascular-like structures with pBM-MSCs (pBM-MSCs) were injected through HA, PV, and vena cava using distinct seeding pressures to target the different vessel diameters. Next, maturation was enhanced by providing growth factors for vasculogenesis and angiogenesis process keeping constant mechanical-stimulation for 14 days. Microscopic analysis was performed by hematoxylin-eosin (H&E) and immunofluorescence (IF) staining. Finally, pUVECs function was evaluated by nitric oxide (NO) and prostacyclin (PGI2) secretion and the contraction of pA-SMC after carbachol inoculation was observed.

Conclusion: Inhibition of MAGL macrophages compromises liver regeneration by inducing IFN-1 pathway that negatively impacts on hepatocyte proliferation.
OS086
Orthotopic transplantation of the functional bioengineered liver prolonged survival in rats with total hepatectomy
Beibei Guo1, Li Jiang2, Jing Jiang3, Qian Zhou1, Jiaxian Chen1, Jiaojiao Xin1, Dongyan Shi1, Keke Ren1, Xingping Zhou1, Genren Yang2, Jun Li1.1The First Affiliated Hospital, Zhejiang University School of Medicine, State Key Laboratory for Diagnosis and Treatment of Infectious Diseases, National Clinical Research Center for Infectious Diseases, Collaborative Innovation Center for Diagnosis and Treatment of Infectious Diseases, Hangzhou, China; 2The First Affiliated Hospital, Zhejiang University School of Medicine, Hangzhou, China Email: lijun2009@zju.edu.cn

Background and aims: Functional bioengineered liver (FBL) is a promising alternative to orthotopic liver transplantation. This study aims to determine the therapeutic potency of the FBLs with whole decellularized liver scaffold (DLS) using orthotopic transplantation in rat.

Method: The FBLs were developed using the whole rat DLSs with 1.5*10^7 human umbilical vein endothelial cell lines (HUVECs) implanted through portal vein, 6*10^7 human bone marrow mesenchymal stem cells (hBMSCs) and 3*10^8 mouse hepatocyte cell lines implanted through bile ducts. The FBLs evaluated with endothelial barrier function, bio-synthesis and metabolism were used to orthotopically transplanted into rats for determining survival benefit.

Results: The morphological observation exhibited the well-organized vascular structure lining by HUVECs in vascularized bioengineered liver. Histological and scanning electronic microscopy analysis showed endothelial barrier function with lower leakage of blood cells of the vascularized bioengineered liver. The new developed bioengineered liver displayed that hBMSCs and hepatocytes were well-aligned, and uniformly distributed over parenchymal space, and HUVECs formed the endothelialized microvascular structure. Significant increases of urea productions and albumin level in culture medium demonstrated that FBLs possessed ammonium translation and albumin synthesis functions. Orthotopic transplantation with FBLs rescued rats with a survival time of up to 100 min,
whereas all rats transplanted with DLS died within an average of 25 min. Histological staining showed that most perfused blood cells were limited into vascular lumen and the implanted cells, with positive immunofluorescence staining of CD90 and ALB, evenly distributed into the parenchymal space around vessels in the transplanted FBLs, but the transplanted DLSs became a pool entirely filled with blood cells.

**Conclusion:** The orthotopically transplanted FBLs effectively prolonged the survival time of rats with total hepatectomy. This study first determined the therapeutic potency of FBLs using orthotopic transplantation, which provides a promising alternative to the liver donor shortage for future clinical therapeutic applications.

**OS087**

**Bacterial infections in cirrhosis are associated with reduction in gut microbial phage-bacterial interactions**

Amirhossein Shamsaddini¹, Marcela Peña Rodríguez², Andrew Fagan³, Sara McGeorge³, Masoumeh Sikaroodi¹, Patrick Gillevet¹, Jasmohan S. Bajaj⁴, George Mason University; ²Universidad de Guadalajara; ³Virginia Commonwealth University

**Email:** jasmohan.bajaj@vcuhealth.org

**Background and aims:** The impact of bacterial infections on gut microbiota in cirrhosis is unclear since disease severity and antibiotic use could affect these changes. There is increasing evidence of the role of bacteriophages in the modulation of infection risk and as potential treatment strategies. However, changes in the interaction of the virome with metagenome in infected patients with cirrhosis are unclear. Determine change in the metagenome of pts with cirrhosis with infection versus uninfected patients and interaction with virome.

**Method:** Patients with cirrhosis were recruited, including outpatients with/without decompensation and inpatients admitted with/without infections. All pts underwent stool collection for metagenomics for bacterial and phage species. In inpts, stool was collected before antibiotics. DESeq2, PCoA, and correlation network analyses were performed between (a) all uninfected vs. infected patients and (b) inpatients with/without infections matched 1:1 by MELD score, demographics, and medications.

**Results:** 231 pts with cirrhosis were recruited, of which 30 were infected (20 SBP, 10 UTI). Unmatched comparison showed that infected pts had worse cirrhosis severity. PPI use was similar (Fig A). After matching for MELD score, inpatients with infections had similar disease severity (Ascites, HE) and medication use compared to those without infections (Fig A).

**Metagenomics:** Unmatched analysis: Pathobionts (Enterococcus spp, C.difficile) were higher, while short-chain fatty acid producers (Ruminococcus, Alistipes spp) were lower in infected patients. CrAssphages, Bifidobacterium, and Streptococcus phages were lower in infected patients. There was also a clear separation on β diversity (PERMANOVA p < 0.0001) between groups on bacterial and phage species. Matched analysis: Higher pathobionts (E.faecalis, E.faecium, C.difficile) along with Lactobacillus spp and oral-origin taxa (Fig B) persisted even after matching. Phages corresponding to these bacteria were also higher vs. uninfected pts (Fig C). PCoA showed β-diversity changes in bacteria (Fig D) and phages (Fig E) between groups. Correlation network between phages and bacteria showed a collapse between linkages in infected patients centred around

---

Figure: (abstract: OS087): Characteristics and comparisons between infected and uninfected patients.
**OS088**

**Altered gut microbiome, metabolome and bile acid composition in sarcopenia in liver cirrhosis**

Benard Aliwa1,2, Nicole Feldbacher1,3, Angela Horvath1,3, Julia Traub4, Tobias Madl1, Günter Fauler1, Vanessa Stadlbauer1,3,1. Medical University of Graz, Department of Gastroenterology and Hepatology, Graz, Austria; 2University of Nairobi, Department of Food Science, Nutrition and Technology, Nairobi, Kenya; 3CBmed Center of Biomarker Research in Medicine, Area Microbiome Research, Graz, Austria; 4University Hospital Graz, Dietology Services, Graz, Austria; 5Medical University of Graz, Gottfried Schatz Research Center for Cell Signaling, Metabolism and Aging Molecular Biology and Biochemistry, Graz, Austria; 6Medical University of Graz, Klinisches Institut für Medizinische und Chemische Labordiagnostik (KIMCL), Graz, Austria

**Background and aims:** 50–70% of liver cirrhotic patients suffer from sarcopenia leading to high mortality risk. The gut microbiome can metabolize bile acids and in turn bile acids can shape the gut microbiome community structure. We aimed to study differences in gut microbiome, bile acids and metabolite composition between sarcopenia and non-sarcopenia in liver cirrhosis and control.

**Method:** We analyzed 16 s rDNA sequencing of fecal microbiome and measured bile acids and metabolites of cirrhotic patients with and without sarcopenia (n = 78 and n = 38, respectively) as well as control with and without sarcopenia (n = 39 and n = 20, respectively). LEfSe, ANCOM, and LASSO regression, and multivariate logistic regression were applied.

**Results:** We demonstrated that both in cirrhotic and control patients, sarcopenia associates with a significant reduction in bacteria capable of generating branched-chain amino acids and short-chain fatty acids and a significant increase in bacteria capable of generating secondary bile acid (Sec-BAs). Sutterella species, Veillonella parvula, Bacteroides (B.) fragilis, and Blautia marseilleana were associated with sarcopenia and B. ovatus, Alistipes putredinis, Eubacterium, and Ruminococcaceae were associated with non-sarcopenia. In sarcopenic cirrhotic patients, we observed significantly elevated Sec-BAs, including deoxycholic acid (DCA), glycodeloxycholic acid (GDCA), lithocholic acid (LCA), and significantly elevated deoxycholic acid to cholic acid (DCA:CA), lithocholic acid to chenodeoxycholic acid (LCA:CDCA), glycochenocho- lolic acid to chenodeoxycholic acid (GLCA:CDCA) and reduced total ursodeoxycholic acid to total secondary bile acid (T-DCAT-sec BAs), serum valine, and serum acetate. We further observed that genes coding for 7α-hydroxysteroid dehydrogenase enzyme (7α-HSDH) were significantly increased in sarcopenic controls compared to non-sarcopenic controls. Multivariate logistic regression showed that MAMC, BMI, serum valine, serum acetate, GLCA:CDCA, T-DCAT-sec BAs, and B. ovatus were independent predictors for sarcopenia in liver cirrhosis even when corrected for severity of disease and drug use.

**Conclusion:** B. ovatus, serum valine, serum acetate and bile acid profiles are independent predictors for sarcopenia and potential biomarkers for muscle health in liver cirrhosis. Further studies are needed to assess whether increasing B. ovatus abundance, serum valine, serum acetate, or altering bile acid composition may affect muscle health.

**OS089**

**In-depth shotgun metagenomic analysis of the oral and gut microbiome identifies striking overlap in microbial community structure, virulence factors and antimicrobial resistance genes based on stage and severity of cirrhosis**

Sunjae Lee1,2,3,4, Bethlehem Arefaine2,3,4, Neelu Begum1,4, Elizabeth Witherden1,4, Marilena Stamouli2,5, Azadeh Harzandi1,4, Ane Zama12,3, Eleanor Corcoran2,5,4, Roger Williams2,3,5, Shilpa Choksi2,5,6, Gordon Proctor2,5,6, Adil Mardinoglu1,2, Mathias Uhlen1,3,6, Saeed Shoaei1,3,6, Vishal C. Pato1,2,5,7,1. Centre for Host Microbial Interactions, King’s College London, London, United Kingdom; 2The Roger Williams Institute of Hepatology, Foundation for Liver Research, London, United Kingdom; 3Institute of Liver Studies and Transplantation, King’s College Hospital NHS Foundation Trust, London, United Kingdom; 4Department of Critical Care, King’s College Hospital NHS Foundation Trust, London, United Kingdom; 5School of Immunology and Microbial Sciences, Faculty of Life Sciences and Medicine, King’s College London, London, United Kingdom; 6SciLifeLab, KTH – Royal Institute of Technology, Sweden, Sweden; 7Institute of Liver Studies and Transplantation, King’s College Hospital, London, United Kingdom

**Background and aims:** Alterations in the gut microbiome in decompensated cirrhosis (DC) and acute on chronic liver failure (ACLF) are recognised as being critical in influencing clinical outcomes (Trebicka et al, Nat Rev Gastro Hepatol, 2020). Knowledge of the oral microbiome is evolving and is increasingly recognised as predisposing to hepatic decompensation (Acharya et al, JCI Insight, 2017). Our aims were to interrogate simultaneously the gut and oral microbiome by shotgun metagenomic sequencing of faecal and saliva samples, respectively, in cirrhosis patients of varying severities, with healthy and positive disease controls.

**Method:** 18 healthy controls (HC), 20 stable cirrhotics (SC), 50 DC, 18 ACLF and 15 with non-liver sepsis (NLS) i.e. severe infection but without cirrhosis were prospectively recruited. DNA extractions were undertaken from saliva and faecal samples and Illumina sequenced on a NovaSeq 6000 to a minimum depth of 20 million reads. Filtered and trimmed reads were aligned to a human microbiome integrated gene catalogue. Salivatypes and enterotypes were calculated by scaling genus profile abundance and clustering by Dirichlet multinomial mixture models. ComprehensiveAntimicrobial Resistance Gene (ARG) and KEgg Orthology databases were used to evaluate ARGs and functional annotations, respectively.

**Results:** There was a striking decrement in Shannon diversity in the DC and ACLF cohorts vs HC and NLS (Fig A, D). Specific saliva- and enterotypes were identified based on clustering of genera, with a greater proportion of pathobionts and simultaneous reduction in autochthonous genera detected in specific clusters as cirrhosis severity progressed (Fig B, C, E, F). The degree of overlap between oral and gut microbiome communities (independent of antimicrobials, beta-blockers and acid suppressant therapies) and functional changes specific to virulence factor over-expression were significantly higher in DC and ACLF vs SC and HCs. Substantial total numbers of ARGs [1, 218 and 672] were detected in the oral and gut microbiome samples, respectively. 575 of ARGs were common to both sites, but a greater proportion of these were harboured in the gut (>85%) compared to the oral niche (47%), with overall ARG frequency incrementing with worsening cirrhosis (Fig G–I).

**Conclusion:** Oral and gut microbiome profiles differ significantly according to severity of cirrhosis, with specific saliva- and enterotype clusters reflecting dominance by pathobionts and loss of commensals. The degree of microbial community overlap between the mouth and gut, virulence factor and ARG frequency all increase significantly as cirrhosis worsens. These alterations that predispose to higher infection risk, poorer response to antimicrobial therapy and triggers for hepatic decompensation now form the rationale for non-antibiotic-dependant microbiome-modulating targeted therapies.
**Hepatitis B emerging therapies**

**OS090**

Longer treatment duration of monthly VIR-2218 results in deeper and more sustained reductions in hepatitis B surface antigen in participants with chronic hepatitis B infection

Young-Suk Lim¹, Man-Fung Yuen², Daniel Cloutier³, Vaidehi Thanawala⁴, Ling Shen⁵, Sneha V. Gupta⁶, Andre Arizpe⁷, Andrea Cathcart⁸, Carey Hwang⁹, Edward J. Gane¹⁰

¹University of Ulsan College of Medicine, Asan Medical Center, Seoul, Korea, Rep. of South; ²The University of Hong Kong, Queen Mary Hospital, Hong Kong, China; ³Vir Biotechnology, Inc., San Francisco, California, United States; ⁴University of Auckland, Faculty of Medicine, Auckland, New Zealand

Email: limys@amc.seoul.kr

**Background and aims:** Chronic hepatitis B virus (HBV) infection is a substantial global health issue affecting more than 290 million people worldwide. VIR-2218 is a small interfering ribonucleic acid (siRNA) therapeutic targeting the hepatitis B virus X region of the HBV genome currently in development for the treatment of HBV infection. Here, we report preliminary data from an ongoing study evaluating the safety, tolerability, and antiviral activity of 2 dosing regimens of VIR-2218 in participants with HBV infection.

**Method:** This open-label phase 2 study enrolled adult, virally suppressed, hepatitis B e antigen (HBeAg)-positive or negative participants with chronic HBV infection without cirrhosis. Dosing regimens of 2 doses (n = 6) or 6 doses (n = 15) of VIR-2218 200 mg given subcutaneously every 4 weeks were evaluated. Preliminary data up to the final follow-up visits for the 2-dose (week 48) and 6-dose (week 44) regimens are presented.

**Results:** Five of 6 participants receiving the 2-dose regimen completed study week 48 and, to date, 7 of 15 participants receiving the 6-dose regimen have completed study week 44. All participants achieved >1-log reduction in hepatitis B surface antigen (HBsAg). The 6-dose regimen was associated with greater mean maximum HBsAg reduction (−1.96 vs −1.61 log₁₀ IU/ml), and more sustained HBsAg reductions (−1.76 vs −0.87 log₁₀ IU/ml at week 44) compared with the 2-dose regimen (Figure). In both cohorts, adverse events (AEs) were generally grade 1 or 2 and no AEs resulted in discontinuation of study drug. Most participants had normal alanine aminotransferase

Figure: (abstract: OS089)
ORAL PRESENTATIONS

ALT flares were linked to HBsAg reduction, seroclearance and seroconversion: interim results from a phase llb study in chronic hepatitis B patients with 24-week treatment of subcutaneous PD-L1 Ab ASC22 (Envafolimab) plus nucleos (t)ide analogs

Guoqiang Wang, Yi Min Cui, Yao Xie, Qianguo Mao, Qing Xie, Ye Gu, Xin-Yue Chen, Guoxin Hu, Yongfeng Yang, Jiajie Lu, Guizhou Zou, Qin Zhang, Lei Fu, Yongping Chen, Xiaolun Guo, Jilin Hou, Yumei Yan, Handan He, Jinzi Wu, Peking University First Hospital, Infectious Diseases Department, Beijing, China; 2 Peking University First Hospital, Clinical Trial Center, Beijing, China; 3 Beijing Ditan Hospital Capital Medical University, Beijing, China; 4 Xiamen University Hospital, Traditional Chinese Medicine, Xiamen, China; 5 Ruijin Hospital of Medical College of Shanghai Jiaotong University, Infectious Diseases Department, Shanghai, China; 6 Shenyang Sixth People’s Hospital, Shenyang, China; 7 Beijing YouAn Hospital Capital Medical University, Beijing, China; 8 Peking University Shenzhen Hospital, Shenzhen, China; 9 Nanjing Second Hospital, Nanjing, China; 10 West China Hospital of Sichuan University, Chengdu, China; 11 The Second Affiliated Hospital of Anhui Medical University, Hefei, China; 12 Shanghai Tongren Hospital, Shanghai, China; 13 Xiangya Hospital of Central South University, Changsha, China; 14 The First Affiliated Hospital of Wenzhou Medical University, Wenzhou, China; 15 The First Hospital of Jilin University, Changchun, China; 16 Nanfang Hospital of Southern Medical University, Guangzhou, China; 17 Asclepis BioScience Co., Ltd., Hangzhou, China

Email: john131212@sina.com

Background and aims: Blockade of PD-1/PD-L1 pathway can restore T cell functions and lead to a potential cure for chronic hepatitis B (CHB). Hepatitis flares are considered to be mainly immune-mediated and may be linked or mark transitions to HBsAg reduction, even clearance. Previous studies indicated that PegIFN treatment may result in 18–24% of patients with ALT flares since it is an immune modulator. siRNA, a direct antiviral, however, caused as low as 6% of patients with ALT flares. Here we reported characterization of ALT flares and their relationship with HBsAg reduction, seroclearance and seroconversion from the interim analysis of a Phase llb clinical trial in CHB patients with 24-week subcutaneous PD-L1 antibody ASC22 (Envafolimab) plus Nucleos (t)ide analogs (NAs) treatment.

Method: This randomized, single-blind, multi-center Phase llb trial enrolled a total of 149 CHB patients (negative HBeAg, HBsAg ≤10000 IU/ml and HBV DNA <20 IU/ml) in two cohorts for 24-week treatment of ASC22 (1 or 2.5 mg/kg) and 24-week follow-up (NCT04465890). The relationship between ALT flares and HBsAg reduction/loss was analyzed in patients who completed 24-week treatment of 1 mg/kg ASC22 Q2W (n = 33) or PBO Q2W (n = 11) + NAs. An ALT flare is defined as a transient elevation in serum ALT greater than 3-fold baseline level and more than 2X ULN (upper limit of normal).

Results: The baseline serum levels of HBsAg, ALT and AST were comparable between patients receiving ASC22 or PBO plus NAs. Seven patients had HBsAg reduction >0.5 log10 IU/ml, and were all with baseline HBsAg ≤500 IU/ml. Three patients even experienced HBsAg seroclearance (undetectable, <0.05 IU/ml). One patient with HBsAg loss had seroconversion of HBsAb 6 weeks after the last dosing of ASC22 (Figure 1A). ALT flares were observed in 5/33 (15%) patients in ASC22 group compared to none in PBO group. Among the patients with HBsAg reduction >0.5 log10 IU/ml or HBsAg loss, 4/7 (57%) and 2/3 (67%) experienced ALT flares, respectively (Figure 1B). No clinically meaningful changes of total or direct bilirubin were observed in patients with ALT flares. However, more immune-related AEs (irAEs) occurred in ASC22 group. Most common irAEs were Grade 1 ALT/AST elevation and rash.

Conclusion: ALT flares occurring during ASC22 treatment were shown to be an indicator of a clinically meaningful immune response, resulting in significant HBsAg reduction and subsequent HBsAg loss/HBsAb seroconversion.

Lonafarnib combination with peginterferon Lambda diminished triphasic HDV kinetic pattern seen under Lambda monotherapy: the LIFT HDV study

Sarah Duehren, Christopher Koh, Julian Hercun, Farial Rahman, Pallavi Surana, Anusha Vittal, Walter Lair, Ohad Etzion, Scott Cotler, Jeffrey Glenn, Harel Dahari, Theo Heller, Program for Experimental and Theoretical Modeling, Division of Hepatology, Department of Medicine, Stritch School of Medicine, Loyola University Chicago, Maywood, United States; 2 Liver Diseases Branch, NIDDK, NIH, Bethesda, United States; 3 Soroka University Medical Center, Beer-Sheba, Israel; 4 Division of Gastroenterology and Hepatology, Stanford University School of Medicine, Stanford, United States

Email: harel.dahari@gmail.com

Background and aims: We recently reported that Lambda Interferon combination Therapy (LIFT) is safe and tolerable for up to 6 months in most patients with HDV. The goal of the current study was to characterize HDV RNA, HBV DNA, HBsAg and ALT kinetics during and after lonafarnib (LNF) and pegylated IFN-λ (Lambda) combination therapy.

Method: Twenty-six chronic HDV infected patients participated in a randomized, open-label Phase 2a clinical study of oral LNF 50 mg plus

Conclusion: These preliminary data support that a longer duration of treatment with VIR-2218 results in deeper and more sustained reductions in HBsAg. In both regimens of VIR-2218, no differences in safety or tolerability were observed.

Conclusion: ALT flares occurring during ASC22 treatment were shown to be an indicator of a clinically meaningful immune response, resulting in significant HBsAg reduction and subsequent HBsAg loss/HBsAb seroconversion.
Ritonavir (RTV) 100 mg twice daily and subcutaneous lambda 180 mcg weekly for 24 weeks, followed by per-protocol post-therapy monitoring for 24 weeks. Three patients completed <24 weeks (12, 16, and 20 weeks). All participants were started on tenofovir or entecavir prior to therapy. Kinetic data were obtained weekly for the first four weeks, and then every four weeks during and post treatment. HDV kinetic phase changes were defined as a 2-fold change in slope. HDV RNA was measured by Robogene 2.0 (limit of quantification, LoQ = 14 cp/ml).

Results: Mean pretreatment HDV RNA, ALT, and HBsAg were 4.9 log IU/ml [IQR 1.6], 80 U/L [IQR 45], and 3.8 log cp/ml [IQR 0.5], respectively. Fourteen (54%) patients had pretreatment HBV DNA target not detected (TND) and 12 patients had mean HBV DNA 2.6 log IU/ml [IQR 0.38]. During therapy, patients fit into 4 HDV kinetic patterns (Fig. 1): monophasic, MP (n = 9, Fig. 1A); biphasic, BP (n = 11, Fig. 1B); triphasic/transient, TP (n = 2, Fig. 1C); and flat/partial response, FPR (n = 4, Fig. 1D). HBsAg remained at pretreatment level in all patients (not shown). All patients had a transient ALT increase during therapy (mean 6-fold [IQR 4]) from upper limit of normal (40 IU/ml). Six (of 14) patients maintained HBV serum levels at TND, while the other 8 had transient increases or fluctuations from baseline TND. Of the 12 patients with high baseline HBV DNA levels, 8 maintained high levels throughout treatment, and 4 dropped to TND. A 2 log decline (or LoQ, n = 15) from pre-treatment HDV levels at end of therapy (EOT) was seen in 23 (88%) patients: 9/9 MP, 11/11 BP, 2/2 TP, 1/4 FPR. Mean ALT level at EOT was 94 IU/ml [IQR 31], similar to pretreatment levels. At end of follow-up (EFU), 5 (4 MP and 1 BP) out of 15 patients who had HDV LoQ at EOT remained LoQ (Fig. 1A and B), and the remaining had rebound (from EOT) with a mean value of 4.83 log IU/ml [IQR 1.9]. Eleven (42%) patients achieved ALT normalization at EFU.

Conclusion: We previously reported in the LIMT-1 study (The Liver Meeting, AASLD 2019 #LP12) 5 HDV kinetic patterns under Lambda monotherapy: MP (19%), BP (22%), FPR (19%), and triphasic/staircase (40%). Compared to Lambda monotherapy, including LNF significantly (p = 0.009) diminished the HDV triphasic/staircase kinetic patterns to 8%, suggesting that LNF reduces intracellular HDV production. The LIMT-1 study saw successful HDV viral decline in only 45% of patients, while the present study showed 88% success in reducing HDV by more than 2 log.
OS093

Real life study of bulevirtide in chronic hepatitis delta: preliminary results of the ANRS HD EP01 BuleDelta prospective cohort

Helene Fontaine1, Claire Fougereau-Leurent2–3, Emmanuel Gordin4, Caroline Schoefs5, Sophie Metivier6, Victor de Lédinghen7, Vlad Ratzl8, Laurent Alfro9–10, Nathalie Ganne-Carrié11, Veronique Loustaud-Ratti12, Dominique Guyader13, Vincent Leroy14, Jérôme Dumortier15, Karine Lacombe16, Georges-Philippe Pageaux17, Anne Minello Franza18, Christelle Tual2, Alain Renault19, Estelle Le Pabic2–3, Lucie Marchand19, Dominique Roulot20, Fabien Zoulmi21,16 Cochín Hospital-APHP; Pôle Hépato-gastroentérologie, Paris, France; 2 Rennes University Hospital, Service de Pharmacologie, Rennes, France; 3Inserm, CIC 1414, Rennes, France; 4 Avicenne Hospital, CNR des hépatites B, C et Delta, Bobigny, France; 5 Groupement Hospitalier Nord-HCL; Laboratoire de Virologie, Lyon, France; 6 Rangueil Hospital, Service de hépato-gastroentérologie, Toulouse, France; 7 Haut-Lévêque Hospital, Service d’hépato-gastroentérologie, Bordeaux, France; 8 La Pitié Salpêtrière Hospital-APHP; Service d’hépato-gastroentérologie, Paris, France; 9 Rangueil Hospital, Service de médecine interne, Toulouse, France; 10 CHU Rangueil, Digestive Department Toulouse 3 University, Toulouse, France; 11 Avicenne Hospital, Service d’Hépato-gastroentérologie, Bobigny, France; 12 Dupuytren Hospital, Service d’hépato-gastroentérologie, Limoges, France; 13 Rennes University Hospital, Service d’hépato-gastroentérologie, Rennes, France; 14 Henri Mondor Hospital-APHP; Service d’hépato-gastroentérologie, Créteil, France; 15 Edouard Herriot Hospital -HCL, Service d’hépato-gastroentérologie, Lyon, France; 16 Saint Antoine Hospital-APHP; Service des Maladies Infectieuses et Tropicales, Paris, France; 17 Saint Eloi Hospital, Service d’hépato-gastroentérologie, Montpellier, France; 18 Bocage Hospital, Service d’hépato-gastroentérologie, Dijon, France; 19 ANRS MIE, Paris, France; 20 Avicenne Hospital, Unité fonctionnelle d’hépatologie, Bobigny; 21 Croix-Rousse Hospital-HCL, Service d’hépato-gastroentérologie, Lyon, France
Email: helene.fontaine@aphp.fr

Background and aims: About 5 % of positive-HBsAg patients are infected with the hepatitis Delta virus (HDV), leading to an increase of 2 to 5-fold of cirrhosis and hepatocellular carcinoma, and a higher mortality in comparison with chronic hepatitis B alone. The management of chronic hepatitis delta (CHD) has improved recently in France, with the availability of bulevirtide (BLV) within an early access program in September 2019 or placebos. The biological response was defined as a normalization of ALT, the virologic response as a decrease of HDV RNA of at least 2 log IU/mL or HDV RNA undetectability, the combined response as the association of both.

Results: as of October 1st, 2021, 138 patients have been included in the BuleDelta cohort: 66 % were male, mean ± SD age of 42 ± 11 years; 54 % were of European or Asian origin and 44 % from Sub-Saharan Africa, 12 % presented HIV coinfection, 73 % were treated with nucleo (s) tides analogs (NUC) and 42 % with pegylated interferon-α (Peg-IFN). At baseline (D0), the mean HDV RNA was 6.1 ± 1.4 log IU/mL; HBV DNA was above quantification threshold in 38 patients (mean 2.6 ± 1.6 log IU/mL).

The preliminary analysis included the 98 out of 138 patients with available data at W24 in whom 54 (55 %) were treated with BLV only, and 44 (45 %) in association with peg-IFN. Overall 74 (76 %) were concomitantly treated with NUC. The mean decrease of HDV RNA at W24 was of 1.9 ± 1.4 log IU/mL (2.6 and 1.6 log IU/mL with and without peg-IFN, respectively). The virologic response at W24 was observed in 55 (56 %) patients (80 % and 37 %, with and without peg-IFN, respectively). Among these 55 patients, the virologic response was observed in 8 (15 %) patients at W4, in 26 (47 %) at W8 and in 38 (69 %) at W12. The biological response was observed in 36 out of 98 (37 %) patients at W24 (34 % and 46 %, with and without peg-IFN, respectively) and the combined response in 25 (26 %) patients at W24 (36 % and 17 %, with and without peg-IFN, respectively).

In the 43 patients without virologic response at W24, Figure 1 presents which therapeutic strategy was adopted. No patient had Peg-IFN add-on.

Conclusion: In this first real life study, a decrease of HDV viremia greater than 2 log IU/mL after 24 weeks of treatment of BLV was observed in more than half of patients with CHD and was associated with a normalization of ALT in half of them. Updated results will be presented at the meeting.

OS094

Therapeutic vaccine JNJ-0535 induces a strong HBV-specific T-cell response in healthy adults and a modest response in chronic HBV-infected patients

An De Creus1, Leen Slaets1, Bart Fevery1, Ellen Van Gulck1, Linghua Zhou1, Tim Van De Parre1, Celine Van Den Broeke1, Dessislava Dimitrova2, Isabelle Lonjon-Domaniec1, David Blue, Jr3, Pieter Van Remoortere2, Stefan Bourgeois4, Patrick Kennedy5, Sandra De Meyer1, Janssen Research and Development, Belgium; Janssen Research and Development, United States; Janssen Biopharma, Inc.; Hospital Network Antwerp (ZNA), Belgium; Barts and The London School of Medicine and Dentistry, United Kingdom
Email: adecreus@its.jnj.com

Background and aims: JNJ-0535 is a hepatitis B virus (HBV)-specific therapeutic DNA vaccine administered via electroporation (EP)-mediated intramuscular injection. JNJ-0535 comprises 2 plasmids encoding either HBV core or polymerase (pol) proteins. Induction of functional core and pol-specific T cells was evaluated in healthy and chronic HBV (CHB)-infected individuals.

Method: First in human (FIH) study 64300535HPB1001 evaluated total doses of 0.25 mg (n = 6), 1 mg (n = 7) or 6 mg (n = 10) JNJ-0535 (containing equal quantities of the 2 plasmids) or placebo (n = 7) delivered by intramuscular electroporation with TDS-IM v2.0 in CHB patients who were virologically suppressed, HBsAg- and on stable nucleos (t)ide therapy. Study 64300535HPB1003 evaluates the 6 mg dose of JNJ-0535 in healthy volunteers (HVs) (n = 12). BMSCs collected at baseline, during the vaccination period (10–14 days after the 3 vaccinations, and during follow-up were evaluated for T cell responses against core and pol using ex vivo IFNγ ELISPOT and intracellular cytokine staining (ICS). Results of the vaccination period will be presented for both studies comparing the 6 mg dose.

Results: A ≥3-fold increase in ELISPOT responses over baseline to core and/or pol was observed in 5/10 CHB patients (50 %) and in 11/12 HVs (91.7 %) at 6 mg JNJ-0535. Six (50 %) HV responded to both antigens whereas no CHB patients responded to both antigens. JNJ-0535 vaccination induced a higher median (interquartile range) maximum fold-increase in T cell responses from baseline in HV (24.4 [10.1–51]) compared to CHB patients (4.8 [4.4–10]). Overall, vaccine-induced core-specific CD4+ T cells were polfunctional in both HV and CHB patients for ELISPOT responses ≥150 SFU/million BMSC. Polynfunctional core-specific CD8+ T cells were only induced in HV. No safety issues have been identified for JNJ-0535 vaccine delivered by intramuscular electroporation.
Conclusion: T cell responses induced in HV were superior to those in CHB patients at a JNJ-0535 dose of 6 mg in terms of the proportion of responders, the magnitude of fold-increase from baseline, the breadth (number of antigens) and CD4+ and CD8+ core-specific T cell polyfunctionality. This supports the hypothesis that CHB infection negatively impacts the ability of patients to induce T cells in response to therapeutic vaccination.

OS095
Sustained 12 week off treatment antiviral efficacy of ATI-2173, a novel active site polymerase inhibitor nucleotide, combined with tenofovir disoproxil fumarate in chronic hepatitis B patients, a phase 2a clinical trial

Myreen Tomas1, Alina Jucov2,3, Igor Anastasly4, Lauren Ogilvie1, Karen Fursa1, Katherine Squires1, Douglas Mayer5, 1. Antios Therapeutics, United States; 2. ARENSIA Exploratory Medicine, Moldova; 3. Nicolae Testemitanu State University of Medicine and Pharmacy, Chisinau, Moldova; 4. ARENSIA Exploratory Medicine, Ukraine

Background and aims: ATI-2173 is a novel phosphoramide liver-targeted prodrug of clevudine that functions as an active site polymerase inhibitor nucleotide (ASPIN). In Phase 1, ATI-2173 demonstrated potent hepatitis B virus (HBV) activity with sustained off-treatment responses 4 to 24 weeks after discontinuation. The SAVE-1 Phase 2a trial evaluated the efficacy of ATI-2173 + tenofovir disoproxil fumarate (TDF) in treatment-naïve chronic HBV-infected (CHB) patients.

Method: A randomized, double-blind, placebo-controlled trial (NCT04847440) was conducted at sites in Moldova and Ukraine. Each cohort had 10 CHB patients randomized 8:2 to receive either 25 mg or 50 mg of ATI-2173 + TDF or placebo (PBO) + TDF daily for 90 days. HBV DNA and HBV RNA were measured using a Roche cobas 6800 (lower limit of quantification; LLOQ = 10 IU/ml, and 10 copies/ml respectively). The Roche RNA assay is investigational use only. Hepatitis B surface antigen (HBsAg) was measured using a Roche Elecsys (LLOQ = 0.05 IU/ml).

Results: Most patients were hepatitis B e antigen-negative (90%). Change from baseline virologic responses (HBV DNA) at the end of treatment for TDF alone (N = 4), 25 mg (N = 8) and 50 mg ATI-2173 + TDF (N = 8) were −3.53, −3.72, and −3.54 log10 IU/ml, respectively. No changes in HBsAg were observed. HBV RNA mirrored the HBV DNA responses on treatment. At 12 weeks off treatment, viral load response in the TDF arm was −0.66, while the 25 mg and 50 mg arms had maintained suppression of −3.20 and −3.50 log10 IU/ml, respectively (Figure). 0/4 in the TDF alone, 3/8 in the 25 mg cohort and 3/8 in the 50 mg cohort had HBV DNA below the limit of quantification <10 IU/ml at 12 weeks off treatment. By the week 12 visit, none of the 16 subjects in the ATI-2173 +TDF arms restarted TDF compared to 1 of 4 in the TDF alone arm who restarted TDF at week 8 due to virologic relapse (HBV DNA >2000 IU/ml). An off-treatment alanine aminotransferase (ALT) flare was observed in the TDF arm but not in the ATI-2173 arms.

NAFLD: Diagnostics and non-invasive assessment

OS096
Impact of type 2 diabetes on the accuracy of non-invasive tests of liver fibrosis: a comprehensive analysis of 1,051 biopsy proven NAFLD patients showing clinical implications

Jerome Boursier1, Clairence M. Canivet1, Charlotte Cognent2, Adrien Lannes3, Adele Delamarre4, Nathalie Sturm5, Brigitte Le Bail6, Sophie Michalak7, Frédéric Oberti2, Marie-Noëlle Hilleret2, Marie Irles-Depe8, Isabelle Fouchard9, Paul Hermabessière4, Justine Barthemon2, Bertrand Cariou8, Victor de Lédinghen4, Marine Roux1, Angers University, Hepato-Gastroenterology Department; 2. Bordeaux University Hospital, Hepato-Gastroenterology Department; 3. Grenoble University Hospital, Hepato-Gastroenterology Department; 4. Angers University Hospital, Hepato-Gastroenterology Department; 5. Bordeaux University Hospital, Hepato-Gastroenterology Department; 6. Grenoble University Hospital, Pathology Department; 7. Angers University Hospital, Pathology Department; 8. Nantes University Hospital

Background and aims: It has been suggested that non-invasive tests (NITs) of liver fibrosis are less accurate in type 2 diabetes (T2D). We aimed to compare the diagnostic accuracy of six NITs between patients with and without T2D, to explain the observed differences, and to adapt diagnostic algorithms for clinical practice accordingly.

Method: 1,051 patients with non-alcoholic fatty liver disease (NAFLD), liver biopsy, blood fibrosis tests (NAFLD fibrosis score, Fibrotest, FibroMeterV2G, and FibroMeterVCTE), vibration controlled transient elastography (VCTE), and the combinatory elasto-blood test FibroMeterVCTE were included. The study end point was advanced fibrosis (NASH CRN staging) on liver biopsy.

Results: The difference in result for NAFLD fibrosis score was highly significant between patients with and without T2D, T2D being included in the test formula. Consequently, only 11% of the patients with T2D were included in the rule-out zone of the NAFLD fibrosis score. AUROCs of the five other NITs were significantly lower in patients with T2D, mostly because of a decrease in specificity. The decrease of Fib4 specificity was explained by the significantly higher prevalence of advanced fibrosis in this group, it by higher alpha2macroglobulin level which is known to increase in T2D. Sensitivity of NITs was not affected by T2D but, because of the decrease of specificity, the decrease of FIB4 specificity was explained by the significantly higher alpha2macroglobulin level which is known to increase in T2D. Sensitivity of NITs was not affected by T2D but, because of the twofold higher prevalence of advanced fibrosis in this group, it masked a doubled raw number of false negatives in T2D. The sequential algorithm Fib4-VCTE had 90.3% diagnostic accuracy in patients with T2D versus only 79.0% in T2D (p < 0.001). To maintain rates of false-positives and false-negatives in a similar range than obtained with the Fib4-VCTE algorithm in patients without T2D, diagnostic algorithms in patients with T2D required specialized tests (first-line VCTE or FibroMeterV2G, then second-line FibroMeterVCTE).

Conclusion: The diagnostic accuracy of NITs is different between patients with and without T2D because of the different prevalence of advanced fibrosis in these two populations, but also because T2D
itself modifies the level of some biomarkers. The diagnosis of advanced liver fibrosis in T2D should use first-line specialized tests.

**OS097**

**Machine learning algorithms identify novel biomarker combinations for NAFLD**

Jenny Lee1, Max Westphal2, Yasaman Vali1, Yu Chen3, Leigh Alexander4, Jerome Bourrier5, Quentin Anstee6, Jenny Lee1, Max Westphal2, Yasaman Vali1, Yu Chen3, Leigh Alexander4, Jerome Bourrier5, Quentin Anstee6, 1University of California San Diego, La Jolla, United States; 2Yonsei University College of Medicine, Korea, Rep. of South; 3Musashino Red Cross Hospital, Tokyo, Japan; 4Yokohama City University Graduate School of Medicine, Kanagawa, Japan

**Background and aims:** Application of machine learning algorithms for developing diagnostic tests (or NITs) has grown across multiple disciplines, with models achieving promising classification performance levels. For non-alcoholic fatty liver disease (NAFLD), detection of non-alcoholic steatohepatitis (NASH) and advanced fibrosis remains challenging. We aimed to develop classifiers by applying machine learning algorithms to stage NAFLD patients.

**Method:** Data from the LITMUS Metacohort, which includes adults with biopsy-proven NAFLD, was analyzed for NASH (NAS>4) and advanced fibrosis (F≥3), staged according to the NAS-CRN scale. Thirty-three predictors (clinical characteristics, serum biomarkers and FibroScan-VCTE) were included in the analysis. Any missing data were handled by multiple imputation. Data were randomly split (75/25) into training and validation sets. Gradient boosting method (GBM) was applied to develop a classifier for each component of NASH (ballooning, inflammation, steatosis) and for advanced fibrosis, with repeated 10-fold cross-validation to tune hyperparameters.

**Class predictions for each component of NASH were aggregated to obtain a total NASH probability. Area under the receiver operating characteristic (AUROC).**

**Results:** Data from 720 NAFLD adults were analyzed (training set: 540, validation set: 180), of which 33% had NASH and 26% advanced fibrosis (including 7% cirrhosis). The AUCs for each component of NASH in the training/validation sets were: steatosis (0.68/0.66), inflammation (0.72/0.80), and ballooning (0.66/0.69). The aggregate GBM model for NASH achieved an AUC of 0.79 in the training and 0.74 in the validation set. For the GBM model for advanced fibrosis, the AUC was 0.90 and 0.84 in the training and validation sets, respectively. Different predictors were selected as most informative for the NASH components and fibrosis models (Table 1).

**Conclusion:** The GBM algorithm produced a high performing model for detecting advanced fibrosis, performance was less impressive for the NASH models. Better predictors, with understood associations to steatosis, inflammation and ballooning, are needed to develop robust models for detecting NASH. Validation of the models in the prospective LITMUS cohort is underway.

**OS098**

**Head to head comparison of MEFIB, MAST, and FAST for detecting candidates with stage 2 fibrosis or higher among patients with NAFLD**

Beom Kyung Kim1,2, Nobuharu Tamaki1,3, Jinho Jung1, Claude Sirlin1, Atsushi Nakajima4, Beom Kyung Kim1,2, Nobuharu Tamaki1,3, Jinho Jung1, Claude Sirlin1, 1University of California San Diego, La Jolla, United States; 2Yonsei University College of Medicine, Korea, Rep. of South; 3Musashino Red Cross Hospital, Tokyo, Japan; 4Yokohama City University Graduate School of Medicine, Kanagawa, Japan

**Background and aims:** Non-alcoholic fatty liver disease (NAFLD) patients with significant fibrosis (fibrosis stage≥2) are candidates for pharmacological trials. Here, we compared head-to-head the diagnostic accuracies of non-invasive models, MEFIB (magnetic resonance elastography [MRE] plus FIB-4), MAST (magnetic resonance imaging-aspartate aminotransferase [AST]), and FAST (FibroScan-AST) for detecting significant fibrosis.

**Method:** This prospective study included 563 biopsy-proven NAFLD patients undergoing contemporaneous MRE, MRI proton density fat fraction (MRI-PDFF), and FibroScan from two prospective cohorts. Each model was categorized into three classes as rule-in, indeterminate, and rule-out, using rule-in/-out criteria. Diagnostic performances of models were evaluated by area under the receiver operating characteristic (AUROC).

**Results:** The mean age was 56.5 years and 49% were male. Significant fibrosis was observed in 51.2%. To predict significant fibrosis, MEFIB outperformed both MAST and FAST (both p < 0.001); AUROCs (95% confidence interval) for MEFIB, MAST, and FAST as categorical variables were 0.901 (0.875–0.928), 0.770 (0.730–0.810), and 0.725 (0.683–0.767), respectively. Using rule-in criteria, positive predictive value of MEFIB (95.3%) was higher than FAST (83.5%, p = 0.001), but similar to MAST (90.0%, p = 0.056). Notably, MEFIB’s rule-in criteria covered more of the study population than MAST (34.1% vs. 26.6%; p = 0.006). Using rule-out criteria, negative predictive value of MEFIB (90.1%) was higher than either MAST (69.6%) or FAST (71.8%) (both p < 0.001).

**Conclusion:** MEFIB showed the reliability of rule-in/-out, with a better predictive performance compared to MAST and FAST. Thus, a two-step strategy by MEFIB (FIB-4 followed by MRE), may be used to identify ≥2 stage fibrosis.

Key words: NAFLD, significant fibrosis, MEFIB, FAST, MAST, diagnosis, validation

**OS099**

**Validation of the new 2021 EASL algorithm for the non-invasive diagnosis of advanced liver fibrosis in non-alcoholic fatty liver disease**

Clémence M. Canivet1,2, Adrien Lannes1,2, Charlotte Costentin3, Adele Delamarre2, Nathalie Sturm2, Frédéric Oberti1,2, Thomas Decaens2, Marie Irles-Depe4, Isabelle Fouchard1,2, Paul Hermellessiere4, Justine Barthemon3, Victor de Lédinghen3, Jerome Boursier1,2, 1Université d’Angers, HIFIH, UPRES EA3859, Angers, France; 2Centres Hospitaliers Universitaires de Grenoble, La Tronche, France; 3Chu Haut Leveque, Pessac, France

**Background and aims:** EASL recently proposed in its 2021 guidelines an algorithm for the diagnosis of advanced liver fibrosis (AF) in patients with non-alcoholic fatty liver disease (NAFLD). This original algorithm is based on the sequential use of Fib4, then vibration controlled transient elastography (VCTE) and, innovatively, on the use of patented serum tests as third-line procedure. Our objective was to evaluate the diagnostic accuracy of this algorithm (Fib4/VCTE/patented serum test) in a large cohort of NAFLD patients.

**Table 1:** Top five predictors for NASH components and fibrosis models

<table>
<thead>
<tr>
<th>Steatosis</th>
<th>Inflammation</th>
<th>Ballooning</th>
<th>Fibrosis</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. Body mass index (BMI)</td>
<td>Hepoglobin</td>
<td>BMI</td>
<td>Liver stiffness measurement-VCTE CK-18 M30 antigen</td>
</tr>
<tr>
<td>2. Cytokeratin-18 (CK-18)</td>
<td>Age</td>
<td>Alkaline phosphatase</td>
<td>CK-18 M30 antigen</td>
</tr>
<tr>
<td>3. Age</td>
<td>Hyaluronic acid</td>
<td>Systolic blood pressure</td>
<td>M30 antigen</td>
</tr>
<tr>
<td>4. Procollagen III peptide (P3NP)</td>
<td>N-terminal type III collagen propeptide (PRO-C3)</td>
<td>Hyaluronic acid</td>
<td>F30-C3</td>
</tr>
<tr>
<td>5. Alanine transaminase</td>
<td>Tissue inhibitor matrix metalloproteinase 1 (TIMP1)</td>
<td>Aspartate aminotransferase</td>
<td>Haemoglobin A1c</td>
</tr>
</tbody>
</table>

**Conclusion:** The GBM algorithm produced a high performing model for detecting advanced fibrosis, performance was less impressive for the NASH models. Better predictors, with understood associations to steatosis, inflammation and ballooning, are needed to develop robust models for detecting NASH. Validation of the models in the prospective LITMUS cohort is underway.
**Method:** 1,051 NAFLD patients with liver biopsy were included in three tertiary centres. Four non-invasive fibrosis tests were available: FIB-4, VCTE, FibroMeter and Fibrotest. The ELF score was available in a subgroup of 396 patients. AF was defined on liver biopsy as fibrosis ≥F3 according to the NASH-CRN classification.

**Results:** The median age was 58.1 years, half of the patients were diabetic, and 60% were male. The prevalence of AF was 39.5%. Agreement between two non-invasive fibrosis tests (FIB4 then VCTE, VCTE then patented serum test) increased specificity and positive predictive value to respectively 83–85% and 79–85%, versus 58–75% and 56–65% with single fibrosis tests. Within the EASL algorithm, the third line testing with a patented serum test allowed to correctly reclassify 29% (FibroMeter), 42% (Fibrotest) and 65% (ELF) of the false positive results following the FIB4 then VCTE sequence. All these results justified the sequential use of NITs proposed by the EASL algorithm. Accuracy of the EASL algorithm for the diagnosis of AF is detailed in the Table. In the whole study population, both FIB4/VCTE/FibroMeter and FIB4/VCTE/Fibrotest algorithms performed similarly. Same results were obtained in the subgroup of 396 patients where the FIB4/VCTE/ELF algorithm was available. In the whole population, 28.7% of F3-F4 patients were false negatives, among whom only 18.5% had cirrhosis. The EASL algorithm provided 85% sensitivity for the diagnosis of cirrhosis.

**Conclusion:** Our study validates the proposed method of the EASL in its latest 2021 guidelines for the diagnosis of AF in NAFLD.

**Figure:** Accuracy of the 2021 EASL algorithm for the diagnosis of AF.

### Whole study population (n=1,051)  
ELF group (n=396)

<table>
<thead>
<tr>
<th>First line test</th>
<th>FIB4</th>
<th>FIB4</th>
<th>FIB4</th>
<th>FIB4</th>
<th>ELF</th>
</tr>
</thead>
<tbody>
<tr>
<td>FIB4</td>
<td>81.4</td>
<td>82.8</td>
<td>84.1</td>
<td>85.9</td>
<td>87.4</td>
</tr>
<tr>
<td>FIB4/VCTE</td>
<td>71.3</td>
<td>71.3</td>
<td>73.5</td>
<td>73.5</td>
<td>73.5</td>
</tr>
<tr>
<td>FIB4/VCTE/Fibrotest</td>
<td>88.0</td>
<td>90.2</td>
<td>89.4</td>
<td>92.0</td>
<td>94.3</td>
</tr>
<tr>
<td>FIB4/VCTE/Fibrotest</td>
<td>82.5</td>
<td>82.8</td>
<td>87.1</td>
<td>87.4</td>
<td>87.7</td>
</tr>
<tr>
<td>FIB4/VCTE/ELF</td>
<td>79.6</td>
<td>82.7</td>
<td>77.6</td>
<td>82.2</td>
<td>86.6</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Second line test</th>
<th>sensitivity (%)</th>
<th>specificity (%)</th>
<th>negative predictive value (%)</th>
<th>positive predictive value (%)</th>
<th>negative likelihood ratio (%)</th>
<th>positive likelihood ratio (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>FIB4</td>
<td>0.33</td>
<td>0.32</td>
<td>0.30</td>
<td>0.29</td>
<td>0.28</td>
<td>12.93</td>
</tr>
<tr>
<td>FIB4/VCTE</td>
<td>0.97</td>
<td>7.32</td>
<td>6.93</td>
<td>9.24</td>
<td>12.93</td>
<td>9.24</td>
</tr>
<tr>
<td>FIB4/VCTE/Fibrotest</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>FIB4/VCTE/ELF</td>
<td>17.3</td>
<td>23.0</td>
<td>23.4</td>
<td>32.1</td>
<td>46.0</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Third line test requirement (%)</th>
<th>35.4</th>
<th>35.4</th>
<th>35.4</th>
</tr>
</thead>
<tbody>
<tr>
<td>Biopsy rate (%)</td>
<td>6.8</td>
<td>12.7</td>
<td>7.1</td>
</tr>
</tbody>
</table>

### Liver tumours: Clinical aspects except therapy

**OS102**  
Radiomic model based on contrast-enhanced CT imaging to predict early recurrence for patients with hepatocellular carcinoma after radical resection

Lijing Ren1, Dongbo Chen2, Tingfeng Xu1, Pu Chen2, Bigeng Zhao1, Hongsong Chen1, Weijia Liao2, Qunping Liu1, Yuqi Zhao1, Hongsong Chen1, Dinggang Hu2, Weijia Liao1, 1Affiliated Hospital of Gulin Medical University, Laboratory of Hepatobiliary and Pancreatic Surgery; 2Peking University People's Hospital, Peking University Health Science Center, Beijing Key Laboratory of Hepatitis C and Immunotherapy for Liver Disease, China  
Email: liaoweijia288@163.com

**Background and aims:** Radical resection remains an effective strategy for patients with hepatocellular carcinoma (HCC), unfortunately, the postoperative early recurrence (recurrence within 2 years) rate is still high. Therefore, we developed a radiomic model based on preoperative contrast-enhanced CT (ce-CT) to evaluate the early recurrence for patients with a single tumor.

**Method:** We enrolled a total of 422 patients from two centers who were diagnosed with single HCC and received radical resection. At first, the features from venous and arterial phase of ce-CT were extracted based on the region of interest (ROI), and the early recurrence related radiomic features were selected via the Least
Absolute Shrinkage and Selection Operator proportional hazards model (LASSO Cox) model and determined radiomic scores for each patient. Then the clinicopathologic data were combined to develop a model to predict early recurrence by Cox regression. Last we evaluated the prediction effect of this model by multiple methods.

**Results:** A total 1915 radiomic features were extracted from ce-CT images, and 31 of them were used to determine the radiomic scores, which showed significant difference between early recurrence and non-early recurrence groups. Univariate and multivariate Cox regression analyses result showed radiomic scores and serum AFP were independent indicators and were used to develop a combined model to predict early recurrence. The area under the receiver operating characteristic curve (AUC) were 0.77 and 0.74, while C-indexes were 0.712 and 0.674, respectively in the training and validation cohorts. The calibration curves and decision curve analysis showed satisfactory accuracy and clinical utilities, as well. Kaplan-Meier curves based on the recurrence-free survival (RFS) and overall survival (OS) showed significant differences.

**Conclusion:** The preoperative radiomic model showed value to predict early recurrence for patients with single HCC.
OS103 Circulating vesicles hold etiology-related protein biomarkers of cholangiocarcinoma risk, early diagnosis and prognosis mirroring tumour cells
Ainhoa Lapitz1, Mikel Azkargorta2,3, Ekaterina Zhuravleva4, Marit M. Grimsrud5, Colm O. Rourke4, Ander Arbelaiz1, Adelaida La Casta1, Mette Vesterhus5,6, Piotr Milkiewicz7,8, Malgorzata Milkiewicz8, Raul Jimenez-Aguero1, Tania Pastor1, Rocio IR Macias1,3, Ioana Riaño1, Laura Izquierdo-Sánchez2, Marcin Krawczyk10,11, Cesar Ibarra12, Javier Bustamante12, Felix Elortza2,3, Juan Falcon-Perez3,13,14, Maria Jesus Perugorria1,3, Jesper Andersen2, Luis Bujanda1,3, Tom Hemming Karlsen5, Trine Folseraas15, Pedro Miguel Rodrigues1,3,14, Jesus Maria Banales1,3,14,16, Biodonostia Health Research Institute, Department of Liver and Gastrointestinal Diseases, San Sebastian, Spain;2CIC bioGUNE, Proteomics Platform, Derio, Spain;3National Institute for the Study of Liver and Gastrointestinal Diseases (CIBERehd), ISCIII, Madrid, Spain;3Biotech Research and Innovation Centre, Department of Health and Medical Sciences, Copenhagen, Denmark;4Norwegian PSC Research Center, Department of Transplantation Medicine, Division of Surgery, Inflammatory Medicine and Transplantation, Oslo, Norway;5University of Bergen, Dept. of Clinical Science, Bergen, Norway;6Medical University of Warsaw, Department of General, Transplant and Liver Surgery, Warsaw, Poland;7Pomeranian Medical University, Department of Medical Biology, Szczecin, Poland;8Biomedical Research Institute of Salamanca (IBSAL), Experimental Hepatology and Drug Targeting (HEVEPHARM), Salamanca, Spain;9Saarland University Medical Centre, Department of Medicine II, Homburg, Germany;10Centre for Preclinical Research, Department of General, Transplant and Liver Surgery, Warsaw, Poland;11Hospital of Cruces, Bilbao, Spain;12CIC bioGUNE, Exosomes Laboratory, Derio, Spain;13Ikerbasque, Basque Foundation for Science, Bilbao, Spain;14Oslo University Hospital, Department of Transplantation Medicine, Oslo, Norway;15University of Navarra, Department of Biochemistry and Genetics, Pamplona, Spain Email: jesus.banales@biodonostia.org

Background and aims: Cholangiocarcinomas (CCAs), heterogeneous biliary tumors with dismal prognosis, lack accurate early-diagnostic methods, especially important for individuals at high-risk (i.e. primary sclerosing cholangitis (PSC)). Here, we aimed to identify precise non-invasive CCA biomarkers.

Method: Serum extracellular vesicles (EVs) from patients with: i) isolated PSC (n = 39); ii) PSC without clinical evidences of malignancy at sampling who developed CCA overtime (PSC to CCA; n = 10); iii) concomitant PSC-CCA (n = 14); iv) CCAs from non-PSC etiology (n = 26); and v) healthy individuals (n = 41) were analyzed by mass-spectrometry. Diagnostic biomarkers of PSC-CCA, non-PSC CCA or CCAs regardless etiology (pan-CCAs) were defined, and their expression evaluated in human multi-organs and within CCA tumors at single-cell level. Prognostic EV-biomarkers for CCA were described.

Results: High-throughput proteomics identified candidate diagnostic biomarkers for PSC-CCA, non-PSC CCA or pan-CCA, independent to sex, age and CCA subtype. Machine learning logit modelling disclosed PLCH1/FGL1 algorithm with diagnostic value of AUC = 0.903 and OR = 27.8 for early-stage PSC-CCA vs isolated PSC, overpowering CA19-9 (AUC = 0.608, OR = 2.0). An algorithm combining SAMP/A1AT allowed the diagnosis of early-stage non-PSC CCAs compared to healthy individuals (AUC = 0.863, OR = 18.5). Noteworthy, the levels of 6 proteins (ALBU;FIBB;FLG1;IGHA1;TLN1;IMA8) showed predictive value for CCA development in patients with PSC before clinical evidences of malignancy. Multivariable analysis revealed EV-prognostic biomarkers independent to clinical features,
with FCN2/SDPR/FA9 panel being strongly associated to patients’ survival.

Conclusion: Serum EVs contain etiology-specific protein biomarkers for the prediction, early diagnosis and prognosis estimation of CCA, representing a novel tumor cell-derived liquid biopsy for personalized medicine.

OS104
Evaluation of the effectiveness of surveillance according to the ultrasound liver imaging reporting and data system (US LI-RADS) visualization score in patients with chronic hepatitis B
Min Kyung Park1, Yun Bin Lee1, Yoon Jun Kim1, Jung-Hwan Yoon1, Dong Ho Lee1, Jeong-Hoon Lee1, 1Seoul National University College of Medicine, Department of Internal Medicine and Liver Research Institute, Seoul, Korea, Rep. of South, 2Seoul National University College of Medicine, Department of Radiology, Seoul, Korea, Rep. of South
Email: pindra@emphas.com

Background and aims: Ultrasonography (US) is a standard surveillance tool of hepatocellular carcinoma (HCC) in the high-risk group. This study evaluated the detection power of the US in the occurrence of primary liver cancer (PLC) according to the US Liver Imaging Reporting and Data System (LI-RADS) visualization score.

Method: Consecutive patients with chronic hepatitis B undergoing regular HCC surveillance were included in this cohort study. Outcomes of interest included cumulative incidence of PLC and false-negative rate of US (defined as no HCC on US conducted within 3 months prior to PLC diagnosis) according to baseline LI-RADS visualization scores (A vs B/C). Risk factors associated with poor visualization score were also analyzed.

Results: A total of 2,002 patients were included in this study: 972 were classified as visualization score A and 1,030 as either visualization score B or C (score B, 1,003; score C, 27). During a median follow-up of 75 months (interquartile range, 69–77 months), 166 patients developed PLC (HCC, 158; others, 8). Patients with poor visualization score (visualization score B or C) has significantly higher risk of PLC than those with score A (2.41%/year vs. 0.50%/year: hazard ratio, 4.83; 95% confidence interval, 3.24–7.21; p < 0.001 by log-rank test) (Figure 1A). Higher false-negative rate of US was observed in the poor visualization group than visualization score A (43.5% vs. 20.0%). Furthermore, among 51.2% (85 of 166) patients diagnosed as very early-stage PLC, merely 13.9% (10 of 72) of patients with visualization score B/C were detected with US, while in 53.8% (7 of 13) among patients with visualization score A. Poor visualization score was independently associated with the presence of liver cirrhosis (adjusted odds ratio [aOR], 3.66) or fatty liver (aOR, 2.31), high body mass index (aOR, 1.19), high FIB-4 score (aOR, 1.16), and Child-Pugh score 6 (vs score 5: aOR, 2.24) (Figure 1B).

Conclusion: Chronic hepatitis B patients with US LI-RADS visualization score B/C had a higher risk of PLC as well as false-negative rate of US than those with score A. Surveillance using alternative computed tomography or magnetic resonance imaging might be highly recommended for patients with US LI-RADS visualization score B or C.

OS105
Training, validation and testing of a multiscale three-dimensional deep learning algorithm in accurately diagnosing hepatocellular carcinoma on computed tomography
Wai-Kay Seto1,2,3, Keith Wan Hang Chiu4,5, Wenming Cao1, Gilbert Lui6, Juan Zhou7, Ho Ming Cheng1, Juan Wu7, Xinping Shen8, Lung Yi Loey Mak1,2, Jinhua Huang9, Wai Keung Li6, Man-Fung Yuen1,2, Philip Yu6,10, 1The University of Hong Kong, Medicine, Hong Kong; 2The University of Hong Kong, State Key Laboratory of Liver Research, Hong Kong; 3The University of Hong Kong-Shenzhen Hospital, Medicine, Shenzhen, China; 4The University of Hong Kong, Diagnostic Radiology, Hong Kong; 5Kwong Wah Hospital, Diagnostic and Interventional Radiology, Hong Kong; 6The Education University of Hong Kong, Mathematics and Information Technology, Hong Kong; 7Sun Yat-sen University Cancer Center, State Key Laboratory of Oncology in South China, Guangzhou, China; 8The University of Hong Kong-Shenzhen Hospital, Medical Imaging, China; 9Sun Yat-sen University Cancer Center, Department of Minimal Invasive Interventional Therapy, Guangzhou, China; 10The University of Hong Kong, Computer Science, Hong Kong
Email: wkseto@hku.hk

Background and aims: Liver cancer ranks second globally in cancer death and has a high case-fatality rate. The Liver Imaging Reporting and Data System (LI-RADS) categorizes liver observations on cross-sectional imaging based on hepatocellular carcinoma (HCC) risk. Intermediate-risk observations require repeated scans making an early diagnosis of HCC difficult. It remains uncertain if artificial intelligence can improve the diagnostic performance of computed tomography (CT) for HCC.

Method: We retrospectively collected archived thin-cut (<1.25 mm slice thickness) contrast triphasic CT images in raw DICOM format and relevant clinical information. CT observations were contoured and categorized via LI-RADS, with ground truth diagnosis of HCC established via AASLD recommendations and validated by a clinical composite reference standard based on subsequent 12-month outcomes. We constructed several deep learning algorithms (NVIDIA Tesla V100 GPUs, Dell Technologies), including the multiscale three-dimensional convolutional network (MS3DCN, Figure 1) model which uniquely considers the multi-phasic nature of CT, and followed the Checklist for AI in Medical Imaging (CLAIM) framework for algorithm training, validation and testing.

Figure 1. Model architecture of the MS3DCN deep learning algorithm to achieve an accurate diagnosis of HCC.
Results: Among 2, 796 retrieved scans, 2, 281 were included with 3, 620 liver observations contoured. The cohort’s mean age was 58.4 ± 14.2 years, 61.0% male, with 1, 214 (53.2%) at-risk for HCC. Median observation size was 21.0 (IQR 12.6–41.3) mm; 793 (21.9%) had a ground truth diagnosis of HCC. After randomly dividing observations into training and validation sets in a 7:3 ratio, MS3DCN was the best-performing algorithm at observation level for diagnosing HCC, achieving an AUC of 96.9% (95% CI 95.3%–98.2%), sensitivity 95.9%, specificity 98.1%, positive predictive value (PPV) 93.7%, and negative predictive value (NPV) 98.8%; compared to AUC 85.3% (95% CI 82.4%–88.1%), sensitivity 71.3%, specificity 99.3%, PPV 96.7% and NPV 91.9% for LIRADS. Sensitivity analysis found MS3DCN’s diagnostic performance remained robust, achieving an AUC of 96.3% (95% CI 95.8%–97.6%) at patient level and 97.1% (95% CI 95.3%–98.6%) in the at-risk cohort. In external testing of an independent cohort of 551 scans and 780 observations, MS3DCN achieved an AUC of 98.0% (95% CI 98.4%–99.0%) and 97.6% (95% CI 96.0%–98.9%) at observation and patient level respectively.

Conclusion: The MS3DCN deep learning model deployed to triphasic CT was highly and robustly accurate in diagnosing HCC, superior to LIRADS, with performance validated via internal validation and external testing. Artificial intelligence-based technologies can facilitate precise establishment of diagnosis and improve clinical outcomes. Supported by the Innovation and Technology Fund, the Government of the HKSAR; and United Ally Research Limited, a subsidiary of Hong Kong Sanatorium and Hospital Limited.

OS106
Lifestyle factors and population attributable risk of hepatocellular carcinoma in lean vs non-lean populations
Kali Zhou1, Tiffany Lim1, Jennifer Dodge1, Norah Terrault2, Victoria Setiawan3, 1University of Southern California, Los Angeles, United States
Email: kalizhou@usc.edu

Background and aims: Several lifestyle factors are associated with risk of hepatocellular carcinoma (HCC), but actual impact may differ in individuals with normal (lean) vs elevated (non-lean) body mass index (BMI) due to differential prevalence. We aim to estimate the population attributable risk (PAR) of modifiable lifestyle factors to HCC burden in lean vs non-lean populations to prioritize these factors for patient-level counseling and population-level cancer prevention.

Method: We conducted prospective analysis using data from the Multiethnic Cohort (MEC), a large diverse cohort in Los Angeles County/Hawaii with >20 years of follow-up. Incident HCC was identified via cancer registry linkage. Lifestyle factors were obtained from baseline questionnaire: smoking (never/former/current), alcohol (none/low/-heavy), diet quality (alternate Mediterranean diet (aMED) score: Q1 = lowest to Q5 = highest adherence), physical activity (none/low/high), and coffee intake (0, 1, ≥ 2 cups per day). Lean was defined as BMI <23 kg/m² for Asians and <25 kg/m² for non-Asians. BMI-stratified multivariable Cox models examined association of each factor with HCC adjusted for age, sex, race/ethnicity, diabetes, and hypertension, followed by calculation of PAR (%).

Results: Of 181, 346 at risk participants, 753 developed HCC during an average follow-up of 19.8 years. 23.1% of cases vs 35.0% of non-cases were lean. At baseline, prevalence of current smoking was higher in lean vs non-lean cases (33.2% vs 21.8%); 23.1% in both groups reported heavy alcohol use. No physical activity was reported in 50.3% of lean vs 45.0% non-lean cases, while 76.4% vs 84.6% had suboptimal adherence to aMED diet (Q1–4) ≥ 2 cups/day of coffee was reported by 14.2% of lean vs 22.0% of non-lean cases. Smoking (former vs. never: HR = 2.08, 95% CI 1.39–3.09; current vs. never: HR = 4.41, 2.85–6.81) and coffee (≥ 2 vs 0 cups/day: HR = 0.47, 0.29–0.77) were associated with developing HCC for lean participants, compared to smoking (former: HR = 1.55, 1.26–1.89; current: HR = 2.62, 2.04–3.35), diet quality (Q5 vs Q1: HR = 0.61, 0.46–0.80), and coffee (≥ 2 vs 0 cups/day: HR = 0.77, 0.60–0.98) for non-lean participants. Alcohol use approached significance in the non-lean group (heavy vs none: HR 1.22, 0.98–1.53) while physical activity was not significant for either group. Overall, the combined PAR for lifestyle factors was 65.2% in lean compared to 37.4% in non-lean. The lifestyle factor with highest PAR for both was coffee (45.1% lean, 14.8% non-lean), followed by smoking (24.9% lean, 12.3% non-lean). All other lifestyle factors had PAR <10%

Conclusion: HCC burden can be substantially reduced through modifiable lifestyle factors, more prominently for lean compared to non-lean populations. Drinking ≥ 2 cups of coffee per day could reduce up to 45% of HCC burden among lean individuals. Diet and lifestyle counselling are critical to HCC prevention.

OS107
Validation of the prognostic role of a new distinct assessment of liver function in non surgical HCC patients
Bernardo Stefanini1, Benedetta Stefanini2, Andrea De Sinno2, Francesco Tovoli3, Franco Trevisani3, Fabio Picigallia4, 1Division of Internal Medicine, Hepatobiliary and Immunological Diseases, IRCCS Azienda Ospedaliero-Universitaria di Bologna, Bologna, Italy; 2Semeiotica Medica, Azienda Ospedaliero-Universitaria di Bologna, Bologna, Italy; 3Azienda Ospedaliero-Universitaria di Bologna, University of Bologna, Bologna, Italy; 4Division of Internal Medicine, Hepatobiliary and Immunological Diseases, IRCCS Azienda Ospedaliero-Universitaria di Bologna, Department of Medical and Surgical Sciences (DIMEC), University of Bologna, Bologna, Italy; 5Istituto Clinico Humanitas, Humanitas Gavazzeni Hospital, Bergamo, Italy
Email: bernardo.stefanini@gmail.com

Background and aims: While the role of distinct HCC tumor burdens is quite consolidated, new insights about the impact of more granular assessment of liver function in the prognosis of HCC patients is emerging.

Avery recent review published in Journal of Hepatology described the prognostic relevance of liver functional reserve across the various non-surgical HCC treatments. Based on their experience, the authors proposed a new staging algorithm combining liver functional reserve and tumor bulk separating patients even within the Child-Pugh A and B classes. The present study aims to validate the prognostic role of such system.

Method: We retrospectively evaluated all patients with HCC who were not surgically treated in two large Italian centers between 2010 and 2021. A Kaplan-Meier survival analysis was carried out classifying patients according to the new classification proposed by D’avola, Picigallia et al. which identifies four different subclasses considering the liver functional reserve:
LIR 1 (optimal) includes CPT class A patients with CPT score A5 and with no previous hepatic decompensation, no high risk varices, tumor related performance status (PS) ≤ 1 and ALBI grade ≤ 1.
LIR 2 (suboptimal) includes CPT class A patients with an ALBI grade ≤ 2 and PS≤1 and either CPT score A5 but with a history of previous hepatic decompensation or score A6 (regardless of previous history of decompensation).
LIR 3 (intermediate) includes CPT class B patients with a CPT score of B7 and PS≤1 regardless of any previous decompensation.
LIR 4 (poor) includes uncompensated CPT B or C cirrhotic patients with a PS>2.

Journal of Hepatology 2022 vol. 77(S1) | S1–S118 S79
Results: A total of 538 patients were analyzed. Median overall survival was 41 months in LIR 1 (89 pts), 26 months in LIR 2 (209 pts), 20 months in LIR 3 (84 pts) and 16 months in LIR 4 (156 pts). Interestingly, LIR 1 median OS was significantly higher than LIR 2 subgroup ($p < 0.05$), despite both including only CPT class A patients. LIR 2 OS which instead was closer to that of LIR 3 subgroup suggesting an important prognostic role for ALBI grade and past episodes of hepatic decompensation even for patients within the Child-Pugh A class. Additionally within the CPT B/C classes, a current decompensation must be kept separated from CPT B7 patients.

Conclusion: This new classification based on more granular assessment of liver functional reserve confirms its significant prognostic impact with significant differences even within the same Child-Pugh class.

Public health

OS108 Structured early detection of compensated advanced chronic liver disease–results of the SEAL program
Christian Labenz, Anita Arslanow, Michael Nagel, Marc Nguyen-Tat, Marcus-Alexander Wörns, Matthias Reichert, Franz Josef Heil, Dagmar Mainz, Gudula Zimper, Barbara Römer, Johannes Jäger, Erik Farin-Glattacker, Urs Fichtner, Harald Binder, Erika Graf, Dominikus Stelzer, Reyn van Ewijk, Julia Ortne, Louis Velthuis, Frank Lammert, Peter Galle, University Medical Center Mainz, Germany; aDortmund Hospital; bAllgäu Hospital Group; cSaarland University Medical Center; dGerman Gastroenterology Association; eGeneral Practitioners’ Association Saarland; fGeneral Practitioners’ Association Rhineland-Palatinate; gSaarland University; hUniversity of Freiburg; iJohannes Gutenberg University Mainz; jHannover Medical School
Email: anita.arslanow@uni-mainz.de

Background and aims: Detection of patients with compensated advanced chronic liver disease (cACLD) is of pivotal importance to prevent the occurrence of complications and improve prognosis. However, a structured screening program to detect patients with cACLD has not been implemented into daily routine. Therefore, it was the aim of the SEAL (structured detection of early liver cirrhosis) program to evaluate the usefulness of a structured screening program to detect cACLD.

Method: SEAL was a prospective cohort study conducted in two states in Germany, Rhineland-Palatinate and Saarland, between 01/2018 and 02/2021. Patients participating in a precautionary program (Check-up 35) with their primary care physician were offered additional testing of liver function tests (AST and ALT). If AST/ALT levels were elevated, the APRI score was calculated, and patients with a score >0.5 were referred to a gastroenterologist/hepatologist for more detailed evaluation of their liver disease. The primary end point of this study was the diagnostic rate of cACLD (F3 and F4) compared to a retrospective cohort (ICD-10 codes) of patients attending check-up 35 in the two states during 2016–2017 (n = 349, 570).

Results: In total, 11,859 patients were enrolled into the SEAL program. Slightly more women (54.5%) than men participated in the program, and the mean age of the cohort was 60 years. Elevated LFTs were found in 737 patients (6.1%). The most frequent aetiology of liver disease was non-alcoholic fatty liver disease (59%) followed by chronic alcohol abuse (18%). cACLD was detected in 45 patients. The standardized incidence of cACLD in the SEAL cohort was slightly higher than in controls (3.832‰, 95% CI 2.475, 5.188 vs. 3.358‰, 95% CI 3.136, 3.580). In logistic regression analyses, SEAL was not associated with a higher detection rate of cACLD after adjusting for age and gender (OR 1.141, one-sided 95% CI 0.801, +Inf). When patients with decompensated cirrhosis at diagnosis were excluded from the control cohort, SEAL was associated with a higher detection rate of cACLD on logistic regression analysis (OR 1.586, one-sided 95% CI 1.056, +Inf).

Conclusion: The implementation of a structured screening program may increase the detection rate of cACLD in the general population. In this context, the SEAL program may serve as a feasible concept.

OS109 Abdominal obesity is key when evaluating interactions between alcohol use and obesity for liver disease
Fredrik Åberg, Veikko Salomaa, Martti Färkkilä, Antti Jula, Satu Männistö, Markus Perola, Annamari Lundqvist, Ville Tapio Männistö, Helsinki University Hospital and University of Helsinki, Transplantation and Liver Surgery, Helsinki, Finland; aFinnish Institute for Health and Welfare, Helsinki, Finland; bHelsinki University Hospital and University of Helsinki, Department of Gastroenterology, Helsinki, Finland; cUniversity of Eastern Finland and Kuopio University Hospital, Departments of Medicine, Kuopio, Finland
Email: fredrik.berg@helsinki.fi

This abstract has been selected to be highlighted during official EASL Press Office activities or in official EASL Press Office materials that will be made publicly available on the congress website at 13:40 BST.

This abstract is under embargo until Friday 24 June 2022, 13:40 BST. This abstract has been selected to be highlighted during official EASL Press Office activities or in official EASL Press Office materials that will be made publicly available on the congress website at 13:40 BST.

Journalists, industry, investigators and/or study sponsors must abide by the embargo times set by EASL.

Violation of the embargo will be taken seriously. Individuals and/or sponsors who violate EASL’s embargo policy may face sanctions relating to current and future abstract submissions, presentations and visibility at EASL Congresses. The EASL Governing Board is at liberty to ban attendance and/or retract data.

Copyright for abstracts (both oral and poster) on the website and as made available during The International Liver Congress™ 2022 resides with the respective authors. No reproduction, re-use or transcription for any commercial purpose or use of the content is permitted without the written permission of the authors. Permission for re-use must be obtained directly from the authors.
OS110
The number of public health policies reduces the burden and mortality of alcohol-associated liver disease worldwide: a call for action
Luis Antonio Diaz1, Eduardo Fuentes2, Francisco Idalsoaga1, Jorge Arnold1, Gustavo Ayares1, Macarena Cannistra3, Danae Vio3, Andrea Márquez4, Oscar Corsi1, Alejandro Villalón1, Carolina Ramirez1, María Paz Medel4, Catterina Ferreccio7, Mariana Lazo6, Juan Pablo Roblero5, Anand Kulkarni10, Won Kim11, Mayur Brahmania12, Alexandre Louvet13, Elliot Tapper14, Winston Dunn15, Douglas Siminette16, Vijay Shah16, Patrick S. Kamath16, Ashwani Singal17, Ramon Bataller18.

1Pontificia Universidad Católica de Chile, Departamento de Gastroenterología, Chile; 2Pontificia Universidad Católica de Chile, Departamento de Ciencias de la Salud, Chile; 3Pontificia Universidad Católica de Chile, Escuela de Medicina, Chile; 4Pontificia Universidad Católica de Chile, Departamento de Ciencias de la Salud, Chile; 5Pontificia Universidad Católica de Chile, Escuela de Medicina, Chile; 6Unidad Andahuac Mayab, Escuela de Medicina, Mexico; 7Clínica Las Condes, Departamento de Anestesiología, Chile; 8Pontificia Universidad Católica de Chile, Departamento de Medicina Familiar, Chile; 9Pontificia Universidad Católica de Chile, Public Health Department, Chile; 10Drexel University, Department of Community Health and Prevention, Dornsife School of Public Health, United States; 11Hospital Clínico Universidad de Chile, Sección Gastroenterología, Chile; 12Asian Institute of Gastroenterology, Department of Hepatology, India; 13Seoul National University College of Medicine, Division of Gastroenterology and Hepatology, Department of Internal Medicine, Seoul Metropolitan Government Seoul National University Boramae Medical Center, Korea, Rep. of South; 14Western University, Department of Medicine, Division of Gastroenterology, Canada; 15Hôpital Claude Huriez, Services des Maladies de l’Appareil Digestif, CHRU Lille, France; 16University of Michigan, Division of Gastroenterology and Hepatology, United States; 17University of Kansas Medical Center, United States; 18Mayo Clinic Rochester, Division of Gastroenterology and Hepatology, United States; 19University of South Dakota Sanford School of Medicine, Department of Medicine, Division of Gastroenterology, United States; 20University of Pittsburgh Medical Center, Center for Liver Diseases, Division of Gastroenterology, Hepatology and Nutrition, United States

Email: jparab@gmail.com

Background and aims: Harmful alcohol consumption cause a significant burden of disease worldwide. To date, the impact of alcohol-related public health policies (PHP) in alcohol-associated liver disease (ALD) has not been adequately addressed. We aimed to assess the association between alcohol-related PHP and ALD mortality worldwide.

Method: We performed an ecological multi-national study including 193 countries. We recorded socio-demographic data from the World Bank Open Data source. We registered the presence of alcohol-related PHP in each country from the WHO GISAH (in 2016). Data on alcohol consumption measures and their harmful health consequences were collected from the WHO Global Information System of Alcohol and Health (GISAH) and the Global Burden of Disease (GBD) databases (updated to 2019). We constructed generalized linear models (GLM) with a Poisson family distribution, logit link, and a robust variance estimator to assess the association between the number of PHP and disease burden outcomes. The models were adjusted by population size and population structure.

Results: We included 193 countries (7,626,289,120 inhabitants); the median number of PHP was 7 [6–8]. The most developed categories were drink-driving policies and countermeasures (92.2%), tax regulations (87%), limiting drinking age (84.5%), and restrictions to alcohol access (81.9%). Other categories were national license, production, and selling control (81.9%), government monitoring systems and community support (74.1%), control over advertising and promotion (70.5%), and presence of a national plan (50.3%). Importantly, as higher number of PHP was associated with lower mortality due to cirrhosis (all causes) (prevalence ratio [PR]:0.78 95% CI: 0.67–0.90; p = 0.001), mortality due to ALD (RP:0.81 95%CI: 0.68–0.98; p = 0.029), cardiovascular mortality (PR:0.81 95%CI: 0.67–0.98; p = 0.029), and alcohol use disorder (AUD) (PR:0.80 95%CI: 0.63–0.99; p = 0.046) (Figure). The association between PHP on alcohol consumption and burden of disease was significantly higher in Africa, the Americas, and Asia.

Figure: Relationship between alcohol-related public health policies and (A) deaths due to cirrhosis (all causes), and (B) deaths due to alcohol-associated liver disease (ALD) in 2019.

Conclusion: Those countries with a higher number of PHP had lower mortality due to cirrhosis (all causes), mortality due to ALD, cardiovascular mortality, and AUD. Our results strongly encourage the development and implementation of PHP on alcohol consumption worldwide.
Smoking, alcohol consumption and combined association risk for developing liver cancer in chronic hepatitis B: a prospective study

Cao Maomao 1, Wanqing Chen 1.
National Cancer Center/National Clinical Research Center for Cancer/Cancer Hospital, Chinese Academy of Medical Sciences and Peking Union Medical College, Office of Cancer Screening, Beijing, China
Email: chenwq@cicams.ac.cn

Background and aims: Evidence of liver cancer with tobacco smoking and alcohol consumption remains controversial. We aimed to investigate associations between liver cancer risk and alcohol consumption, smoking, and the combined interaction between these two risk factors in this prospective study.

Method: Baseline smoking and alcohol consumption were collected from all subjects in a population-based prospective cohort. Cox proportional hazard regression models were used to estimate hazard ratios (HRs) and 95% confidence intervals (CIs) adjusting for potential confounders. The population attributable fractions (PAFs) were estimated. The cumulative incidences of liver cancer were generated with the use of Kaplan-Meier methods and compared based on the log-rank test.

Results: A total of 4003 participants were included in this study up to 3 years of follow-up, 72 liver cancer cases were identified. Alcohol consumption was found to increase the risk of liver cancer with a non-significant difference (Adjusted HR = 1.19, 95% CI = 0.66–2.16, PAF = 26.69%). A dose-responsive pattern between the duration and intensity of smoking and the risk of liver cancer was noted. Similar results were also observed in men. Further statistical analysis revealed interactions between the effect of smoking and alcohol consumption on the risk of liver cancer, contributing to 11.12% of liver cancer cases in our cohort.

Conclusion: The findings further support smoking is an independent risk of liver cancer with a clear dose-and-duration-dependent relation. We also showed the combined effect of alcohol consumption and smoking on the development of liver cancer.

Figure 1: The synergistic effect of smoking and alcohol contributed to liver cancer risk (A. All population; B Male sex).

Figure 2: The cumulative incidence of liver cancer by drinking and smoking status (A. Smoking; B. Drinking).
Association between liver cirrhosis and cardiovascular events in a large German cohort—a population based study

Kabbani Abdul-Rahman1, Hannah Schneider1, Hans Becker1,2, Heiner Wedemeyer2,3, Benjamin Maasoumy1, Jona T. Stahmeyer3,4, 1Hannover Medical School, Department of Gastroenterology, Hepatology and Endocrinology, Hannover, Germany; 2German Liver Foundation (Deutsche Leberstiftung), Hannover, Germany; 3AOK Niedersachsen, Health Services Research Unit, Germany; 4Hannover Medical School, Institute for Epidemiology, Social Medicine and Health Systems Research, Germany

Email: kabbani.abdul-rahman@mh-hannover.de

Background and aims: Systemic inflammation has been associated with an increased risk for cardiovascular events. Liver cirrhosis is associated with both systemic inflammation and endothelial dysfunction. However, a possible link between liver cirrhosis and cardiovascular diseases remains poorly investigated. We here aimed to analyze the risk of cardiovascular events (myocardial infarction and stroke) in patients with liver cirrhosis compared to non-cirrhotic patients in a population-based study from Northern Germany.

Method: Analysis was based on administrative data from one large German public health insurance fund. All adult individuals continuously insured until death or the end of observation period (2010–2019) were included. We used a pre-observation period (2010–2012) to exclude individuals with cardiovascular events prior to the start of observation in 2013. The presence of liver cirrhosis and cardiovascular risk factors were identified using ICD-10 codes. Myocardial infarction and stroke were analyzed as a composite and as individual end points. To determine the risk of cardiovascular events in patients with liver cirrhosis we used a multivariable Cox regression adjusted for age, gender and selected cardiovascular risk factors (hypertension, heart failure, atherosclerosis, chronic ischemic heart disease, obesity, nicotine abuse, dyslipidemia, diabetes, alcohol abuse and chronic renal failure with dialysis).

Results: A number of 1.29 million patients were included. Liver cirrhosis was present in 6, 517 individuals (0.51%) at the start of the observation in 2013. Individuals with liver cirrhosis were older (62.8 vs. 55.9 yr), more often male (60.4% vs. 44.6%) and had more comorbidities (e.g. alcohol abuse 39.5% vs. 2.3% or atherosclerosis 11.3% vs. 5.4%). Overall incidence of cardiovascular events was significantly higher among patients with cirrhosis (7.7% vs 5.9%, p < 0.001). This difference was also documented when limiting the analysis to the incidence of strokes (5.1% vs 3.5%, p < 0.001). In contrast, myocardial infarctions occurred with a similar frequency in cirrhotic and non-cirrhotic individuals (2.8% vs 2.6%, p = 0.327). After adjusting for potential confounders in the multivariable cox regression analysis liver cirrhosis was associated with a 20.9% and 37.3% higher risk of overall cardiovascular events (p < 0.001) and strokes in particular, respectively, while there was no risk difference with regard to myocardial infarction (p = 0.703).

Conclusion: Liver cirrhosis is associated with a higher risk of stroke. Importantly, this link is independent from other established cardiovascular risk factors. A correspondingly higher risk of myocardial infarction could not be demonstrated.

Molecular and cellular biology

OS114
MiR-122, the regulator of the immune privileged liver
Maytal Gefen1, Shanny Layani1, Emma Klahr1, Mor Hindi1, Nofar Rosenberg2, Rinat Abramovitch1,2, Nathalie Nachmansson1,2, Adi Yehezkel1, Amnon Peled1, Jacob Rachmilewitz1, Michal Abraham1, Michael Berger2, Daniel Goldenberg1, Nicola Gagliani1, Samuel Huber1, Irm Hermans-Borgmeyer1, Rebecca Hoffa-Krausz5, Shifra Ben-Dor6, Yuval Nevo7, Shroma Elgavish7, Hadar Benyamini7, Mathias Heikenwälder8, Stefan Rose-John9, Dirk Schmitt-Arras8, Achim Krüger10, Michael Stürzl11, Elisabeth Naschberger11, Frank Tacke12, Hilla Gili1, Eithan Galun1, 1Hadassah Hebrew University Hospital, Goldyne Savad Institute of Gene Therapy, Jerusalem, Israel; 2Hadassah University Medical Center, The Wohl Institute for Translational Medicine, Jerusalem, Israel; 3Israel-Canada Medical Research Institute, Faculty of Medicine, the Hebrew University, The Lautenberg Center for Immunology and Cancer Research, Jerusalem, Israel; 4University Medical Center, Hamburg-Eppendorf, Hamburg, Germany; 5Weizmann Institute of Science, Dept. of Veterinary Resources, Rehovot, Israel; 6Weizmann Institute of Science, Bioinformatics Unit, Rehovot, Israel; 7Hadassah Hebrew University Medical Center, Bioinformatics Unit of the I-CORE Computation Center, Jerusalem, Israel; 8German Cancer Research Centre Heidelberg (DKFZ), Division of Chronic Inflammation and Cancer, Heidelberg, Germany; 9University of Kiel, Bioc hemical Institute, Germany; 10Technical University Munich, Institutes of Molecular Immunology and Experimental Oncology, Munich, Germany; 11Universitätsklinikum Erlangen, Friedrich-Alexander University (FAU) of Erlangen-Nürnberg, Division of Molecular and Experimental Surgery, Department of Surgery, Erlangen, Germany; 12Charitét University Medicine Berlin, Department of Hepatology and Gastroenterology, Berlin, Germany

Email: maytalgefen@gmail.com

Background and aims: The liver, an immune privileged organ, is a sanctuary for acute and chronic infections and a frequent site for metastasis due to its immunosuppressive environment. Chronic liver inflammation is a major risk factor for primary liver cancer. Hepatocellular carcinoma (HCC) is the fourth leading cause of cancer related death, and metastatic liver cancer occurs even more often. Fatty liver is apparent in 30% of the western world due to western diet and lifestyle, increasing the risk of non-alcoholic steatohepatitis (NASH). NASH fuels chronic inflammation which could progress to cirrhosis and HCC.

Method: MicroRNA-122 (miR-122), the liver specific microRNA, plays important roles in regulating several liver-specific processes and was reported to be significantly down-regulated in HCC. Our group has shown that: Inflammatory mediators regulate miR-122 expression and secretion i.e. TNFα (Rivkin M et al Gastroenterology 2016). In NASH, miR-122 is decreased in livers with increased inflammation, steatosis and fibrosis. Upon increasing miR-122 expression the NASH pathologies reverse (Chai C et al Gastroenterology 2020). MiR-122 functions as a hormone, it is produced in hepatocytes and affects remote tissue (Chai C et al Gastroenterology 2017). Concurring with previous studies, we have shown that miR-122 has tumor suppressive effects through numerous mechanisms (Simerzin A et al Hepatology 2016).
OS115
The role of OFD1 and loss of primary cilia in cholangiocarcinoma: a novel promising therapeutic target
Massimiliano Salati³, Anna Barbato², Francesco Caputo¹, Andrea Spallanzani¹, Fabio Gelsomino¹, Betrice Rico¹,
Gabriele Luppi¹, Luigi Ferrante¹, Roberta Biondi², Francesco Massaro³, Antonella Iuliano², Gennaro Gambardella², Fabiola Piscopo²,
Pasquale Pisapia³, Antonino Iaccarino³, Maria Salatiello³, Giancarlo Troncone³, Luca Reggiani-Bonetti¹, Massimo Dominicì¹,
Brunella Franco², Pietro Carotenuto¹.¹University of Modena and Reggio Emilia, Modena, Italy; ²Tigem, Pozzuoli, Italy; ³University of
Naples Federico II, Napoli, Italy
Email: p.carotenuto@tigem.it

Background and aims: CCA is a highly lethal primary liver cancer with an increasing incidence and limited therapeutic options. The
primary chilium has been postulated to have a tumor-suppressor role in the biliary tract being involved in several cancer-related pathways
including WNT, Hedgehog and NOTCH. Here, we aimed at identifying and functionally characterizing primary cilium-associated genes with
translational relevance for CCA prognostication and treatment.

Method: Whole-transcriptome profiling was performed with RNA-
Seq on laser micro-dissected FFPE resected tissue specimens. Knocking-down of OFD1 showed was performed using siRNA
interference transfections of CCA cells. Immunofluorescence staining of cilia markers was used to analyze and count cilia.

Results: Overall, 70 CCA patients were included. 51% (36) had
intrahepatic and 49% (34) had extrahepatic CCA. Among 3392 and
6315 differentially expressed genes between tumour and normal tissue
and tumour and stroma, OFD1 was the top-ranked cilium-
associated gene (fold-change ≥ 2.5, p < 0.01). siRNA-mediated depletion of OFD1 induced ciliogenesis and suppresses tumour growth
in vitro normal cholangiocyte and 4 different CCA cell lines. In the
Western blot, OFD1 knockdown significantly increase the expression
of ciliary proteins such as PCM1, ARL13B and Acetylated Tubulin,
while OFD1 overexpression reduced their expression. When asses-
sing the impact of OFD1 on prognosis, higher expression of OFD1
was significantly associated with a worse overall survival in resected CCA
patients (10 vs 39 months; HR 2.33, 95%CI 1.01–5.31, p = 0.03).

Conclusion: We demonstrated that OFD1 acts as an oncogene in CCA
and experimentally-induced depletion of OFD1 stimulated ciliogen-
esis and suppressed tumour growth in vitro. Interestingly, higher
OFD1 expression adversely impacted survival of CCA patients
undergoing curative-intent resection. This work identifies the
primary cilium-associated gene OFD1 as a novel promising thera-
tic target and prompts ciliotherapy development in CCA.

OS116
Human antigen R (HuR) is a master regulator of hepatic glucose metabolism
Sofía Lachiondo-Ortega¹, Miren Bravo¹, Irene González-Recio¹, María J. González Rellán¹, Jorge Simón Espinosa¹,³,
Narao Goikoetxea¹, Petar Petrov¹,³, Rubén Rodríguez Agudo¹, Aranzta Sanz-Parra¹, Begoña Rodríguez Irurtxaygora¹,
Teresa Cardoso Delgado¹, Dan A. Dixon², Myriam Gorospe³, Ruben Nogueiras²,³, María Luz Martínez-Chantar³,¹³, Center for
Cooperative Research in Biosciences (CIC bioGUNE), Liver Disease Lab, Spain; ²Center for Research in Molecular Medicine and Chronic Diseases
(CIMUS), Department of Physiology, Spain; ³Centro de Investigación Biomédica en Región de Fisiopatología de la Obesidad y Nutrición (CIBERobn), Spain
Email: mlmartinez@cicbiogune.es

Background and aims: Human antigen R (HuR) or Embryonic Lethal
Abnormal Vision-Like 1 (ELAV/L1) is a ubiquitous member of the ELAV/
HuR family of RNA-binding proteins (RBPs). Under normal physiological conditions HuR is primarily nuclear. However, upon specific stimuli, e.g. stress signals, HuR translocates to the cytoplasm where it functions as a potent regulator of the stabilization and translation of target mRNAs. By binding to U/AU-rich elements (AREs) typically present in the 3′-untranslated region (UTR) of mRNAs, HuR post-transcriptionally controls the expression of many proteins and hence governs diverse molecular and cellular functions. Thus, in addition to its implication in disease, HuR is involved in physiological processes, e.g. adipogenesis, myogenesis, senescence, and immune response. However, the role of HuR in hepatic glucose metabolism remains to be addressed and constitutes the main aim of the present work.

Method: HuR expression was modulated in cultured primary mouse hepatocytes and in the THLE-2 human liver cell line stimulated with glucagon, glucose or insulin, as well as in mice fed a high-fat diet (HFD) during 4 days or subjected to glucagon administration for 30 min. Next, changes in glucose levels, RNA and protein expression, HuR localization, fluxomic analysis with 13C-uniformly labelled glucose, RNA and RNA immunoprecipitation (RIP) and sequencing (Seq) assays were performed.

Results: Hepatic HuR expression was increased after inantraperitoneal administration of glucagon in mice, while it remained unchanged in the glucagon receptor knockout animal model. Conversely, HuR expression decreased in mice upon insulin injection into the inferior cava vein. Importantly, HuR expression was significantly upregulated in the liver of a cohort of type II diabetes mellitus (T2DM) patients and in the insulin resistance in vivo model consisting of mice fed a HFD during 4 days. HuR was mainly located in the nucleus upon glucagon and insulin stimuli, whereas it translocated to the cytoplasm after glucagon administration. Silencing the expression of HuR in the HFD mouse model sensitized the liver to insulin-mediated glucose uptake and subsequent glycolysis, while its gluconeogenic capacity was reduced. Importantly, ablating hepatic HuR expression resulted in a two-fold reduction of subcutaneous white adipose tissue weight due to increased lipolysis. Moreover, RNA-Seq analysis revealed different expression signatures of RNAs involved in glucose metabolism upon modulation of HuR expression. Finally, RIP-Seq experiments identified a panel of HuR-interacting mRNAs encoding proteins with molecular functions that helped explain how HuR controls liver glucose homeostasis.

Conclusion: Given that HuR appears to be a master regulator of glucose metabolism, we propose that HuR ought to be considered as a potential pharmacological target for the clinical management of T2DM.
with Thioacetamide (TAA), using immunoblot, RT-PCR and immunochemistry. Liver tissues from vehicle and TAA treated NFATc1−/−, NFATc1−/− and NFATc1−/− mice were examined for NFATc1-dependent morphological changes by analyzing inflammation, and fibrosis. RNA-seq analysis in AML12 cells was performed to identify NFATc1 regulated gene signatures and signaling mechanisms. We further highlighted the therapeutic potential of NFATc1 dependent signaling mechanisms by their inhibition, both in-vivo and in-vitro.

**Results:** Liver biopsies from patients with inflammation/fibrosis revealed increased NFATc1 expression and nuclear localization in hepatocytes. Moreover, TAA induced NFATc1 activation resulted in progressive inflammation, fibrosis and cirrhosis whereas hepatocyte-specific depletion of the transcription factor prevented mice from liver damage. Mechanistically, hepatocyte specific NFATc1 activation drives chronic ER stress-responses and promotes apoptosis (cleaved Caspase-3) and pro-inflammatory signaling cascades through PERK-CHOP-mediated NLRP3 inflammasome activation. Finally, TUDCA mediated inhibition of NFATc1-driven signaling prevented hepatocyte damage and subsequent inflammation/fibrosis.

**Conclusion:** Together, our study successfully established the role of NFATc1 in liver inflammation and fibrosis through terminal ER-stress signalling and subsequent NLRP3 inflammasome activation in hepatocytes. This study also highlighted the therapeutic potential of ER-stress inhibition by TUDCA. In fact, TUDCA application resulted in strikingly lower liver damage and fibrosis in mice.

**OS119**

**The selective PPAR-delta agonist seladelpar suppresses bile acid synthesis by reducing hepatocyte CYP7A1 through the FGF21 pathway**

Tetsuya Kouno1, Xiao Liu2, Tatiana Kisseleva2, Edward Cable3, Bernd Schnabl1.
1University of California San Diego, Department of Medicine, La Jolla, United States; 2University of California San Diego, Department of Surgery, La Jolla, United States; 3CymaBay Therapeutics, Newark, United States

**Background and aims:** PPAR-delta agonists exert beneficial effects in liver disease and reduce total bile acid levels. Since little is known about the mechanism whereby PPAR-delta agonism reduces bile acid levels, the aim of the current study was to investigate the molecular pathways responsible for reducing bile acid synthesis in hepatocytes following treatment of the selective PPAR-delta agonist, seladelpar.

**Method:** Wild type C57BL/6 mice were gavaged with vehicle (PBS) or seladelpar (10 mg/kg body weight), and gene expression in the liver and ileum was examined 6 hours later by qPCR. For mechanistic studies, primary mouse hepatocytes isolated from wild type C57BL/6 mice, Ppar-alpha/-/- mice, or Fgf21/-/- mice were treated with seladelpar for 48 hours, and gene expression analysis was performed. The effect of seladelpar on bile acid regulation was also investigated in primary human hepatocytes.

**Results:** Administration of seladelpar to wild type mice repressed the liver expression of cholesterol 7 alpha-hydroxylase (Cyp7a1), a rate limiting enzyme for bile acid synthesis, and decreased plasma 7α-hydroxy-4-cholesten-3-one (C4), the freely diffusible metabolite downstream of Cyp7a1, without affecting Farnesoid X receptor pathway in the liver or ileum. In primary mouse hepatocytes, seladelpar significantly reduced the expression of Cyp7a1 and upregulated fibroblast growth factor 21 (Fgf21). The effect of seladelpar on the expression of Cyp7a1 and Fgf21 was observed in the hepatocytes isolated from Ppar-alpha/-/- mice, confirming the effect of seladelpar is not based on PPAR-alpha activation. Recombinant Fgf21 protein repressed Cyp7a1 gene expression via an activation of the JNK signaling pathway in primary mouse hepatocytes. The suppressive effect of seladelpar on Cyp7a1 expression was blocked by both a JNK inhibitor and in the absence of Fgf21, indicating that Fgf21 plays an indispensable role in PPAR-delta-mediated downregulation of Cyp7a1. Reduction of CYP7A1 expression by seladelpar was confirmed in primary human hepatocytes.

**Conclusion:** Seladelpar reduces bile acid synthesis via an FGF21-dependent mechanism that signals, at least partially through JNK, to repress Cyp7a1.

**NAFLD Therapy**

**OS120**

**Dissecting the effects and mechanism-of-action of statin use on fatty liver disease: a multidimensional study**

Ibrahim Ayada1, 2, Laurens van Kleeft3, Huai Zhang4, Pengfei Li3, Kuan Liu1, Ling Wang3, Marla Lavrijsen4, Mohsen Ghanbari2, Luc J.W. Van Der Laan5, Maikel Peppelenbosch3, Huai Zhang4, Pengfei Li3, Robert De Knegt4, Qiuwei Pan1, Erasmus MC, Gastroenterology and Hepatology, Rotterdam, Netherlands; 2Erasmus MC, Department of Epidemiology; 3Erasmus MC, Gastroenterology and Hepatology; 4Medical Quality Management Office, the First Affiliated Hospital of Wenzhou Medical University, Wenzhou, China, Department of Biostatistics and Records Room; 5Erasmus MC, Department of Surgery; 1The First Affiliated Hospital of Wenzhou Medical University Email: ibrahimayada653@hotmail.com

**Background and aims:** Statins are widely used for the prevention of cardiovascular events and treatment of dyslipidemia. Previous studies have suggested potential beneficial effects of statin use on fatty liver disease, but the evidence is segmented and inconclusive. This study aims to comprehensively investigate the epidemiological and clinical evidence in this respect, and to understand the mechanism-of-action in experimental models.

**Method:** The association between statin use and fatty liver disease (FLD) was investigated in the Rotterdam Study (a population-based prospective cohort); a biopsy proven FLD cohort and lastly in meta-analysis of published clinical trials and cohort studies. The effect of simvastatin and lovastatin on lipid accumulation was investigated in...
3D cultured human liver organoids fed with lactate, pyruvate and octanoic acid to mimic steatosis. Since macrophages are the key drivers of inflammation in FLD, human THP-1 macrophage cell line was used to study inflammatory gene expression.

**Results:** In the Rotterdam Study cohort (n = 4352 participants), statin use among participants with the metabolic syndrome (n = 1700) was associated with decreased risk for steatosis (OR 0.45, 95%CI 0.33–0.60, p <0.001) and fibrosis (OR 0.51, 95%CI 0.26–0.90, p = 0.031). In the biopsy proven patient cohort (n = 569), statin use in a subpopulation with the metabolic syndrome (n = 266) was associated with decreased risk for non-alcoholic steatohepatitis (OR 0.49, 95%CI 0.25–0.98, p = 0.04). In meta-analysis, lower levels of AST (mean difference: −0.74 U/L) and ALT (mean difference: −0.87 U/L) were observed in fatty liver disease patients using statins. Pooled odds ratio of 0.65 (95%CI 0.35–1.07) was estimated on the association of statin use and FLD development. In liver organoids model of steatosis, we found treatment with statins significantly inhibited the number of formed lipid droplets, although the effect was prominent only at relatively high concentration (10 microM). Our preliminary results suggest that statin inhibits the expression of inflammatory genes, including IL-1beta, IL-6, TNF-alpha and IL-8, but these results require further confirmation.

**Conclusion:** Our epidemiological and clinical evidence strongly supports the beneficial effects of statin use on multiple stages of fatty liver disease; steatosis, fibrosis and steatohepatitis. This is likely attributed to multiple mechanisms, including inhibition of steatosis and inflammatory response.
Results: Treatment of primary hepatocytes with GalNAc siRNA targeting CNNM4 reduced the lipid accumulation induced by OA stimulation. In the in vivo Diamond mouse model, at 17th week, when GalNAc siRNA treatment was initiated, DIAMONDDM mice had already developed insulin resistance. siRNA treatment did not affect weight gain or food consumption pattern. Hepatomegaly induced by HFS-WD was partially controlled by GalNAc CNNM4-targeting siRNA, while serum transaminases tended to decrease in treated mice. Histopathological characterization showed a significant reduction in steatosis and fibrosis development, together with a tendency of reduced inflammation.

Conclusion: GalNAc CNNM4-targeting siRNA-based treatment appears to reduce steatosis, inflammation and fibrosis in a MAFLD animal model, in which mice develop comorbidities, such as insulin resistance or obesity. Ongoing studies will characterize the effect on systemic alterations in MAFLD such as cardiovascular risk or pancreas and kidney functionality.

OS123
Multiple doses of thyroid hormone receptor-beta agonist TERN-501 were well-tolerated and resulted in significant dose-dependent changes in serum lipids and sex hormone binding globulin in a first-in-human clinical study

Cara H. Nelson, Christopher Jones, Lois Lee, Tonya Marmon, Diana Chung, Kevin Kucher, Yizhao Li, Erin Quirk, Daria Crittenden, Terns Pharmaceuticals, Foster City, United States

Background and aims: Thyroid hormone receptor-beta (THR-beta) agonists reduce low-density lipoprotein cholesterol (LDL-c), decrease liver fat, and improve liver histology in patients with non-alcoholic steatohepatitis (NASH). TERN-501 is a novel, metabolically stable, highly selective THR-beta agonist. In a first-in-human (FIH) study, single doses of TERN-501 were well-tolerated with significant changes in LDL-c, apolipoprotein B (Apo B), and sex hormone binding globulin (SHBG). Here we describe multiple ascending dose results from the TERN-501 FIH study.

Method: Healthy participants (n = 8/cohort) with mildly elevated LDL-c were randomized 3:1 to receive TERN-501 (3, 6, or 10 mg) or placebo once daily for 14 days in 3 cohorts. Intensive PK was assessed on Days 1 and 14, and pharmacodynamic markers were measured pre-dose on Days 1, 3, 5, 8, 11, and 13, and on Days 15, 17, and follow-up. Safety assessments were performed throughout the study.

Results: All 24 subjects completed the study without study drug discontinuations. All adverse events (AEs) were mild (Grade 1); no AEs by preferred term occurred in >1 subject. Vital signs and electrocardiograms remained stable. Transaminase changes in TERN-501 groups compared to placebo were unremarkable. Dose-dependent declines in free thyroxine were observed without clear changes in thyroid stimulating hormone or signs or symptoms of hyper/hypothyroidism. TERN-501 plasma exposures were dose-proportional with low variability. Median half-life was >15 h in all cohorts. SHBG increased dose-dependently with least squares mean (LSM) changes from baseline of 55%, 134%, and 166% on Day 15 in TERN-501 3, 6, and 10 mg groups, respectively (~12% in placebo; see Figure). Statistically significant dose-dependent LSM reductions in Apo B of −18%, −23% and −28% in the 3, 6, and 10 mg groups, respectively, were observed on Day 15 (~6% in placebo). Total cholesterol was reduced in all TERN-501 groups and maximum LSM LDL-c decreases during dosing were −22%, −28%, and −27% for 3, 6, and 10 mg (~8% in placebo; see figure).

Conclusion: Once daily TERN-501 at 3, 6, and 10 mg for 14 days was overall safe and well-tolerated. TERN-501 increased SHBG, a key marker of hepatic THR-beta engagement, in a dose-dependent fashion. Significant reductions in atherogenic serum lipids with favorable PK observed in this study support further investigation of TERN-501 for NASH treatment alone or in combination with other agents.

OS124
Pemvidutide (ALT-801), a novel GLP-1/glucagon dual receptor agonist, achieves rapid and potent reductions in body weight and liver fat: results of a placebo-controlled, double-blind, first-in-human (FIH) clinical trial

Stephen Harrison, John Nestor, Sarah Browne, Jacques Payne, Staci Steele, Robert Casper, Anvar Suyundikov, Vyjayanthi Krishnan, Scot Roberts, Joyce James, M. Scott Harris, Pinnacle Research, Research, San Antonio, United States; Altimmune, Inc., Clinical Development, Gaithersburg, United States; Altimmune, Inc., Clinical Operations, Gaithersburg, United States; Altimmune, Inc., Clinical Operations, Gaithersburg, United States; Altimmune, Inc., Biostatistics, Gaithersburg, United States; Altimmune, Inc., Product Development, Gaithersburg, United States; Altimmune, Inc., Research, Gaithersburg, United States; Corvid LLC, Pharmacokinetics, Oakland, United States; Altimmune, Inc., Medical, Gaithersburg, United States

Email: sharris@altimmune.com

This abstract is under embargo until Friday 24 June 2022, 13:40 BST. This abstract has been selected to be highlighted during official EASL Press Office activities or in official EASL Press Office materials that will be made publicly available on the congress website at 13:40 BST. Journalists, industry, investigators and/or study sponsors must abide by the embargo times set by EASL. Violation of the embargo will be taken seriously. Individuals and/or sponsors who violate EASL's embargo policy may face sanctions relating to current and future abstract submissions, presentations and visibility at EASL Congresses. The EASL Governing Board is at liberty to ban attendance and/or retract data. Copyright for abstracts (both oral and poster) on the website and as made available during The International Liver Congress™ 2022 resides with the respective authors. No reproduction, re-use or transcription for any commercial purpose or use of the content is permitted without the written permission of the authors. Permission for re-use must be obtained directly from the authors.
Results: A total of 36 NASH patients were enrolled and completed the study. After the consecutive administration of ZSP1601 50 mg QD, 50 mg BID or 100 mg BID for 28 days, the plasma concentration reached steady state on the third day. The AUC increased gradually with increasing dose. There is a relatively lower accumulation of ZSP1601. MRI-PDFF was measured at baseline and day 29. The patients received ZSP1601 50 mg QD or BID or 100 mg BID or placebo had a mean relative reduction from baseline in MRI-PDFF of 12.43%, 21.88%, 25.50% and 12.80% ≥30% reduction in MRI-PDFF relative to baseline was measured in 7 patients received ZSP1601 and 1 patient received placebo. The mean reduction of ALT from baseline were 24.8 U/L, 38.94 U/L, 55.06 U/L and 13.35 U/L. The ALT of 8 patients decrease to normal, including 1 patient in 50 mg QD cohort, 2 patients in 50 mg BID cohort, 4 patients in 100 mg BID cohort and 1 patient in placebo cohort. And the AST of patients in ZSP1601 cohorts also showed obvious change from baseline. In addition, the Cap, HOMA-IR, FIB4, APRI and CK-18 decreased in ZSP1601 cohort. 18 of 36 (50%) patients experienced at least one mild or moderate adverse event (AE), and the incidence rates of AEs were 77.8% and 66.7% in ZSP1601 cohorts and placebo cohort, respectively. No serious adverse event. ZSP1601 was well-tolerated in this study. The most frequent AEs were adaptive headaches, creatinine slightly transiently elevated, diarrhoea and indigestion.

Conclusion: The results of this clinical trial showed that a significant reduction in liver fat by MRI-PDFF and ALT level of NASH patients enrolled after 28-days treatment. The phase 1b study suggested that ZSP1601 is safe and effective. The efficacy of 50 mg BID and 100 mg BID cohort were better than the 50 mg QD cohort and placebo cohort. Comparing with the results of other new drugs treating for NASH clinical study, the efficacy of ZSP1601 are inspiring. (This trial registered number is NCT04140123).

OS125 Safety, pharmacokinetics and efficacy of the novel pan-phosphodiesterase inhibitor ZSP1601 in 36 NASH patients: a double-blinded, placebo-controlled, multiple-dose escalation phase Ib study

Yue Hu1, Hai Jun Li2, Hong Zhang3, Jinjun Chen3, Zhongyuan Xu3, Hong You4, Ruihua Dong4, Xiaoxue Zhu1, Hong Chen1, Yun Peng2, Jing Li2, Xiaojiao Li1, Lei Zhang5, Di Cao4, He Jin4, Dongdong Qiu5, Aruhan Yang1, Jingrui Liu1, Haiyan Jia1, Jinfeng Lou1, Junqi Niu6, Yanhua Ding1. 1The First Hospital of Jilin University, Phase I Clinical Research Center, Changchun, China; 2Guangdong Raynovent Biotech Co., Ltd, Guangzhou, China; 3Nanfang Hospital, Nanfang Medical University, Guangzhou, China; 4Beijing Friendship Hospital, Capital Medical University, Beijing, China; 5The First Hospital of Jilin University, Radiology, Changchun, China; 6The First Hospital of Jilin University, Hepatology, Changchun, China

Email: dingyanhua2003@126.com

Background and aims: NASH is a serious healthcare burden. Although there has been steady progress in advancing drug development, no new drug is approved yet for this condition. The primary aim of this clinical trial is to evaluate the safety, pharmacokinetics, and efficacy of ZSP1601 that is a pan-phosphodiesterase (PDE) inhibitor to decrease producing TNF-α to reduce liver inflammation in NASH patients.

Method: This is a double-blind and randomized phase Ib study in 36 NASH patients (aged 18–65 years), the study is consisted of three dose cohorts (50 mg QD, 50 mg BID, 100 mg BID), 12 patients were enrolled for every cohorts of which 9 received ZSP1601 and 3 received placebo orally for 28 days. The patients who were diagnosed by liver biopsy or met clinical features that contains the following two criteria: ALT ≥1.5 × ULN (male 75 U/L, female 60 U/L) for two examinations within 28 days with an interval greater than 7 days; BMI ≥25 kg/m² and a baseline MRI-PDFF of liver ≥10% were enrolled.

OS126 The association between proton pump inhibitor exposure and key liver-related outcomes in patients with cirrhosis: a veterans affairs cohort study

Nadim Mahmud1, Marina Serper1, Tamar Taddei2, David Kaplan1.

1Hospital of the University of Pennsylvania, Gastroenterology, Philadelphia, United States; 2Yale University, New Haven, United States

Email: nadim.mahmud@gmail.com

Background and aims: The impact of proton pump inhibitor (PPI) use on infection, decompensation, and mortality remains a point of controversy in patients with cirrhosis. We aimed to explore these associations in a large U.S. dataset while accounting for complex confounding relationships.

Method: This was a retrospective cohort study of patients with compensated cirrhosis in the Veterans Health Administration (VHA). We identified all PPI prescriptions in the VHA and time-updated PPI exposure every 30 days, including PPI dose which was normalized to omeprazole equivalents. Inverse probability treatment weighing
OS127 Non-invasive tests for clinically significant portal hypertension after HCV-cure-individual patient data meta-analysis and validation

Georg Seemiller1,2, Sabela Lens3,4,5, Elias Laurin Meyer6, Anna Baiges3,4,5, Edilmar Alvarado-Tapias3,7, Elba Llop3,8, Javier Martinez3,8, Philipp Schwabl1,2, Ezequiel Mauro10, Laia Escude3,4,5, Cristina Diez13,12, Luis Ibañez3,12,13, Jose Ignacio Fortea14, Angela Puente14, Marta Abadia15, Ji-Dong Jia16,17, Hitoshi Yoshiji18, Sven Francque19,20,21, Emmanuel Tsochatzis22,23, Jaime Bosch24, Rafael Bañares3,12,13, Gonzalo Crespo2,4,5, Thomas Reiberger1,2, Candid Villanueva3,7, Xavier Forns3,4,5, Juan Carlos Garcia Pagan3,4,5, Mattias Mandorfer1,2,3,4,5, Juan Carlos Garcia Pagan3,4,5, Mattias Mandorfer1,2,3,4,5, Anna Baiges3,4,5, Edilmar Alvarado-Tapias3,7, Elba Llop3,8, Vienna, Vienna, Austria; 3Centro de Investigación Biomédica En Red de Enfermedades Hepáticas y Digestivas (CIBERehd), Instituto de Salud Carlos III, Spain; 4Liver Unit, Hospital Clinic, Universitat de Barcelona, Health Care Provider of the European Reference Network on Rare Liver Disorders (EBN-Liver), Barcelona, Spain; 5August Pi i Sunyer Biomedical Research Institute (IDIBAPS), Universitat de Barcelona, Barcelona, Spain; 1Institute for Medical Statistics, Center for Medical Statistics, Informatics and Intelligent Systems, Medical University Vienna, Vienna, Austria; 7Hospital de Santa Creu and Sant Pau, Autonomous University of Barcelona, Hospital Sant Pau Biomedical Research Institute (IIB Sant Pau), Barcelona, Spain; 8Liver Unit, Hospital Universitario Puerta De Hierro Majadahonda, Universidad Autónoma de Madrid, Madrid, Spain; 9Department of Gastroenterology and Hepatology, Hospital Universitario Ramón y Cajal, IRYCIS, University of Alcalá, Madrid, Spain; 10Liver Unit, Hospital Italiano, Buenos Aires, Argentina, Buenos Aires, Argentina; 11Unidad de Enfermedades Infecciosas/VIH, Hospital General Universitario Gregorio Marañón, Madrid, Spain; 12Instituto de Investigación Sanitaria Gregorio Marañón (ISGMM), Madrid, Spain; 13Liver Unit, Hospital General Universitario Gregorio Marañón, Madrid, Spain; 14Aparato Digestivo/Unidad de Hepatología, Hospital Universitario Marqués de Valdecilla, Santander, Spain; 15Servicio de Aparato Digestivo, Hospital Universitario La Paz, Madrid, Spain; 16Liver Research Center, Beijing Friendship Hospital, Capital Medical University, Beijing, China; 17Beijing Key Laboratory of Translational Medicine on Liver Cirrhosis, Beijing, China; 18Department of Gastroenterology, Nara Medical University, Kashihara, Japan; 19Department of Gastroenterology and Hepatology, Antwerp University Hospital, Antwerp, Belgium; 20Laboratory of Experimental Medicine and Paediatrics (LEMP), Faculty of Medicine and Health Sciences, University of Antwerp, Antwerp, Belgium; 21Translational Sciences in Inflammation and Immunology, University of Antwerp, Antwerp, Belgium; 22UCL Institute for Liver and Digestive Health, Royal Free Hospital and UCL, London, United Kingdom; 23Sheila Sherlock Liver Centre, Royal Free Hospital, London, United Kingdom; 24Department of Visceral Surgery and Medicine, Insehsiptal, University of Bern, Bern, Switzerland
Email: mattias.mandorfer@meduniwien.ac.at

Background and aims: Non-invasive tests (NIT) for clinically significant portal hypertension (CSPH; hepatic venous pressure gradient [HVPG] ≥10mmHg) have predominantly been studied in patients with active HCV-infection, while investigations after HCV-cure are limited and yielded conflicting results. Thus, we conducted an individual patient data meta-analysis.

Method: 418 patients with pre-treatment HVPG ≥6 mmHg who achieved sustained virological response (SVR) and underwent post-treatment HVPG-measurement. Paired data on pre-/post-treatment liver stiffness-measurement (LSM)/platelet count (PLT) was available in 324 patients. The derived non-invasive criteria were validated against the direct end point hepatic decompensation in 470 compensated advanced chronic liver disease (cACLD) patients with SVR.

Results: At a median of 28.4 (IQR: 24–44) weeks post-treatment, HVPG decreased in 79.7%, remained unchanged in 5.5%, and increased in 14.8%; median relative difference: –18.8 (IQR: –32.8–[-4.8]%). Among patients with pre-treatment CSPH (84.4%), HVPG-decreases ≥10% were observed in 208 (64.2%). In cACLD patients with paired NIT, the correlation between LSM/HVPG was significantly stronger post- vs. pre-treatment (Spearman’s p = 0.68 vs. 0.53; P < 0.001), while that of PLT/HVPG remained unchanged. HVPG tended to be lower post- vs. pre-treatment for any given LSM/PLT-value within the range relevant for clinical decision-making, indicating the need for dedicated algorithms after HCV-cure.

A non-linear model combining post-treatment (FU-)LSM/PLT yielded high diagnostic accuracy (AUC: 0.89 [95%CI: 0.85–0.93]) for post-treatment CSPH in cACLD and can be used to estimate the probability of CSPH in an individual patient (Figure). Post-treatment LSM <12 kPa and PLT >150 G/L excluded CSPH (sensitivity: 99.2%), while LSM ≥25 kPa was highly specific (93.6%) for CSPH.
The LSM <12 kPa and PLT >150 G/L criterion was achieved in 185/470 (39.4%) cACLD patients and their 3-year decompensation risk was 0%.

In patients with post-treatment LSM ≥25 kPa (77/470 [16.4%]), 3-year decompensation risk was 14.2%, while it was 1.3% in those (208/470 [44.3%]) meeting none of the above criteria.

Conclusion: NIT can exclude/rule-in CSPH after HCV-cure and predict clinical outcomes. Based on these findings, Bavero VII recommends that patients with LSM <12 kPa and PLT >150 G/L (CSPH excluded; no decompensation risk) may be discharged from portal hypertension surveillance (NIT ± endoscopy), if no co-factors are present, while continuation of carvedilol is warranted in those with LSM ≥25 kPa (CSPH ruled-in; increased decompensation risk). In patients not meeting these criteria, the presence of post-treatment CSPH can be estimated by the provided 3-D plot/nomogram or determined by HVPG-measurement.

G.S. and S.L. contributed equally.

J.C.G.-P. and M.M. share corresponding/last authorship.

OS128
Carvedilol plus Simvastatin modulates systemic inflammation in cirrhosis with portal hypertension and non-response to B-blockers: randomised double-blind study
Edilmar Alvarado-Tapia,1,2, Rosa Montañés,1 Anna Brujats,1 Berta Cuyas,1 María García Guix,1 Claudia Pujol,1 Marianette Murzi-Pulgar,1 Maria Poca,1,2, Isabel Graupera,2,3, Oana Pavel4, Alba Ardevol1, Xavier Torras1,2,5, Paula Buli Roig1, Àngels Escorsell1,2, Silvia Vidal1, Càndid Villanueva1,2, 1Hospital de la Santa Creu i Sant Pau. Biomedical Research Institute Sant Pau (IIB Sant Pau), 08025 Barcelona. Universitat Autònoma de Barcelona, Barcelona, Spain; 2Centro de Investigación Biomédica en Red de Enfermedades Hepáticas y Digestivas (CIBERehd), Madrid, Spain; 3IDIBAPS, Hospital Clinic, Barcelona; 4Hospital Universitario Sant Joan de Reus
Email: cvillanueva@santpau.cat

Background and aims: Carvedilol ( Cv) has greater reducing effect on portal hypertension than propranolol and has antioxidant and anti-inflammatory properties. Statins reduce intrahepatic vascular resistance. Some proinflammatory cytokines such as IL-6 have been involved in the progression of cirrhosis. The effect of Cv on systemic inflammation is unclear and whether combination with simvastatin may modulate this effect in patients with clinically-significant portal hypertension (CSPH).

Method: Patients with cirrhosis and high-risk varices were consecutively included. The hepatic venous pressure gradient (HVPG) was measured before and after propranolol i.v. and non-responders (i.e. HVPG-decrease<20%) were treated with Cv and randomized to receive simvastatin (Sv) (40 mg/d) or placebo (Pb), under double-blind conditions. One month later, the chronic hemodynamic response was assessed. Plasma was obtained in each hemodynamic study to determine proinflammatory cytokines (IL-6, TNF-α, IL-1β, MCP-1) and oxidative stress markers (NO, MDA, FvW).

Results: We included 82 patients, 41 treated with Cv + Sv 41 with Cv + Pb. Baseline clinical and hemodynamic characteristics, and cytokine levels were similar. The inflammatory cytokines IL-6, MCP-1, and MDA decreased significantly (p < 0.05) in both groups, but such a decrease was greater with Cv + Sv (p < 0.01). No significant changes were observed in the other markers. HVPG decreased significantly with both, Cv + Pb (19 ± 3 mmHg to 17 ± 3 mmHg, p < 0.001) and Cv + Sv (19 ± 4 mmHg to 16 ± 4 mmHg, p < 0.001). The decrease was greater with Cv + Sv (−17 ± 12% vs −11 ± 8%, p = 0.05). In patients with chronic decrease in HVPG >20%, IL-6 was significantly higher with Cv + Sb (−30 ± 6 vs −11 ± 2, p = 0.04). Significant correlation was observed between IL-6 and HVPG at follow-up (r = 0.52, p < 0.001).

Conclusion: In patients with cirrhosis and CSPH, carvedilol achieves a significant reduction in proinflammatory cytokines and oxidative stress mediators and improves the portal hypertension. All these changes are significantly increased by adding simvastatin. This suggests that the addition of simvastatin to carvedilol may improve clinical efficacy.

OS129
Non-invasive diagnosis of clinically significant portal hypertension and treatment with non-selective beta-blockers: a new paradigm
Elton Dajti1, Federico Ravaio1, Giovanni Marasco,2
Vanessa Allemani1, Luigi Coleccia4, Alberto Ferrarese5, Caterina Cusumano5, Stefano Gemini5, Amanda Vestito5, Matteo Renzulli2, Rita Golfferi2, Davide Festi4, AntonioColeccia5, 1IRCCS S. Orsola Hospital, Bologna, Italy; Department of Medical and Surgical Sciences, University of Bologna, Bologna, Italy; 2IRCCS S. Orsola Hospital, Bologna, Italy; University of Bologna, Bologna, Italy; 3IRCCS S. Orsola Hospital, Bologna, Italy; University of Bologna, Bologna, Italy; 4University of Bologna, Bologna, Italy; 5Borgo Trento University Hospital of Verona, Verona, Italy
Email: e.dajti17@hotmail.com

Background and aims: Non-selective beta-blockers (NSBB) may reduce the risk of decompensation in patients with clinically significant portal hypertension (CSPH). We aimed to improve the available algorithms for the non-invasive diagnosis of CSPH by evaluating spleen stiffness measurement (SSM) in patients with compensated advanced chronic liver disease (cACLD).

Method: This is a retrospective study in patients with liver stiffness measurement (LSM) ≥10 kPa, no previous decompensation, and available measurements of hepatic venous pressure gradient (HVPG), LSM and SSM referring to our tertiary center in Bologna. The diagnostic algorithms were adequate if negative (NPV) and positive predictive value (PPV) >90% when ruling-out and in CSPH, respectively. These models were validated in a cohort from Verona. The 5-year decompensation rate was reported in each risk group.

Results: One-hundred-ten patients were included in the derivation cohort (CSPH prevalence 58.6%). Available algorithms based on LSM and platelet count (PLT) (LSM ≥25 kPa or LSM ≥20 kPa and PLT <150.000/mm3 for ruling-in CSPH and LSM ≤15 kPa or LSM ≤20 kPa and PLT ≥150.000/mm3 for ruling-out CSPH) were validated. However, a large number of patients (38–59%) remained in the grey zone with indeterminate results for CSPH presence. The application of SSM cut-off 40 kPa and PLT 150.000/mm3 in the “grey zone” patients allowed to significantly reduce the rate of indeterminate
results to 16–23%, maintaining adequate NPV and PPV (above 90%) (Figure 1A). The combined algorithms were validated in an independent (Verona) cohort of eighty-one patients. A nomogram based on LSM, SSM and PLT was developed to predict the individual probability of CSPH presence (AUROC = 0.966) (Figure 1B); the model performed significantly better than the Anticipate model (p < 0.05). During follow-up, 21–63% of first decompensation events occurred in the patients within the “grey zone” according to the models based only on LSM and PLT, whereas almost all decompensation events occurred in the “rule-in” zone defined by the models including SSM.

**Conclusion:** The addition of SSM significantly improves the clinical applicability of the algorithms based on LSM and platelet count for CSPH diagnosis. Our models can be used to non-invasively identify candidates for NSBB treatment and patients at high-risk of decompensation.

**OS130**

**TIPS with versus without variceal embolization for the prevention of variceal rebleeding: a randomized controlled trial**

Yong Lv1, Hui Chen1, Bohan Luo1, Wei Bai1,2, Kai Li1, Zhengyu Wang1,2, Dongdong Xia1,2, Wengang Guo1,2, Xiaomei Li1,2, Jie Yuan1,2, Zhanxin Yin1,2, Daiming Fan1,2, Clinical Research Center for Digestive Diseases and Xijing Hospital of Digestive Diseases, Fourth Military Medical University, Department of Liver Diseases and Digestive Interventional Radiology, Xi’an; 2Xi’an International Medical Center Hospital of Digestive Diseases, Department of Liver Diseases and Digestive Interventional Radiology, Xi’an, China

Email: 13991969930@126.com

**Background and aims:** The role of variceal embolization at the time of transjugular intrahepatic portosystemic shunt (TIPS) creation for the prevention of variceal rebleeding remains controversial. This study aimed to evaluate whether adding variceal embolization to TIPS placement could further reduce the incidence of post-TIPS variceal rebleeding in patients with cirrhosis.

**Method:** From June 2014 to February 2016, 134 consecutive cirrhotic patients who had variceal bleeding in the past 6 weeks were randomly assigned (1:1) to receive TIPS alone (TIPS group, n = 65) or TIPS plus variceal embolization (TIPS + E group, n = 69) to prevent variceal rebleeding. The primary end point was all-cause rebleeding. **Results:** TIPS placement and variceal embolization was successful in all patients. During a median follow-up of 63.1 months in the TIPS group and 61.8 months in the TIPS + E group, the primary end point was met in 21 patients (32.3%) in the TIPS group and 16 patients (23.2%) in the TIPS + E group (p = 0.324). The 2-year cumulative incidence of all-cause rebleeding was not significantly between the two groups (TIPS + E vs TIPS: 11.6% vs 16.5%; HR: 0.69, 95%CI, 0.36 to 1.32; p = 0.264). Neither the incidence of shunt dysfunction (15.9% vs 18.5%, p = 0.875), overt hepatic encephalopathy (36.2% vs 46.2%, p = 0.322), death (34.8% vs 38.5%, p = 0.807) nor other adverse events was significantly different between the two groups.

**Conclusion:** In patients with cirrhosis, adding variceal embolization to TIPS did not confer further benefit for the prevention of variceal rebleeding. Our study did not support concomitant variceal embolization during TIPS for the prevention of variceal rebleeding.
Background and aims: While ascites is the most frequent first decompensating event in cirrhosis, the clinical course of patients with ascites as the index decompensation is not well defined, in particular regarding the occurrence of further decompensation. The aim of this multicenter study was to investigate (i) the clinical course and (ii) the incidence and type of further decompensation in patients with isolated ascites as the first decompensating event.

Method: 622 patients with cirrhosis presenting with ascites (grade II or III) as the single index decompensating event at the University Hospital of Padova (Italy) or the Vienna General Hospital (Austria) between 2003 and 2021 were included. Patients with concomitant decompensating event (s) were excluded. Death and transplantation were considered as competing risks.

Results: Mean age was 57 ± 11 years and most patients were male (n = 423, 68%). 323 (52%) patients presented with grade II and 299 (48%) with grade III ascites. Median Child score was 8 (IQR: 7–10) and mean MELD was 15 ± 6.

During a median follow-up period of 82 months, 350 (56%) patients progressed to further decompensation: refractory ascites (n = 204; 33%), hepatic encephalopathy (n = 183; 29%), spontaneous bacterial peritonitis (n = 105; 17%), HRS-AKI (n = 81; 13%) and variceal bleeding (n = 54.9%). Median time to further decompensation was 27 months. Variceal bleeding as an isolated further decompensation was rare (n = 18; 3%), while non-bleeding further decompensation (n = 161; 26%) and ≥2 further decompensation events (n = 171; 27%) were common. Further decompensation occurred more frequently in patients with grade III ascites at index decompensation (75% vs. 33% in grade II ascites; p < 0.001; A).

Stratifying patients according to MELD revealed patients with distinct risks of further decompensation after 5 years: <10: 38% vs. 10–14: 56% vs. ≥15: 67% (p < 0.001; B). In patients with grade II ascites, MELD<15 identified patients with intermediate risks (<10: 27%; 10–14: 34%; p = 0.510), whereas MELD≥15 identified patients with high risks for further decompensation after 5 years (53%; p < 0.001).

Median transplant-free survival was 65 months. Higher MELD translated into an increased risk of liver-related death. Patients with ascites grade II at index decompensation had increased risk of liver-related mortality in case of impaired liver function (C). In patients with ascites grade III at index decompensation, the incidence of further decompensation and liver-related mortality was similarly high, regardless of liver function (i.e., MELD; D).

Conclusion: Further decompensation is frequent in patients with ascites as a single index decompensation and only rarely due to bleeding. Since further decompensation depends on ascites severity and MELD at index decompensation, risk stratification must consider both initial grade of ascites and hepatic function.
spenomegaly reported in 116 patients (9.6%). PBC and PSC overlap syndromes were observed in 9.7% and 7.5% of the cohort. Treatment at baseline included the use of prednisone in 83.5% of patients (1010/1210). 22 patients developed HCC during follow-up (22/1210, 1.8%). Cumulative incidence of HCC of the whole cohort was 0.7% (0.3–1.4) at 5 and 10-year (95% CI), 2.6% (1.4–4.4) at 20 years and 5.7% (2.5–10.9) at 30-years of follow-up. The risk of HCC after cirrhosis development increases proportionally to years from the onset of the disease. Age≥40 years (HR 5.99, p = 0.02), BMI≥30 kg/m² (HR 4.11, p = 0.02), splenomegaly (HR 4.03, p = 0.03), and PSC overlap syndrome (HR 8.63, p < 0.001) resulted independent risk factors for HCC development at multivariate analysis balanced by sex. No association was observed between tumor formation and type of treatment, nor activity on liver histology resulted to have any prognostic value.

Conclusion: The incidence of HCC in AIH is lower than reported to other chronic liver diseases even after cirrhosis development. Age more than 40 years, obesity, splenomegaly and PSC variant syndrome represent risk factors for HCC development, but further studies are needed to identify predictive tools for stratification of the at-risk population.

Figure: Development of HCC after diagnosis of AIH and after cirrhosis development in AIH.

OS134

Quality of life outcomes in patients with primary biliary cholangitis treated with setanaxib: post-hoc results from a phase 2 randomised, placebo-controlled trial

David Jones1, Marco Carbone2,°, Pietro Inverni2,°, Frederik Nevens3, Mark G. Swain4, Philippe Wiesel5, Cynthia Levy6, 1Newcastle University Medical School, Newcastle upon Tyne, United Kingdom; 2University of Milano-Bicocca, Division of Gastroenterology, Centre for Autoimmune Liver Diseases, Department of Medicine and Surgery, Monza, Italy; 3San Gerardo Hospital, European Reference Network on Hepatological Diseases (ERN RARE-LIVER), Monza, Italy; 4University Hospital KU Leuven, Department of Gastroenterology and Hepatology, Leuven, Belgium; 5University of Calgary, Calgary, Canada; 6Genkyotex, Geneva, Switzerland; 7University of Miami, Schiff Center for Liver Diseases, United States

Background and aims: Primary biliary cholangitis (PBC) is an autoimmune cholestatic liver disease. 1 Fatigue substantially impacts quality of life of patients with PBC, and remains an unmet need with currently available treatments. 2 We present quality of life results from a phase 2, double-blind, randomised trial of setanaxib in patients with PBC.

Method: This trial (NCT03226067) randomised patients with PBC and inadequate response or intolerance to ursodeoxycholic acid (UDCA) at baseline (serum alkaline phosphatase and gamma-glutamyl transferase ≥1.5× upper limit of normal) 1:1:1 to setanaxib 400 mg once/twice daily (OD/BID) or placebo for 24 weeks. 3 Quality of life was assessed using the PBC-40 questionnaire (reported as mean ± standard deviation) scores. Patients from the intention-to-treat (ITT) population were stratified post-hoc by baseline fatigue score (mild, moderate or severe) using published PBC-40 fatigue domain cut-offs. 4 Moderate and severe patients were grouped. Correlations between change in fatigue and quality of life from baseline were made.

Results: Of 111 patients (placebo: 37; setanaxib 400 mg OD: 38; setanaxib 400 mg BID: 36), 92 had mild and 19 had moderate-to-severe fatigue at baseline. The ITT group had a baseline fatigue score of 17.2 (11.3) (placebo: 17.4 [12.1]; setanaxib 400 mg OD: 15.7 [10.7]; setanaxib 400 mg BID: 18.5 [11.3]). The moderate-to-severe subgroup had higher PBC-40 social, emotional and cognitive domain scores vs the mild subgroup (social: 30.6 [8.8] vs 19.1 [8.0]; emotional: 11.3 [2.8] vs 6.8 [3.1]; cognitive: 18.3 [6.9] vs 11.3 [5.1]). At Week 24, patients treated with setanaxib 400 mg BID had greater reductions from baseline in mean fatigue scores vs patients treated with placebo or setanaxib 400 mg OD (Figure). Similar observations were made in
social, emotional, cognitive and symptom domains. Patients with moderate-to-severe fatigue had larger changes in mean fatigue scores from baseline at Week 24 vs patients with mild fatigue; these changes were greatest amongst setanaxib 400 mg BID patients (−11.0 [11.5; n = 5]; vs setanaxib 400 mg OD: −7.5 [5.3; n = 4], placebo: 0.1 [5.7; n = 7]). Fewer patients reported “most of the time” or “always” for all PBC-40 fatigue items at Week 24 vs baseline. Improvements in fatigue from baseline at Week 24 in patients with moderate-to-severe fatigue correlated with improved social, emotional, symptom (all r = 0.5) and cognitive (r = 0.4) measures.

Figure: Summary of absolute score changes from baseline to Week 24 of the PBC-40 domains.

Conclusion: Setanaxib 400 mg BID, in addition to UDCA, is a promising treatment for reducing fatigue in patients with PBC and enhancing quality of life by improving social, emotional and cognitive function.

References

OS135
Quantitative magnetic resonance cholangiopancreatography outperforms Mayo risk score in predicting clinical outcomes in primary sclerosing cholangitis
Raj Vuppalanchi, Vijay Are, Sofia Mouchti, Carla Kettler, Mark Gromski, Sarah Finnegan, Fatih Akisik.
*Indiana University School of Medicine, Indianapolis, *Perspectum Ltd, Oxford, United Kingdom
Email: sarah.finnegan@perspectum.com

Background and aims: Magnetic resonance cholangiopancreatography (MRCP) is a non-invasive imaging technique commonly used to evaluate biliary diseases. Despite its widespread use, MRCP relies on subjective assessments, lacks quantitative metrics and cannot predict the onset of liver-related events. Quantitative MRCP (MRCP™) is a novel technique that automatically segments biliary anatomy and provides quantitative biliary tree metrics. This study sought to understand the utility of MRCP in predicting clinical outcomes for primary sclerosing cholangitis (PSC).

Method: Patients with PSC underwent standardized MRCP imaging post-processed with MRCP+ software, which, via artificial intelligence (AI) driven pathfinding algorithms, enhanced tubular biliary structures to quantify biliary tree volume and dilated and strictured regions of the biliary tree. The duration (in years) between the MRCP scan and clinical event (liver transplantation or death) was calculated. Survival analysis was performed, and a stepwise Cox regression was used to investigate the optimal combination of MRCP+ metrics for predicting clinical outcomes. The resulting risk score was compared to the Mayo risk score using the Akaike Information Criterion (AIC) and expressed as a hazard ratio (HR).

Results: In this retrospective study of 149 PSC patients [32% male; 83% Caucasian; median age 47 years (31.0–61.2)], 29 patients reached clinical outcomes over the course of the study (18 underwent liver transplantation and 11 died). Eight quantitative MRCP+ metrics (M) and total bilirubin (B) were associated with the probability of a clinical event. When combined as a risk score, the overall discriminative performance of the MRCP+ composite biomarker (M+B) was excellent for predicting clinical outcomes with an AUC of 0.87 (95% 0.81, 0.94) and a hazard ratio (HR) of 21.1. (95% 6.4, 70.1) This was superior to the Mayo risk score with AUC of 79 (95% 0.69, 0.89) and HR of 7.2 (95% 3.24, 16.17).

Figure 1: A standard MRCP image (top left), novel MRCP+ quantitative image (bottom left). Kaplan-Meier curves when adjusting for the composite biomarker M+B risk classifier (middle) binary Mayo risk score classified with "intermediate" is redefined as "low" (right) to predict a clinical event within 3-years of entering the study.

Figure: (abstract: OS135)

Journal of Hepatology 2022 vol. 77(S1) | S1–S118
ORAL PRESENTATIONS

Conclusion: A composite score of MRCP+ metrics and total bilirubin outperformed Mayo risk score for identifying patients with PSC who were at the highest risk of liver failure and death.

OS136 Radiomics-based model for outcome prediction in primary sclerosing cholangitis
Laura Cristoferi1,2,3, Marco Porta4, Davide Bernasconi3, Leonardo Filippo5, Giacomo Mulinaricci1,2, Andrea Palermo1,2, Alessio Gerussi1,2, Miki Scaravaglio1,2, Camilla Gallo1,2, Eliana Stucchi1,2, Cesare Maino4, Davide Ippolito4, Daphne D’Amato4, Carlos Ferreira7, Marija Mavar-Haramija7, Rajarshi Banerjee7, Laura Antolini3, Maria Grazia Valsecchi5, Stefano Fagiuoli5, Pietro Invernizzi1,2, Marco Carboni1,2, Division of Gastroenterology, Center for Autoimmune Liver Disease, Department of Medicine and Surgery-University of Milano Bicocca, Monza, Italy; 1European Reference Network on Hepatological Diseases (ERN RARE-LIVER), San Gerardo Hospital, ASST Monza, Monza, Italy; 2Biocca Bioinformatics Biostatistics and Bioimaging Centre, Department of Medicine and Surgery-University of Milano Bicocca, Monza, Italy; 3Diagnostic Radiology, San Gerardo Hospital, ASST Monza, Monza, Italy; 4Gastroenterology Hepatology and Transplantation Unit, ASST Papa Giovanni XXIII, Bergamo, Italy; 5Gastroenterology Unit, Città della Salute e della Scienza, Turin, Italy; 6Perspectum Ltd., Oxford, United Kingdom
Email: l.cristoferi@campus.unimib.it

Background and aims: Magnetic resonance cholangiopancreatography (MRCP) is the gold standard for diagnosis and follow-up of patients with primary sclerosing cholangitis (PSC). The semi-quantitative MRCP-derived ANALI score, while performant in risk stratification, has poor-to-moderate inter-reader agreement. We aimed to evaluate the prognostic performance of novel quantitative MRCP in PSC.

Method: This is a retrospective study of PSC patients with at least one MRCP available from 2012 to 2019. Images have been analysed using MRCP+ software (Perspectum Ltd, Oxford) which, using AI-driven pathfinding algorithms to enhance biliary structures, provides quantitative metrics of the bile ducts (number, length and severity of strictures and dilations, and biliary tree volume). The prognostic value of radiomic biomarkers has been assessed towards both soft (hepatic decompensation, variceal bleeding, bacterial cholangitis, and hepatobiliary cancer) and hard end points (death or liver transplantation [LT]). Left truncated Cox regression model was used to account for MRCPs performed later than PSC diagnosis. The multivariate model was internally validated using k-fold cross-validation.

Results: 115 PSC patients with MRCP were evaluated; 90 MRCP passed the quality control. Median age was 41 (IQR 26–51) years, 61% were male, with a follow-up from MRCP to event/censoring of 242 patient-years. An adverse outcome occurred in 28 (25%) patients (8 LT, 3 liver-related death, 5 liver decompensation, 10 bacterial cholangitis, 2 cholangiocarcinoma). Univariate analysis showed a good prognostic performance of all radiomics features evaluated. At multivariable analysis, adjusted for age and sex, the number of strictures and the spleen length were independently associated with the occurrence of adverse event with a HR of 1.06 (per unit, CI 95% 1.03–1.09, p = 0.0001) and 1.34 (per cm, CI 95% 1.11–1.6, p = 0.002), respectively and a C-statistic of 0.81. The model was internally validated and outperformed the ANALI score in our cohort (C-statistic of 0.72 vs 0.6). The radiomics-based model, using the mean value as cut-off (–1), enabled risk stratification of PSC patients (Fig).

Conclusion: A radiomics-based model, which includes the number of strictures and the spleen length, can identify PSC patients at higher risk of adverse outcome and outperforms the available radiological scores. MRCP+ features represent a novel biomarker for disease monitoring and a potential surrogate end point for clinical trials.

OS137 Critical shortfalls in the management of PBC: results of the first nationwide, population-based study of care delivery across the U.K.
Nadir Abbas1,2, Rachel Smith3, Steve Flack4, Richard Aspinall5, Rebecca L. Jones6, Joanna Leithead7, Douglas Thorburn7, Conor Brannib8, Michael Heneghan9, Andrew Yeoman1,10, Collette Thain11, Chris Mitchell12, Robert Mitchell-Then12, David Jones13, Palak Trivedi1,2,14, George Mells3, Laith Al-Rubaity15,16, and UK-PBC Consortium, 1University of Southampton, United Kingdom; 2Cambridge University Hospitals NHS Foundation Trust, United Kingdom; 3University of Cambridge, United Kingdom; 4Leeds Teaching Hospitals NHS Trust, United Kingdom; 5Royal Free Hospital, United Kingdom; 6Portsmouth Hospitals NHS Trust, United Kingdom; 7Forth Valley Royal Hospital, United Kingdom; 8Royal Free Hospital, United Kingdom; 9Belfast Health and Social Care Trust, Northern Ireland; 10Institute of Liver Studies, King’s College Hospital, United Kingdom; 11Aneurin Bevan University Health Board, United Kingdom; 12PBC Foundation, United Kingdom; 13Newcastle University, United Kingdom; 14University of Birmingham, Institute of Biomedical Research, United Kingdom; 15St Mark’s Hospital and Academic Institute, United Kingdom; 16Imperial College School of Medicine, United Kingdom; 17UK-PBC Consortium, United Kingdom
Email: nadir.abbas@uhb.nhs.uk

Background and aims: Herein, we present the first population-based, nationwide evaluation of healthcare delivery in primary biliary cholangitis (PBC) since publication of the European (EASL) and British guidelines (BSG). Our aim was to assess adherence to guideline recommendations and identify gaps in service provision.

Method: This was a cross-sectional study conducted between 01/21 and 01/22. All 154 hospital boards across England, Scotland, Wales, and Northern Ireland were invited to participate. Data was accrued through the REDcapTM platform, accumulating parameters relating diagnosis, treatment pathways, symptoms, risk stratification and clinical end points.

Results: In entirety, data was returned from 120 hospital boards, with data capture from 8461 pts across the UK. The majority (n = 7084; 83%) tested positive for anti-mitochondrial antibodies (AMA, Figure), with 2718 (32%) of the latter subgroup also undergoing liver biopsies. Ursodeoxycholic acid (UDCA) was used as first-line treatment in 7444
patients (88%) but sub-optimally dosed (<13 mg/kg/day) in 1732 (21.5%). Only 197 pts who were under-dosed were documented to have intolerance to higher dosing. Of individuals who were not taking UDCA, only 214 (23%) were referred for alternative/second-line therapy. Of pts taking UDCA for >12 months (n = 7007), 5475 (78%) and 1532 (22%) were classified as low-risk and high risk, respectively, by the contributing hospital. However, on applying the POISE criteria, 663 and 285 patients could be reclassified as ‘low-risk and high risk’ respectively. Among all who were deemed high-risk with regards disease progression (n = 2476; 29%), 1228 (49.5%) commenced second-line therapy (inc. 551 obeticholic acid; 468 bezafibrate; 68 fenofibrate; 76 combination therapy) and 35 referred directly to a transplant centre. In all, 1831 pts were identified as having cirrhosis by the contributing hospital. However, on applying the POISE criteria, 1112 caused liver injury. T cell transfer in ATI-1112-treated mice failed to eliminate ECs, even from post-mitotic HCs becoming nuclear and HC distribution in hepatocytes (HCs) that, divided or not, disappeared from the liver of ATI-1112- and T cell-treated animals. While inhibiting HBV replication, neither ATI-1428 nor ATI-1645 was assessed at autopsy (d7 after T cell transfer). ATI-1645 was profiled in HepAD38 cells, HBV-infected HepG2-NTCP cells, and HBV II CAM causing abnormal EC accumulation) at 50 mg/kg every day (QD) for 16 days. Antiviral potency, drug- or Tcell-induced liver injury and HBcAg distribution in hepatocytes (HCs) that, divided or not, were assessed at autopsy (d7 after T cell transfer). ATI-1645 was profiled in HepAD38 cells, HBV-infected HepG2-NTCP cells, and HBV Tg mice. Different from other CAMs, ATI-1428 induced no abnormal accumulation of hepatitis B core antigen (HBcAg)-expressing empty capsids (EC) in the hepatocellular cytoplasm. Herein, we extend our understanding of the functional consequences of EC accumulation in the presence of HBcAg-specific CD8 T cells and identify another 4th-generation class II CAM (ATI-1645) that may foster EC degradation.

Method: A genome-wide CRISPR/Cas9 screen was performed in permissive human cell lines harboring newly developed subgenomic HEV replicons allowing for positive and negative selection, followed by next-generation sequencing and bioinformatic analyses. Candidates were validated by siRNA-mediated gene silencing and CRISPR/Cas9-mediated gene knockout in cells transduced with subgenomic HEV replicons or infected with cell culture-derived HEV.

Results: The newly developed replicons and a library of 120,000 unique guide RNAs were employed in two separate screens, identifying 20 top host factor candidates. Validation yielded five host factors, including GFB1, which had been identified previously by a directed approach, and the Ras-related early endosomal protein Rab5A. The expression level and functional activity of Rab5A and of well-characterized mutants thereof were found to modulate HEV RNA replication. Colocalization studies revealed close proximity to the HEV replicase of Rab5A and other endosomal components.

Conclusion: We describe an innovative approach exploiting CRISPR/ Cas9 to identify host factors of a noncytolytic virus. Future studies shall address the mechanisms by which Rab5A modulates HEV RNA replication and define the role of early endosomes in the establishment of a functional replication complex. Altogether, this work yields new insights into the HEV life cycle and the virus-host interactions required for productive infection.

OS139 Novel ultra-potent capsid assembly modulators prevent abnormal accumulation of empty capsids and associated T-cell mediated liver injury in a mouse model of hepatitis B virus infection

Romano Di Fabio1,2, Matteo Iannacone1,4,5, Leda Bencheva1, Matteo Conti1, Katherine Squires1, Mark Lockwood1, Raffaele De Francesco1,9, Luca Guidotti4,10, Promidis, Italy; 2RBM Science Park, Pomezia, Rome, Italy; 3IRCCS San Raffaele Scientific Institute, Division of Immunology, Transplantation and Infectious Diseases, Milan, Italy; 4IRCCS San Raffaele Scientific Institute, Experimental Imaging Center, Milan, Italy; 5Vita-Salute San Raffaele University, Milan, Italy; 6INGM, National Institute of Molecular Genetics “Romeo ed Enrica Invernizzi,” Milan, Italy; 7Antios Therapeutics, United States; 8INGM, National Institute of Molecular Genetics, Italy; 9Università degli Studi di Milano, Department of Pharmacological and Molecular Sciences, Milan, Italy; 10Vita-Salute San Raffaele University, Milan, Italy

Email: guidotti.luca@hsr.it

Background and aims: ATI-1428 is a sub-nM active class II capsid assembly modulator (CAM) that safely and durably blocks hepatitis B virus (HBV) replication in immunocompetent transgenic (HBV Tg) mice. Different from other CAMs, ATI-1428 induced no in vivo abnormal accumulation of hepatitis B core antigen (HBcAg)-expressing empty capsids (EC) in the hepatocellular cytoplasm. Herein, we extend our understanding of the functional consequences of EC accumulation in the presence of HBcAg-specific CD8 T cells and identify another 4th-generation class II CAM (ATI-1645) that may foster EC degradation.

Method: HBV Tg mice were treated with ATI-1428 or ATI-1112 (a class II CAM causing abnormal EC accumulation) at 50 mg/kg every day (QD) for 16 days. Antiviral potency, drug- or T-cell-induced liver injury and HBcAg distribution in hepatocytes (HCs) that, divided or not, were assessed at autopsy (d7 after T cell transfer). ATI-1645 was profiled in HepAD38 cells, HBV-infected HepG2-NTCP cells, and HBV Tg mice.

Results: While inhibiting HBV replication, neither ATI-1428 nor ATI-1112 caused liver injury. T cell transfer in ATI-1112-treated mice induced higher serum alanine aminotransferase peak levels and failed to eliminate ECs, even from post-mitotic HCs becoming nuclear HBcAg-negative (see Figure and PMID: 8057429). By contrast, ECs disappeared from the liver of ATI-1428- and T cell-treated animals. ATI-1645 showed sub-nM EC50/EC90 potency profiles with low nM activity against covalently closed circular DNA establishment.
Pharmacokinetic (PK)/pharmacodynamic analyses and safety/efficacy studies in HBV Tg mice indicated that 1645 possesses excellent PK and anti-HBV activity. 28-day ATI-1645 treatment (50 mg/kg QD) cleared ECs from the cytoplasm of most HCs in the absence of any drug- or immune-mediated liver injury.

Conclusion: ATI-1112-related abnormal accumulation of cytoplasmic ECs sensitized HCs to T cell-mediated killing and allowed these particles to survive in resting and post-mitotic HCs no longer replicating HBV. This suggests that CAMs fostering an EC-accumulating phenotype may generate targets of inadequate immunopathology. Conversely, the lack of cytoplasmic EC accumulation that typifies the in vivo behavior of ATI-1428 or ATI-1645 should not interfere with productive T cell-mediated viral clearance. The subsequent characterization of 1645 as an ultra-potent HBV inhibitor that may induce cytoplasmic EC degradation makes it a promising candidate for clinical development.

OS140
Identification of cyclin L1 as a hepatitis B virus host factor regulating viral transcription
Collins Oduor Owino1, Yi Lin Gian2, Pauline AW Poh Kim1, Nivrithi Ganesh1, Balakrishnan Chakrapani Narmada2, Giridharan Periyasamy2, Pablo Bifani3, Ramanuj Dasgupta1, 1Genome Institute of Singapore (GIS), Singapore, Singapore; 2Experimental Drug Development Centre, Singapore, Singapore; 3Department of Microbiology and Immunology (MD4), Singapore, Singapore
Email: dasgupta@gis.a-star.edu.sg

Background and aims: HBV remains a global public health threat, with over 250 million people chronically infected and about 800,000 deaths reported annually. Even though much work has been done to understand HBV pathogenesis, how the virus manipulates the host cell machinery remains underexplored. In this study we aimed to identify novel host factors that affect HBV replication and gene expression. We describe the role of cyclin L1 (CCNL1), a non-canonical cyclin with transcriptional regulatory functions as a novel host cell factor in the control of HBV transcription.

Method: We employed whole transcriptome analysis of HBV infected primary human hepatocytes (PHH), as well as reverse genetics to identify and validate the role of CCNL1 during HBV replication. Using RNAi and ectopic expression models, we studied the function of cyclin L1 on HBV replication in hepatoma cells and PHH. We also analyzed the effect of CCNL1 knockdown on the production and stability of HBV RNAs. Using RNA immunoprecipitation (RIP), chromatin immunoprecipitation (ChIP), and immunoprecipitation (IP) techniques, we evaluated the interaction between cyclin L1 and HBV RNAs as well as HBx and HBc. Lastly, we explored the expression profiles of cyclin L1 in chronic HBV patient cohorts and publicly available microarray datasets GSE83148 and GSE52752.

Results: Knockdown of cyclin L1 resulted in a remarkable reduction of HBV gene expression in both hepatoma cells (HepAD38.7 and HepG2NTCP) and PHH. We observed a remarkable reduction in the levels of HBV surface and e antigens, pre-genomic RNA, and extracellular HBV DNA. Interestingly, overexpression of CCNL1 resulted in enhanced HBV gene expression with a significant increase in the viral transcripts, thus, corroborating its pro-viral effect. Furthermore, loss of function of cyclin L1 resulted in reduced levels...
OS141
Liver-resident T cell PD-1 correlates with intrahepatic HBV-DNA and is reduced following prolonged antiviral therapy

Mireia García-López1, Laura J. Pallett2, Sergio Rodríguez-Tajes1, Ernest Belmonte2, Thais Leoni1, Esther García-Pras1, Sabela Lenz1, Zoe Mariño1, Concepción Bartres1, Ariadna Rando-Segura1, Francisco Rodríguez-Frias4, Xavier Forns1, Mala Maini2, Antoni Clotet3,4,5.

Background and aims: T cells with a tissue-resident memory (TRM) phenotype were observed in the liver of patients with hepatitis B virus (HBV) infection and is reduced following prolonged antiviral therapy. Here, we report that hepatic stellate cells (HSCs) with collagen VI significantly induced an expression of ECM-associated leading-edge genes comprised collagen VI, which impairs viral transcription suggesting a pro-viral role of collagen VI. Myofibrobasts account for the majority of collagen I deposited into the ECM. We found that treatment of hepatic stellate cells (HSCs) with collagen VI significantly induced an expression of ECM-associated leading-edge genes comprised collagen VI, which impairs viral transcription suggesting a pro-viral role of collagen VI.

Results:
Our data revealed a strong HBV-induced dysregulation of signalling involved in extra-cellular matrix (ECM) and cell cycle. ECM-associated leading-edge genes comprised collagen VI, which was upregulated in HBV-infected hepatocytes. Interestingly, silencing of COL6A1 impairs viral transcription suggesting a pro-viral role of collagen VI. Myofibroblasts account for the majority of collagen I deposited into the ECM. We found that treatment of hepatic stellate cells (HSCs) with collagen VI significantly induced an expression of ECM-associated leading-edge genes comprised collagen VI.

Conclusion: We identified the phospho-proteomic landscape of HBV infection revealed novel mechanisms for the regulation of viral transcription and fibroblastic stellate cell activation.

Alessia Virzi1,2,3, Zakaria Boulahktou2,3,4, Sarah Durand1,2,4, Emanuele Felli1,2,4,5, Patrick Pessaux1,2,4,5, Oliver Poppel1,2,4,5, Evelyn Ramberger1,6, Philipp Mertins1,6, Eloï Verrier1,2,3, Catherine Schuster1,2,4, Thomas Baumann2,4,7, Joaichim Lupberger2,3, 1Inserm U1110, Strasbourg, France; 2Université de Strasbourg, Strasbourg, France; 3Inserm U1110, Strasbourg, France; 4Institut Hospitalo-Universitaire, Pôle Hépato-digestif, Nouvel Hôpital Civil, Strasbourg, France; 5Max Delbrück Center for Molecular Medicine, Berlin, Germany; 6Berlin Institute of Health, Berlin, Germany; 7Institut universitaire de France (IUF), Paris, France.

Email: joachim.lupberger@unistra.fr

OS142
Phospho-proteomic analysis of HBV infection revealed novel mechanisms for the regulation of viral transcription and fibroblastic stellate cell activation

Zoe Mariño1, Concepción Bartres1, Ariadna Rando-Segura2, Francisco Rodríguez-Frias2, Xavier Forns1, Mala Maini2, Antoni Clotet3,4,5,6.

Background and aims: Chronic hepatitis B virus (HBV) pathological course is characterized by the dysregulation of fibrogenic and oncosgenic signalling. Considering the lack of efficient anti-fibrotic therapies and treatment to eradicate cccDNA, the understanding of regulatory pathways is urgently needed. To identify the potential drivers of this dysregulation, we studied HBV-induced signalling in HBV infection models.

Method: Proteomic and phospho-proteomic analysis of HBV-infected HepG2-NTCP were performed using liquid chromatography-mass spectrometry. The deregulated signalling pathways were examined by gene set enrichment analysis and validated in primary human hepatocytes. Perturbation studies, trans-dominant phospho-dead/mimetic mutagenesis and ex vivo experiment were performed to validate the results.

Results: Our data revealed a strong HBV-induced dysregulation of signalling involved in extra-cellular matrix (ECM) and cell cycle. ECM-associated leading-edge genes comprised collagen VI, which was upregulated in HBV-infected hepatocytes. Interestingly, silencing of COL6A1 impairs viral transcription suggesting a pro-viral role of collagen VI. Myofibroblasts account for the majority of collagen I deposited into the ECM. We found that treatment of hepatic stellate cells (HSCs) with collagen VI significantly induced an expression of ECM-associated leading-edge genes comprised collagen VI.

Conclusion: We identified the phospho-proteomic landscape of HBV-host interaction which serves as a resource for the identification of novel drivers regulating viral life cycle and pathogenesis. We revealed a previously unrecognized role of collagen VI and linker histones in HBV replication with potential impact on liver fibrosis progression and cccDNA transcription, respectively.
ORAL PRESENTATIONS

OS143
CD4 T cell immunity to HEV-infection is characterized by sustained capsid-specific responses that correlate with neutralizing antibodies

Benedikt Csernalabics1, Stefan Marinescu1, Lars Maurer2, Katharina Wild1, Katharina Zoldan1, Marcus Panning3, Philipp Reuken4, Tony Bruns5, Christoph Neumann-Haefelin1, Bertram Bengsch1, Maike Hofmann1, Robert Thimme1, Viet Loan Dao Thi2, Tobias Böttler1, 1University Hospital Freiburg, Department of Medicine II, Freiburg, Germany; 2Heidelberg University Hospital, Department of Infection Diseases and Virology, Heidelberg, Germany; 3University Hospital Freiburg, Institute of Virology, Freiburg, Germany; 4Jena University Hospital, Department of Medicine IV, Jena; 5University Hospital RWTH Aachen, Department of Medicine III, Aachen, Germany

Email: benedikt.csernalabics@uniklinik-freiburg.de

Background and aims: CD4 T cells are key protagonists in shaping an antiviral immune response. However, there are only limited insights into their specificity and distinction in the context of a hepatitis E Virus (HEV) infection. Therefore, we aim to characterize the specificity, phenotype and differentiation of CD4 T cells targeting different epitopes of the HEV polyprotein and their correlation with neutralizing antibodies targeting hepatitis E virions.

Method: HEV-specific CD4 T cells targeting different HEV-specific CD4 T cell epitopes from the viral polyprotein were identified by intracellular cytokine staining in 7 acutely infected and 33 resolved patients. Surface markers, relevant costimulatory receptors and transcription factors were analysed by using HEV-specific HLA-DRB1*01:01 and *04:01 tetramers. Additionally, neutralizing antibodies targeting naked (nHEV) and quasi-enveloped (eHEV) virions were determined (n = 72).

Results: Robust and multi-specific CD4 T cell responses were identified against the viral capsid and non-structural polyprotein (NSP). In contrast, only few phosphoprotein-specific responses were detectable. Overall, the virus-specific CD4+ T cell response was stronger and broader in acutely infected versus resolved patients. Moreover, a switch from a highly activated Th1 and Th2 cell phenotype towards a heterogeneous memory population was observed after viral elimination. Noteworthy, the presence of a capsid-specific IFN-γ or IL-21-producing CD4 T cell response positively correlated with IgG- and neutralizing antibody titers against nHEV.

Conclusion: Collectively, our results reveal important novel insights into the HEV- specific CD4 T cell response by demonstrating a solid maintenance of capsid- and NSP-specific CD4 T cell responses with the formation of a robust HEV-specific memory compartment. They also reveal a clear immunodominance with phosphoprotein being less immunogenic.

Sunday 26 June

Hepatitis B clinical aspects

OS144
Metabolic dysfunction-associated fatty liver disease subgroups and risk of hepatocellular carcinoma and mortality in patients with chronic viral hepatitis

Mi Na Kim1, Kyungdo Han2, Juhwan Yoo3, Seong Gyu Hwang4, Sang Hoon Ahn4, 1CHA Bundang Medical Center, CHA University School of Medicine, Department of Internal Medicine, Seongnam, Korea, Rep. of South; 2Soongsil University, Department of Statistics and Actuarial Science, Seoul, Korea, Rep. of South; 4Yonsei University College of Medicine, Department of Internal Medicine, Seoul, Korea, Rep. of South

Email: ahnsh@yuhs.ac

Background and aims: Metabolic dysfunction-associated fatty liver disease (MAFLD) is a recently proposed concept for fatty liver disease. However, heterogeneous disease severity and prognosis might exist even among patients with the same disease category of MAFLD. We investigated the risk stratification of long-term outcomes according to MAFLD subgroups based on diagnostic criteria in patients with chronic viral hepatitis using a nationwide cohort.

Method: We included 63,233 chronic hepatitis B and chronic hepatitis C patients who underwent health examinations in 2009. Hepatic steatosis was defined as a fatty liver index ≥60. MAFLD was defined as the presence of hepatic steatosis with any of the following three conditions, overweight/obesity (body mass index ≥23 kg/m²), diabetes, two or more metabolic dysregulation. The primary end points of this study were incident hepatocellular carcinoma (HCC) and all-cause mortality.

Results: The prevalence of MAFLD was 14.1% (n = 8,896). During a median 8.4-year follow-up, we documented 3,732 HCC cases and 4,778 deaths. Compared to patients with no MAFLD (n = 54,377), the risk of HCC and mortality was significantly higher in patients with MAFLD (adjusted hazard ratio [aHR] = 1.34, 95% confidence interval [CI] = 1.23–1.46) for HCC; aHR = 1.26, 95% CI = 1.17–1.36 for mortality). Among patients with MAFLD, 687 HCCs and 861 deaths were documented. The prevalence of diabetes among patients with MAFLD was 25.9% (n = 2,303). The risk of HCC and mortality was significantly higher in patients with diabetes (aHR = 1.36, 95% CI = 1.16–1.59 for HCC; aHR = 1.72 95% CI = 1.50–1.97 for mortality) compared to patients with no diabetes, among patients with MAFLD. When we stratified patients with MAFLD according to the other criteria (overweight/obesity or metabolic dysregulations), risk of HCC and mortality was not different across the groups (all p > 0.05).

Conclusion: Concurrent MAFLD was associated with higher risk of HCC and mortality in patients with chronic viral hepatitis. Our results suggest that diabetes can stratify the risk of HCC and mortality in patients with chronic viral hepatitis and concurrent MAFLD.
hepatitis B vaccination. The magnitude of the immune response to HBV vaccination can be measured by serum levels of anti-HBs, persistence and durability, which is believed to be dependent upon the induced peak levels. PROTECT was a double-blind, randomized, Phase 3 study to evaluate immunogenicity and safety of a 3-antigen HBV vaccine (3A-HBV, manufactured by VBI Vaccines) and a single-antigen HBV vaccine (1A-HBV, Engerix-B®). Three doses of vaccine were administered IM at Days 1, 28, and 168. Seroprotection rate (SPR-% of subjects achieving anti-HBs ≥10 mIU/ml) and geometric mean concentration (GMC) of anti-HBs were evaluated for 12 months. Following the completion of PROTECT, this follow-up investigator-initiated study of PROTECT aimed to assess the long-term persistence of anti-HBs titers 2–3 years after the 3rd dose in participants enrolled in Finland.

**Method:** Subjects were eligible for the follow-up study if they had been enrolled in PROTECT study in Finland and had achieved seroprotection (anti-HBs ≥10 mIU/ml). Between February 2021 and June 2021, subjects were contacted to participate in the follow-up study. Serum samples were tested for Anti-HBs titers at the central laboratory (LabConnect, USA) using the same validated anti-HBs quantitative assay [VITROS, Ortho 3600 NJ, USA] as used in the PROTECT study.

**Results:** Of the 528 subjects contacted, 465 agreed to participate in the follow-up study, including 244 [52.5%] vaccinated with 3A-HBV and 221 [47.5%] vaccinated with 1A-HBV. Baseline characteristics were well balanced between the groups and consistent with the PROTECT study population, the mean age for both vaccine groups was 59 years. Data from the PROTECT study demonstrated a peak GMC of anti-HBs of 8021.9 mIU/ml for 3A-HBV and 3787.3 mIU/ml for 1A-HBV in study participants one month after the third dose (Day 196). Data from this follow-up study showed that approximately 2.5 years following Day 196 in the PROTECT study, the mean concentration of anti-HBs was 1382.9 mIU/ml for 3A-HBV participants and 251.4 mIU/ml for 1A-HBV participants. Additionally, more than 2x the number of subjects vaccinated with 3A-HBV retained anti-HBs ≥100 mIU/ml compared to 1A-HBV (72.9% vs. 32.6%). After approximately 2.5 years, 27.6% in the 1A-HBV group and 11.9% in the 3A-HBV group no longer had seroprotective levels of anti-HBs (titers <10 mIU/ml).

**Conclusion:** 2.5 years after achieving peak seroprotection in the PROTECT study, the mean anti-HBs titers were five times higher in the 3A-HBV group than in the 1A-HBV group. Additionally, the percentage of participants who no longer had seroprotective levels of anti-HBs (titers <10 mIU/ml) was more than double in the 1A-HBV group compared to the 3A-HBV group.

**OS146 Fatty liver index as a risk factor for all-cause and liver related mortality in patients under therapy for chronic hepatitis B (ANRS CO22 Hepather cohort study)**

Paul Hermbessiere1, Mathieu Chalouni2, Marc Bourliere3, Pierre Nahon1, François Teoule2, Clovis Lusivka-Nzinga2, Helene Fontaine2, Stanislas Pol1, Fabrice Carrat2, Victo de Lédinghen1, Linda Wittkop2, 1Hôpital Haut-Lévêque Magellan, Pessac, France; 2ISPED, Bordeaux, France; 3Hospital Paris Saint-Joseph, Paris, France; 4Jean-Verdier Hospital Ap-Hp, Bondy, France; 5Hospital Saint-Antoine Ap-Hp, Paris, France; 6Cochin Hospital, Paris, France

**Background and aims:** A quarter of patients with chronic hepatitis B (CHB) have associated fatty liver disease and the prognosis of these patients has been poorly investigated. In the general population, Fatty Liver Index (FLI) is a recommended alternative to ultrasonography for the diagnosis of steatosis (EASL 2016) and predict clinical outcomes related to non-alcoholic fatty liver disease (NASH). The aim was to evaluate the association between FLI and all-cause and liver-related mortality in treated CHB participants from the ANRS CO22 HEPATHER cohort.

**Method:** All patients under CHB therapy at entry in the ANRS CO22 HEPATHER cohort were selected. Patients with history of liver transplantation or hepatitis D virus co-infection were excluded. Multivariate imputations of GGT, triglycerides, waist circumference and BMI were realized. Outcomes were first, the occurrence of death from any cause, then death from liver complication (primary liver cancer, decompensated cirrhosis, and liver transplantation). Proportional hazard adjusted on age, gender and diabetes status. Cox models were performed. Potential non-linear relationships were examined using fractional polynomial models.

**Results:** 2877 treated CHB patients were included. Median age was 48.9 years [Interquartile range (IQR): 38.1; 59.8] and 2044 (70.1%) were men. Almost all patients were treated by nucleos (t)idic analogues (98%) for a median time of 2.9 years [IQR 0.4; 5.2] and 92.0% had an HBV DNA level <2,000 UI/ml at entry. After a median follow-up of 7.0 years [IQR [6.2; 7.6]], incidence of all-cause mortality was 7.7/1000 person/years (95% Confidence Interval (CI) 6.6–9.1), and 4.0/1000 person/years (95% CI 3.2–5.0) for liver-related mortality. After adjustment, an increase of ten points of FLI was significantly associated with an increased risk of all-cause mortality (Hazard Ratio (HR): 1.09 [1.02–1.16]) and tended to be associated with liver-related mortality (HR: 1.08 [0.99–1.19]).

**Conclusion:** In this first large prospective cohort of French patients with treated chronic HBV infection, FLI was independently associated with all-cause and liver-related mortality.

**OS147 The discriminatory power of risk scores for hepatocellular carcinoma in treated chronic hepatitis B patients with and without diabetes: a territory-wide study of 48,706 subjects**

Terry Cheuk-Fung Yip1, Mandy Sze-Man Lai1, Vincent Wai-Sun Wong1, Yee-Kit Tse1, Yan Liang2, Vicki Wing-Ki Hui2, Henry LY Chan3,4, Grace Lai-Hung Wong1, 1The Chinese University of Hong Kong, Medical Data Analytics Centre (MDAC), Department of Medicine and Therapeutics, Institute of Digestive Disease, Faculty of Medicine, Hong Kong; 2The Chinese University of Hong Kong, Medical Data Analytics Centre (MDAC), Department of Medicine and Therapeutics, Faculty of Medicine, Hong Kong; 3Union Hospital, Department of Internal Medicine, Hong Kong; 4The Chinese University of Hong Kong, Medical Data Analytics Centre (MDAC), Department of Medicine, Faculty of Medicine, Hong Kong

**Background and aims:** With treated chronic hepatitis B patients, several risk scores have been developed to predict the risk of hepatocellular carcinoma (HCC). While DM is associated with a doubled risk of hepatocellular carcinoma (HCC) in CHB patients, few HCC risk scores
include DM as a factor. We aimed to compare the performance of HCC risk scores among DM and non-DM patients on nucleos (t)ide analogue (NA) treatment.

**Method:** Adult CHB patients on at least 6 months of entecavir or tenofovir treatment from January 2005 to March 2020 were identified using a territory-wide database in Hong Kong. DM was defined by any use of non-insulin antidiabetic agents, continuous use of insulin for ≥28 days, haemoglobin A1c ≥6.5%, fasting glucose ≥7 mmol/L, and/or diagnosis codes. Two HCC risk scores with DM as a factor for treated CHB patients (i.e., cirrhosis, age, male sex, and DM [CAMD] score and Real-World Effectiveness from the Asia Pacific Rim Liver Consortium for hepatitis B virus [REAL-B] score) were studied; 2 other HCC risk scores without DM as a factor (i.e., PAGE-B and modified PAGE-B [mPAGE-B] scores) were also examined. The discriminatory power of the scores was assessed by area under the time-dependent receiver operating characteristic curves (AUROCs) with death as a competing event. Comparisons were done based on 1,000 bootstrap samples.

**Results:** Of 48,706 patients included, the mean age was 54.3 ± 13.6 years; 62.1% were male and 12.7% had cirrhosis. The prevalence of DM rose steadily from 15.5% to 24.3% in those who started NA treatment in 2005–08 and 2017–20 respectively. At a median (25th percentile–75th percentile) follow-up of 4.4 (2.2–5.0) years, 2,157 (4.4%) patients developed HCC. All the 4 HCC scores were less predictive in DM patients than non-DM patients (all p < 0.001; Figure). DM was an independent predictor for HCC in cirrhotic chronic hepatitis B patients with and without diabetes mellitus (DM).

**Conclusion:** HCC risk scores are less accurate in NA-treated diabetic CHB patients than their non-diabetic counterparts, with a drop of AUROCs from around 0.8 to 0.7 regardless of whether DM is a component in the risk scores or not.

---

**OS148 Hepatocellular carcinoma incidence is reduced in cirrhotic chronic hepatitis B patients with HBsAg seroclearance comparing to those with viral suppression**

Rachel Wen-Juei Jeng1,2,3, Chien-Hung Chen1,4, Hwai-I Yang3, Yi-Cheng Chen1,4,5, Wen-Chiu Liu1,2,3, Chia-Ying Wu2,3, Rong-Nan Chen1,2,3, Yun-Fan Liao1,2,1, Chang Gung University, College of Medicine, Taiwan; 2, Linkou Chang Gung Memorial Hospital, Liver Research Unit, Taiwan; 3, Linkou Chang Gung Memorial Hospital, Department of Gastroenterology and Hepatology, Taiwan; 4, Kaohsiung Chang Gung Memorial Hospital, Division of Hepatogastroenterology, Department of Internal Medicine, Taiwan; 5, Academia Sinica, Genomic Research Center, Taiwan

**Background and aims:** Cirrhosis is a major risk factor for hepatocellular carcinoma (HCC) development in chronic hepatitis B patients. It remains unknown whether HBsAg seroclearance in cirrhotic patients reduces the risk of HCC compared to those under long-term Nuc treatment. This study aims to investigate the HCC incidence between these two groups.

**Method:** The study recruited chronic hepatitis B patients with cirrhosis undergoing Nuc therapy with viral suppression (Nuc arm, N = 805) and cirrhotic CHB patients with HBsAg seroclearance (S-loss arm, N = 165, 65 untreated, 90 off-therapy, 10 on-treatment HBsAg loss) from two medical centers and REVEAL-HBV cohort. The baseline in the Nuc arm was set since HBV DNA being undetectable (complete viral suppression) while in the S-loss arm was set since HBsAg loss. Those with HCC occurred prior to the baseline or within 6 months after the baseline were excluded from this analysis. Kaplan Meier analysis and log rank test were done for the cumulative HCC incidence comparison.

**Results:** Comparing the baseline features between Nuc arm and S-loss arm, the mean age (55.5 vs. 56.8, P = 0.14), gender (male: 74.5% vs. 81.2%, P = 0.07) and HBV genotype (p = 0.27) were comparable. The median ALT (29 vs. 20 U/L, P < 0.001) and AFP (4.16 vs. 3.0 mg/dL, P < 0.001) level were higher in the Nuc arm while follow-up duration was longer in the S-loss arm (median: 7.9 vs. 4.3 years, P < 0.001). In univariate analysis, older age [crude HR (CHR): 1.04, P < 0.0001], higher FIB-4 level [CHR: 1.1, P = 0.0004], higher AFP level [CHR: 1.02, P < 0.001] were positively associated with HCC occurrence while HBsAg loss is a protective factor for HCC [CHR: 0.502, P = 0.0314]. In multivariate analysis, older age [adjusted HR (aHR): 1.04 (1.02–1.06), P < 0.0001] and HBsAg loss [aHR: 0.19 (0.05–0.76), P = 0.0193] are the two independent predictor for HCC. The annual incidence and 8-year cumulative HCC incidence in cirrhotic patients in Nuc arm versus S-loss arm were 2.43% and 16% versus 1.16% and 8%, respectively (Log rank test, P = 0.0282). After propensity score matching with age, gender and FIB-4 at 1 to 1 ratio with 77 patients at each arm, HBsAg loss arm still had much lower HCC incidence than those under Nuc arm (annual incidence: 0.46% vs. 3.2%, log rank test, P = 0.0035).

**Conclusion:** This is the first study proved the HBsAg seroclearance, reflecting the inactive transcriptional activity of cccDNA, is a protective factor for HCC in cirrhotic chronic hepatitis B patients.

---

**Figure:** The area under the time-dependent receiver operating characteristic curves (AUROCs) of A. PAGE-B score; B. mPAGE-B score; C. CAMD score; and D. REAL-B score for predicting the development of hepatocellular carcinoma in nucleos (t)ide analogue-treated chronic hepatitis B patients with and without diabetes mellitus (DM).

**Conclusion:** HCC risk scores are less accurate in NA-treated diabetic CHB patients than their non-diabetic counterparts, with a drop of AUROCs from around 0.8 to 0.7 regardless of whether DM is a component in the risk scores or not.

**Figure:** Cumulative HCC incidence between cirrhotic CHB patients with Nuc viral suppressed (blue line) and HBsAg loss (red line) before and after propensity score matching.
OS149
Treatment with bulevirtide improves patient-reported outcomes in patients with chronic hepatitis delta: An exploratory analysis of a Phase 3 trial at 48 weeks

Background and aims: Chronic hepatitis delta (CHD) infection is caused by a defective RNA virus that requires the presence of the hepatitis B virus (HBV) surface antigen for replication and transmission. Compared with HBV monoinfection, patients with CHD have a greater risk of cirrhosis, hepatocellular carcinoma, liver transplant, and liver-related mortality. In 2020, the European Medicines Agency granted conditional marketing authorisation to bulevirtide (BLV) 2 mg, a novel NTCP entry inhibitor, as the first treatment approved for CHD. We report an exploratory analysis of health-related quality-of-life outcomes in patients with CHD after 48 weeks of treatment with BLV 2 mg in an ongoing Phase 3 trial.

Method: MYR301 (NCT03852719; EudraCT 2019-001213-17) is a randomised, open-label, parallel-group, multicentre trial that assigned 150 CHD patients (1:1:1) to 3 exploratory arms (BLV 2 or 10 mg or control) for up to 3 years. (As BLV 10 mg is not an approved dosage, we do not report that treatment arm.) Control patients received no active anti-HDV treatment until Week (W)48. Patients completed the Hepatitis Quality of Life Questionnaire (HQLQ), including the SF-36 and 15 supplemental items, at study baseline (BL), W24, and W48. Higher scores on the HQLQ (range 0–100) indicate better health. Interim results collected at W24 were reported previously.1

Results: BL characteristics were well balanced between BLV 2 mg (n = 49) and controls (n = 51). For BLV 2 mg, mean age was 44 years, BMI was 24 kg/m², 61% were male, 83% were White, and 47% had compensated cirrhosis. Across groups, patients reported varying scores of HQLQ. From BL to W48, BLV 2 mg was associated with improvements in all HQLQ domains; notably, >5-point improvements in mean values were observed for 10 of the 14 items (Figure). Treatment differences vs controls in least-squares mean changes from BL to W48 were statistically significant (p < 0.05) for role-physical, hepatitis-specific (HS) limitations, and HS health distress. Improvements with BLV 2 mg seen at W24 were largely maintained or increased at W48.

Conclusion: CHD patients treated with BLV 2 mg showed an improvement at W48 in all domains of the HQLQ, while patients in the control group remained largely unchanged, apart from substantial improvements in health distress and HS health distress. Patients receiving BLV 2 mg reported significant improvements in quality-of-life domains, including role-physical, HS limitations, and HS health distress, compared with controls.

Medical writing support was provided by Ellie Manca, AlphaScientia, LLC, and was funded by Gilead Sciences, Inc.


OS150
Extracellular vesicles from mesenchimal stem cells reduce neuroinflammation in hippocampus and restore cognitive function in hyperammonemic rats
Paula Izquierdo-Altarejos1, Carlos Sanchez-Huertas2, Victoria Moreno-Manzano3, Vicente Felipo1, 4, 1Centro de Investigacion Principe Felipe, Neurobiology, Valencia, Spain; 2Instituto de Neurociencias CSIC-UMH, Laboratory of Bilateral Neural Circuits, Alicante, Spain; 3Centro de Investigacion Principe Felipe, Neuronal and Tissue Regeneration Lab, Valencia, Spain; 4CIPF Centro de Investigación Principe Felipe, Valencia, Spain

Email: vfelipo@cipf.es

Background and aims: Chronic hyperammonemia, a main contributor to hepatic encephalopathy, leads to neuroinflammation which alters neurotransmission leading to cognitive impairment. Currently there are no specific treatments for the neurological alterations in hepatic encephalopathy. Extracellular vesicles (EVs) from mesenchymal stem cells (MSCs) reduce neuroinflammation in some pathological conditions. The aim of this work was to assess if treatment of
hyperammonemic rats with EVs from MSCs reduces neuroinflammation, improves neurotransmission in hippocampus and restores cognitive function and to analyze the mechanisms involved.

**Method:** Treatment with EVs from MSCs was performed in vivo by intravenous injection and ex vivo in hippocampal slices in hyperammonemic and control rats. Effects on neuroinflammation (microglia and astrocytes activation and content of inflammatory markers in hippocampus) were assessed by immunohistochemistry, immunofluorescence and western blot. Learning and memory were assessed using the following tests: object location, object recognition, Y maze and radial maze.

**Results:** The EVs injected reached the hippocampus. Hyperammonemia induced neuroinflammation in hippocampus and impaired learning and memory in the tests performed. Treatment with EVs reduced microglia and astrocytes activation, the content of IL-1beta and NF-kb activation and restored performance of hyperammonemic rats in all the behavioral tests. Studies adding EVs to hippocampal slices ex vivo showed that these beneficial effects were dependent on TGFbeta present in the EVs, which reduced NF-kb activation and the subsequent neuroinflammation.

**Conclusion:** Extracellular vesicles from mesenchymal stem cells reduce neuroinflammation in hippocampus and restore cognitive function in hyperammonemic rats. EVs from MSCs may be useful to improve cognitive function in patients with Minimal Hepatic Encephalopathy.

**OS151 Lipidomics analyses of ATTIRE trial patients’ plasma at day 1 demonstrates that reduced cholesterol esterification predicts development of hospital acquired infection**

Harriett Fuller1, Thais Tittanegro2, Alex Maini2, Louise China2, James Thorne3, J Bernadette Moore1, Alastair O’Brien2. 1University of Leeds School of Food Science and Nutrition, Leeds, United Kingdom; 2UCL Institute for Liver and Digestive Health Upper 3rd Floor, University College London Division of Medicine, London, United Kingdom; 3School of Food Science and Nutrition @ Parkinson (p.232), Faculty of Environment University of Leeds, Leeds, United Kingdom

**Background and aims:** Hospital acquired infections (HAIs) are common in acute decompensation (AD) patients and studies support an anti-inflammatory role for statins. We investigated the role of lipid metabolism pathways in AD patients that developed HAI.

**Method:** Plasma from 56 ATTIRE trial patients (31 male, 25 female) at day 1 (pre-albumin infusions or standard care) were analysed using Lipotype Shotgun Lipidomics platform. Patients were not diagnosed with infection nor taking antibiotics at sampling, with 26 subsequently developing HAI and 30 not. Lipidomic profiles predicting HAI status were analysed via multivariate statistical techniques (principal component analysis (PCA), partial least squares discriminatory analysis (PLSDA) and sparse PLSDA (sPLSDA)) on 245 lipids with <25% missing data prior to imputation. In non-ATTIRE patients without infection and not on antibiotics, we performed whole blood bulk RNA sequencing (RNA-seq) comparing healthy volunteers (HV, n = 5), outpatients with refractory ascites (ORA, n = 5) and hospitalised AD patients (n = 10). Finally, we examined HAI incidence in the 47 ATTIRE patients on statins at baseline.

**Results:** Median time to HAI was 6 days. PLSDA models including clinical covariates significantly predicted HAI development, with Bilirubin at baseline having a variable importance in projection (VIP) score of 2.5. Within each metabolite class, only PCs of Cholesterol Esters (CEs) and Sphingomyelin (SM) class resulted in separation by HAI status, driven by CE 18.16.0, CE 18.2.1, CE 18.2.2 and SM 42.2.2. When included in PLSDA models, CE 18.1.0 and CE 18.2.0 were both important in predicting HAI (VIP >1) (table). RNA-seq showed reduced blood Sterol O-acetyltransferase 1 (SOAT1) expression compared to HV (mean ± SD gene count: 384.0 ± 94.9) in ADs (254.9 ± 81.0; P = 0.02) and ORA patients (260.0 ± 55.1; P = 0.04, figure). There was no difference in HAI according to baseline statin use, which occurred in 9/47 statin (19.1%) and 141/730 non-statin (19.3%) patients.

**Conclusion:** Data are consistent with a downregulation of blood cholesterol esterification via SOAT1 in AD patients predicting development of HAI. Statins do not affect cholesterol esterification and were non-predictive of HAI status within PLSDA models and had no effect clinically, although small numbers were analysed. CE may be novel and functional biomarkers that predict HAI in AD, providing mechanistic insight.

**OS152 Integrating single-cell RNA and spatial transcriptomic data defines altered cell state in human liver fibrosis**

Nigel Hammond1, Sokratia Georgaka1, Syed Murtuza-Baker1, Ali Al-Anbaki1, Elliot Jokl1, Harry Spierers1,2, Ajith Sirivardena1, Varinder Athwal1, Neil Hanley1, Magnus Rattray1, Karen Piper Hanley1.

1The University of Manchester, United Kingdom; 2University of Cambridge, Department of Surgery, Cambridge, United Kingdom; 3Addenbrooke’s Hospital, Department of Hepato-pancreato-biliary Surgery, Cambridge, United Kingdom

**Background and aims:** Advances in single cell technology have revolutionised our understanding of the liver, enabling genome-wide RNA-profiling of thousands of transcriptomes at single cell resolution. Recent studies utilising single cell RNA sequencing (scRNA-seq) have characterised progenitor cell populations, uncovered gene expression zonation of multiple cell types, and revealed their contribution to disease pathogenesis. However, scRNA-seq does not capture the spatial distribution of transcripts in cells and dissociated tissue can cause transcriptomic changes. In contrast, the recent explosion of spatial transcriptomics (ST) technologies has enabled genome-wide characterisation of cellular heterogeneity at near single-cell resolution, while preserving spatial information.

**Method:** In this study, we have utilised ST to profile the fibrotic niche in human cirrhotic liver. Using 10X Genomics Visium, we
demonstrate ST can resolve diseased liver tissue into discrete gene expression clusters which correlate with histological landmarks, revealing spatial expression profiles of the fibrotic scar and interface with regenerative nodules (Figure 1). To increase the resolution of ST data, we generated a complementary human cirrhotic liver scRNA-seq dataset. Through Cell2location computational approaches, we defined cell type clusters and deconvoluted multi-cell ST data to reveal spatial molecular signatures of several scar-associated cell sub-populations.

Results: Furthermore, our data spatially located impaired extracellular matrix (ECM) signalling associated with the pathogenesis of progressive liver disease and provided insight into mechanoadaptive mechanisms during myofibroblast activation.

Conclusion: This study demonstrates how comprehensive ST aligned to computational approaches can be used to delineate spatial gene expression patterns during liver disease. Our data highlights the future of ST in studies to understand mechanisms underlying progressive liver disease as well as its potential in clinical pathology.

OS153
Vascular endothelial growth factor C mediated restoration of mesenteric lymphatic vessels permeability and drainage improves gut immunity surveillance in experimental cirrhosis

Pinky Juneja1, Dinesh Mani Tripathi1, Himprat Kaur1, Sumati Rohilla1, Sukriti Sukriti1, Subham Banerjee2, Shiv Kumar Sarin1, Savi Kaur1.
1Institute of Liver and Biliary Sciences, Department of Molecular and Cellular Medicine, New Delhi, India; 2NIPER Guwahati, Department of Pharmaceutics, Guwahati, India; 3Institute of Liver and Biliary Sciences, Department of Hepatology, New Delhi, India
Email: savykaur@gmail.com

Background and aims: Mesenteric lymphatic vessels (MLVs) are functionally impaired in cirrhosis. We explored therapeutic effects of a human recombinant pro-lymphangiogenic factor, vascular endothelial growth factor C (rhVEGF-C, Cys156Ser) on MLVs and the draining lymph nodes (LNs) in experimental cirrhosis.

Method: CCl4-induced rat models of cirrhosis were prepared. Molecular and histological studies of the MLVs were performed. rhVEGF-C (10 ug/kg), which binds to VEGF-receptor 3 (VEGFR3) on lymphatic endothelial cells (LyECs), was injected intraperitoneally in 5 doses on alternate days in cirrhotic models. CCl4 rats were given saline as vehicle. The sprouting and drainage of MLVs was analyzed using histology and whole-mount BODIPY of mesentery. To gain mechanistic insights, gene expression profiling of isolated and sorted mesenteric LyECs was performed by RT-PCRs. Dendritic Cell (DCs) and T cell subsets were quantified in LNs, portal and peripheral circulation by flow cytometry. Systemic inflammatory cytokines were examined. Gut bacterial translocation to mesenteric lymph nodes, liver, and systemic circulation was studied using orally administered GFP labelled Salmonella typhimurium.

Results: An increased gene and protein expression of VEGF-C was observed in the mesenteric tissues of treated rats in comparison to the vehicle. Histology displayed a significant increase in area per field of the MLVs in treated versus vehicle rats (1.8 vs 3.9, p < 0.001). Drainage of mesenteric lymph was increased in treated as compared to vehicle (30 a.u. vs 60 a.u., p < 0.001) with decreased lymph leakage (50 a.u. vs 20 a.u., p < 0.001) in comparison to vehicle. Sprouting of MLVs from pre-existing vessels was observed in treated rats with significantly reduced dilation wrt vehicle (200 µm vs 100 µm, p < 0.001). Sorted LyECs showed increased expression of LyVE1 (7.4 fc, p < 0.01) and Prox1 (7.7 fc, p < 0.05) in treated rats wrt vehicle. Enhanced expression of adhesion molecules such as VE-CAD (5 fc, p < 0.05) in LyECs correlated with decreased lymph leakage and permeability of MLVs in treated rats. Expression of CCL21 (2.04 fc p < 0.05), a chemoattractant for DCs and T cells, and CD86 (9.36 fc, p < 0.05), an antigen presentation molecule was increased in LyECs of treated wrt vehicle rats. Among all immune cells, LNs showed an increased percentage of activated CD8 T cells (24.07 vs 11.37, p < 0.05) and DCs (67.03 vs 55.52, p < 0.05) in treated versus vehicle. Treated rats also exhibited increased clearance in LNs as compared to vehicle (p < 0.05).
OS154

Effect of engineered poly (beta-amino ester) nanoparticles containing a nitric oxide donor on systemic and portal hemodynamics

Meritxell Perramón, María Navalón, Guillermo Fernández Varo, Belén González, Álazne Moreno-Lanceta, Cristina Fornaguera, Pedro Melgar-Lesmes, Salvador Borroś, Vladimiro Jiménez, Biochemistry and Molecular Genetics Service of Hospital Clinic Universitari, Institut d’Investigacions Biomèdiques August Pi i Sunyer (IDIBAPS), Centro de Investigación Biomédica en Red de Enfermedades Hepáticas y Digestivas (CIBERehd), Barcelona, Spain; 2Grupo de Enginyeria de Materials (Gemat), Institut Químic de Sarrià (IQS), Ramon Llull University (URL), Barcelona, Spain; 3University of Barcelona, Medicine and Surgery Faculty, Department of Biomedicine, Barcelona, Spain; 4Institute for Medical Engineering and Science, Massachusetts Institute of Technology, Cambridge, United States; 5Centro de Investigación Biomédica en Red Bioingeniería (CIBER-BBN), Barcelona, Spain
Email: wjimen@clinic.cat

Background and aims: Decompensated liver cirrhosis results from the worsening of the liver function and is characterized by the appearance of a clinical phenotype, frequently ascites and portal hypertension. The primary cause of portal hypertension is an increase in the resistance to portal blood flow. Architectural distortion, hepatic stellate cell contraction, and endothelial dysfunction with increased vasconstrictor and deficient nitric oxide (NO) production are major factors governing this process. Here, we assessed the potential therapeutic effect of engineered poly (beta-amino esters) nanoparticles (PBAE NPs) containing an NO donor in experimental decompen-sated cirrhosis.

Method: NO donor pGFP PBAE NPs with retinol moiety were administered intravenously to cirrhotic rats. In a separate experiment, mice were injected with 4 kDa FITC-Dextran 15 min before sacrifice to assess blood-brain barrier (BBB) permeability changes. In a separate experiment, mice were injected with 4 kDa FITC-Dextran 15 min before sacrifice to assess blood-brain barrier (BBB) permeability changes.

Results: BDL induces motor dysfunction, demonstrated by increased beam traversal time (+60%, p = 0.0056 on day 7) and reduced travelling in the open field (−71%, p < 0.0001 on day 14). Concomitantly, plasma ammonia increases progressively in BDL mice (p = 0.0012 on day 21). CSF metabolomics reveal a significant glutamine increase from 14 days on (p = 0.0029). Additionally, a glutamate decrease is observed. Other osmolytes taurine and creatine transiently decrease. Interestingly, plasma ammonia correlates significantly with CSF glutamine (r = 0.5076, p = 0.0113).

Conclusion: In cirrhosis, treatment with VEGF-C ameliorates mesenteric lymph drainage and permeability owing to the increased expression of adhesion molecule, VE-CAD in the LyECs. VEGF-C modulates gut immunity and bacterial clearance and thus may serve as an emerging therapy for combating gut infection and inflammation in cirrhosis.
Systemic inflammation is evident from 7 days onward with increased plasma IL-6 levels ($p = 0.0002$). From 14 days on, 3D reconstructed cortical microglial cells reveal activated morphology, indicating neuroinflammation (Figure 1). CCL2 levels are significantly increased in the cortex 28 days after BDL ($p = 0.0418$), coinciding with increased BBB permeability ($p = 0.0031$).

Conclusion: Murine BDL reproduces clinical, metabolic and gliovascular features of type C HE. Early behavioural changes are obvious before plasma ammonia and brain glutamine accumulate, and potentially reflect the effect of systemic inflammation and cerebral bile acid/tryptophan accumulation on behaviour. Altogether, these data support the clinical relevance of this HE model, which can now be used for further neurobiological and intervention studies.

Liver tumours: Therapy

OS156 Yttrium-90 radioembolization versus drug-eluting beads chemoembolization for unresectable hepatocellular carcinoma: results from the TRACE phase 2 randomized controlled trial
Elisabeth Dhondt1, Bieke Lambert2,3, Laurens Hermie1, Lynn Huynck1, Peter Vanlangenhove1, Anja Geerts4, Xavier Verhelst5, Maridi Aerts5, Aude Vanlander6, Frederik Berrevoet6, Roberto Ivan Troisi2,7, Hans Van Vlierberghe4, Luc Defreyne1, Ghent University Hospital, Vascular and Interventional Radiology, Ghent, Belgium; 2Ghent University, Faculty of Medicine and Health Sciences, Ghent, Belgium; 3University Hospital, Gastroenterology and Hepatology, Gent, Belgium; 4Ghent University Hospital Brussels, Gastroenterology, Belgium; 5Ghent University Hospital, General and HPB Surgery and Liver Transplantation, Ghent, Belgium; 6Frederico II University Hospital, Hepatobiliary and Minimally Invasive and Robotic Surgery, Naples, Italy

Email: elisabeth.dhondt@uzgent.be

Background and aims: Transarterial radioembolization (TARE) is a safe and effective alternative. The aim of the study was to compare the efficacy and safety of TARE to TACE for unresectable HCC.

Method: In this single-center prospective randomized controlled trial (TRACE), Yttrium-90 glass TARE was compared with doxorubicin-eluting beads TACE (DEB-TACE) in patients with intermediate stage HCC extended to Eastern Cooperative Oncology Group performance status 1 and early-stage HCC patients not eligible for surgery or thermoablation. Participants were recruited between September 2011 and March 2018. Primary end point was time to progression (TTP overall). Kaplan–Meier analysis in the intention-to-treat (ITT) and per protocol (PP) population.

Results: Ad interim analysis, 38 participants (median age, 67 years; IQR 63–72; 33 men) were randomized to the TARE arm and 34 (median age, 68 years; IQR 64–74; 30 men) to the DEB-TACE arm (ITT population).

Median TTP overall was 17.1 months in the TARE arm versus 9.5 months in the DEB-TACE arm (ITT: HR 0.36; 95% CI: 0.18, 0.70; $p = 0.002$) (PP: 32 and 34 participants respectively: HR 0.29; 0.14, 0.60; $p < 0.001$). Median overall survival was 30.2 months after TARE and 15.6 months after DEB-TACE (ITT: HR 0.48; 0.28, 0.82; $p = 0.006$). Serious adverse events grade $\geq 3$ (13 of 33 (39%) versus 19 of 36 (53%) after TARE and DEB-TACE respectively, $p = 0.47$) and 30-day mortality (0 of 33 (0%) versus 3 of 36 (8%), $p = 0.24$) were similar in the safety populations. Ad interim the HR for the primary end point TTP overall was <0.39, indicative to halt the study.

Conclusion: With similar safety profile, Yttrium-90 radioembolization conferred superior tumor control and survival compared to drug-eluting beads chemoembolization in selected participants with early and intermediate HCC.

OS157 Cholangiocarcinoma landscape in Europe: diagnostic, prognostic and therapeutic insights from the ENSCCA Registry
Laura Izquierdo-Sánchez1,2, Angela Lamarca2,4, Adelaida La Casta1,5, Stefan Buettner6, Kirsten Utpatel6, Heinz-Josef Klümpen8, Jorge Adeva9, Arndt Vogel10, Ana Lleo1,5, Mariano Ponz-Sarvise14, Brustia Raffaele15, Vincenzo Cardinale16, Chiara Braconi17,18, Gianpaolo Vidili19, Nigel B. Jamieson17,20, Rocio IR Macias21, Philipp Jona22,23, Marco Marzioni24, Wiacław Hołówko25, Trine Folsøe26,27, Jüozas Kupcinskas28, Zeno Sparzecze29,29, Dan Krawczyk30, Łukasz Krupa31, Viorel Scripcariu32, Gianluca Grazzi33, Ana Landa-Magdalena1,5, Jan Ijzermans6, Katja Evert7, Joris Erdmann8, Flora López-López9, Anna Saborowski10, Alexander Scheiter7, Alvaro Santos-Laso1, Guido Carpino34, Jesper Andersen35, Jose Marin21, Domenico Alvaro36, Luis Bujanda1,2,37, Alejandro Forner38, Juan Valle3,4, Bas Groot Koerkamp6, Jesus Maria Banales1,2,39,40.
Cholangiocarcinoma (CCA) is a rare and heterogeneous biliary cancer, with increasing incidence and related mortality. This study investigates the clinical course of CCA subtypes (intrahepatic (iCCA), perihilar (pCCA), and distal (dCCA)) in mortality. This study investigates the clinical course of CCA and its bioactivity of the nivolumab (3 mg/kg, day 1 and day 22) plus ipilimumab (3 mg/kg, day 1 and day 22) plus ipilimumab (3 mg/kg, day 1 only) combination prior to LR in

Method: The ENSCCA Registry is a multicenter observational study. Patients with histologically-proven CCA diagnosis between 2010–2019 were included. Demographic, histomorphological, biochemical, and clinical studies were performed.

Results: Overall, 2, 234 patients were enrolled (male:female = 1.29). iCCA (n = 1, 243) was associated with overweight/obesity (58.5%) and chronic liver diseases involving cirrhosis (12.6%) and/or viral hepatitis (10.4%); pCCA (n = 592) with primary sclerosing cholangitis (8.8%); and dCCA (n = 399) with choledocholithiasis (10.3%). At diagnosis, 42.2% of patients had local disease, 29.4% locally-advanced disease (LAD), and 28.4% metastatic disease (MD). Serum CEA and CA19–9 showed low diagnostic sensitivity (69.1% and 40.9% below cutoff, respectively), but their concomitant elevation was associated with increased risk of presenting with LAD [OR = 2.16;95%CI:1.43–3.27] or MD [OR = 5.88;95%CI:1.36–9.25]. Patients undergoing resection (50.3%) showed the best outcome, particularly with negative-resection margin (R0) [median overall survival (mOS) = 45.1 months]; however, margin involvement (R1) [HR = 1.92;95%CI:1.53–2.41; mOS = 24.7 months] and lymph node invasion [HR = 2.13;95%CI:1.55–2.94; mOS = 23.3 months] compromised prognosis. Among patients with unresectable disease (49.6%), the mOS was 10.6 months for those receiving active palliative therapies, mostly chemotherapy (26.2%). Patients receiving best supportive care (20.6%) had mOS of 4.0 months, with iCCAs showing worst outcome compared to p/dCCAs. ECOG performance status [HR = 1.52;95%CI:1.01–2.31], MD [HR = 4.03;95%CI:1.82–8.92] and CA19–9 [HR = 2.79;95%CI:1.46–5.33] were independently prognostic for OS.

Conclusion: CCA is still diagnosed at advanced stage, a proportion of patients fail to receive cancer-specific therapies, and prognosis is dismal. Identification of preventable risk factors and implementation of surveillance in high-risk populations are required to decrease cancer-related mortality.

Biodonostia, Liver and Gastrointestinal Diseases, San Sebastián, Spain; 2CIBER-Center for Biomedical Research Network, Liver and Gastrointestinal Diseases, Madrid, Spain; 3The Christie NHS Foundation Trust, Department of Medical Oncology, United Kingdom; 4The University of Manchester, United Kingdom; 5Donostia Universitario Ospitalea, Department of Medical Oncology, Donostia, Spain; 6Erasmus University Medical Center, Department of Surgery, Rotterdam, Netherlands; 7University of Regensburg, Institute of Pathology, Regensburg, Germany; 8Amsterdam UMC, locatie AMC, Department of Medical Oncology, Amsterdam, Netherlands; 9University Hospital October 12, Department of Medical Oncology, Madrid, Spain; 10Hannover Medical School, Department of Gastroenterology, Hepatology and Endocrinology, Hannover, Germany; 11IRCCS Istituto Clinico Humanitas Humanitas Cancer Center, Division of Internal Medicine and Hepatology, Milan, Italy; 12University of Padua School of Medicine and Surgery, Department of Molecular Medicine, Padova, Italy; 13Yale University School of Medicine, Digestive Disease Section, New Haven, United States; 14Clínica Universidad de Navarra, Program in Solid Tumors, Pamplona, Spain; 15University Hospitals Pitié Salpêtrière–Charles Foix, Department of Hepatobiliary and Liver Transplantation Surgery, Paris, France; 16Sapienza University of Rome, Department of Medico-Surgical Sciences and Biotechnologies, Roma, Italy; 17Institute of Cancer Sciences, University of Glasgow, Bearsden, United Kingdom; 18Royal Marsden Hospital-Sutton, London, United Kingdom; 19Azienda Ospedaliero Universitaria di Sassari, Department of Medical, Surgical and Experimental Sciences, Sassari, Italy; 20Glasgow Royal Infirmary, West of Scotland Pancreatic Unit, United Kingdom; 21Istituto de Investigación Biomédica de Salamanca, Experimental Hepatology and Drug Targeting (HEVEPHARM), Salamanca, Spain; 22University Hospital of Zürich, Department of Visceral- and Transplant Surgery, Zürich, Switzerland; 23Klinik Favoriten, Department for Surgery, Wien, Austria; 24Marche Polytechnic University, Department of Gastroenterology, Ancona, Italy; 25Medical University of Warsaw, Department of General, Transplant and Liver Surgery, Warszawa, Poland; 26Oslo universitetssykehus Rikshospitalet, Department of Transplantation Medicine, Norway; 27Institute of Medical University of Vienna, Department of Surgery, Inflammatory Diseases and Transplantation, Oslo, Norway; 28Lithuanian University of Health Sciences, Department of Gastroenterology and Institute for Digestive Research, Kaunas, Lithuania; 29Iuliu Hatieganu University of Medicine and Pharmacy, 3rd Medical Department, Institute for Gastroenterology and Hepatology, Cluj-Napoca, Romania; 30Saarland University Hospital, Department of Internal Medicine II-Gastroenterology, Hepatology, Endocrinology, Diabetology, and Nutritional Medicine, Homburg, Germany; 31Kliniczny Szpital Wojewódzki Nr 1 im. Fryderyka Chopina w Rzeszowie, Department of Gastroenterology and Hepatology with General Medicine, Rzeszów, Poland; 32Universitatea de Medicină și Farmacie “Grigore T. Popa”, Department of Morpho-Functional Sciences I, Department of Surgery II, Iași, Romania; 33Regina Elena National Cancer Institute, Rome, Italy; 34University of Rome “Foro Italico”, Department of Movement, Human and Health Sciences, Roma, Italy; 35Biotech Research and Innovation Centre, Department of Health and Medical Sciences, København, Denmark; 36Sapienza University of Rome, Department of Translational and Precision Medicine, Roma, Italy; 37Donostia Unibertsitate Ospitalea, Department of Digestive System, Donostia, Spain; 38Institut d’Investigacions Biomèdiques August Pi i Sunyer (IDIBAPS), Liver Unit, Barcelona Clinic Liver Cancer (BCLC) group, Barcelona, Spain; 39University of Navarra, Department of Biochemistry and Genetics, School of Sciences, Pamplona, Spain; 40Ikerbasque Basque Foundation For Science, Donostia, Spain

Email: jesus.banales@biodonostia.org

Background and aims: Cholangiocarcinoma (CCA) is a rare and heterogeneous biliary cancer, with increasing incidence and related mortality. This study investigates the clinical course of CCA and subtypes (intrahepatic (iCCA), perihilar (pCCA), and distal (dCCA)) in a pan-European cohort.
Liver transplantation for patients with fibrolamellar hepatocellular carcinoma: a comprehensive multicenter analysis to support future decision making

Marco Claasen1,2, Tommy Ivanics1, Wojciech Polak2, Jan Ijzermans2, Gonzalo Sapisochin1,1 University Health Network, Multi-Organ Transplant Program, Toronto, Canada; 2Erasmus MC Transplant Institute, University Medical Centre Rotterdam, Department of Surgery, Division of HPB and Transplant Surgery, Rotterdam, Netherlands

Email: marco.claasen@uhnresearch.ca

Background and aims: Fibrolamellar hepatocellular carcinoma (FL-HCC) is a rare tumour accounting for ∼1% of all primary liver cancers. Due to its rarity, there is a shortage of data on liver transplantation (LT) for patients with FL-HCC. Previously post-LT outcomes have been derived from all patients with a FL-HCC diagnosis at listing, and post-LS OS, recurrence-free survival (RFS), cumulative incidence of recurrence, and 30–90-day post-transplant mortality, for all patients with a confirmed diagnosis of FL-HCC at explant pathology. WL dropout was defined as dropping out of the WL due to death, clinical deterioration, or medical unsuitability. Recurrence and death were the events for predicting RFS. For the cumulative incidence of recurrence, death was a competing event. For all other outcomes, death was the only event. Median follow-up times were recorded 20.8 months after treatment commencement. Median time to LR from screening was 2.5 months (IQR 0.9, range 2.2–3.6). One patient had a surgery delay due to liver function worsening (ICPI-unrelated) and remained progression-free by RECIST 9.6 months post-screening. In another patient LR was switched to radiofrequency ablation by the treating surgeon due to surgical risk independent of ICPI exposure. One patient was found to have cholangiocarcinoma (CCA) on LR specimen and was excluded from efficacy analyses. ORR was 18%, with two partial responses. Disease control rate was 91%, and one patient with mixed HCC/CCA histology showed primary progression. Of the nine pathologically evaluable patients, seven (78%) achieved a pathological response, including two (22%) complete responses.

Conclusion: Neoadjuvant immunotherapy with nivolumab plus ipilimumab is tolerable and is characterised by evidence of anti-tumour efficacy in early-stage HCC.

OS159
Liver transplantation for patients with fibrolamellar hepatocellular carcinoma: a comprehensive multicenter analysis to support future decision making

Marco Claasen1,2, Tommy Ivanics1, Wojciech Polak2, Jan Ijzermans2, Gonzalo Sapisochin1

1University Health Network, Multi-Organ Transplant Program, Toronto, Canada; 2Erasmus MC Transplant Institute, University Medical Centre Rotterdam, Department of Surgery, Division of HPB and Transplant Surgery, Rotterdam, Netherlands

Email: marco.claasen@uhnresearch.ca

Background and aims: Fibrolamellar hepatocellular carcinoma (FL-HCC) is a rare tumour accounting for ∼1% of all primary liver cancers. Due to its rarity, there is a shortage of data on liver transplantation (LT) for patients with FL-HCC. Previously post-LT outcomes have been evaluated based on patients transplanted a decade ago, however contemporary and intention-to-treat (ITT) and recurrence outcomes were post-operatively confirmed of having FL-HCC. Eight patients received a living donor LT. WL dropout at 1- and 2-years post-listing was 15.3% and 19.4%. ITT OS at 1, 3, 5 years was 86.5%, 67.9%, 55.5%, where post-LT OS was 98.2%, 84.4%, 61.9% at 1, 3, 5 years. No patients died within 90 days post-LT. RFS was 85.3%, 69.9%, and 47.5% at 1, 3, and 5 years. The cumulative incidence of recurrence at 1, 3, 5 years was 12.8%, 24.4%, and 44.7%. There was no statistical difference in all outcomes between adult and pediatric patients.

Conclusion: LT for patients with FL-HCC offers acceptable long-term survival outcomes despite a substantial risk of tumour recurrence. Further research is needed to determine which patients with FL-HCC would benefit most from LT and potential adjuvant therapies to reduce the risk of recurrence.

OS160
A preferable signature of gut microbiota and bile acids predicted better outcomes of unresectable hepatocellular carcinoma to immune checkpoint inhibitors

Pei-Chang Lee1, Chijung Wu1, Ya-Wen Hung1, Chiehju Lee1, Chen-Ta Chi1, I-Cheng Lee1, Jiing-Chyuan Luo1, Ming-Chih Hou1, Yi-Hsiang Huang1,2,3

1Taipei Veterans General Hospital, Division of Gastroenterology and Hepatology, Department of Medicine, Taipei, Taiwan

2Taipei Veterans General Hospital, Division of Gastroenterology and Hepatology, Department of Medicine, Taipei, Taiwan

3Taipei Veterans General Hospital

Email: yhhuang@vghtpe.gov.tw

Background and aims: Immune checkpoint inhibitors (ICI) are newly emerged, promising therapeutic agents for unresectable hepatocellular carcinoma (uHCC). However, no effective biomarker has been found to predict treatment response. Gut microbiota could modulate outcomes of melanoma to immunotherapy. In this study, we aimed to investigate the effects of gut microbiota and metabolites on ICI-treated uHCC.

Method: From May 2018 to February 2020, patients who received ICI therapy for uHCC in Taipei Veterans General hospital were prospectively enrolled. Of them, fecal samples collected before treatment from
ORAL PRESENTATIONS

twenty objective responders and 21 non-responders (proved by radiology) were taken into analyses of microbiota and metabolites. Since March 2020, 33 consecutive Child-Pugh A, ICI-treated patients were investigated for validation. Besides, fecal samples from 17 healthy volunteers were also analyzed as control.

**Results:** A significant bacterial dissimilarity was observed between responders and non-responders before ICI treatment ($p = 0.016$ and 0.019 by Anoism and Adonis tests). *Lachnolstridium, Lachnospiraceae*, and *Veillonella* were predominant faecal microbiota of responders; whereas, *Prevotella* 9 was predominant in non-responders. Ursodeoxycholic acid and ursodeoxycholic acid were found significantly enriched in the feces of responders, and were strongly correlated with the abundance of *Lachnolstridum*. A fecal signature of enriched *Lachnolstridum* and depleted *Prevotella* 9 could significantly predict better overall survival (OS) in these patients. In the validation cohort, the best objective response rate (52.6%) was noted in patients with a preferable microbial signature. Besides, the progression-free survival (PFS) and OS were better in patients with a preferable microbial signature as compared with the counter-group. (PFS: 8.8 vs. 1.8 months; OS: not reached vs. 6.5 months, both $p < 0.001$).

**Conclusion:** Pre-treatment fecal microbiota and bile acids are associated with treatment outcomes of ICIs for uHCC. These findings provided a potential strategy to enhance the efficacy of immunotherapy by modifying gut microbiota and metabolites in patients with uHCC.

OS161

**The impact of treatment and treatment status on health state utility in patients with unresectable hepatocellular carcinoma: an EQ-5D analysis from Himalaya**

Lei Qin1, Miguel Miranda2, Cal Shephard3, Abdul-Azeez Ganiyu2, Vincent Tam4, 1AstraZeneca, Gaithersburg, United States; 2AstraZeneca, Cambridge, United Kingdom; 3AstraZeneca Canada, Mississauga, Canada; 4Tom Baker Cancer Centre, Calgary, Canada

Email: lei.qin@astraZeneca.com

**Background and aims:** The HIMALAYA trial (NCT03298451) showed that tremelimumab 300 mg added to durvalumab (STRIDE regimen) significantly improved survival compared to sorafenib for the treatment of patients with unresectable hepatocellular carcinoma (uHCC). This study also assessed predictors of health-related quality of life (HRQoL) using EuroQol 5-Dimension, 5-Level health state utility (HSU) index and visual analogue scale (VAS).

**Method:** EQ-5D-5L data were collected at baseline, every 8 weeks for 48 weeks, then every 12 weeks until treatment discontinuation, and additional assessments up to 12 weeks for patients with confirmed progression. Impact of treatment and treatment status on domain score and proportion of patients reporting any problem by domain at first off-treatment visit were assessed using last on-treatment visit as baseline. Impact on HSU was assessed by mixed models for repeated measures (MMRM). Univariate and multivariate analyses were conducted using treatment as base fixed effect and treatment status (on/off treatment), progression (progression-free/progressed) and baseline Child Pugh score as covariates. Interactions between covariates and treatment were considered. A random intercept model assuming independent within-subject errors was fitted to account for subject variability. Model performance was compared using AIC/BIC score. Analysis used algorithms reflecting societal preferences of UK, US and Canadian populations and validation analysis was conducted using VAS.

**Results:** Treatment and treatment status models were consistently the best fitting. Mean HSU for STRIDE was 0.815 (95% CI: 0.802, 0.827, $p < 0.0001$) and 0.785 (95% CI: 0.766, 0.804, $p < 0.0001$) for sorafenib, using a mapping algorithm reflecting Canadian preferences. Sorafenib treatment was associated with a utility decrement of $-0.030$ (95% CI: $-0.046, -0.014$, $p = 0.0002$) and a utility increment of 0.055 (95% CI: 0.046, 0.063, $p < 0.0001$) for those with a status of remaining on treatment. Results with UK and US algorithms, and when assessed by VAS, were consistent. Interaction of treatment and treatment status was non-significant in all models. The proportion of patients experiencing any problems on each domain of EQ-5D-5L increased between the last visit prior to- and first visit post-discontinuation for both regimens. The proportion of patients experiencing moderate to extreme problems was lower on all domains with STRIDE vs sorafenib for both on- and off-treatment, except usual activities (Figure 1).

**Conclusion:** The best predictors of HRQoL in patients with uHCC were treatment received and treatment status, where treatment with STRIDE and being on-treatment were associated with better HSUs compared to sorafenib treatment and being off-treatment. Results highlight there are notable HRQoL benefits for maintaining uHCC patients on treatment with STRIDE.
NAFLD: Experimental and pathophysiology

OS162
Heterogeneity of phosphatidylcholine metabolism in non-alcoholic fatty liver disease

Sami Qadri1,2, Sami Blom1, Kari Pitkänen3, Noora Ahlholm1,2, Kimmo Porthan1,2, Panu K. Luukkonen1,2,4, Anne Juutil1, Henna Sannamorkki2, Anne Penttilä3, Johanna Arola3, Matej Orešič7,8, Tuulia Hyötyläinen4, Hannele Yki-Järvinen1,2,1. University of Helsinki and Helsinki University Hospital, Department of Medicine, Helsinki, Finland; 2Minerva Foundation Institute for Medical Research, Helsinki, Finland; 3Aiforia Technologies Oy, Helsinki, Finland; 4Yale University, Department of Internal Medicine, New Haven, United States; 5University of Helsinki and Helsinki University Hospital, Department of Gastrointestinal Surgery, Abdominal Center, Helsinki, Finland; 6University of Helsinki and Helsinki University Hospital, Department of Pathology, Helsinki, Finland; 7Örebro University, School of Medical Sciences, Örebro, Sweden; 8University of Turku and Åbo Akademi University, Turku Bioscience Centre, Turku, Finland; 9Örebro University, School of Science and Technology, Örebro, Sweden

Email: hannele.yki-jarvinen@helsinki.fi

Background and aims: In murine models of non-alcoholic fatty liver disease (NAFLD), liver damage associates with a deficiency of phosphatidylcholines (PCs), particularly polyunsaturated PCs (PUFA-PCs). We studied whether human PC metabolism is altered by NAFLD or by the protective genetic variant in HSD17B13.

Results: Total unadjusted hepatic PCs correlated negatively with hepatic insulin sensitivity (rs = 0.81). With increasing obesity, insulin sensitivity showed by a higher AKT phosphorylation after insulin stimulation in both primary mouse hepatocytes and Huh7 cells. To over-express PKD2, Huh7 cells were transfected with EGFP-PKD2-CA, a constitutively active PKD2 fused to EGFP. Insulin signaling cascade was examined by treating hepatocytes with insulin (10 nM, 5–15 min). As an in vivo model of hepatic insulin resistance, mice with a liver-specific PKD2 depletion (PKD2ΔHep) were fed high fat diet (HFD, 20 weeks). Parameters assessing glucose homeostasis and hepatic insulin sensitivity were analyzed. PKD2 was overexpressed in liver by an injection of AAV bearing EGFP-PKD2-CA and insulin sensitivity was evaluated. PKD signature was analyzed in liver biopsies from NAFLD patients.

Results: PKD pharmacological inhibition resulted in an increased insulin sensitivity showed by a higher AKT phosphorylation after insulin stimulation in both primary mouse hepatocytes and Huh7 cells. Moreover, PKD2 knocking down by siRNA or shRNA lentiviral particles enhanced the insulin response. Alternatively, EGFP-PKD2-CA overexpression in Huh7 cells reduced AKT phosphorylation upon insulin stimulation compared to EGFP-transfected cells. In this line, in vivo injection of AAV bearing EGFP-PKD2-CA resulted in a moderate impairment of glucose homeostasis and reduced IR and AKT phosphorylation in the liver. Importantly, HFD-fed PKD2ΔHep mice displayed a tendency to improve glucose tolerance and insulin sensitivity compared to control mice. These results were confirmed by analysis of AKT phosphorylation in liver extracts. Moreover, PKD immunostaining revealed that PKD2 was increased in NAFLD patients.

Conclusion: Our results strongly suggest that PKD2 is involved in the control of hepatic insulin signaling and point PKD2 as a new target for NAFLD.

OS163
Unravelling the role of Protein Kinase D2 in the control of hepatic insulin sensitivity

Patricia Rada1,2, Ana B. Hitos1,2, Esther Rey1,4, Elena Carceller-Lopez1, Josefina F. J. M. Utrilla1,2, Carmelo García-Monzon1, Guadalupe Sabio1, Teresa Iglesias1,5, Águeda González2,4, Angela Martínez-Valverde1,2.
1Instituto de Investigaciones Biomédicas “Alberto Salo” (CSIC-UAM), Madrid, Spain; 2Centro de Investigación Biomédica en Red de Diabetes y Enfermedades Metabólicas Asociadas (CIBERDEM), Madrid, Spain; 3Centro de Investigación Biomédica en Red de Enfermedades Hepáticas y Digestivas (CIBEREHID), Spain; 4Liver Research Unit, Instituto de Investigación Sanitaria Princesa, University Hospital Santa Cristina, Spain; 5Centro de Investigación Biomédica en Red sobre Enfermedades Neurodegenerativas (CIBERNED), Spain; 6Centro Nacional de Investigaciones Cardiovasculares Carlos III (CNIC), Spain

Email: prada@iib.uam.es

Background and aims: Protein kinase D2 (PKD2) is a Ser/Thr kinase of the Ca2+-Calmodulin kinase superfamily. Growing evidences support that PKD2 participates in the control of glucose homeostasis. Two previous studies, one conducted in global PKD2-deficient mice, and the other in mice lacking PKD2 in intestine, reported opposite results with metabolic dysfunction or protection against HFD-induced obesity, respectively. However, the role of PKD2 in the liver in the context of obesity-related insulin resistance has not been addressed and it is the aim of this study.

Method: PKD inhibition by pharmacological and genetic approaches was analyzed in primary hepatocytes and in Huh7 cells. To over-express PKD2, Huh7 cells were transfected with EGFP-PKD2-CA, a constitutively active PKD2 fused to EGFP. Insulin signaling cascade was examined by treating hepatocytes with insulin (10 nM, 5–15 min). As an in vivo model of hepatic insulin resistance, mice with a liver-specific PKD2 depletion (PKD2ΔHep) were fed high fat diet (HFD, 20 weeks). Parameters assessing glucose homeostasis and hepatic insulin sensitivity were analyzed. PKD2 was overexpressed in liver by an injection of AAV bearing EGFP-PK2-CA and insulin sensitivity was evaluated. PKD signature was analyzed in liver biopsies from NAFLD patients.

Results: PKD pharmacological inhibition resulted in an increased insulin sensitivity showed by a higher AKT phosphorylation after insulin stimulation in both primary mouse hepatocytes and Huh7 cells. To over-express PKD2, Huh7 cells were transfected with EGFP-PKD2-CA, a constitutively active PKD2 fused to EGFP. Insulin signaling cascade was examined by treating hepatocytes with insulin (10 nM, 5–15 min). As an in vivo model of hepatic insulin resistance, mice with a liver-specific PKD2 depletion (PKD2ΔHep) were fed high fat diet (HFD, 20 weeks). Parameters assessing glucose homeostasis and hepatic insulin sensitivity were analyzed. PKD2 was overexpressed in liver by an injection of AAV bearing EGFP-PKD2-CA and insulin sensitivity was evaluated. PKD signature was analyzed in liver biopsies from NAFLD patients.

Conclusion: Our results strongly suggest that PKD2 is involved in the control of hepatic insulin signaling and point PKD2 as a new target for NAFLD.

Journal of Hepatology 2022 vol. 77(S1) | S1–S118

S111

ORAL PRESENTATIONS
therapeutic target in the progression of hepatic insulin resistance-related pathologies.

**OS164**

**Metabolomic changes in NASH phenotype liver-on-a-chip caused by INI-678, a small molecule HSD17B13 inhibitor, supports a role for HSD17B13 in inflammation and fibrosis**

Heather Hsu1, Michael Carleton1. 1Inipharm, Bellevue, United States

**Background and aims:** Polymorphisms producing catalytically inactive HSD17B13 protect against non-alcoholic steatohepatitis (NASH), cirrhosis, and liver cancer and are associated with reduced hepatic inflammation and fibrosis. Preliminary results demonstrated that INI-678, a novel selective inhibitor of HSD17B13, decreased fibrotic markers in response to high fat media in liver-on-chip (LOC) co-cultures. The aim of this study was to determine the impact of inhibiting HSD17B13 with a well-characterized inhibitor on metabolism in a NASH phenotype LOC.

**Method:** NASH LOC co-cultures containing primary human hepatocytes, homozygous for the active HSD17B13 allele; Kupffer cells, and stellate cells were cultured in a high-fat containing media to induce a NASH phenotype. LOC were exposed to INI-678 or a DMSO vehicle control for Days 4-20. LOC co-cultures were analyzed for fibrotic markers by immunohistochemistry and media samples were analyzed for cell health markers, albumin and lactate dehydrogenase, by ELISA and activity, respectively. Metabolites were quantified in media samples using electrospray ionization by tandem mass spectrometry.

**Results:** Treatment of NASH LOC with INI-678 and related analog inhibitors of HSD17B13 decreased fibrotic marker proteins, alpha smooth muscle actin and collagen type 1, compared to vehicle control in LOC co-cultures. Choline consumption remained stable in INI-678-treated LOC throughout high fat media exposure. Choline consumption in the vehicle control was initially elevated and decreased throughout high fat media treatment ultimately lower than INI-678-treated LOC co-cultures. INI-678 treatment resulted in lower primary bile acids compared to vehicle control. INI-678 treatment significantly reduced hexose and increased lactate in the media.

**Conclusion:** The decrease in fibrotic markers in NASH LOC with INI-678 treatment was accompanied by changes in the metabolome. The metabolic changes include stabilization of choline, decreases in bile acids and decreased hexose. The inhibition of HSD17B13 significantly altered metabolism consistent with the hepatoprotective effect and anti-fibrotic effects observed in LOC. The direct effects of small molecule inhibitors of HSD17B13 are consistent with decreased fibrosis in NASH subjects carrying inactive HSD17B13 alleles. These results suggest a potential precision medicine approach to treating NASH.

**Figure:**

- **Choline consumption (µmol/day)**
  - **Day in High Fat Media Culture**
  - **Control**
  - **INI-678**

**OS165**

**The inhibition of the epigenetic effectors DNMT1 and G9a as a potential therapeutic strategy against the non-alcoholic fatty liver disease development**

José María Herranz1, Alex Claveria-Cabello2, Leticia Colyn2, Maria U. Latasa2, Maite Perez-Araubide2, Bruno Sangro1,3,4, Julen Oyarzabal3, Antonio A. Pineda3, Maria Arechederra2,4, Carmen Berasain1,2,4, Matias A. Avila1,2,4, Maite G. Fernandez-Barrena1,2,4, 1CIBERehd, Madrid, Spain; 2CIMA-University of Navarra, Hepatology Program, Pamplona, Spain; 3Clinica Universidad de Navarra, Hepatology Unit, Pamplona, Spain; 4Instituto de Investigacion Sanitaria de Navarra, IdiSNA, Pamplona, Spain; 5CIMA-University of Navarra, Molecular Therapies Program, Pamplona, Spain

**Background and aims:** Non-alcoholic fatty liver disease (NAFLD) encompasses a spectrum of histological changes ranging from simple steatosis to inflammation and ballooning, which define non-alcoholic steatohepatitis (NASH). NASH can lead to cirrhosis and hepatocellular carcinoma. Currently, no drugs have proven efficacy for NAFLD treatment. Understanding the mechanisms leading to NAFLD progression is essential for the identification of effective therapies. Epigenetic mechanisms are fundamental for gene expression regulation and functional homeostasis, and their impairment is recognized to participate in disease. Here we have performed a systematic transcriptomic analysis of epigenetic genes in human liver tissues from patients with different stages of NAFLD. We identified marked alterations in a significant number of epigenetic effectors, including DNA methyltransferase 1 (DNMT1) and its epigenetic cofactor UHRF1. DNMT1 and UHRF1 work in concert with the histone methyltransferase G9a in DNA methylation and gene expression regulation. We evaluated the potential relevance of the DNMT1/G9a/UHRF1 complex in in vitro and in vivo models of NAFLD.

**Method:** We analyzed four publicly available liver transcriptome datasets integrating more than 520 patients. In vitro studies were performed in HepG2 cells challenged with a NASH cocktail. Cells were treated with the DNMT1/G9a/UHRF1 complex small molecule inhibitor CM272. In vivo studies were performed in C57BL6 mice fed with normal chow diet (ND) or high-fat diet (HFD, 45% fat) for 4 or 9 months and different regimes of CM272 treatment (one month and one week, respectively). Transcriptionic profiling, biochemistry and histological analyses were performed.

**Results:** Inhibition of DNMT1 and G9a with CM272 significantly reduced serum triglyceride and free fatty acids, and hepatic lipids accumulation in the two HFD models. Liver tissues transcriptomic analyses revealed that CM272 modulated metabolic pathways fundamentally involved in fatty acids and cholesterol metabolism and, intriguingly also the expression of genes involved in immune pathways, such as antigen presentation and processing. DNMT1 and G9a inhibition also caused significant changes in the expression of genes involved in energy expenditure and lipid metabolism in brown and white adipose tissue. In vitro studies confirmed most of the in vivo findings, including a robust induction by CM272 of carboxylesterase 1 (CES1), a key enzyme in the liver triglyceride metabolism.

**Conclusion:** A profound dysregulation in the expression of epigenetic effectors characterizes human NAFLD progression. We show that the pharmacological modulation of the epigenetic complex DNMT1/G9a/UHRF1 markedly affects the course of this disease in its early stages. Our findings suggest that characterization of epigenetic pathways in NAFLD may help to understand the disease and to expose new targets.
OS166
Molecular characterization of metabolic associated fatty liver disease as an immune-mediated inflammatory disease: IMID associated fatty liver disease
Enrique García-Nieto1, Juan Carlos Rodriguez-Duque1,2, Paula Iruzubia1,2, Agustín García-Blanco1, Coral Rivas1,2, María Luisa Cagigal1, Javier Rueda-Gotor1, Montserrat Rivero1,2, Susana Armesto1, Marcos Antonio Gonzalez-Lopez5, Carlos Duran-Vian1, Anna Esteve Codina1, Marta Guti1, José Pedro Vaqué1,2, Javier Crespo1,2, María Teresa Arias Loste1,2.
1Research institute Marqués de Valdecilla (IDIVAL), Group of Clinical and Translational Research in Digestive Diseases Infection, Immunity and Digestive Pathology Group, Santander, Spain; 2University Hospital Marqués de Valdecilla, Gastroenterology and Hepatology Department, Santander, Spain; 3University Hospital Marqués de Valdecilla, Pathological Anatomy Service, Santander, Spain; 4University Hospital Marqués de Valdecilla, Division of Rheumatology, Santander, Spain; 5University Hospital Marqués de Valdecilla, Dermatology Department, Santander, Spain; 6CNAG-CRG, Centre for Genomic Regulation (CRG), Barcelona Institute of Science and Technology (BIST), Universitat Pompeu Fabra (UPF), Barcelona, Spain; 7University of Cantabria, Molecular Biology Department, Santander, Spain
Email: javiercrespo1991@gmail.com

Background and aims: Growing evidence support an increased prevalence of metabolic associated fatty liver disease (MAFLD) in the context of immune-mediated inflammatory diseases (IMIDs) that can occur independently of classic metabolic risk factors. We aimed to characterize clinically and mechanistically a prospective cohort of IMID-MAFLD patients compared to regular MAFLD patients.

Method: Cross-sectional, case-control study including a subset of IMID patients (inflammatory bowel disease, psoriasis, hidradenitis, and spondyloarthritides). Controls from a random sample drawn from the general population were age, gender, type 2 diabetes, and BMI matched in a 1:2 ratio. MAFLD was established by the controlled attenuation parameter. Liver biopsies were collected when MAFLD with significant liver fibrosis was suspected. Total RNA was obtained from frozen cases and analyzed by RNA-Seq. Differential gene expression was performed with limma-voom. Gene set enrichment analysis (GSEA) was performed with fgsea R package with a pre-ranked gene list. Serum protein concentrations were obtained using Quantikine ELISA Kit and fibrosis severity. Gene set enrichment analysis (GSEA) was performed on transfected cells. We observed that EphB2 was upregulated in IMID-MAFLD patients. A GSEA analysis detected the most relevant gene set of EphB2 and its ligands.

Results: 1435 IMID patients and 2918 controls were included. MAFLD prevalence was significantly higher among IMID patients than controls, as well as the prevalence of advanced-MAFLD (LSM >9.7 kPa). In multivariate analysis, concomitant IMID was an independent and the strongest predictor of advanced-MAFLD. We observed 87 highly significant genes differentially expressed between the two groups. Whereas genes like MT1M or MT1G were downregulated, genes like IGFBP2 showed a upregulated expression in IMID-MAFLD, others like DGR5 or the Metallotioneins MT1M, MT1G and MT1F were downregulated. Normalized expression values of significantly expressed genes and specific clustering of IMID-MAFLD and MAFLD cases are shown in Figure. A GSEA analysis detected the most relevant cellular activities in IMID-MAFLD vs. MAFLD. IMID-MAFLD cases displayed an enriched expression of genes implicated in pro-tumoral activities like signaling by Rho-GTPases or the control of the Cell Cycle concomitant with a negative expression of genes related to the metabolism. IGFBP-2 protein levels in serum samples from IMID-MAFLD and MAFLD validated the transcriptional data.

Conclusion: MAFLD has a disproportionately high tendency to occur in IMID populations, which may be explained by its distinctive chronic inflammatory burden. Supporting this, we provide a functional explanation to distinguish between MAFLD groups, and show that IMIDs can trigger a pro-tumoral liver condition that can lead to an aggressive form of MAFLD independently of classic metabolic pathways.

OS167
EphB2 is a novel signaling receptor in non-alcoholic steatohepatitis liver fibrosis
Patrice Mimche1, Severin Donald Kamdem1, Erika Egal1, Quinian Johanson1, Tuan Pham2, Kimberley Evason3, Sihem Boudina4, Michael Ortiz2, Francis Sprouse5, Chinthaka Mahesh Udumulle Gedara3, Karina Cortez3, Mahmoud Ahmed6, Hesham Sadek6, Mark Henkemeyer5, 1University of Utah, Department of Pathology, Salt Lake City, United States; 2University of Utah, Department of Internal Medicine, Division of Gastroenterology, Hepatology and Nutrition, Salt Lake City, United States; 3University of Utah and Huntsman Cancer Institute, Department of Pathology, Salt Lake City, United States; 4University of Utah, Department of Nutrition and Integrated Physiology, Salt Lake City, United States; 5UT Southwestern Medical Center, Department of Neuroscience, Dallas, United States; 6UT Southwestern Medical Center, Department of Internal Medicine and Molecular Biology, Dallas, United States
Email: patrice.mimche@path.utah.edu

Background and aims: Emerging evidence suggests that the EphB2 receptor tyrosine kinase regulates tissue inflammation and fibrosis. However, its role in diet-induced non-alcoholic steatohepatitis (NASH) fibrosis has not been explored. We aimed to decipher the contribution of EphB2 to non-alcoholic steatohepatitis (NASH) development in mouse NASH models and in patients at various stages of non-alcoholic fatty liver disease progression.

Method: In NASH patients, hepatic EphB2 and serum sEphrinB2 ligand were evaluated. Disease phenotyping was performed in male and female wild type (WT), EphB2+/−, EphB2-kinase-dead (EphB2F620D), EphB2-kinase-overactive (EphB2K661R) mice, and in hepatic stellate cell (HSC) specific EphB2−/− mice fed the obesogenic Gubra-Amylin NASH (GAN) diet for 22–28 weeks and the Choline Deficient Amino-acid improved (CDAA) high-fat diet for 10–12 weeks. The crosstalk between EphB2 and TGFβ signaling in primary human HSC was investigated in vitro. Pharmacological inhibition of EphB2 for the treatment of NASH was also evaluated in vivo.
Histology, flow cytometry, qPCR, biochemical assays, bulk RNA sequencing, and single cell RNA-sequencing were used to dissect the molecular mechanism underlying EphB2 function in NASH.

**Results:** Hepatic EphB2 was strongly upregulated in NASH patients and correlated with NASH fibrosis score. Serum sEphrinB2 was also elevated in NASH patients. In mouse models of NASH, EphB2−/− knockout mice showed a significant reduction in liver steatosis, inflammation, and fibrosis compared to WT mice. EphB2 forward signaling is likely the main driver of NASH progression as depicted by rhTGF-β1, 2, and 3 upregulating EphB2 in human HSC and its silencing with EphB2-siRNA abrogates TGFβ-mediated HSC transdifferentiation into myofibroblasts-producing collagen. Finally, pharmacological inhibition of EphB2 reduced NASH fibrosis in mice.

**Conclusion:** We have identified EphB2 as a key player in the pathogenesis of diet-induced fatty liver disease in human and mouse and showed that therapeutic targeting of this receptor mitigates NASH fibrosis.

**Liver transplantation and Acute liver failure: Clinical aspects**

**OS168**

**Cumulative exposure to tacrolimus and incidence of cancer after liver transplantation**

Manuel Rodríguez-Perálvarez,1 Gonzalo Crespo,2 Jesús Rivera,3 Antonio González-Rodríguez,4 Estefanía Berge Garrido,4 Mikel Gastañ6,4 Patricia Ruiz,6 Anna Curell5, Cristina Dopazo5, Ainhoa Fernández-Yunquera,4 Fernando Díaz,4 Ana Sánchez Martínez,2 María Luisa Ortíz,2 Marina Berenguer,2 Tommaso Di Maira4, José Ignacio Herrero,4 Mercedes Iñarrairaegui9, Carolina Almohalla10, Esteban Fuentes Valenzuela11, Sara Lorente Perez,8, Cristina Borao,7, Fernando Casafont12, Emilio Fabrega13, Sonia Pascual13, Patricio Más-Serrano13, María Angeles Lopez Garrido14, Rocío González-Grande15, Javier Zamora1, Rafael Alejandre1, Antonio M. Gómez-Orellana16, Carmen Bernal17, Miguel Ángel Gómez Bravo17,1 Hospital Universitario Reina Sofía, University of Córdoba, IMIBIC, CIBERehd, Department of Hepatology and Liver Transplantation, Córdoba, Spain; 2Hospital Clinic Barcelona, IDIBAPS, CIBERehd, Univ. of Barcelona, Spain; 3Hospital Universitario Ntra. Sra. de Candelaria, Spain; 4Hospital Universitario Cruces, Biocrues Bizkaia Health Research Institute, Spain; 5Hospital Universitario Vall d‘Hebron, Spain; 6Hospital General Universitario Gregorio Marañón, CIBERehd, Spain; 7Hospital Universitario Virgen de la Arrixaca, IMIB, Spain; 8Hospital Universitari i Politècnic La Fe, CIBERehd, Spain; 9Clínica Universidad de Navarra, CIBERehd, IDISNA, Spain; 10Hospital Universitario Río Hortega, Spain; 11Hospital Luciano Blesa, Spain; 12Marqués de Valdecilla University Hospital, Idiex, Spain; 13Hospital General Universitario Alicante, CIBERehd, Spain; 14Hospital Universitario Virgen de las Nieves, Spain; 15Hospital Regional Universitario de Málaga, Spain; 16University of Córdoba, Department of Computer Science and Numerical Analysis, Spain; 17Hosp. Univ Virgen del Rocío, Spain

**Email:** ropeml@hotmail.com

**Background and aims:** Cancer, either de novo or recurred, is the leading cause of death after liver transplantation (LT). We aimed to evaluate the effect of maintenance immunosuppression on post-LT malignancy.

**Method:** Multicentre case-control nested study involving 16 LT institutions. The eligible cohort included adult patients undergoing LT (2010–2015) who received tacrolimus-based immunosuppression. Patients developing malignancy after LT, either de novo or recurred, formed the group of cases. Controls were selected among patients without cancer after an identical follow-up period. Cases and controls were matched by propensity score based on age, gender, smoking habit, aetiology of liver disease and hepatocellular carcinoma (HCC) before LT. The exposure to immunosuppressive drugs within the first year after LT was recorded. Cumulative exposure to tacrolimus (CET) was calculated by the area under curve of trough levels (PMID: 31107827). The relationship between the immunosuppression protocol and the risk of post-LT malignancy was evaluated using multivariate logistic and Cox’s regression.

**Results:** The eligible cohort included 2, 495 patients. The study cohort comprised 425 patients who developed post-LT malignancy and 425 matched controls. The most frequent types of malignancy were: HCC recurrence (24%), non-melanoma skin cancer (16.1%), lung cancer (13.7%) and head and neck tumors (12.6%). Cases and controls were comparable in terms of age, gender, smoking habit, aetiology of liver disease and presence of HCC before LT. The immunosuppression protocol was similar in cases and controls (p > 0.51), and there were no differences in terms of individual drugs. Patients with post-LT malignancy had increased CET as compared with matched controls, both within the first 3 months (p = 0.002) and within the first 12 months (p = 0.009). An increased CET was the only independent predictor of post-LT malignancy after controlling for clinical features and concomitant immunosuppressive drugs: the hazard ratio (HR) of post-LT malignancy for a 20% increase of CET was 1.11 (95% CI 1.05–1.19; p = 0.001) at 3 months, and 1.10 (95% CI 1.03–1.17; p = 0.004) at 12 months. These results were consistent when considering exclusively de novo malignancy (CET at 3 months HR = 1.09; p = 0.020 and CET at 12 months HR = 1.10; p = 0.016).

**Conclusion:** CET is the most important immunosuppression-related risk factor of cancer after LT, thus highlighting the relevance of tacrolimus minimization.
Background and aims: Infections caused by bacteria resistant to 3 or more antibiotic families (multidrug-resistant bacterial infections or MDRBIs) are an increasing healthcare issue. Our aim was to analyze the prevalence, burden, and risk factors associated with MDRBIs after liver transplantation (LT).

Method: Retrospective multi-center cohort study including adult patients who underwent LT from January 2017 to December 2019. Risk factors related to pre-LT liver disease, surgical procedure, and post-operative stay were recorded. A multivariate logistic regression analysis was performed to identify independent predictors of MDRBIs within the first 90-days after LT.

Results: We included 1,089 LT (1,004 patients) performed in 9 tertiary Spanish hospitals. Mean age was 56.83 ± 9.31 years, 72.5% (801 patients) were men. Thirty-three percent (358 infections, 50.7%) were considered MDRBIs (358 infections, 50.7%). Treatment with AAT in hypoxia exposed ICOs failed to attenuate apoptosis but switched it into necroptosis. We further identified clinical-grade alpha-1 antitrypsin (AAT) as a potent inhibitor of hypoxia-induced apoptosis without necroptotic switch (p < 0.05). Treatment of ICOs with AAT in hypoxia exposed ICOs increased the cell viability (p < 0.05) and partially restored the Ki67 expression (p < 0.05). Treatment of ICOs with AAT in hypoxia exposed ICOs increased the cell viability (p < 0.05) and partially restored the Ki67 expression (p < 0.05).
Background and aims: Among cancer patients on checkpoint inhibitors (CPI), 1–16% develop checkpoint inhibitor-induced liver injury (ChILI). However, there are limited accurate reports of the incidence rate of ChILI as assessed by time on treatment. Using a prospective database and review of patient records, we estimated the risk and incident rate of ChILI in all melanoma and renal cancer patients who received CPI at Nottingham University Hospitals (NUH) from 2011–2021.

Method: Using ‘ChemoCare’, a prospective oncology prescribing database, we identified all adult patients who received CPI for adjuvant or metastatic melanoma or metastatic renal cell carcinoma (RCC) since 2011. Prescription event monitoring was performed using patient-related records and digital records; ChILI, other immune-related adverse events (irAE) and response to rechallenge were recorded. International Expert Working Group (EWG) for drug-induced liver injury case definitions were used to define ChILI cases and grade severity. Causality was assessed using Roussel Uclaf Causality Assessment Method (RUCAM).

Results: Out of 432 patients, ChILI occurred in 38 (8.8%). RUCAM was ‘possible’ in 9, ‘probable’ in 22 and ‘highly probable’ in 7 cases. The incidence rate of ChILI was 10.93 (95% CI 5.66–18.75) per 1000 patient-months of CPI exposure, with most cases occurring in patients treated with dual checkpoint inhibition. ChILI severity was ‘mild’ in 11 and ‘moderate’ in 27 (based on EWG grading); 36 of 38 (94.7%) received corticosteroids. Mean time to resolution of ChILI was 77 days ±9 following steroid therapy compared to 49 days ±2 in those untreated. Of 38 ChILI cases, 15 (39.5%) were re-treated with a single CPI, and only one patient developed recurrent ChILI. However, three developed colitis, one each developed hyponaditis and severe neuropathy.

Table: Risk and incidence rate of ChILI per CPI regime.

<table>
<thead>
<tr>
<th>Cancer</th>
<th>CPI Regime</th>
<th>Number of Patients</th>
<th>Mean number of cycles</th>
<th>Person-Time at risk (months)</th>
<th>ChILI cases</th>
<th>Risk</th>
<th>Incidence rate per 1000 patient-months</th>
</tr>
</thead>
<tbody>
<tr>
<td>Melanoma</td>
<td>Ipilimumab</td>
<td>88</td>
<td>3</td>
<td>210.53</td>
<td>2</td>
<td>2.27%</td>
<td>9.50 (95% CI 5.73–17.25)</td>
</tr>
<tr>
<td>RCC</td>
<td>Ipilimumab folowed by Nivolumab</td>
<td>102</td>
<td>3</td>
<td>combination 8 Nivolumab</td>
<td>7</td>
<td>1</td>
<td>2.56%</td>
</tr>
<tr>
<td>RCC</td>
<td>Nivolumab</td>
<td>22</td>
<td>12</td>
<td>281.20</td>
<td>0</td>
<td>0%</td>
<td>0.00 (95% CI 0.00–0.01)</td>
</tr>
<tr>
<td>RCC</td>
<td>Pembrolizumab</td>
<td>108</td>
<td>9</td>
<td>1035.37</td>
<td>3</td>
<td>2.78%</td>
<td>2.90 (95% CI 2.32–3.64)</td>
</tr>
<tr>
<td>RCC</td>
<td>Adjuvant Pembrolizumab</td>
<td>39</td>
<td>7</td>
<td>316.70</td>
<td>1</td>
<td>2.56%</td>
<td>3.16 (95% CI 2.08–4.38)</td>
</tr>
<tr>
<td>RCC</td>
<td>Ipilimumab + Nivolumab folowed by Nivolumab maintenance</td>
<td>19</td>
<td>3</td>
<td>160.10</td>
<td>2</td>
<td>10.53%</td>
<td>12.49</td>
</tr>
<tr>
<td>RCC</td>
<td>Total</td>
<td>54</td>
<td>12</td>
<td>524.70</td>
<td>1</td>
<td>8.8%</td>
<td>19.10 (95% CI 16.2–21.8)</td>
</tr>
</tbody>
</table>

Conclusion: Prescription event monitoring provides an accurate estimate of the risk of ChILI as well as its outcomes. Rechallenge with single-agent CPI is feasible, with most patients not having a recurrence of ChILI. However, there is a risk of developing other irAE, especially colitis. The benefits and risks of corticosteroid therapy should be evaluated in a larger cohort of ChILI patients.

Background and aims: MELD 3.0 improves upon MELD-Na by incorporating sex and albumin alongside bilirubin, creatinine, INR, and sodium, updating the existing coefficients, adding relevant factors to better predict mortality and the incidence of complications in patients with liver disease.

Methods: We applied MELD 3.0 to a prospective cohort of patients undergoing liver transplantation at our centre. We compared the performance of MELD 3.0 with MELD-Na using receiver operating characteristic (ROC) curves and Kaplan-Meier survival analysis.

Results: The median MELD score was 12.5 (IQR: 8.5–17.5) in the overall cohort. The ROC curves showed that MELD 3.0 had a higher area under the curve (AUC) than MELD-Na (0.95 vs 0.88). Kaplan-Meier survival analysis revealed that patients with a MELD score >20 had a higher 1-year survival rate with MELD 3.0 compared to MELD-Na (91% vs 85%).

Conclusion: MELD 3.0 provides a more accurate prediction of mortality and complications in patients with liver disease, improving the selection of candidates for liver transplantation.
Figure: (abstract: OS171)
interactions, and resetting the upper bound of serum creatinine to 3.0 from 4.0 mg/dL. In the US liver allocation system, previous versions of MELD including MELD-Na have been capped at 40. We study the impact of increasing MELD score beyond this threshold on liver transplant outcomes.

**Method:** Adult waitlist registrations for liver transplantation from 15 Jan 2016 to 30 Jun 2021 were identified using OPTN data. MELD 3.0 = 1.33 (if female) + 4.56*loge (bilirubin) + 0.82* (137–Na) – 0.24* (137–Na)*loge (bilirubin) + 9.09*loge (INR) + 11.14*loge (creatinine) + 1.85* (3.5-albumin) – 1.83* (3.5-albumin)*loge (creatinine) + 6. Survival analysis evaluated the effect of increasing MELD 3.0 beyond 40 on 30-day waitlist mortality. Individual follow-up time started from the first qualifying MELD score ≥40; patients were censored after 30 days of follow-up, at the time of an approved death, or liver transplant, whichever occurred first. In a sensitivity analysis, the Cox regression model was performed to consider MELD 3.0 as a time-dependent covariate if MELD remained ≥40. 2-year posttransplant outcomes were also assessed.

**Results:** There were 54, 060 new waitlist registrations during the study period, 2476 (4.6%) with MELD-Na ≥40 and 2820 (5.2%) with MELD 3.0 ≥40 at listing. 23.9% of candidates with MELD ≥40 met clinical criteria for acute-on-chronic liver failure. An additional 3, 254 candidates recorded MELD 3.0 ≥40 during their waiting time. 30-day waitlist mortality was higher for each point increase in MELD 3.0 (HR 1.15), with a linear relationship from MELD 3.0 of 40 up to 55. 30-term waitlist mortality was higher for each increasing MELD stratum, from 65.6% to 88.7% for those with MELD 40–44 compared to MELD 50+ (Figure). Results were similar when MELD 3.0 was considered as a time-dependent covariate. Posttransplant outcomes were comparable across MELD strata including MELD 35–39.

**Conclusion:** MELD 3.0 is anticipated to increase the proportion of patients reaching or surpassing the maximum allocation score of 40. Patients with MELD ≥40 may derive greater survival benefit from LT compared to MELD 40 without necessarily worse post-transplant outcome. Increasing the maximum score for MELD 3.0 may improve risk stratification of waitlist mortality and better represent liver transplant urgency for the sickest patients, including those with acute-on-chronic liver failure.

**OS174**
Bile duct on a chip: engineering a microfluidic platform for studying biliary epithelium in a dish
Jorke Willemse1, Mees N.S. de Graaf2, Gilles van Tienderen1, Luc J.W. van der Laan1, Valeria Orlova2, Jeroen de Jonge1, Monique M.A. Verstegen1, 1Erasmus MC Transplant Institute University Medical Center, Department of surgery, Rotterdam, Netherlands; 2Leiden University Medical Center, Department of Anatomy and Embryology, Netherlands
Email: j.willemse@erasmusmc.nl

**Background and aims:** Biliary complications that may arise after liver transplantation, such as non-anastomotic strictures and diffuse bile leakage, are challenging and complex. Ischemia-related cell death and impaired regeneration of damaged biliary epithelium is known to be involved in causing these complications. Intrahepatic cholangiocyte organoids (ICO) allow for the expansion and study of cholangiocyte-like cells, but access to the lumen of the organoids is limited and can only be studied after disrupting the 3D structure. There are currently no in vitro models mimicking the circumstances as exposure of bile ducts to warm ischemia time or cold storage, and therefore we aimed to establish a microfluidic bile-duct-on-chip (BDOC) platform for studying the effect of these conditions on biliary epithelium in vitro.

**Method:** ICO were initiated from human liver biopsies (N = 5) obtained during liver transplant procedures. Three-channel BDOC (dimensions: length 1 cm, width and height 500 μm) were prepared by casting polydimethylsiloxane (PDMS) into a mold. Subsequently, plasma treated PDMS chips were bonded to glass slides. The BDOC channels were filled with collagen type I pre-gel and viscous finger patterning procedures were used to create channels inside these collagen hydrogels. ICO-derived cells (25·103 cells/channel) were introduced into the channels and ICO expansion medium was added to the reservoirs. The BDOC were incubated for up to 21 days. Growth of epithelial cells was monitored using confocal microscopy and histology.

**Results:** ICO-derived cells populated the entire surface of the channels with a single layer of cells within 7 days after seeding. Whole mount confocal imaging revealed that cells were columnar in shape and morphologically looked like biliary epithelium. Zonula Occludens-1 (ZO-1) staining showed cholangiocyte-like polarization of cells in honey comb patterns. The cells express the cholangiocyte markers cytokeratin 7 and 19 on gene and protein level.

**Conclusion:** The results show that microfluidic approaches combined with cholangiocyte-like (KRT 7 and 19-positive) cells from ICO can be used to create healthy small diameter intrahepatic bile duct structures in vitro. This model allows for detailed analysis of epithelial damage and regeneration during warm and cold ischemic conditions that are known to cause post transplantation complications to the biliary system, and also to study onset and progression of biliary diseases.

<table>
<thead>
<tr>
<th>MELD 3.0</th>
<th>n Transplanted</th>
<th># of deaths</th>
<th>30-day mortality</th>
<th>Median survival time in days (95% CI)</th>
</tr>
</thead>
<tbody>
<tr>
<td>40–44</td>
<td>5015</td>
<td>3463</td>
<td>1304</td>
<td>65.6% (18 (17–20)</td>
</tr>
<tr>
<td>45–49</td>
<td>872</td>
<td>525</td>
<td>327</td>
<td>81.2% (13 (11–14))</td>
</tr>
<tr>
<td>50+</td>
<td>187</td>
<td>74</td>
<td>109</td>
<td>88.7% (5 (3–7)</td>
</tr>
</tbody>
</table>

Figure: Kaplan-Meier curves: 30-day survival of patients with MELD 3.0 ≥40 at any time on waitlist.
Thursday 23 June

Alcoholic liver disease

THU001
Heavy alcohol intake along with ALDH2 polymorphism increases the risk of hepatocellular carcinoma and mortality in hepatitis B virus-related cirrhosis
Chih-Wen Lin1, Ming Chao Tsai2, Sien-Sing Yang3, Chih-Che Lin2, Wen-Lung Wang2, Yao-Chun Hsu2, Yaw-Sen Chen2, Ming-Lung Yu4, Jui-Ting Hu4, 1E-Da Hospital, Medicine, Kaohsiung, Taiwan; 2Kaohsiung Chang Gung Memorial Hospital, Kaohsiung, Taiwan; 4Kaohsiung Medical University Chung-Ho Memorial Hospital, Kaohsiung, Taiwan

Background and aims: Hepatitis B virus (HBV) infection and alcoholism are risk factors for hepatocellular carcinoma (HCC) and mortality. We investigated the effect of heavy alcohol intake, ALDH2 polymorphism, and HBV infection on clinical outcomes and risk factors in cirrhotic patients.

Method: We enrolled 1515 cirrhotic patients (342 patients with HBV infection and alcoholism, 796 patients with HBV infection, and 373 patients with alcoholism) from three tertiary hospitals in Taiwan between 2005 and 2020.

Results: Of patients with concomitant HBV infection and alcoholism, HBV infection alone, and alcoholism alone, 81 (23.7%), 134 (16.8%), and 55 (14.6%) patients developed HCC and 151 (45.3%), 322 (40.5%), and 150 (39.8%) patients experienced mortality, respectively. The 15-year cumulative incidences of HCC (66.4% vs. 46.8%, 54.8%, P < 0.001) and mortality (88.9% vs. 81.9%, 90%, P < 0.001) were significantly higher in cirrhotic patients with HBV infection and alcoholism than in those with HBV infection alone or alcoholism alone before and after propensity score matching. The ALDH2 polymorphism (allele GA/AA) with heavy alcohol intake significantly increased the risk of HCC and mortality in HBV-related cirrhotic patients. Risk factors for HCC were baseline serum HBV DNA (HR = 4.08), antiviral therapy (HR = 0.13), alcohol intake (HR = 1.77 and 1.49), abstention (HR = 0.41), and ALDH2 polymorphism (HR = 5.09). Risk factors for mortality were abstention (HR = 0.22), ALDH2 polymorphism (HR = 1.49), Child-Pugh class (HR = 1.43 and 1.98), serum albumin (HR = 0.62), and HCC development (HR = 1.57) in cirrhotic patients with HBV infection and alcoholism.

Conclusion: Heavy alcohol intake along with the ALDH2 polymorphism significantly increased the risk of HCC and mortality in HBV-related cirrhotic patients.

THU002
Biomarkers for prediction of alcohol-related liver cirrhosis in the Swedish general population
Gustav Jakobsson1,2, Mats Talbäck2, Göran Walldius1, Niklas Hammar2, Ying Shang3, Hannes Hagström1,4,5, 1Division of Hepatology, Department of Upper GI, Karolinska University Hospital, Stockholm, Stockholm, Sweden; 2Department of Medicine Capio St Göran’s hospital, Stockholm, Stockholm, Sweden; 3Unit of Epidemiology, Institute of Environmental Medicine, Karolinska Institutet, Stockholm, Sweden; 4Department of Medicine, Huddinge, Karolinska Institutet, Stockholm, Sweden; 5Clinical Epidemiology Unit, Department of Medicine, Solna, Karolinska Institutet, Stockholm, Sweden

Background and aims: Alcohol-related liver cirrhosis (ARLC) is a severe and well-known complication to chronic alcohol overconsumption. There are several known biomarkers associated with increased intake of alcohol and liver damage. There is limited knowledge on which biomarkers that have the best predictive capabilities for future ARLC, especially in a general population setting. Here, we investigated this in a large, population-based Swedish cohort.

Method: We used data from the AMORIS cohort, a general population cohort with blood samples from routine health care and outpatient visits in primary or occupational care collected from 1985 through 1996. The cohort consists of 812 073 individuals, approximately 35% of the total population in Stockholm county, Sweden, during this period. We included all persons above 18 years old, with a baseline blood sample of Alanine transaminase (ALT) and Aspartate transaminase (AST). We excluded subjects with known liver cirrhosis at baseline.

We ascertained incident cases of ARLC by linking the AMORIS cohort to Swedish national health registers. All subjects were followed until a first event of ARLC, death, emigration or end of the study period, December 31, 2011. Biomarkers were standardized to increase comparability. Associations between biomarkers and incident ARLC were analyzed with Cox regression models and discrimination was assessed using C-statistics.

Results: We identified 537 479 individuals with a mean follow-up time of 19.0 years. The biomarkers with the best predictive capabilities in both unadjusted and adjusted analyses were gamma-glutamyl transferase (GGT) and mean corpuscular volume (MCV), with an adjusted C-index of 0.81 and 0.85 respectively. The AST/ALT-ratio showed a lower predictive value, with a C-index of 0.70 (Table 1).

Table 1: Hazard ratios (HR) reflect an increase of one standard deviation for each parameter. *Unadjusted; **Adjusted for sex and age. Harrell’s C-index.

<table>
<thead>
<tr>
<th>biomarker</th>
<th>Number</th>
<th>HR</th>
<th>95% CI</th>
<th>C-index</th>
<th>HR</th>
<th>95% CI</th>
<th>C-index</th>
</tr>
</thead>
<tbody>
<tr>
<td>ALT</td>
<td>537 479</td>
<td>1.05</td>
<td>1.05–1.05</td>
<td>0.81</td>
<td>1.05</td>
<td>1.05–1.05</td>
<td>0.75</td>
</tr>
<tr>
<td>AST</td>
<td>537 479</td>
<td>1.04</td>
<td>1.03–1.04</td>
<td>0.85</td>
<td>1.03</td>
<td>1.03–1.04</td>
<td>0.76</td>
</tr>
<tr>
<td>GGT</td>
<td>515 958</td>
<td>1.14</td>
<td>1.14–1.15</td>
<td>0.90</td>
<td>1.14</td>
<td>1.13–1.14</td>
<td>0.81</td>
</tr>
<tr>
<td>Bilirubin</td>
<td>121 260</td>
<td>0.71</td>
<td>0.68–0.74</td>
<td>0.58</td>
<td>0.70</td>
<td>0.66–0.73</td>
<td>0.72</td>
</tr>
<tr>
<td>Albumin</td>
<td>470 915</td>
<td>1.19</td>
<td>1.17–1.21</td>
<td>0.62</td>
<td>1.18</td>
<td>1.16–1.20</td>
<td>0.71</td>
</tr>
<tr>
<td>MCV</td>
<td>172 891</td>
<td>2.14</td>
<td>2.07–2.21</td>
<td>0.80</td>
<td>2.10</td>
<td>2.03–2.17</td>
<td>0.85</td>
</tr>
<tr>
<td>AST/ALT-ratio</td>
<td>537 479</td>
<td>0.97</td>
<td>0.93–1.02</td>
<td>0.52</td>
<td>1.08</td>
<td>1.05–1.11</td>
<td>0.70</td>
</tr>
</tbody>
</table>
Conclusion: The best predictive biomarkers for ARLC in the general population were MCV and GGT, whereas the commonly used AST/ALT ratio had a lower predictive capability.

THU003
A history of bariatric surgery is independently associated with a younger age at onset of severe alcoholic hepatitis

Luukas Van Melkebeke,1,2 Annelotte Broekhoven,3 Tessa Ostryn,3 Minneke Coenraad4, Hannelie Korf4, Tania Roskams4, Lukas Van Melkebeke4, Hannelie Korf4, Tania Roskams4, Schalk van der Merwe1,2, Frederik Nevens1,2, Jef Verbeek1,2, KU Leuven, Laboratory of Hepatology, Belgium; 2University Hospitals Leuven, Department of Gastroenterology and Hepatology, Belgium; 3Leiden University Medical Center, Department of Gastroenterology and Hepatology, Netherlands; 4KU Leuven, Department of Imaging and Pathology, Translational Cell and Tissue Research, Belgium

Email: luukas.vanmelkebeke@kuleuven.be

Background and aims: Patients with prior bariatric surgery (BS) are at risk to develop an alcohol use disorder (AUD). We assessed the effect of prior BS on disease profile and outcome of patients with severe alcoholic hepatitis (sAH).

Method: From 01/2008 to 04/2021, consecutive patients admitted to our tertiary referral center with biopsy-proven sAH were included in a prospective database. Student’s t-test, Wilcoxin rank sum test and Fisher’s exact test were used. A p value <0.05 after multiple testing correction was considered significant.

Results: sAH patients (n = 158) were identified with a median follow-up of 366 (68–1656) days. Out of this cohort, 28 (18%) patients had a history of BS (BS-group): 27 (96%) underwent bypass surgery and 1 patient gastric banding. No patient underwent sleeve gastrectomy. The proportion of patients with BS increased significantly over time reaching a number of 4 (8%) within the first 5 years, 11 (19%) within the following 5 years and 13 (28%) during the last 4 years (p = 0.02) of the follow-up period. An important finding from our analysis was that patients in the BS-group were significantly younger at diagnosis of sAH, were more frequently female, featured an elevated body mass index (BMI) and advanced steatosis upon histological evaluation of the liver biopsy (Table 1). Furthermore, there were no differences in sAH disease severity (histological and Maddrey) or corticosteroid response (Lille score) (Table 1). Importantly, the correlation between BS and a younger age at diagnosis remained significant after correction for sex, steatosis and BMI in a multivariate regression analysis (p <0.001). Notably, survival determined after 28 or 90 days following the onset of sAH remained unchanged (Table 1).

<table>
<thead>
<tr>
<th>Age</th>
<th>BS-group (n = 28)</th>
<th>Other (n = 130)</th>
<th>p value</th>
</tr>
</thead>
<tbody>
<tr>
<td>BMI</td>
<td>44.3 ± 8.1</td>
<td>50.4 ± 10.3</td>
<td>0.005</td>
</tr>
<tr>
<td>Sex (male)</td>
<td>15 (54)</td>
<td>81 (63)</td>
<td>0.02</td>
</tr>
<tr>
<td>BMI</td>
<td>29.7 ± 4.9</td>
<td>29.6 ± 5.0</td>
<td>0.2</td>
</tr>
<tr>
<td>Steatosis</td>
<td>35–66%</td>
<td>35–66%</td>
<td>NS</td>
</tr>
<tr>
<td>Polymorphonuclear infiltration</td>
<td>No or mild</td>
<td>Severe</td>
<td>NS</td>
</tr>
<tr>
<td>Mitral valves</td>
<td>2 (7%)</td>
<td>17 (13%)</td>
<td>NS</td>
</tr>
<tr>
<td>Ballooning</td>
<td>29 (100%)</td>
<td>130 (100%)</td>
<td>NS</td>
</tr>
<tr>
<td>Medry score</td>
<td>1 (4%)</td>
<td>13 (10%)</td>
<td>NS</td>
</tr>
<tr>
<td>Lille score</td>
<td>6 (5.7–7.2)</td>
<td>53.6 (45–70.9)</td>
<td>NS</td>
</tr>
<tr>
<td>Survival 90 days</td>
<td>29 (100)</td>
<td>29 (100)</td>
<td>NS</td>
</tr>
<tr>
<td>Survival 180 days</td>
<td>29 (100)</td>
<td>29 (100)</td>
<td>NS</td>
</tr>
</tbody>
</table>

Conclusion: The proportion of sAH patients with prior BS has increased 3-fold over the last 15 years. Bypass surgery is independently associated with younger age of sAH onset but not with corticosteroid response or short-term survival. These novel findings indicate the need for early and effective prevention of AUD and sAH in patients who underwent bypass surgery.

THU004
Cyclophilin inhibitor CRV431 as a potential therapy for alcohol-related liver disease

Elena Palma1,2, Sara Campinoti1,2, Una Rastovic1,2, Nicola Harris1,2, Tsin Shue Koay1,2, Lola Ajayi1,2, Bruna Almeida1,2, Sandra Phillips1,2, Daren Ure3, Melissa Preziosi4, Marjorie Yumol5, Rosa Mique6, Yoh Zen7, Andreas Prachalias1, Krishna Menon8, Nigel Heaton4, Luca Urbani1,2, Shilpa Chokshi1,2, 1The Roger Williams Institute of Hepatology, London, United Kingdom; 2King’s College London, Faculty of Life Sciences and Medicine, London, United Kingdom; 3Hepion Pharmaceuticals, United States; 4Institute of Liver Studies, King’s College London, United Kingdom

Email: e.palma@researchinliver.org.uk

Background and aims: Cyclophilins are peptidyl-prolly isomerases that facilitate protein folding and regulate several biological processes with isoforms A, B, D being best characterised. Cyclophilin inactivation via therapeutic inhibition or genetic manipulation has been shown beneficial at various stages of liver disease, including steatosis, fibrosis, inflammation, cell injury and in hepatocellular carcinoma. CRV431 is a pan-cyclophilin inhibitor (non-immunosuppressant cyclosporin derivative) that is currently in clinical development for NASH (Phase 2A). Our study aims to evaluate the effects of CRV431 in human experimental models of Alcohol-related Liver Disease (ALD) and on fibrosis in primary hepatic stellate cell (HSC) cultures.

Method: Patient-matched Precision Cut Liver Slices (PCLS) and primary HSCs were prepared from human liver specimens (different fibrotic stages, n = 8). PCLS were exposed to hepatotoxic insults including ethanol 250 mM, fatty acids 0.1 mM, LPS 10 µg/mL individually and/or combined for up to 5days and HSCs activated with TGF-β1 for up to 10days, in the presence/absence of 5 µM CRV431. Tissue functionality was evaluated by histology, cytokeratin-18 release and mitochondrial assays. In PCLS and HSCs, fibrosis/HSC activation status was assessed by gene expression, immunofluorescence and secretion of fibrotic markers. Pro-inflammatory cytokines were quantified by Luminox.

Results: Features of alcoholic steatohepatitis were observed in human PCLS exposed to the insults, and CRV431 profoundly reduced the expression and secretion of pro-fibrogenic markers and restored a balanced cytokine profile. CRV431 alone was not hepatotoxic and did not induce cell death. In HSCs, CRV431 reduced αSMA and collagen deposition/expression when added simultaneously or after TGF-β1 activation. In addition, alignment of collagen fibers deposited by HSCs was significantly affected by the drug treatment.

Conclusion: Our results confirm the role of cyclophilins in liver fibrosis, including HSC activation, collagen deposition and orientation. These data reveal for the first time the potential for the cyclophilin inhibitor CRV431 to reduce ALD-induced fibrosis and suggest the possibility of using this drug as a therapy in ALD patients.

THU005
UK national service evaluation of transplant assessments for patients with alcohol related liver disease

Christopher Oldroyd1, Varuna Aluvihare2, Yun Chew3, Andrew Holt4, Steven Masson5, Richard Parke2, Nesil Rajorija6, Liz Shepherd6, Kenneth J. Simpson7, Clare Wai1, Ian Webzell2, Christopher Oldroyd1, 2, Varuna Aluvihare2, Yun Chew3, Andrew Holt4, Steven Masson5, Richard Parke2, Nesil Rajorija6, Liz Shepherd6, Kenneth J. Simpson7, Clare Wai1, Ian Webzell2, Michael Allison1, 3, Cambridge Liver Unit, Addenbrooke’s Hospital, Cambridge, United Kingdom; 2Institute of Liver Studies, King’s College Hospital NHS Foundation Trust, London, United Kingdom; 3The Liver Unit, St James’s University Hospital, Leeds, United Kingdom; 4The Liver Unit, Queen Elizabeth Hospital, Birmingham, United Kingdom; 5The Liver Unit, Freeman Hospital, Newcastle, United Kingdom; 6The Sheila Sherlock Liver Unit, Royal Free Hospital, London, United Kingdom; 7Scottish Liver Transplant Unit, Royal Infirmary of Edinburgh, Edinburgh, United Kingdom

Email: christopher.oldroyd@nhs.net

Background and aims: Alcohol-related liver disease (ArLD) is responsible for 60% of all liver disease and 84% of liver related
death in the UK. Although we know how many patients with ArLD are registered for a liver transplant, it is not known how many people with ArLD are being assessed for liver transplantation.

**Method:** Prospective data was collected for all patients with a diagnosis of ArLD assessed at the seven UK liver transplant centres from 1st Aug 2020 to 31st July 2021. This included; gender, age category, indication for transplant, United Kingdom Model for End-Stage Liver Disease Score (UKELD), co-factors for liver disease, duration of abstinence from alcohol at assessment, listing decision and reasons for decline or deferral.

**Results:** 568 patients were included. Median UKELD was 54 (range 41–76). 144 patients (25%) were female. Median duration of abstinence was 12 months (range 0–240), with 18.4% of assessments having ≤6 months abstinence. 329 (58%) were listed for liver transplantation, with 204 (36%) not listed, and 35 (6%) deferral. Indications for assessment were: UKELD ≥49 (90%), ascites (32%), hepatic encephalopathy (19%), hepatocellular carcinoma (16%) and other (11%) with most patients having multiple indications. The most common co-factor was non-alcoholic steatohepatitis (n = 57) with hepatitis C virus infection second most common (n = 24). Most common reasons for not listing were: medical co-morbidities (29%), potential recoverability (20%), too early to need transplant (19%), active or recent alcohol use (12%), concern about return to harmful drinking (11%) and surgical risk (5%). Comparing patients listed for transplant with those not listed we noted higher UKELD (Mean 55.66 vs 53.77 p <0.001), longer duration of abstinence (Median 12 vs 11 months U = 35751, p = 0.018) and no significant differences between gender (Chi Sq p = 0.258) or age distribution (Chi Sq p = 0.53).

**Conclusion:** This study provides a complete representation of all patients with ArLD assessed for liver transplantation over a 12-month period in the UK. Future work is planned to investigate outcomes of patients not listed for transplant and better understand reasons for patients being declined transplantation.

**THU006**

Fibroblast growth factor 21 (FGF21) is the main alcohol responsive peptide hormone in healthy humans and we show greater plasma concentrations after alcohol intake (0.7 g per kg body weight) in 12 individuals. Subsequently, plasma FGF21 concentrations were evaluated before, during and for 10 hours after alcohol exposure (0.5 g per kg body weight ingested over 10 minutes) in 15 males diagnosed with AUD (Group A), 15 males with paternal AUD (Group B), and 15 males without any predisposition to AUD (Group C). The desire for alcohol was assessed by visual analogue scale.

**Results:** Out of 1,472 proteins, only 11 changed after alcohol exposure in the 12 individuals, with FGF21 increasing the most (10-fold, p <0.0001) (Fig. 1A). The three groups were similar with regards to age and body mass index, and all participants had normal plasma concentrations of transaminases and bilirubin. Baseline plasma FGF21 concentrations did not differ between groups (p = 0.10). Peak plasma concentration of FGF21 was significantly higher in Group A (mean ± standard deviation: 4.0 ± 0.8 ng/ml) compared to Group C (1.8 ± 0.4 ng/ml) (p = 0.03) but not compared to Group B (2.2 ± 0.5 ng/ml) (p = 0.08) (Fig. 1B). Area under the curve for FGF21 was greatest in Group A (763 ± 150 ng/ml × min) followed by Group B (488 ± 120 ng/ml × min) and Group C (356 ± 77 ng/ml × min) with borderline statistical significant difference between Group A and C (p = 0.05) (Fig. 1B). Group A exhibited a greater desire to drink alcohol than seen in Group B (p = 0.02) and C (p = 0.01).

**Conclusion:** We show that FGF21 is the main alcohol responsive peptide hormone in healthy humans and we show greater plasma FGF21 concentrations after alcohol intake in individuals suffering from AUD compared to healthy individuals and individuals predisposed to AUD, respectively, implicating FGF21 in the pathophysiology of AUD.

**THU007**

**Background and aims:** Recent data have implicated gut-derived virulence factors in the pathogenesis of ArLD. However, it is not clear how virulence factors gain access to portal circulation. We investigated if gut-derived proteases enable bacterial translocation in...
patients with ArLD including patients with severe alcohol-related hepatitis (sAH).

Method: Protease activity of faecal water (FW) was assayed using fluorescently-labelled casein. Madin Darby Canine Kidney (MDCK) cells grown to confluent monolayers on Transwell plate inserts were used to create a model of gut barrier function validated against Caco-2 cells. FW was applied to the apical surface of the insert and the transepithelial electrical resistance (TEER), a marker of monolayer integrity, was measured at 120 min. Enterococcus faecalis (GelE+) supernatant served as a high-protease positive control while phosphate buffered solution (PBS) was a negative control. Zymography allowed differentiation of proteases in FW by substrate protein and molecular weight. Next, MDCK cells were grown to confluence on histology slides. FW was applied and the slides fixed and stained for the tight junction protein zonulin-1 (ZO-1). Finally, patient FW aliquots were plated on to protease-indicator agar and the bacterial isolates were plated on to protease-indicator agar and the bacterial isolates used to create a model of gut barrier function validated against CACO-2.

Results: FW samples were obtained from 38 subjects: sAH n = 14, decompenstated ArLD n = 11 and control subjects n = 13. Protease activity in FW correlated with change in TEER (ΔTEER) for all subjects (r = −0.5888, p < 0.001) (Fig. 1). Interestingly, ΔTEER correlated with liver function (r = −0.472, p = 0.0036 for MELD) with the greatest change in TEER seen in sAH FW samples. Strikingly, a broad-spectrum protease inhibitor added to the FW abolished the correlation between ΔTEER and protease activity (r = 0.0897, p = 0.644) (Fig. 1) and MELD score (r = −0.0645, p = 0.754). ZO-1 staining was markedly decreased in slides treated with sAH FW samples vs controls (Fig. 1b+c). Zymography showed the altered pattern of proteases within the FW of sAH patients. Protease-differential agar culture identified E. faecium, S. epidermidis and E. coli as the putative source of proteases responsible for tight junction damage.

Conclusion: Protease activity in patient FW can cause tight junction damage and increased gut permeability in vitro and correlates strongly with liver function. This points to a potential mechanism for gut derived virulence factors to reach the liver in ArLD, and particularly in sAH.

THU008 Incident acute kidney injury in severe alcohol-related hepatitis is strongly associated with mortality and can be predicted using micro-RNAs and markers of systemic inflammation
Luke D. Tyson1,2, Stephen Atkinson1,2, Michael Allison3, Andrew Austin4, Lily Cross5, James Dear6, Ewan Forrest7, Tong Liu1, Emma Lord1, Stephen Masson7, Joao Nunes8, Paul Richardson9, Stephen Ryder10, Mark Wright11, Mark Thursz12, Nikhil Vergis1,2
1Imperial College London, Department of Metabolism, Digestion and Reproduction, London, United Kingdom; 2St Mary’s Hospital, The Liver Unit, London, United Kingdom; 3Addenbrooke’s Hospital, Cambridge, United Kingdom; 4Royal Derby Hospital, United Kingdom; 5University of Edinburgh, United Kingdom; 6Glasgow Royal Infirmary, United Kingdom; 7Newcastle Freeman Hospital, High Heaton, United Kingdom; 8Meso Scale Diagnostics, Gaithersburg, United States; 9The Royal Liverpool University Hospital, Liverpool, United Kingdom; 10Queens Medical Centre, Nottingham, United Kingdom; 11University Hospital Southampton NHS Foundation Trust, United Kingdom
Email: luke.tyson@nhs.net

Background and aims: Acute kidney injury (AKI) can complicate severe alcohol-related hepatitis (sAH) and has been associated with increased mortality. However, the relative impact of AKI at baseline compared to AKI that develops on treatment has not been evaluated. Moreover, treatments that may modulate the risk of AKI are poorly defined. A range of biomarkers have shown promise to predict the development of AKI, but few have been independently validated in sAH.

Method: Data was available from 1051 sAH patients recruited to the STOPAH trial. AKI was defined by an adapted International Club of Ascites definition as either: an increase in creatinine >26.5 micromol/L above or 1.5x the lowest recorded; creatinine >133 micromol/L; or new renal replacement therapy. Incident AKI was defined as AKI at day 7 without baseline AKI. We compared baseline and incident AKI to 90-day mortality using Kaplan-Meier survival analysis and binary logistic regression. Further, we identified factors associated with baseline and incident AKI by multivariable models. Finally, we tested previously published and novel serum biomarkers and a micro-RNA panel measured by PCR array to predict incident AKI using AUROC analyses.

Results: Baseline AKI was present in 198/1051 (19%) patients and associated with increased D90 mortality (OR 1.42, 95% confidence interval 1.02–2.00, p = 0.038). Excluding 282 patients alive at D7 without D7 creatinine available, incident AKI developed in 119/769 (15%) patients and was associated with higher D90 mortality (OR 2.61, 1.72–3.96, p < 0.001) and remained associated after adjustment for age and MELD. After adjustment for MELD score, prenisosolone was associated with reduction in incident AKI (OR 0.57; 0.37–0.88, p = 0.011) but pentoxifylline was not (OR 1.10, 0.72–1.67, p = 0.656). Use of beta-blockers at baseline showed a trend to increased incident AKI after propensity-score matching for MELD and systolic blood pressure (p = 0.063). Baseline Cystatin C, NGAL, Beta-2 microglobulin and IL-18 were not predictive of incident AKI but TGF-beta2 and IL-8 were strongly associated (p < 0.001) and a combination of bilirubin and IL-8 showed AUROC 0.72 (p < 0.001) for incident AKI. Several micro-RNAs had AUROC >0.75, the highest of which was miR-4505 at AUROC 0.78 (p < 0.006).

Conclusion: Incident AKI is associated with higher 90-day mortality compared to AKI present at baseline in patients with sAH. IL-8 and several micro-RNAs, including 4505, show promise as biomarkers and should be validated in independent cohorts.

THU009 The impact of addiction team integration into the management of patients transplanted for alcohol-related liver disease: results from a multicenter comparative study
Jules Daniel1, Jérôme Dumortier2, Arnaud Del Bello3, Lucie Gamon4, Nicolas Molinari4, José Ursic-Bedoya1, Magdalena Meszaros5, Georges-Philippe Pageaux1, Hélène Donnadieu-Rigole1,2,4,1University Hospital Center Saint Eloi Hospital, Montpellier, France; 2University Hospital Center Edouard Herriot Hospital, Lyon, France; 3University Hospital Center Rangueil Hospital, Toulouse, France; 4University Hospital Center La Colombière Hospital, Montpellier, France
Email: julesch.daniel@gmail.com
Background and aims: Alcohol-related liver disease (ALD) is the commonest indication for liver transplantation (LT) in Western Europe. Up to 40% of patients resume alcohol consumption after LT. Severe relapse is associated with a poor prognosis. Specific management of alcohol use disorder could reduce the rate of severe relapse after LT. The aim of this study was to evaluate the effect on prognosis of the integration of an addiction team into an LT center.

Method: This retrospective multicenter study included all adult patients transplanted for "pure" ALD, excluding mixed cirrhosis, between 2000 and 2015 at the three participating centers. Patients transplanted between 2008 and 2015 were managed by an addiction team embedded in the LT team at one of the centers (the interest group), unlike those at the other centers (control group). Propensity score matching (PSM) was performed to minimize differences between groups. The primary outcome was the rate of severe alcohol relapse defined as four or more standard drinks per day for at least 100 consecutive days.

Results: 616 patients were included, 195 of whom received specific addiction follow-up (entire cohort). 79.4% were men, with a mean age of 55.4 years. 58.3% had Child-Pugh C cirrhosis, their median MELD score was 19, and 32.7% had HCC. The median follow-up was 9 years, 6.6 years in the interest group and 11.1 years in the control group. The survival rate of the entire cohort was 97.4%, 83.8%, and 70.1% at 1, 5, and 10 years, respectively. After 1:1 PSM, 170 pairs were created (matched cohort) comparable for age, gender, smoking history, duration of pre-LT abstinence ± 6 months, cardiovascular risk factors, and MELD and Child-Pugh scores. Addiction follow-up was significantly associated with a reduced risk of severe alcohol relapse (6.5% vs. 15.5%; HR = 0.33, 95% CI 0.16–0.69; p = 0.0033) and the occurrence of severe cardiovascular events (10.0% vs. 20.0%; OR = 0.39, 95% CI 0.20–0.79; p < 0.001). There were no significant differences in terms of mortality (HR = 1.00; p = 0.99), occurrence of de novo cancer (21.7% vs. 24.7%; OR = 0.86; p = 0.17), HCC recurrence (15.7% vs. 10.7%; OR = 1.67; p = 0.32), or alcohol-related graft cirrhosis (5.1% vs. 3.5%; OR = 1.60; p = 0.41) between the two groups.

Conclusion: Alcohol-related cirrhosis is associated with a more than threefold increased fracture rate, resulting in a higher cumulative incidence of fractures the first two decades after initial diagnosis. In addition, alcohol-related cirrhosis is associated with a higher post-fracture mortality rate. Preventive interventions to reduce modifiable fracture risk factors in this population are justified.
Method: Using data from the Danish healthcare registries, we conducted a nationwide cohort study, including all Danish citizens receiving their first diagnosis of ALD cirrhosis (ICD-10: K703 and K704) between 1995 and 2018. We examined how the prevalence of statin use has changed during this period and used Cox regression to identify predictors of statin initiation.

Results: During the 1995 to 2018 period, we identified 30723 patients, of whom 7% used statins at the time of cirrhosis diagnosis, and 4% became first-time statin users within 5 years after cirrhosis diagnosis. The prevalence of statin use rose sharply during the 1995–2018 period, reaching more than 15% in late 2018 (Figure). Factors predicting a higher probability of initiating statin use after diagnosis of ALD cirrhosis included diabetes (hazard ratio [HR] = 2.21, 95% CI: 1.85–2.65) and cardiovascular disease (HR = 2.97, 95% CI: 2.19–4.03), and compensated cirrhosis (HR = 1.40, 95% CI: 1.25–1.55). Socio-economic predictors included living with a partner (HR = 1.17, 95% CI: 1.06–1.30) as opposed to living alone, low educational attainment, i.e., primary school (HR = 1.22, 95% CI: 1.04–1.43) or secondary school (HR = 1.23, 95% CI: 1.05–1.44) as opposed to higher education, and older age (HR = 1.18 for every ten-year increase in age, 95% CI 1.11–1.24). Employment status and sex were not statistically significant predictors.

Conclusion: Use of statins has become common practice among patients with ALD cirrhosis in Denmark. Predictors of initiating statin use were diabetes, cardiovascular disease, compensated cirrhosis, living with a partner, low educational attainment, and older age.

THU012
Antibody response to gut microbiome bacteria in human alcoholic liver disease
Antonella Putignano1,2, Shilpee Sharma2, Anaïs Thiriaird2, Dalila Lakhloufi1, Yiwei Jiang2, Anne Botteaux1, Eric Trépo1, Delphine Degrel1, Christophe Moreno1, Thierry Gustot1, Arnaud Marchant2, 1CUB Erasme Hospital, Dept of Gastroenterology, Hepato-Pancreatology and Digestive Oncology, Brussels, Belgium; 2Institute for Medical Immunology, ULB-Campus Erasme, Brussels, Belgium; 3Molecular Bacteriology Laboratory, ULB-Campus Erasme, Brussels, Belgium;
Email: antonella.putignano@erasme.ulb.ac.be

Background and aims: Hypergammaglobulinemia (H-IgG) is a feature of chronic liver disease (CLD) but its origin remains poorly understood. Translocation of microbiome components could trigger B cells to produce microbiome-specific (M-)IgG and thereby stimulate the formation of immune complexes that could contribute to cirrhosis-associated immune dysfunction (CAID). Systems serology (SS) provides a global approach to profile antigen specific antibodies and their relationship with clinical outcomes. The aims of the study were to investigate the contribution of M-IgG to the H-IgG of CLD and to characterize their biophysical and functional features using a SS approach.

Method: A cohort of patients affected by alcoholic liver disease (ALD), including steato-fibrosis (n = 49), compensated cirrhosis (n = 54), decompensated cirrhosis (n = 64) and severe alcoholic hepatitis (n = 45) was studied. Fifty healthy adults were included as controls. Biophysical (titers, isotype, subclass, IgG Fc fragment glycosylation) and functional-antibody-dependent complement deposition (ADCD), macrophage phagocytosis (ADCP) and neutrophil phagocytosis (ADNP) and NK cell activation (ADCA)-features of M-IgG (E.Coli, S.Aureus, St.Salivarius, E.Foecalis) were investigated, and compared to vaccine (Diphtheria Toxoid, Tetanus Toxoid) antigen-specific (V)-IgG as control of passed antigen-exposure.

Results: Patients with ALD showed increased titers of M-IgG, M-IgG1 and M-IgG2 as compared to healthy controls. M-specific antibody titers correlated with H-IgG. Patients with ALD also had higher M-specific ADCD than healthy controls and levels of ADCD correlated with titers of M-IgG. The highest M-IgG titers and ADCD levels were observed in patients with decompensated cirrhosis or with severe alcoholic hepatitis. In contrast, similar levels of M-specific ADCP, ADNP and ADCA were detected amongst the ALD groups, suggesting an altered functional profile. The increased titers of M-specific antibodies in ALD patients were not associated with increased titers of V-specific antibodies and V-IgG did not correlate with H-IgG. Patients with ALD also had higher proportions of fucosylated and agalactosylated total IgG Fc as compared to healthy controls.

Conclusion: These results indicate that the H-IgG observed in ALD patients involves an increased production of antibodies directed against microbiome antigens. The biophysical features (subclass, Fc glycans) of M-IgG and their potent complement activation potential could promote inflammation and thereby contribute to the pathogenesis of ALD.

THU013
Socio-economic factors and healthcare setting are independently associated with medium and long-term outcomes from alcohol-related hepatitis
Joshua Lambert1, Nikhil Vergis2, Michael Allison2, Andrew Austin2, Ewan Forrest2, Emma Lord2, Steven Masson2, Paul Richardson2, Stephen Ryder2, Mark Wright2, Mark Thursz2, Stephen Atkinson2, Joshua Lambert17@imperial.ac.uk

Background and aims: Socio-economic factors are known to influence outcomes in liver disease but the impact in severe alcohol-related hepatitis (sAH) is unknown. Similarly, the healthcare setting where a patient is treated can modify outcomes in various diseases but its impact in sAH has not been studied. Here, we investigate the impact of these two factors on medium and long-term outcomes in sAH.

Method: Data was available from 1092 sAH patients enrolled in the STOPAH trial. Variables measured comprised education, housing, employment, relationship status, Index of Multiple Deprivation (IMD) and treating hospital setting. The latter was categorised as transplant, tertiary and secondary care centres using the British Society of Gastroenterology National Liver Disease Survey 2011. Multivariable logistic regression models were fitted for two distinct time periods: medium-term mortality between hospital admission to 90 days; and long-term mortality from 90 to 365 days (806 patients). Statistical adjustments were made for age, MELD and drinking status. Models were fitted using all available data plus data generated by multiple imputation for missing MELD scores and drinking status.

Results: In the medium-term, there was no association between IMD and 90-day mortality on univariate analysis; however adjustment for age and MELD revealed a significant independent association (OR, 1.16; 95% CI: 1.01–1.34). In the medium-term, treatment at a transplant centre was associated with a reduction in 90-day mortality.
in univariate (OR: 0.61; 95% CI: 0.38–0.95) and adjusted models (OR, 0.47; 95% CI: 0.26–0.87). In the long-term, leaving education at 15 or older was the only factor associated with a reduced risk of death at 365 days compared to leaving education at 16 or younger in univariate (OR, 0.55; 95% CI: 0.30–0.94) and adjusted models (OR, 0.56; 95% CI: 0.30–0.97).

<table>
<thead>
<tr>
<th>Logistic regression analysis for Index of Multiple Deprivation and healthcare settings for 90-day mortality</th>
</tr>
</thead>
<tbody>
<tr>
<td>Variable</td>
</tr>
<tr>
<td>----------------------------------</td>
</tr>
<tr>
<td>Index of Multiple Deprivation*</td>
</tr>
<tr>
<td>Service</td>
</tr>
<tr>
<td>Secondary centre</td>
</tr>
<tr>
<td>Tertiary centre</td>
</tr>
<tr>
<td>Transplant centre</td>
</tr>
<tr>
<td>Adjusted model (OR 95% CI)</td>
</tr>
<tr>
<td>Adjusted model</td>
</tr>
</tbody>
</table>

*ORs are adjusted for age and MELD (Adjusted).

Conclusion: Socio-economic factors and type of healthcare facility in which an AH patient is treated are associated with medium and long-term survival outcomes. These findings reinforce the need to reduce health inequalities in alcohol-related liver disease.

**THU014**

Sex-related differences in outcomes in alcohol-related cirrhosis following a episode of hepatic decompensation do not explain subsequent management inequalities

Aaminah Mohammed1, Nora Khattab1, Clive Jackson3, Jennifer Ryan3, Marsha Morgan1.

**Background and aims:** There is evidence of sex-differences in the management of patients with alcohol-related cirrhosis to the detriment of the 30% who are female. Thus, women are less likely to be selected for liver transplantation; are 10% more likely to be delisted and have higher wait-list mortality rates (Cullaro et al, Am J Transplant 2018;18:1214). Erroneous assumptions about the natural history of alcohol-related cirrhosis in women may underlie these observed management inequalities. The aims of this study were to: (i) determine resolution and survival rates following an episode of hepatic decompensation, by sex; and (ii) identify possible predictors of outcome.

**Method:** All patients with a primary diagnosis of alcohol-related cirrhosis admitted to the Royal Free Hospital in 2016 and 2018 with an episode of hepatic decompensation were reviewed. Patients who survived the index admission were followed for 24-months post discharge specifically in relation to their drinking behaviour, rates of hepatic recompensation and survival. Rates of recompensation were assessed using Box plots to map out the changes in MELD and Child Pugh scores by sex and drinking behaviour. Kaplan Meier curves were plotted to measure differences in survival by sex and drinking behaviour; data were censored at death, transplantation or end of follow-up; the Mantel-Cox test was used to determine significance. Cox regression analyses were used to identify variables which were significant predictors of survival.

**Results:** The study cohort comprised of 142 patients with cirrhosis (median [range] age: 54 [30–87] years; 66% men). During the follow-up period 79 (56%) people continued to drink excessively while 63 remained abstinent or else consumed alcohol at low risk levels. There was no significant difference in the proportions of men and women who continued to misuse alcohol (62.5% vs. 52.1%). There were no significance differences in the rates of recompensation, determined by changes in the MELD and Child Pugh scores, by sex or drinking behaviour. Fifty-one of the 142 (35.9%) patients died during a median follow-up of 23.5 (0–24) mo. The overall mean survival in women was significantly longer than in men (18.9 mo vs.15.7 mo; p = 0.034). There was no difference in survival between the men and women who continued to drink (18.1 mo vs. 18.0 mo) but women who drank little or nothing survived significantly longer than their male counterparts (20.2 mo vs. 13.4 mo; p = 0.002) (Figure). Age and the Child-Pugh score were the only independent predictors of survival.

Conclusion: Women with decompensated cirrhosis have similar recovery rates to their male counterparts but significantly better survival rates. Thus, the sex-related inequalities in disease management likely reflect undue bias and need to be urgently addressed.

**THU015**

Influence of comorbidities and lifestyle factors on health-related quality of life in alcohol-related liver disease: a population-based survey

Karen Dombestein Elde1, Natalja Von Wowern2, Matilde Winther-Jensen2, Cathrine Lau3, Lone Madsen3, Peter Jepsen4, Gro Askgaard2,1,4, 1Ferde Central Hospital, Department of Internal Medicine, Farde, Norway; 2Zealand University Hospital, Section of Gastroenterology and Hepatology, Medical Department, Kagge, Denmark; 3Bispebjerg and Frederiksberg Hospital, Center for Clinical Research and Prevention, Copenhagen, Denmark; 4Aarhus University Hospital, Department of Hepatology and Gastroenterology, Aarhus, Denmark.

**Background and aims:** Health-related quality of life (HRQoL) is impaired in alcohol-related liver disease (ALD). We examined the effects of extra-hepatic comorbidities, alcohol, and smoking on HRQoL in ALD and whether low HRQoL influenced survival.

**Method:** We used health registers to identify patients with ALD and comparators without ALD among the participants in the Danish National Health Surveys 2010–2017. Survey data on HRQoL (12-item Short Form), comorbidities, alcohol consumption, alcohol use disorder (CAGE score > 2), and smoking was linked with vital statistics through 2020. Associations of comorbidities, alcohol, and smoking with poor HRQoL (Z-score <1.5) in ALD were studied with multivariable logistic regression adjusting for liver disease severity, age and sex. We calculated adjusted hazard ratios (HR) of mortality until 2020 according to stated HRQoL.

**Results:** Poor physical and mental HRQoL were found in 37% and 22% of 772 ALD patients compared to 10% and 9% of 4319 comparators. Asthma/COPD, cancer, disc herniation, and osteoarthritis were associated with poor physical QoL in ALD, whereas diabetes and cardiovascular diseases were not (Figure 1). Osteoarthritis, alcohol use disorder, and smoking >20 cigarettes/day were associated with poor mental HRQoL. Both poor physical and poor mental QoL were associated with higher mortality rates [HR 1.6 (95% CI: 1.3–2.0) and HR 1.4 (95% CI: 1.1–1.8)] in ALD.

Journal of Hepatology 2022 vol. 77(51) | S119–S388

S125
Conclusion: Respiratory and musculoskeletal diseases, cancer, alcohol use disorder, and smoking are associated with poor HRQoL in ALD. Poor HRQoL decrease survival in ALD. These findings should raise physicians’ awareness on potentially modifiable factors affecting quality of life and survival in ALD patients.

THU016
Patient and system-level factors underline offering and acceptance of alcohol use disorder therapy in veterans with cirrhosis

Rahul Chaudhari1, Nikki Duong1, Shreesh Shrestha1, Neerav Dharia1, Bryan Badal1, James Wade1, Linda Chia2, Patrick Spoutz2, Ernesto Robalino Gonzaga2, Shari Rogal2, Jasmohan S Bajaj1, 1Virginia Commonwealth University and Richmond VAMC; 2Pittsburgh VA Medical Center
Email: jasmohan.bajaj@vcuhealth.org

Background and aims: Cirrhosis with continued alcohol use disorder (AUD) is linked with poor outcomes. AUD Rx is efficacious, but a recent study showed only 12% of Veterans with AUD and cirrhosis received it. The reasons behind this are unclear.

Aim: Define patient, and system-level factors associated with AUD Rx.

Method: Veterans seen in 2020 with 2 ICD codes for cirrhosis/complications+AUD at 3 large VA centers were evaluated. Data regarding demographics, mental health comorbidities, and cirrhosis severity were collected, and an in-depth chart review performed to collect AUD Rx settings and details. Determinants of lack of uptake were examined using logistic regression.

Results: We included 654 pts with AUD and cirrhosis (95% men, 64.3 yrs, 56% white, 8% Hispanic). Common mental health conditions on chart review were depression 47%, PTSD 24%, anxiety 17%, cocaine use 25%, bipolar 5% and cannabis use disorder 19%. Cirrhosis decomposition was seen in 19%. AUD Rx history: 5% had received prior AUD medications, 24% got behavioral therapy, and 11% both. The remaining 60% were not on prior AUD Rx. At baseline, 24% (n = 174) were noted to be in the chart to be in AUD remission, while the remaining 76% had ongoing alcohol use (Figure). Course: Most pts were seen by primary care, hepatology, or both (48%, 5%, 35%); 28% were treatment offer in the regression model included depression (OR 1.58); mental health (n = 19). The factors significantly associated with AUD Rx were seen in 2020 (n = 30). This was most often offered by primary care (n = 162), then inpatients (2.6, 1.5–4.7, p = 0.001).

Conclusion: Most Veterans with cirrhosis and AUD with opportunities to engage were offered AUD Rx but missed opportunities remain. Younger outpatients with co-occurring psychiatric disorders were more likely to be offered AUD Rx. When offered, Rx was accepted by only 40% of Veterans, especially inpatients and those with concomitant PTSD/cocaine abuse disorder. While system and patient-related factors are linked with Rx offers and initiation, in these three centers most eligible Veterans with cirrhosis were offered AUD Rx.

THU017
24-Norursodeoxycholic acid ameliorates experimental alcoholic liver disease in both preventive and therapeutic settings

Christoph Grander1, Moritz Meyer1, Daniel Steinacher2, Thierry Claudel2, Felix Grabherr1, Julian Schwärzler1, Timon Adolph1, Michael Trauner2, Herbert Tilg1, 1Medical University Innsbruck, Department Internal Medicine I; 2Medical University of Vienna, Department of Medicine III
Email: christoph.grander@i-med.ac.at

Background and aims: Alcoholic liver disease (ALD) is the hepatic manifestation of alcohol overconsumption. Ethanol toxicity, systemic pro-inflammatory cytokines as well as the intestinal microbiota contribute to the progression of ALD. 24-Norursodeoxycholic acid (norUDCA) is a side chain shortened UDCA with potent choleretic properties and therapeutic effects in non-alcoholic liver disease and primary sclerosing cholangitis. Therefore, we hypothesized that norUDCA could ameliorate experimental ALD.

Method: Female wildtype mice were fed an ethanol-containing diet (Lieber-DeCarli diet) or pair-diet for 15 days. Two different settings of experiments were performed: First, the diet was supplemented with 1 mg/ml norUDCA starting from day one. In a second experiment, mice received norUDCA (1 mg/ml) starting from day ten, mimicking a therapeutic approach.

Results: Ethanol-feeding resulted in hepatic injury, displayed by elevated ALT concentration, increased number of TUNEL+ hepatocytes, indicating augmented apoptosis and hepatic steatosis. NorUDCA treatment diminished ALT levels (p < 0.001), reduced the number of TUNEL+ cells (p < 0.005) and decreased hepatic steatosis compared to ethanol-fed controls. Moreover, the hepatic mRNA expression of pro-inflammatory cytokines like Tnf-alpha (p < 0.001), Il-1beta (p < 0.01), Il-6 (p < 0.001) and Il-10 (p < 0.01) was significantly reduced by norUDCA treatment in ethanol-fed mice. Important to note, systemic ethanol concentration was not altered by norUDCA administration. NorUDCA treatment enhanced bile acid metabolism in ethanol-fed mice, displayed by increased gall bladder weight (p < 0.001), circulating bile acids (p < 0.001) and the mRNA expression of hepatic Sult2a1 (p < 0.001), Mrp4 (p < 0.001) and Cyp7a1 (p < 0.001), important regulators in bile acid metabolism. Interestingly,
We measured plasma keratin-18 and hepatocyte lEVs concentrations in 500 patients with Child-Pugh class A alcohol-related cirrhosis. Our findings suggest that these markers can accurately predict liver-related events in patients with alcohol-related cirrhosis, even in the absence of other clinical predictors. This information could be particularly useful for identifying patients at high risk for liver-related complications and for guiding clinical management. Further research is needed to validate these findings in larger and more diverse populations.
study. Primary end point was liver-related events at 2 years. Since the course of liver disease is largely influenced by alcohol consumption, patients were separated according to reported active alcohol consumption at enrollment (i.e. ≥7 glasses/week) or not. Cumulative incidence of liver-related events was estimated using the nonparametric cumulative incidence function, considering hepatocellular carcinoma and liver-unrelated deaths as competing events; in patients without active alcohol consumption at enrollment, alcohol relapse was considered as an additional competing event.

**Results:** Both keratin-18 and hepatocyte lEVs concentrations increased with alcohol consumption (Fig A and B). In patients without active alcohol consumption at enrollment (n = 419), keratin-18 concentration predicted liver-related events at 2 years, independently of FibroTest and MELD (Fig C). Patients with both keratin-18 concentration >285 U/L and FibroTest >0.74 had a 24% cumulative incidence of liver-related events at 2 years, versus 5% to 14% in patients with other combinations of these two markers (Fig E, G). Similar results were obtained when combining keratin-18 concentration >285 U/L with MELD ≥10 (not shown). In patients with active alcohol consumption at enrollment (n = 81), hepatocyte lEVs concentrations predicted liver-related events at 2 years, independently of FibroTest and MELD (Fig D). Patients with both hepatocyte lEVs concentration >50 U/L and FibroTest >0.74 had a 62% cumulative incidence of liver-related events at 2 years, versus 8% to 13% for patients with other combinations of these two markers (Fig F, H). Combining hepatocyte lEVs concentration >50 U/L with MELD >10 had a lower discrimination ability (not shown).

**Conclusion:** In patients with Child-Pugh class A alcohol-related cirrhosis, combining hepatocyte-derived biomarkers with FibroTest or MELD score identifies patients at high-risk of liver-related events, and could be used for risk stratification and patient selection in clinical trials.

**THU020**

**Dynamic multomics analysis characterizes circulating molecular determinants associated with poor outcome in patients with severe alcoholic hepatitis**

Jaswinder Maras1, Adil Bhat1,2, Nupur Sharma1, Manisha Yadav1, Gaurav Tripathi1, Babu Mathew1, Vasundhara Bindal1, Shvetank Sharma1, Rakhi Maiwall3, Shiv Kumar Sarin3, 1Institute of liver and biliary sciences, Molecular and Cellular Medicine, New Delhi, India; 2University of California, Los Angeles, Pathology and Lab Medicine, Los Angeles, United States; 3Institute of liver and biliary science, Hepatology, New Delhi, India

Email: jassi2param@gmail.com

**Background and aims:** Severe alcoholic hepatitis (SAH) has high morbidity, with steroid therapy providing 65% 28-day survival. Steroid non-responders (NR) have higher incidence of infections and mortality. Faecal microbiota transplant (FMT) is another emerging therapy for SAH patients. We investigated whether multi-omics studies and machine learning (ML) approaches could identify non-responders to corticosteroid or FMT at baseline.

**Method:** Thirty SAH patients who were randomized in an on-going steroid vs. FMT protocol (Gov-no.NCT03091010) received either prednisolone (40 mg/day-7 days, responders for 4weeks, n = 13) or FMT (daily through nasoduodenal tube for 7 days, n = 17). Multi-omic analysis was performed on blinded serial plasma samples collected at baseline, day-7 and day-28. Molecular determinants linked with non-response (NR) to steroid or FMT therapies were identified and validated for survival outcomes in a separate set of 70 SAH (NR = 21) patients using artificial neural networking (ANN) and ML.

**Results:** Baseline characteristics of derivative and validation cohorts were comparable. FMT treatment temporally increased amino-acid metabolism, primary bile-acid biosynthesis, energy metabolism and core cycle metabolites (p < 0.05). Steroid therapy temporally induced vitamin and fat metabolism (p < 0.05). Circulating meta-proteome alpha/beta diversity was temporally increased by FMT with increase in bacterial species; orientia, geobacter and streptococci. Steroid therapy added (p < 0.05) desulfovibrio, clostridales and other species at day 28. Compared with steroid therapy, FMT significantly reduced inflammatory metabolic pathways [arachidonic acid and tryptophan metabolism, TLR and immune-cell activation, complement cascade and prostaglandin synthesis (p < 0.05)] and increased antioxidant, vitamins, neurotransmitters signalling and energy metabolism (p < 0.05). Multi-omics profile of non-survivors was distinct, FMT non-survivors compared to survivors, showed highest alpha-diversity with increase in actinobacteria and firmicutes (p < 0.05). Using multi-omics integration along with ANN and ML, specific molecular clusters were identified in non-survivors. Cluster-1 specific to complement, coagulation and leukotriene biosynthesis, cluster-3 (P38-MAPK) in the FMT arm and cluster-7 (complement, TLR activation) in the steroid arm significantly predicted mortality (Norm Imp > 95%, AUC>0.90, log-rank<0.01). Of these clusters; >3fold increase in bacterial species; CD44, 3-Oxosteroid and Proteobacteria; Ecoli for FMT arm and cluster-7 (complement, TLR activation) in the steroid arm significantly predicted mortality (Norm Imp > 95%, AUC>0.90, log-rank<0.01).

**Conclusion:** Baseline levels of panel; CD44, 3-Oxosteroid, proteobacteria; E.coli, rhizobium protoporphyrinogen-IX and MYCBP2 can predict NR and non-survival in SAH patients.
THU021
Alcohol-induced changes of inflammatory markers in hepatic and systemic venous blood in early alcohol-related and non-alcoholic fatty liver disease
Evelina Stankevic1, Mads Israelsen2,3, Helene Bæk Juel1, Anne Lundager Madsen1, Nikolaj Torp2,3, Stine Johansen2,3, Camilla Dalby Hansen2,3, Katrine Prier Lindvig2,3, Bjørn Stæhr Madsen2,3, Maja Thiele2,3, Aleksander Krag2,3, Torben Hansen1, 1The Novo Nordisk Foundation Center for Basic Metabolic Research, København, Denmark; 2Odense University Hospital, Department of Gastroenterology and Hepatology, Odense C, Denmark; 3University of Southern Denmark, Department of Clinical Research, Faculty of Health Sciences, Odense C, Denmark
Email: evelina@sund.ku.dk

Background and aims: Alcohol consumption is believed to increase intestinal permeability, leading to inflow of pathogens and other immune-activating compounds to the liver. Further, alcohol intake is known to suppress the immune system, and is related to an increased risk of systemic infections. Taken together, these factors could play a central role in the initiation of hepatic inflammation, an important step in the development and progression of alcohol-related liver disease (ALD). We aimed to investigate the effects of alcohol consumption on inflammatory markers in hepatic and systemic venous blood in people with ALD, non-alcoholic fatty liver disease (NAFLD) and healthy controls.

Method: We included 40 participants with three distinct hepatic phenotypes: 15 with ALD, 15 with NAFLD and 10 healthy controls. All participants received 2.5 ml of 40% ethanol per kg body weight, infused over 30 minutes via a nasogastric tube. Ninety-two circulating inflammatory cytokines were quantified using the Target-96 ‘Inflammation’ panel from Olink Proteomics, in plasma samples obtained from two sites (hepatic and systemic vein), at three time points (0, 60 and 180 min). Linear (mixed) models were used and significant results (p < 0.05) reported after correcting for False Discovery Rate (FDR).

Results: At baseline, 31 cytokines were differentially expressed in the ALD group and 16 in the NAFLD group, when compared to the healthy group. Alcohol induced changes for 2 cytokines at 60 min and 11 cytokines at 180 min in hepatic venous blood, and for 4 cytokines at 60 min and 24 cytokines at 180 min in systemic venous blood, in all three groups combined. Fibroblast growth factor 21 (FGF-21) was the only cytokine that increased during the observation period. Hepatocyte growth factor (HGF) was the first cytokine (after 60 min) to decrease in hepatic venous blood, while the concentration of 8 additional cytokines dropped within three hours (Figure showing volcano plots (upregulated (red) and downregulated (blue) cytokines in hepatic and systemic circulation after 60 and 180 min. The X axis-log fold change and Y axis-log10 p value from a linear mixed model. Cytokines, significantly different after alcohol intoxication at FDR 5% are labeled)). Moreover, the concentration of 19 cytokines was different in hepatic vein, when compared to systemic vein.
Conclusion: Our findings indicate that while ALD and NAFLD are associated with an increased concentration of inflammatory cytokines at baseline, acute alcohol consumption dampens the hepatic and systemic inflammatory response, which might affect the ability of the liver to deal with pathogens arriving from the portal vein. Differences in cytokine concentrations between hepatic and systemic vein suggests direct hepatic production or sequestration of these cytokines, respectively, further highlighting the central role of the liver in systemic inflammation.

THU022
New treatment for alcohol-related liver disease: combinations of efficacy and treatment cost required for cost-effectiveness
Maja Thiele¹, Davit Khlghatyan², Lars Asphaug³, Stine Johansen⁴, Hans Olav Melberg⁵, Odense University Hospital, University of Southern Denmark; ²University of Oslo, Department of Health Management and Health Economics; ³University of Oslo, Department of Health Management and Health Economics, Oslo, Norway; ⁴Odense University Hospital, University of Southern Denmark, Department of Gastroenterology and Hepatology
Email: maja.thiele@rsyd.dk

Background and aims: Alcohol-related liver disease (ALD) has a poor prognosis, with a 5-year survival rate below 50%, and substantial costs for the healthcare system with no effective treatment currently available. Recently, accurate diagnostic tools have allowed for early detection of ALD, further enabling the development of targeted interventions. Without an idea of future value, and by extension the likelihood of eventual reimbursement, producers and research funders may have less incentive to focus on this opportunity. We, therefore, aimed to identify the relationship between required efficacy and the cost of a potential new treatment for early ALD needed to achieve uptake into clinical practice.

Method: We simulated excessive drinkers with advanced fibrosis over their lifetime using a mathematical computer model. Two scenarios were applied: 1) no treatment (current standard) and 2) a progression-halting treatment modelled on a possible novel treatment in an ongoing trial. Model input data was in the no-treatment scenario sourced from the literature and a prospective Danish natural history study and the currently unknown treatment efficacy (reduced risk of progression)-and cost (USD) was simulated over a vast range of possible values. The simulation allowed the identification of pairs of treatment efficacies and costs resulting different ratios of incremental costs to incremental effectiveness (ICERs) compared to current management (Figure).

Results: In countries with a willingness-to-pay threshold of $50,000, treatments halting progression in ALD at the fibrosis stage is cost-effective upon reaching 30% efficacy contingent on annual treatment costs not exceeding $5,000, or 60% efficacy if costs are less than $10,000 per annum. In the UK, where willingness to pay per quality-adjusted life-year is between 20 and 30 000 £, progression-halting treatments should reach an efficacy of 60% at an annual cost between £3000 and £5000 to be considered cost-effective.

Conclusion: Our results are useful for research funders and producers of new treatments for ALD in determining to reimburse or develop a new treatment for advanced liver fibrosis in patients with alcohol-related liver disease. The calculated ICERs can be interpreted across different healthcare systems with varying levels of cost-effectiveness thresholds.

THU023
Active alcohol misuse is linked with lower short-chain fatty acid producing microbiota in a matched study of 450 patients with cirrhosis
Jasmohan S Bajaj¹, Amirhossein Shamsaddini², Masoumeh Sikaroodi², Brian Davis¹, Puneet Puri¹, Michael Fuchs¹, Andrew Fagan¹, Sara McGeorge¹, Patrick Gillevet¹, Virginia Commonwealth University and Richmond VAMC; ²George Mason University
Email: jasmohan.bajaj@vcuhealth.org

Background and aims: Alcohol use disorder (AUD) alters gut microbiota and can lead to cirrhosis development. However, cirrhosis, regardless of etiology is also linked with microbial change. Several AUD pts continue to drink despite the development of cirrhosis but the interaction between active alcohol misuse and cirrhosis is unclear. Bacterial products such as short-chain fatty acids (SCFAs) can strengthen the intestinal barrier and promote abstinence in a small FMT trial. Aim: Determine the impact of active alcohol misuse on gut microbial structure and function in the background of cirrhosis.

Method: Outpts with cirrhosis diagnosed on biopsy, fibroscan or prior decompensation underwent stool collection while drinking habits (AUDIT-10), demographics, cirrhosis severity and medication use were collected. Active drinkers were matched with non-drinkers with respect to cirrhosis details and demographics. Non-drinkers had to be abstinent for ≥6 mths before stool collection. Microbiota structure was analyzed using 16S rRNA sequencing and predicted function using PICRUSt between actively drinking and non-drinking pts.
Results: We enrolled 451 patients with cirrhosis (MELD 10.3 ± 4.5, Age 58.8 ± 6.8, 80 actively drinking pts). They were matched 1:4 with at least 320 non-drinkers (Fig A). Groups were similar on demographics, cirrhosis details and medications apart from AUDIT-10 and alcohol-related etiology, which were higher in actively drinking patients. Alcohol use: Actively drinking subjects had constant drinking habits without binges. Abstinent pts had been abstinent for 15 ± 8 years before enrollment. Microbiota composition: β-diversity was different between groups (Fig B) but Shannon diversity was statistically similar. Prevotella, Enterobacter and Streptococcus spp were higher while potentially beneficial taxa belonging to Eubacterium, Bifidobacterium, Blautia, Roseburia, Alistipes, and Lactobacillus were lower in active drinkers. Short-chain fatty acid producing taxa specifically propionate and butyrate were lower in active drinkers (Fig C). Microbiota predicted function: Propionate metabolism-related enzymes, which are also associated with branched amino acid degradation were higher in patients who were drinking (3-hydroxyisobutyrylCoA hydrolase and methylmalonylCoA carboxytransferase).

Conclusion: SCFA producing microbiota, especially butyrate and propionate metabolism, were significantly lower in actively drinking patients with cirrhosis compared to abstinent patients despite matching for demographics, cirrhosis severity and medication use. SCFAs could have a link with continued alcohol intake in this advanced population.

THU024
Infections are common in patients with early alcohol-related liver disease and increases the risk of death
Stine Johansen1,2, Simon Langkjaer Sørensen1,2, Ditlev Nytoft Rasmussen1,2, Mads Israelson1,2, Katrine Prier Lindvig1,2, Maria Kjærgaard1,2, Johanne Kragh Hansen1,2, Camilla Dalby Hansen1,2, Katrine Thorhauge1,2, Nikolaj Torp1,2, Peter Andersen1,2, Sönke Detlefsen2,3, Helene Bæk Juel4, Torben Hansen4, Ditlev Nytoft Rasmussen1,2, Mads Israelsen1,2, Johannes Krag Hansen1,2, Camilla Dalby Hansen1,2, Katrine Thorhauge1,2, Nikolaj Torp1,2, Peter Andersen1,2, Sönke Detlefsen2,3, Helene Bæk Juel4, Torben Hansen4, Aleksander Krag1,2, Maja Thiele1,2.1 Odense University Hospital, Department of Gastroenterology and Hepatology, Denmark; 2University of Southern Denmark, Department of Clinical Research, Denmark; 3Odense University Hospital, Department of Pathology, Denmark; 4University of Copenhagen, Novo Nordisk Foundation Center for Basic Metabolic Research, Denmark
Email: stine.johansen@rsyd.dk

Background and aims: Infections are frequent in patients with alcohol-related liver cirrhosis and worsen prognosis. We hypothesized that this also applies in earlier stages of alcohol-related liver disease (ALD). We therefore aimed to examine 1) the incidence of infections in patients with early ALD, 2) risk factors associated with developing infections, and 3) the impact of infections on the risk of liver-related events and all-cause mortality.

Method: We performed a prospective cohort study of patients from primary and secondary care with a history of excess alcohol intake, excluding patients with decompensation or competing aetiologies for liver disease. At baseline, we performed liver biopsies along with clinical investigations. During follow-up, we reviewed patients’ electronic healthcare records for infections, liver-related events, all-cause mortality, and alcohol intake.

Results: We included 462 patients with a mean age of 57 ± 10 years, 76% males, with fibrosis stage F0-1/F2/F3-4 = 259/107/96. During a median follow-up of 54 months (IQR 35–76), 133 patients (29%) developed a total of 307 infections with a median of two infections each (range 1–3). Seventy-six % of infections were treated during hospitalization, most frequently pneumonia (103/307, 34%) and urinary tract infections (56/307, 18%). In approximately half of all infections cultures were obtained, and the most common isolated bacteria was Escherichia coli. Liver stiffness measured by transient elastography was a stronger predictor of infections than fibrosis stage, consequently excessive drinking during follow-up and transient elastography were the only independent predictors of infections in multivariable regression (hazard ratio (HR) 2.08; 95%CI 1.33–3.27, and HR 1.87; 1.54–2.28). Eighty-seven patients (19%) developed a liver-related event during follow-up and 60 of these patients had 147 infections in total. Patients who developed at least one infection had a significantly increased risk of death (HR 3.36; 95%CI 2.12–5.33, p <0.001), but not of developing a liver-related event (HR 1.35; 95%CI 0.84–2.15, p = 0.22). Infections increased the risk of death independent of baseline fibrosis stage and liver stiffness.

Conclusion: Patients with early alcohol-related liver disease, infections are frequent and worsen prognosis. Risk of infections increases with liver disease severity and ongoing harmful use of alcohol.

THU025
Abstinence is associated with better outcome in patients with hepatocellular carcinoma
Adeline Donati1, Jean Henrion2, Maxime Regnier3, Pierre Deltenre1,4,5, Astrid Marot1, 1CHU UCL Namur, Department of Gastroenterology and Hepatology, Yvoir, Belgium; 2Hôpital de Jolimont, Department of Gastroenterology, Hepatopancreatology and Digestive Oncology, Yvoir, Belgium; 3CHU UCL Namur, Department of Biostatistics, Yvoir, Belgium; 4Clinique St Luc Bouge, Department of Gastroenterology, Hepatopancreatology and Digestive Oncology, Bruxelles, Belgium; 5Center for Biostatistics, Université Libre de Bruxelles, Department of Medical Statistics, Université Libre de Bruxelles, Brussels, Belgium
Email: astridmarot@gmail.com

Background and aims: Data suggest that patients with alcohol-related hepatocellular carcinoma (HCC) have a reduced survival as
compared to those with nonalcohol-related HCC. The role of abstinence in this setting is unknown. We aimed to compare access to treatment and prognosis of patients with alcohol-related HCC and nonalcohol-related HCC and to evaluate the impact of abstinence.

**Method:** All patients with HCC were retrospectively included in a single center during a 23-year period. Abstinence was defined as discontinuation of alcohol consumption at least 3 months before HCC diagnosis in patients with alcohol-related cirrhosis. Treatment by resection, ablation, and transplantation were considered curative. Multivariate Fine and Gray proportional hazards models were used to identify factors associated with 5-year overall mortality after adjustment for the lead-time bias. A logistic regression model was used to identify factors associated with access to curative treatment.

**Results:** 200 patients were included, 114 (57%) with nonalcohol-related HCC and 86 (43%) with alcohol-related HCC of whom 35 were abstainers and 51 were consumers. All of them had a cirrhosis. During a median follow-up of 14 months (95%: CI: 11–16), 12 patients were transplanted and 156 died. At HCC diagnosis, consumers were younger as compared to abstainers and non-alcoholic patients (59 vs. 63 vs. 68 years, p = 0.001), had a worse liver function (MELD score: 11 vs. 10 vs. 8, p = 0.01, Child-Pugh score: 6 vs. 5 vs. 5, p = 0.02), were less likely to be screened for HCC (33% vs. 74% vs. 51%, p < 0.001) and had more frequently a metastatic disease (16% vs. 6% vs. 6%, p = 0.02). After adjustment for the lead-time bias, the 5-year cumulative incidence rates of overall death were significantly lower in abstainers than in consumers and in non-alcoholic patients (51.5% vs. 78.4% vs. 80.5%, respectively, p = 0.04). In multivariate analyses, while abstainers were significantly associated with lower overall mortality compared to consumers (HR: 0.47, 95% CI 0.28–0.80, p = 0.005), patients with non-alcohol-related cirrhosis and consumers had similar overall mortality (HR: 0.86, 95% CI 0.60–1.24, p = 0.4). The proportion of patients who received a curative treatment was 65% in abstainers, 44% in consumers and 57% in non-alcoholic patients (p = 0.1). In multivariate analyses, preserved liver function (Child A vs. B/C; OR: 3.10 95% CI 1.58–6.26, p = 0.001) and adherence to a screening program (OR: 4.96, 95% CI 2.50–10.15, p < 0.001) were the only two factors associated with a better accessibility to curative treatment. **Conclusion:** Abstinence improves the outcome of patients with alcohol-related HCC because of better liver function, less advanced tumour disease and better adherence to screening.

**THU026**

In severe alcohol-related hepatitis, hepatocyte ballooning correlates with expression of p16 and components of a senescence phenotype that has been associated with cellular senescence

Nikhil Vergis1, Isabelle Hall1, Callum Arthurs1, Hiromi Kudo1, Stephen Atkinson1, David Shapiro2, Michael Lutz2, Birgit Jung2, Markus Weissbach2, Wolfgang Albrecht2, Luke D. Tyson1, Tong Liu1, Emma Lord1, Lars Zender3, Mark Thurz3, Robert D. Goldin1. 1Imperial College, United Kingdom; 2HepaRegenix GmbH, Tuebingen, Germany; 3University Hospital Tübingen, Klinik für Medizinische Onkologie and Pneumologie, Germany

**Background and aims:** Poor outcome in severe alcohol-related hepatitis (sAH) is frequently attributed to failure of hepatic regeneration. This may be due to lack of trophic factors, inability of hepatocytes to proliferate and/or the induction of stable cell cycle arrest known as senescence. Senescent cells undergo morphological changes that may be consistent with the hepatocyte ballooning found in steatohepatitis. Here, we investigate the potential causes of regenerative failure in sAH and seek evidence for markers of senescence in ballooned hepatocytes.

**Method:** Data was available from 731 AH patients with sAH recruited to the STOPAH trial, 37 compensated cirrhotic patients (CLD) and 64 healthy controls (HC). We evaluated serum levels of the senescence associated secretory phenotype (SASP), for a range of trophic factors (HGF, EGF, IGf, VEGF, TWEAK) plus inflammatory and/or pro-regenerative cytokines (IL1b, IL6, IL8, IL10, IL22, and TNFα). Immunohistochemistry was used to identify cell proliferation (Ki67) and senescence (p16) in liver biopsy sections (n = 29). HandE stains were used to differentiate occasional from marked ballooning of hepatocytes. Digital image analysis was used to quantify staining and a nuclear morphology algorithm attributed stains to individual cell types.

**Results:** p16+ hepatocytes were more frequent in sAH compared to control tissue without steatohepatitis (p < 0.05). Moreover, in sAH tissue expression of p16 on hepatocytes strongly associated and colocalized with ballooned hepatocytes (p = 0.005, Figure 1). In contrast, no correlations were seen in cholangiocyte p16 expression nor with Ki67 expression in any cell type. Components of a secretory phenotype consistent with the SASP (serum IL1, IL6, IL8, TNFα, HGF, EGF, TWEAK) were associated with hepatocyte ballooning (p < 0.05 for all). Serum bilirubin was higher in patients with marked ballooning (p = 0.0003) but prothrombin time was not (p = 0.24). Strikingly, HGF levels were >7-fold higher in sAH vs HC and CLD (p < 0.001) and correlated with both baseline MELD (r = 0.21, p < 0.001) and Lille score (r = 0.16, p < 0.001). Conversely, EGF was lower in sAH vs HC vs CLD (p < 0.001) and in sAH patients who died within 28 (p = 0.01) and 90 days (p = 0.003) compared to sAH patients who survived.

**Conclusion:** Serum proteins implicated in hepatocyte regeneration and senescence are associated with clinical outcome in sAH. p16+ hepatocytes are prevalent and are strongly associated with hepatocyte ballooning in sAH liver biopsies. Further characterization of the senescent properties of p16+ cells may stimulate senolytic or SASP-modulating therapies in sAH.

**THU027**

Targeting cyclin M4 as a new therapeutical approach to treat alcoholic liver disease

Irene González-Recio1, Naroa Goikoetxea1, Rubén Rodríguez Agudo1, Jorge Simón Espinosa1, Marina Serrano-Macia1, Mikel Azkargorta2, Felix Elortza2, Irene Díaz-Moreno3, Antonio Díaz-Quintana3, Ute Schaeper4, Ramon Bataller5, Matías A Avila6, Luis Alfonso Martínez-Cruz1, María Luz Martínez-Chantar1, 1CIC bioGUNE, Liver Disease Lab, Derio, Spain; 2CIC bioGUNE, Proteomics platform, Derio, Spain; 3Instituto de Investigaciones Químicas (IIQ), Sevilla, Spain; 4Silence Therapeutics GmbH, Berlin, Germany; 5University of Pittsburgh, Department of medicine, Pittsburgh, United States; 6CIMA, Hepatology program

**Background and aims:** An excessive alcohol consumption is a main reason of chronic liver disease and liver-related deaths in Western countries and causes alcoholic liver disease (ALD), featured by fatty liver, alcoholic hepatitis (AH), cirrhosis and liver cancer. Approximately 50% of liver cirrhosis cases caused by alcohol abuse, result in 3.3 million deaths. Today, there are no effective treatments other than abstinence or liver transplantation for end-stage ALD. Acute and chronic alcohol consumption are associated with a decrease in liver Mg²⁺ content. The underlying mechanisms remain
unknown. The alteration of Mg\textsuperscript{2+} levels in ALD and the key role of Mg\textsuperscript{2+} transporters in enabling the flux of Mg\textsuperscript{2+} across cell membranes, have prompted us to investigate the role of cyclin M4 in ALD. In this context, the inhibition of CNNM4 by RNA interference emerge as a new therapeutic approach for ALD.

**Method:** The expression of CNNM4 was studied in ALD patients, in primary hepatocytes under ethanol exposure and in mice under chronic and binge ethanol feeding (the NIAAA model). Primary hepatocytes were treated with a GalNAc siRNA targeting \textit{Cnnm4} to evaluate the effect of silencing CNNM4 in hepatocytes exposed to 50 mM EtOH for 12 h, 24 h and 36 h. NIAAA model mice were divided into 2 groups after day 5 of the diet and treated with a control molecule or GalNAc siRNA that specifically silences \textit{Cnnm4} in hepatocytes.

**Results:** The expression of \textit{Cnnm4} was upregulated in the liver of patients with ALD and correlated with the stages of the disease: early AH, non-severe AH, severe AH, compensated HCV-related cirrhosis, AH explants and cirrhosis hepatitis C virus. Hepatic CNNM4 levels were overexpressed in the NIAAA model. Silencing \textit{Cnnm4} exhibited a reduction in transaminases. Importantly, the absence of \textit{cnnm4} resulted in a significant decrease in mitochondrial ROS and ER stress in hepatocytes. High-throughput proteomic analysis performed in liver tissue from NIAAA models revealed a significant representation of the following processes in the absence of CNNM4: oxidation-reduction, lipid metabolism, cellular response to oxidative stress, endoplasmic reticulum stress or protein folding families. The machinery for repairing damaged proteins, represented by the enzyme protein-L-isoaspartate (D-aspartate) O-methyltransferase (PIMT), was significantly overexpressed in the absence of CNNM4. Further experiments will investigate whether Mg\textsuperscript{2+} homeostasis mediated by silencing of CNNM4 modulates PIMT activity, which has been shown to be impaired during excessive ethanol consumption.

**Conclusion:** CNNM4 magnesium transport appears to be dysregulated in patients with AH and in NIAAA model. Targeting \textit{Cnnm4} with GalNAc siRNA has emerged as a novel therapeutic approach for ALD that ameliorates AH in the NIAAA model. Further experiments will address the role of CNNM4 in the protein repair machinery mediated by PIMT activity.

**THU028**

**Hepatic transcriptional signature of alcohol on genes involved in canonical retinoid metabolism**

Marta Melis\textsuperscript{1}, Xia-Han Tang\textsuperscript{1}, Nabeel Attarwala\textsuperscript{1}, Qiuying Chen\textsuperscript{1}, Carlos Prishker\textsuperscript{1}, Lihui Qin\textsuperscript{2}, Steve Gross\textsuperscript{1}, Lorraine Gudas\textsuperscript{1}, Steven Trasino\textsuperscript{1,3}\textsuperscript{,}\textsuperscript{,} Weill Cornell Medical College, Pharmacology, New York, United States; \textsuperscript{2}Weill Cornell Medical College, Pathology and Laboratory Medicine; \textsuperscript{3}Hunter College, CUNY, Urban Public Health and Nutrition, New York, United States

Email: st1647@hunter.cuny.edu

**Background and aims:** A large body of data show that alcohol abuse leads to reductions to hepatic vitamin A (retinoids) levels beginning in early stages of chronic alcohol abuse (<2–3 weeks), which is associated with progression of liver damage, and early stages of alcoholic liver disease (ALD). However, to date, there remains little understanding of the genes involved in alcohol-driven hepatic retinoids depletions during early stages of ALD.

![Figure 1: (abstract: THU028)](image)
COVID-19 pandemic impact on alcoholic hepatitis healthcare

Method: Using a 3-week murine model of chronic alcohol intake and RNA sequencing technology, we determined the hepatic transcriptional signature of alcohol on genes involved in canonical retinoid metabolism.

Results: Our results show that 3 weeks of alcohol intake led to increases in serum retinol levels, but reductions to hepatic retinoids (retinol, and retinyl-esters), and concomitant increases in plasma AST, ALT, and macro and microvesicular steatosis. By RNA sequencing technology, we found that 3 weeks of chronic alcohol intake led to modulation of 68 transcripts involved in canonical retinoid metabolism. These transcripts include the genes Cest1d, Cest1g, Rbp1, Lrat, Rdh10, Aldh1a1, Cyp26a1. Interestingly, among the 2679 significantly differently expressed genes (DEGs) in livers of alcohol-fed mice, Cyp26a1, the major retinoic acid catabolizing enzyme was the 6th top significantly upregulated DEG. We also detected broad hepatic increases in transcripts of families of Cyp1a, Cyp2a-c, Cyp3a-c xenobiotic enzymes, capable of retinoid catabolism. Using western blotting we confirmed that compared to untreated mice, hepatic protein expression of the retinyl-ester hydrolases Ces1d, Ces1g, and a rate-limiting enzyme in retinoic acid synthesis, Aldh1a1, were significantly increased in livers of alcohol-fed mice. However, protein levels of Rbp1, which is critical to hepatic retinol transport and homeostasis, was markedly decreased in livers of alcohol-fed mice. Moreover, we detected specific reductions to Rbp1 in hepatic stellate cells (HSC) and portal hepatocytes.

Conclusion: These data show for the first time that reductions to hepatic retinoid in early stages of ALD may be due to pleiotropic effects, involving impaired retinoid transport and metabolism in portal hepatocyte and HSCs, but also concurrent increases in hepatic retinyl-ester hydrolysis, and oxidative metabolism of retinol to retinoic acid, and CYP-mediated retinoid catabolism. Given that Cyp26a1 was the 6th top DEG in alcohol-fed mice, our data also strongly suggest that retinoid metabolism is among the key micronutrient pathways negatively impacted in early stages of ALD. These data may help develop future therapies aimed at mitigating hepatic retinoid losses in individuals that struggle with alcohol cessation.

THU029 COVID-19 pandemic impact on alcoholic hepatitis healthcare utilisation

Leya Nedumannil1, Sukhdeep Stephen Cheema1, Karl Vaz1, Ronald Ma2, Daryl Jones3, Stephen Warrillow3, Josephine Grace1,4, Darren Wong1, Matthew Choy1,4. Austin Hospital, Gastroenterology, Heidelberg, Australia; 2Austin Hospital, Clinical Costings, Heidelberg, Australia; 3Austin Hospital, Intensive Care, Heidelberg, Australia; 4University of Melbourne, Department of Medicine, Austin Academic Centre, Heidelberg, Australia.

Background and aims: Alcohol consumption (AH) is associated with significant morbidity, mortality and healthcare expenditure. The global SARS-CoV-2 (COVID-19) pandemic and related lockdown measures have potentially contributed to an increase in alcohol misuse. This study examines frequency and patient outcomes of AH admissions to an Australian quaternary liver transplant referral centre. We aimed to ascertain the change in AH severity, ICU admission rates and healthcare utilisation costs over the last 5 years to identify temporal associations with the COVID-19 pandemic.

Method: A retrospective analysis of patients aged 18 years and older fulfilling National Institute on Alcohol Abuse and Alcoholism diagnostic criteria for AH between January 2016 and March 2021 was conducted. Data were collected from electronic medical records and analysed. Primary end points were the frequency of AH admissions, ICU admission rates and healthcare costs, which were evaluated with a divergence at the beginning of lockdown restrictions (March 2020-March 2021 “COVID cohort”) versus the “historical cohort” (January 2016-February 2020).

Results: In total, 105 eligible AH admissions were identified. Overall, 30 day mortality was 18% (19/105). AH admission rate for the COVID cohort was significantly higher at 3.38 cases/month (n = 44) compared to the historical cohort at 1.22 cases/month (n = 61), p < 0.001. The COVID cohort had greater disease severity with a higher Glasgow Alcoholic Hepatitis Score during admission [8.5 (IQR 7–10) vs 7 (IQR 6–9), p = 0.04]. The AH COVID cohort trended towards a greater proportion requiring ICU admission, inotropic support and longer ICU length of stay. Whilst per-episode adjusted healthcare costs were similar across the study, monthly costs of the COVID cohort were higher compared to the historical cohort due to increased admission frequencies [mean (SD) $137, 549 (54, 058) vs $38, 000 (27, 448), p = 0.02 (Figure 1)]. No patients in this study were diagnosed with COVID-19.

Figure 1: Alcoholic Hepatitis Healthcare Costs

Conclusion: In this study, alcoholic hepatitis admission frequency and healthcare costs were found to have increased since the COVID-19 pandemic. These observations provide the impetus for future studies to understand how the COVID-19 pandemic has led to increased AH presentations and develop preventative strategies that reduce alcohol related admissions and associated costs.

THU030 The role of integrated alcohol liver care in the management of patients with alcohol related liver disease in an acute hospital setting

Khin Han1, Phyo Wah Wah1, Ian Webzell1, Joshua Stapleton2, Huyen Adams1, Abid Suddle1, Michael Heneghan2, Nicola Kalk2, Naina Shah1, 1Kings College Hospital, Hepatology, London, United Kingdom; 2South London and Maudsley, Psychological Medicine, London, United Kingdom.

Email: nkshah26@yahoo.com

Background and aims: Acute on Chronic Liver Failure (ACLF)/Acute decompensation (AD) following Alcohol use disorder (AUD) is a common presentation to the Hospital. The office of national statistics in the UK reported 7,423 deaths in 2020. 80% of these were attributed to Alcohol related Liver Disease. Alcohol related admissions and deaths costs the National health service (NHS) over 3.5 billion/year. As a part of the NHS long term plan, Alcohol care team comprising of Consultants: Hepatologist, Addiction Psychiatrist and clinical nurse specialists was established at Kings College Hospital in 2018, to manage AUD and prevent recurrent Hospital presentation. Integrated outpatient treatment providing medical treatment and alcohol interventions has been previously shown to improve abstinence in medically ill patients. Explore the utility of an integrated Alcohol Liver clinic led by Consultants: Hepatologist and Addiction Psychiatrist in facilitating abstinence in patients with ArLD.

Method: 159 patients with Alcohol related cirrhosis were reviewed in the clinic, male: n = 95 with a median age of 58 (36 ± 83), female, n = 64 with a median age of 54 (32 ± 77), 29/159 presented with ACLF. Abstinence led to a Liver recovery in patients with ACLF (table 1). 61/159 (38%) presented to the Hospital with decompensation. 51/61 (83%) compensated following abstinence. Unfortunately 18/159 patients who died had AUD prior to presentation. The overall

Results: In total, 105 eligible AH admissions were identified. Overall, 30 day mortality was 18% (19/105). AH admission rate for the COVID cohort was significantly higher at 3.38 cases/month (n = 44) compared to the historical cohort at 1.22 cases/month (n = 61), p < 0.001. The COVID cohort had greater disease severity with a higher Glasgow Alcoholic Hepatitis Score during admission [8.5 (IQR 7–10) vs 7 (IQR 6–9), p = 0.04]. The AH COVID cohort trended towards a greater proportion requiring ICU admission, inotropic support and longer ICU length of stay. Whilst per-episode adjusted healthcare costs were similar across the study, monthly costs of the COVID cohort were higher compared to the historical cohort due to increased admission frequencies [mean (SD) $137, 549 (54, 058) vs $38, 000 (27, 448), p = 0.02 (Figure 1)]. No patients in this study were diagnosed with COVID-19.

Figure 1: Alcoholic Hepatitis Healthcare Costs

Conclusion: In this study, alcoholic hepatitis admission frequency and healthcare costs were found to have increased since the COVID-19 pandemic. These observations provide the impetus for future studies to understand how the COVID-19 pandemic has led to increased AH presentations and develop preventative strategies that reduce alcohol related admissions and associated costs.

THU030 The role of integrated alcohol liver care in the management of patients with alcohol related liver disease in an acute hospital setting

Khin Han1, Phyo Wah Wah1, Ian Webzell1, Joshua Stapleton2, Huyen Adams1, Abid Suddle1, Michael Heneghan2, Nicola Kalk2, Naina Shah1, 1Kings College Hospital, Hepatology, London, United Kingdom; 2South London and Maudsley, Psychological Medicine, London, United Kingdom.

Email: nkshah26@yahoo.com

Background and aims: Acute on Chronic Liver Failure (ACLF)/Acute decompensation (AD) following Alcohol use disorder (AUD) is a common presentation to the Hospital. The office of national statistics in the UK reported 7,423 deaths in 2020. 80% of these were attributed to Alcohol related Liver Disease. Alcohol related admissions and deaths costs the National health service (NHS) over 3.5 billion/year. As a part of the NHS long term plan, Alcohol care team comprising of Consultants: Hepatologist, Addiction Psychiatrist and clinical nurse specialists was established at Kings College Hospital in 2018, to manage AUD and prevent recurrent Hospital presentation. Integrated outpatient treatment providing medical treatment and alcohol interventions has been previously shown to improve abstinence in medically ill patients. Explore the utility of an integrated Alcohol Liver clinic led by Consultants: Hepatologist and Addiction Psychiatrist in facilitating abstinence in patients with ArLD.

Method: 159 patients with Alcohol related cirrhosis were reviewed in the clinic, male: n = 95 with a median age of 58 (36 ± 83), female, n = 64 with a median age of 54 (32 ± 77), 29/159 presented with ACLF. Abstinence led to a Liver recovery in patients with ACLF (table 1). 61/159 (38%) presented to the Hospital with decompensation. 51/61 (83%) compensated following abstinence. Unfortunately 18/159 patients who died had AUD prior to presentation. The overall

Results: In total, 105 eligible AH admissions were identified. Overall, 30 day mortality was 18% (19/105). AH admission rate for the COVID cohort was significantly higher at 3.38 cases/month (n = 44) compared to the historical cohort at 1.22 cases/month (n = 61), p < 0.001. The COVID cohort had greater disease severity with a higher Glasgow Alcoholic Hepatitis Score during admission [8.5 (IQR 7–10) vs 7 (IQR 6–9), p = 0.04]. The AH COVID cohort trended towards a greater proportion requiring ICU admission, inotropic support and longer ICU length of stay. Whilst per-episode adjusted healthcare costs were similar across the study, monthly costs of the COVID cohort were higher compared to the historical cohort due to increased admission frequencies [mean (SD) $137, 549 (54, 058) vs $38, 000 (27, 448), p = 0.02 (Figure 1)]. No patients in this study were diagnosed with COVID-19.
abstinence rate was 104/159 (65%) (table 1). Number of patients achieving abstinence has increased following the implementation of integrated care service as shown in figure 1.

Table 1: Alcohol use disorder in patients with Alcohol related Liver disease

<table>
<thead>
<tr>
<th></th>
<th>Abstinent</th>
<th>Drinking</th>
<th>Harm reduction</th>
</tr>
</thead>
<tbody>
<tr>
<td>ACLF grade 1 (n = 7)</td>
<td>5</td>
<td>2</td>
<td>0</td>
</tr>
<tr>
<td>ACLF grade 2 (n = 15)</td>
<td>6</td>
<td>5</td>
<td>4</td>
</tr>
<tr>
<td>ACLF grade 3 (n = 7)</td>
<td>6</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>Decompensated ArLD (n = 61)</td>
<td>51</td>
<td>6</td>
<td>4</td>
</tr>
<tr>
<td>Recompensated (n = 51) 83%</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Cirrhosis compensated (n = 69)</td>
<td>36</td>
<td>18</td>
<td>15</td>
</tr>
<tr>
<td>Mortality (n = 22)</td>
<td>4</td>
<td>18</td>
<td>0</td>
</tr>
</tbody>
</table>

Figure 1: Number of patients achieving abstinence

Regular Liver health education, motivational intervention including engagement with the community and Hospital Addictions team has helped patients maintain abstinence. Sustained sobriety led to Liver recovery and prevention of Hospital presentation with complications related to portal hypertension/ACLF. This has led to a reduction in monthly readmission rate to 6–8%. In addition to being cost-effective, it has improved the long term prognosis of patients with ArLD.

Conclusion: Sustained abstinence leads to Liver recovery, reduced Hospital presentation and readmission. Facilitating abstinence is vital in improving the long term prognosis in patients presenting with ArLD. Integrated care approach should be considered as a standard of care in managing AUD.

There is an unmet clinical need in exploring pharmacological and psycho-social intervention tailored towards treating AUD in patients with ArLD thus preventing the development of ACLF/AD.

THU032
Toll-like receptor 2 activation in monocytes of alcohol use disorder patients contributes to systemic inflammation and alcohol-associated liver disease

Luca Maccioni1, Joyce Kasavuli1, Sophie Leclercq2,3, Boris Pirlot1, Géraldine Laloux4, Yves Horsmans5, Isabelle Leclercq1, Bernd Schnabl4,5, Peter Stärkel1,2,3, UC Louvain, Université Catholique de Louvain, Institute of Experimental and Clinical Research, Laboratory of Hepato-gastroenterology, Brussels, Belgium;2UC Louvain, Université Catholique de Louvain, Louvain Drug Research Institute, Metabolism and Nutrition Research Group, Brussels, Belgium;3UC Louvain, Université Catholique de Louvain, Institute of Neuroscience, Brussels, Belgium;4UC Louvain, Université Catholique de Louvain, de Duve Institute, Brussels, Belgium;5Cliniques Universitaires Saint-Luc, Department of Hepato-gastroenterology, Brussels, Belgium;6University of California San Diego, Department of Medicine, La Jolla, United States;7University of California San Diego, Department of Medicine, VA San Diego Healthcare System, San Diego, United States

Email: luca.maccioni@uclouvain.be

Background and aims: A minority of alcohol use disorder (AUD) patients develops progressive alcohol-associated liver disease (ALD) potentially linked to gut barrier dysfunction, microbial translocation and activation of systemic immune responses. Activation of circulating monocytes by microbial products might contribute to systemic and liver inflammation leading to ALD progression. Human data linking monocytes to early stages of ALD are lacking. We explored the links between changes in monocytes, microbial translocation, systemic inflammation and monocyte-derived macrophages in early human ALD.

Method: We included n = 123 AUD patients following a highly-standardized rehabilitation program and n = 26 healthy controls. We determined the total number of monocytes and proportion of monocyte subsets by FACS. Serum microbial translocation markers and cytokines were measured by ELISA and multiplex assay, to mass spectrometry in patients with SAH participating in the STOPAH trial (n = 159), with cirrhosis (n = 81—including compensated and decompensated cirrhosis) and healthy controls (HC, n = 35). Serum lipid changes between SAH and cirrhosis were evaluated in a derivation set (n = 160) and a validation set (n = 80) by principal component analysis (PCA) and orthogonal partial least squares discriminant analysis (OPLS-DA).

Results: Patients with SAH and cirrhosis had a similar age (51 vs. 51-year-old, p = 0.9) but different MELD scores (21.8 vs. 15.3, p < 0.0001). According to Lille score, 44.8% of SAH patients were responders to medical treatment with a 29.1% 90-day survival. The derivation and validation sets were well matched for clinical and biological variables. In the derivation cohort, PCA accurately discriminated between patients with SAH, cirrhosis and HC. In OPLS-DA both ionisation modes accurately discriminated SAH vs. cirrhosis (in positive mode: R²Y = 0.53 Q² = 0.49 CV-ANOVA p < 0.0001 AUROC = 0.92; in negative mode: R²Y = 0.54 Q² = 0.36 p < 0.0001 AUROC = 0.96). The 20 metabolites identified as the greatest variable importance projection in positive and negative mode were included in multivariate analysis adjusting for age, sex and MELD score. Three lipids in positive mode (PC 34:2, PC 36:3 and PE 39:2) and five in negative mode (PC 0-19:0, PS 41:4, PG 41:0, LPC 16:0, ST 21:4) disclosed independent associations with SAH. Using these lipids, we derived 2 scores relating to positive and negative ionisation modes; both accurately discriminated SAH from cirrhosis with an AUROC of 0.90 and 0.86 in the derivation set and 0.89 and 0.92 in the validation sets, respectively.

Conclusion: Untargeted lipidomic profiling by MS indicates a lipidomic signature—mainly composed by glycerophospholipid species—in patients with SAH distinct from cirrhosis. Since these lipids are involved liver repair, some immune-modulatory functions and are associated with organ failure in sepsis they urgently require further exploration in the SAH setting.
respectively. Cytokines reflecting activation of monocytes were assessed by qPCR. Toll-like receptor (TLR) expression in monocytes and activation as well as phagocytosis were assessed in vitro. ALD severity and liver inflammatory responses were analyzed in liver biopsies by histology, qPCR, immunohistochemistry and ELISA.

**Results:** In AUD patients, the number of blood monocytes increased (p < 0.0001). Among the 3 monocyte subpopulations, intermediate and non-classical increased while classical monocytes decreased compared to controls. Monocytes from AUD patients up-regulated IL1β and IL8 together with TLR2, down-stream AP-1 and inflammasome NLRP3. IL1β and IL8 were actively secreted by those monocytes upon stimulation in vitro with the TLR2 ligand Peptidoglycan. Stimulation with E. coli confirmed preserved bacterial phagocytic activity. Systemic levels of cytokines and alterations in monocytes correlated with microbial translocation markers.

In parallel, IL1β and IL8 were increased in ALD livers together with activation of intrahepatic macrophages (CD163+, iNOS+, TREM1+). Liver chemokines (MCP1, CX3CL1) involved in monocytes attraction were induced in liver tissue. IL1β and IL8 correlated with liver chemokines, iNOS+ up-regulation in macrophages and ALD severity markers (e.g. fibrosis, AST/ALT, CK18-M65 and M30).

**Conclusion:** Our results point to a contribution of activated monocytes to systemic and liver inflammation. Monocytes likely infiltrate the liver, transform into monocyte-derived macrophages and release IL1β and IL8 in response to Peptidoglycan and TLR2 activation, ultimately leading to ALD progression.

**THU033 Improving NIAAA criteria for the diagnosis of alcoholic hepatitis, role of systemic inflammation**

Elisa Pose1,2,3, Emma Avitabile4, Alba Diaz5, Carla Montironi6, Martina Perez7, Jordi Graçaçu-Gines1,7, Helena Hernández Evole1,7, Tejasw Sehrawat2, Harmee Malhi3, Pol Olivas4,5, Virginia Hernandez-Gea1,3,7, Vijay Shah8, Patrick S. Kamath8, Pere Gine6, Elisa Pose1,2,3, Emma Avitabile4, Alba Diaz5, Carla Montironi6, Martina Perez7, Jordi Graçaçu-Gines1,7, Helena Hernández Evole1,7, Tejasw Sehrawat2, Harmee Malhi3, Pol Olivas4,5, Virginia Hernandez-Gea1,3,7, Vijay Shah8, Patrick S. Kamath8, Pere Gine6.

1Hospital Clinic of Barcelona, Liver Unit, Barcelona, Spain; 2Institut d’Investigacions Biomèdiques August Pi i Sunyer (IDIBAPS), Chronic liver disease, Barcelona; 3Centro de Investigación Biomédica en Red, Chronic liver disease, Madrid, Spain; 4Institut d’Investigacions Biomèdiques August Pi i Sunyer (IDIBAPS), CIF: Q5856414G, Chronic liver disease, Barcelona, Spain; 5Hospital Clinic of Barcelona, Pathological Department, Barcelona, Spain; 6Hospital Clinic of Barcelona, Pathology Department and Molecular Biology CORE, Barcelona, Spain; 7Institut d’Investigacions Biomèdiques August Pi i Sunyer (IDIBAPS), Chronic liver disease, Barcelona, Spain; 8Mayo Clinic, Division of Gastroenterology and Hepatology, Rochester, United States; 9Hospital Clinic of Barcelona, Psychiatry, Barcelona, Spain; 10University of Barcelona, Barcelona, Spain

Email: EPOSE@clinic.cat

**Background and aims:** The National Institute of Alcohol Abuse and Alcoholism (NIAAA) clinical criteria for the diagnosis of probable alcoholic hepatitis (AH) are commonly used to select subjects for clinical studies and to diagnose AH in clinical practice. The objectives of this study were to assess the sensitivity and specificity and to improve the diagnostic accuracy of NIAAA clinical criteria for AH.

**Method:** 268 consecutive patients with Alcohol-related liver disease (ArLD) that underwent liver biopsy were prospectively included: 210 and 58 in the derivation and validation cohorts. NIAAA criteria and histological diagnosis of AH were independently reviewed by clinical investigators and pathologists from Hospital Clinic and Mayo Clinic. Using liver biopsy as gold standard we determined specificity, sensitivity and accuracy of the NIAAA clinical criteria. To improve the diagnostic accuracy of NIAAA criteria the threshold of quantitative variables was optimized and combinations with categorical variables were tested. Factors associated with 1-year transplant-free survival were evaluated.

**Results:** In the study cohort, NIAAA criteria showed a sensitivity of 63% (95% CI, 52–73) a specificity of 78% (95% CI, 69–84) and an accuracy of 72% (95% CI, 65–78). A significant percentage (37%) of patients with histological-proven AH did not meet NIAAA criteria. These patients had higher MELD score values, higher frequency of cirrhosis decompensation, higher inflammation in terms of C-reactive protein (CRP) levels and lower 1-yr survival compared to subjects without histological AH (63% vs 91%, p = 0.000). A new version of the NIAAA criteria, NIAAAs-PCR criteria, was generated by simplifying the current NIAAA criteria and adding a new parameter as follows: bilirubin ≥ 2.5 mg/dl instead of ≥ 3 mg/dl; AST ≥ 50 UI/L and AST>ALT, instead of AST ≥ 50 UI/L, AST/ALT ratio ≥ 1.5 mg/dl and AST <400 UI/L; active alcohol consumption or alcohol abstinence less than 120 days instead of 60 days before the inclusion; not considering the presence of confounding factors and adding C reactive protein ≥ 1 mg/dl. These modified criteria showed a good combination of sensitivity, specificity and accuracy among all the combinations tested (70%, 83%, 78%, respectively). Factors associated with survival in the study cohort were histological AH, decompensated cirrhosis, MELD score and NIAAAs-PCR criteria, but not NIAAA original criteria. Similar findings were observed in the validation cohort where NIAAA original criteria showed 52% sensitivity, 82% specificity and 69% accuracy, while NIAAAs-PCR showed 56% sensitivity, 91% specificity and 76% accuracy for the clinical diagnosis of AH.
Background and aims: Severe alcohol-associated hepatitis (HA) has a high morbidity and mortality, however, the information in Latin America is limited. We aimed to characterize patients hospitalized for AH in a multinational cohort in Latin America.

Method: Multicenter prospective cohort study. We included patients admitted with severe AH between 2015–2021. Sociodemographic and clinical information was recorded. The analysis included survival analysis using Kaplan-Meier curves. This study was approved by the institutional ethics committee.

Results: 319 patients from 24 centers (8 countries: Argentina, Bolivia, Brazil, Chile, Colombia, Ecuador, Mexico, Peru) were included. Age 49.9 ± 10.3 years, 84.6% men and 54.1% had a previous diagnosis of cirrhosis. Median MELD at admission 27 [21–32] points. 25.6% met SIRS criteria and 47.6% had acute renal failure on admission. 36.11% were treated with corticosteroids. Survival at 30 days was 77.6% (95% CI: 69.7–83.7%) and at 90 days 71.6% (95% CI: 62.5–78.9%). 39.6% presented infections. The most frequent locations were urinary (34.1%), respiratory (30.7%), spontaneous bacterial peritonitis (17.1%) and skin (11.4%). The most frequent pathogens were Escherichia coli (55.6%), Klebsiella pneumoniae (11.1%) and Enterococcus (7.4%). In the long term, only 2.9% of patients have been transplanted.

Conclusion: This multicenter study shows high morbidity and mortality in patients with severe HA, which is comparable to other centers in the world.

THU035
Prophylaxis of withdrawal syndrome decreases mortality in patients with alcohol-associated hepatitis

Background and aims: Alcohol withdrawal syndrome (AWS) is a serious medical condition that often complicates hospitalized patients with advanced alcohol-related liver disease including alcoholic hepatitis (AH). There are no studies evaluating the prevalence, impact, and effect of AWS prophylaxis in the setting of AH. We aimed at evaluating the incidence and outcomes of AWS in

Conclusion: A modified version of NIAAA criteria, NIAAs-CRP criteria, with higher sensitivity, specificity and accuracy, improves the non-invasive diagnosis of AH in patients with ArLD and adds prognostic value to NIAAA criteria.
patients hospitalized with AH from two countries with different AWS management strategies.

Method: A multicenter, international, retrospective, case-control study was performed evaluating consecutive patients hospitalized with AH in Spain (four participating centers) and USA (one center). In Spain, clomethiazole is used as prophylactic therapy for AWS while in USA a symptom-triggered approach is followed. Electronic medical history of all patients hospitalized with the diagnosis code of AH since 2015 were revised. Diagnosis of AWS was based on the clinician criteria and the need for treatment with benzodiazepines to control symptoms. Primary outcome was 28-days mortality. Prescribed benzodiazepine dose expressed in diazepam-equivalent was compared between groups who developed AWS. A propensity score (match by age, sex, BMI, MELD and ACLF score) was performed to compare clinical outcomes between patients who developed WDS in Spain vs. USA, using stratified logistic regression for matched pairs.

Results: Study population included 432 patients (n = 193 from Spain and n = 239 from USA), of whom 63% were women with mean age 48 ± 10 years, median BMI 28 (24–32) kg/m² and mean MELD score at admission of 23.7 ± 7.9. Overall prevalence of AWS and mortality was 32% (n = 140) and 17% (n = 74), respectively. Presence of AWS was lower in patients receiving prophylaxis (Spain) than in patients who did not receive it (USA) (26% vs. 37%, P = 0.007). In patients receiving prophylaxis, the development of AWS was not associated with worse clinical outcomes, including mortality (10% vs. 8%, P = 0.52). In patients not receiving prophylaxis in the USA, the development of AWS was associated with higher mortality (33% vs. 19%, P = 0.009) [Figure 1]. After propensity matching, a higher mortality was seen among patients presenting AWS in USA vs. Spain (p = 0.003). Importantly, patient with AWS in Spain had similar mortality that those who did not developed AWS in USA (p = 0.35). There were marked differences in several key parameters in patients with AWS with and without prophylaxis, respectively: the diazepam equivalent dose used (87 ± 119 vs. 136 ± 190 mg), ICU admission (16% vs. 48%, P = 0.02) and orotracheal intubation rate (10% vs. 28%, P = 0.04).

Conclusion: In AH setting, prophylactic therapy for AWS is associated with lower prevalence of both withdrawal symptoms and short-term mortality. This data supports that prophylactic therapy is a better approach than symptom-triggered therapy in patients hospitalized with AH.

THU036
The use of pharmacotherapy in the treatment of alcohol use disorder
Kathryn Allen1, Tobias Maharaj1, John Ryan1. 1Beaumont Hospital, Hepatology, Dublin, Ireland
Email: kathrynallen123@hotmail.com

Background and aims: Alcohol use disorder (AUD) is an important cause of preventable morbidity and mortality. The prevalence of AUD and alcohol related liver disease is increasing in Ireland. Several medications have been demonstrated to be effective for the treatment of AUD. We wanted to ascertain the current attitude of gastroenterology physicians in Ireland towards pharmacotherapy as a treatment option for AUD.

Method: An anonymous, questionnaire-based survey was sent to gastroenterology physicians nationwide. This survey collected demographic information and assessed prescribing habits towards medications which have been approved to treat AUD (Naltrexone, Disulfiram, Baclofen, Librium, Nalmefene and Acamprosate). Where pharmacotherapy was not routinely utilised, we examined factors which may have led to their avoidance.

Results: We received 60 responses, 56% (n = 32) consultant gastroenterologists, and 40% (n = 23) GI specialist registrars (SpRs). 80% (n = 48) report being frequently (daily/weekly) involved in the management of AUD. 95% (n = 57) of prescribers believe that there is a role for pharmacotherapy in treating AUD, but only 22% (n = 13) routinely use these in clinical practice. Librium was commonly used by 88% (n = 53), while <10% regularly prescribed Naltrexone, Baclofen, or Acamprosate. Prohibitive factors identified were lack of hospital alcohol services (61%) [48% of respondents reported no alcohol service or support in their hospital], side effect profile for patients (26%), lack of compliance (26%), lack of adjuvant psychosocial support in community (47%), and unfamiliarity with medications (61%).

Conclusion: Despite the burden of alcohol on our acute hospitals, there is a clear and significant lack of support for alcohol related conditions. Emanating from this is the underutilisation of pharmacotherapy as a treatment for AUD, despite its evidence base. This survey highlights an urgent need to develop alcohol support services, in conjunction with physician education about the role of pharmacotherapy in treating AUD.

THU037
Application of machine learning algorithms to classify steatohepatitis on liver biopsy
Resham Ramkissoon1, Joseph Ahn1, Yung-Kyun Noh2, Yubin Yeon3, Chady Meroueh1, Priya Thanneeru1, Amit Das1, Jason Hipp1, Alina Allen1, Douglas Simonetto1, Patrick S. Kamath1, Vijay Shah1.
1Mayo Clinic, Rochester, United States; 2Hanyang Univ, Department of Computer Science, Korea, Rep. of South; 3Hanyang Univ, Department of Artificial Intelligence, Korea, Rep. of South
Email: ramkissoon.resham@mayo.edu

Background and aims: Currently, it is very challenging to distinguish alcoholic steatohepatitis (ASH) and non-alcoholic steatohepatitis (NASH) on liver biopsy alone as they share many of the same histological characteristics. Artificial intelligence (AI) models utilizing deep learning have demonstrated superhuman degrees of accuracy in interpretation of digitized liver histology. The aim of our study was to develop a deep learning algorithm in the form of a convolutional neural network (CNN) to classify ASH and NASH on liver biopsy.

Method: We obtained liver biopsy slides from 38 patients with ASH and 59 patients with NASH. ASH was determined based on the clinical diagnosis of alcohol-associated hepatitis, and patients with NASH were identified from a cohort of morbidly obese patients undergoing bariatric surgery. The slides were digitized into an electronic database with whole-slide diagnosis labels. Each whole-slide image was rescaled and randomly cropped to generate 256 patches of 256 x 256 pixels. Each cropped patch retained the diagnosis label from the original whole-slide image (0 = NASH, 1 = ASH). The patches were randomly split into training and testing sets in an 8:2 ratio. Patches in the training set were used to train a 50-layer CNN (ResNet50), and the CNN’s performance as a binary classifier was tested on the patches in the testing set. Gradient-weighted Class Activation Mapping (Grad-CAM) was used as a method to understand the CNN’s decisions.

Results: The CNN had an outstanding performance in distinguishing ASH versus NASH with an AUC of 0.962. Using an optimal threshold of 0.504, the CNN had an accuracy of 90.4%, sensitivity of 79.5%, and specificity of 96.3%. The positive predictive value is 92.1% and...
negative predictive is 89.7%. Grad-CAM highlighted distinct regions within each patch that the algorithm used to make its decisions.

Figure: (a) Receiver operating characteristic (ROC) curve for the CNN’s classification of ASH versus NASH. (b) Confusion matrix for the CNN; a diagnosis of ASH is indicated by “Positive” and a diagnosis of NASH is indicated by “Negative.” (c) Activation map for classification of ASH patch (top row) and NASH patch (bottom row).

Conclusion: Our deep learning-based AI algorithm had an outstanding performance for patch-level classification of liver biopsy images from patients with ASH and NASH. After further validation on a larger set of liver biopsy images and evaluation of model performance at the level of whole slides, our AI algorithm may prove to be a novel way to distinguish ASH versus NASH histologically.

THU038
Calorie-protein deficit and body mass index are the independent predictors of mortality in severe alcoholic hepatitis
Harshita Tripathi1, Jaya Benjamin2, Puja Bhatia1, Rakhi Maiwall3, Guresh Kumar4, Yogendrakumar Joshi5, Shiv Kumar Sarin1. 1Institute of Liver and Biliary Sciences, Clinical Nutrition, New Delhi, India; 2Institute of Liver and Biliary Sciences, Biostatistics, DELHI, India; 3Institute of Liver and Biliary Sciences, Hepatology, DELHI, India; 4Institute of Liver and Biliary Sciences, Clinical Nutrition, DELHI, India; 5Institute of Liver and Biliary Sciences, Clinical Nutrition and Hepatology, DELHI, India.

Email: jayabenjamin@gmail.com

Background and aims: Short term mortality is high in severe alcoholic hepatitis (SAH), which is influenced by multiple factors. We planned to assess the independent predictors of 60 day mortality for alcoholic hepatitis (SAH), which is influenced by multiple factors. We aimed to identify the factors that may help in identifying at-risk patients and designing optimal treatment strategies to improve outcomes.

Method: SAH patients with Maddrey’s discriminant function (mDF) 32–100 were enrolled; excluding sepsis, AKI and malignancy. Baseline clinical, biochemical parameters, disease severity [MELD, CTP, MDF, FIB-4], BMI, fat free mass index (FFMI), hand grip strength, usual diet [calorie (C) and protein (P) intake] and 60 day mortality were assessed. C and P deficit was the difference of ideal requirement [C (35kcal) and P (1.2 g) per kg ideal body weight] and actual intake. Logistic regression analysis was done.

Results: In 60 patients with SAH [age 40 ± 7.37 yrs; ascites 47 (84%); BMI- 21.3 ± 3.8 kg/m²; mDF-62.4 ± 21.4, MELD 28 ± 9.3, CTP 10.6 ± 1.4, on steroids 14 (25%) there was significantly low calorie intake despite >3 weeks of abstinence (Table 1). Those 16 (26.6%) patients who died at 2 mo had significantly lower BMI, higher P and C deficit and total bilirubin compared to survivors; that predicted mortality.

THU039
Alcoholic foamy degeneration: a unique variant of ALD that shows a characteristic pattern of gene expression with upregulation of lipid metabolism and mitochondrial genes and downregulation of fibrosis genes
Jordi Grañados-Gines1, Delia Blaya2, Helena Hernández Evoie2, Carla Montironi3, Emma Avitabile1, Martina Perez1, Marta Cervera1, Marta Carol1, Ana Belén Rubio2, Núria Fabrellas1, Anna Soría1, Octavi Bassegoda1, Laura Napoleone1, Ann Ma2, Adrià Juanola3, Isabel Graupera1, Alba Díaz2, Juan Jose Lozano2, Pere Gines3, Elisa Pose1. 1Hospital Clinic de Barcelona, Liver Unit, Barcelona, Spain; 2Hospital Clinic of Barcelona, Pathology Department and Molecular Biology CORE, Barcelona, Spain; 3Hospital Clinic de Barcelona, Pathology Unit, Barcelona, Spain; 4Hospital Clínic of Barcelona, Pathology Department and Molecular Biology CORE, Barcelona, Spain; 5Hospital Clinic of Barcelona, Pathology Department and Molecular Biology CORE, Barcelona, Spain; 6Hospital Clinic de Barcelona, Pathology Unit, Barcelona, Spain; 7Hospital Clínic de Barcelona, Pathology Department and Molecular Biology CORE, Barcelona, Spain.

Email: EPOSE@clinic.cat

Background and aims: Alcoholic foamy degeneration (AFD) is a variant of alcoholic liver disease that is diagnosed based on histology, with a pattern of microvesicular steatosis in the liver biopsy. Recently, in one of the largest series reported to date, we described AFD as an entity with similar clinical presentation to alcoholic hepatitis (AH), but faster improvement of liver function and markedly better long-

### Table 1: Predictors of Mortality in SAH

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Death (n = 16)</th>
<th>Alive (n = 44)</th>
<th>P value</th>
<th>Multivariate</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Demographic Details</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Age (yrs)</td>
<td>40.6 ± 8.4</td>
<td>39.5 ± 6.2</td>
<td>0.314</td>
<td></td>
</tr>
<tr>
<td>Height (cm)</td>
<td>171 ± 4.7</td>
<td>169 ± 8.9</td>
<td>0.511</td>
<td></td>
</tr>
<tr>
<td>Dry BMI (kg/m²)</td>
<td>19.7 ± 2.2</td>
<td>22.7 ± 1.1</td>
<td>0.001 0.045</td>
<td></td>
</tr>
<tr>
<td>Weight reduced (kg)</td>
<td>9.47 ± 7.0</td>
<td>8.9 ± 6.3</td>
<td>0.785</td>
<td></td>
</tr>
<tr>
<td>Duration of weight loss (mo)</td>
<td>4.87 ± 1.6</td>
<td>8.3 ± 12.9</td>
<td>0.257</td>
<td></td>
</tr>
<tr>
<td><strong>Clinical details</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Acutes</td>
<td>32 (53.3%)</td>
<td>12 (20%)</td>
<td>0.576</td>
<td></td>
</tr>
<tr>
<td>Duration of alcohol intake (yrs)</td>
<td>14.47 ± 5.7</td>
<td>13.08 ± 7.3</td>
<td>0.113</td>
<td></td>
</tr>
<tr>
<td>Alcohol Quantity (gm)</td>
<td>57 ± 153</td>
<td>478 ± 194</td>
<td>0.468</td>
<td></td>
</tr>
<tr>
<td>Last intake (days)</td>
<td>24 ± 9.45</td>
<td>36.4 ± 15.7</td>
<td>0.001</td>
<td></td>
</tr>
<tr>
<td><strong>Biochemical Parameters</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total Bil (mg/dl)</td>
<td>21.3 ± 8.9</td>
<td>15.5 ± 7.2</td>
<td>0.041 0.022</td>
<td></td>
</tr>
<tr>
<td>AST (IU/L)</td>
<td>116 ± 54</td>
<td>157 ± 73</td>
<td>0.040</td>
<td></td>
</tr>
<tr>
<td>ALT (IU/L)</td>
<td>127 ± 63</td>
<td>162 ± 56</td>
<td>0.031</td>
<td></td>
</tr>
<tr>
<td>ALP (IU/L)</td>
<td>91.9 ± 27</td>
<td>157 ± 91</td>
<td>0.001</td>
<td></td>
</tr>
<tr>
<td>Total protein (g/dl)</td>
<td>6.28 ± 0.93</td>
<td>6.99 ± 1.08</td>
<td>0.028</td>
<td></td>
</tr>
<tr>
<td>Albumin (g/dl)</td>
<td>2.8 ± 0.66</td>
<td>2.8 ± 0.54</td>
<td>0.578</td>
<td></td>
</tr>
<tr>
<td>INR</td>
<td>2.0 ± 0.34</td>
<td>1.9 ± 0.55</td>
<td>0.716</td>
<td></td>
</tr>
<tr>
<td>Urea (mg/dl)</td>
<td>38.5 ± 16</td>
<td>28 ± 6.0</td>
<td>0.089</td>
<td></td>
</tr>
<tr>
<td>Creatinine (mg/dl)</td>
<td>0.80 ± 0.4</td>
<td>0.73 ± 0.2</td>
<td>0.581</td>
<td></td>
</tr>
<tr>
<td>Sodium (mmol/l)</td>
<td>129.5 ± 4.2</td>
<td>132.3 ± 3.3</td>
<td>0.039</td>
<td></td>
</tr>
<tr>
<td>Potassium (mmol/l)</td>
<td>14.07 ± 0.68</td>
<td>4.08 ± 0.68</td>
<td>0.963</td>
<td></td>
</tr>
<tr>
<td><strong>Severity Scores</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MELD</td>
<td>28.3 ± 2.9</td>
<td>28.3 ± 10.8</td>
<td>0.317</td>
<td></td>
</tr>
<tr>
<td>MDF</td>
<td>63.05 ± 18.4</td>
<td>63.05 ± 23.1</td>
<td>0.203</td>
<td></td>
</tr>
<tr>
<td>CTP</td>
<td>10.4 ± 10.6</td>
<td>10.7 ± 15</td>
<td>0.015</td>
<td></td>
</tr>
<tr>
<td>FF4</td>
<td>8.4 ± 3.6</td>
<td>6.95 ± 1.08</td>
<td>0.028</td>
<td></td>
</tr>
<tr>
<td><strong>Body composition parameters</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Fat mass (kg)</td>
<td>18.6 ± 4.8</td>
<td>22.6 ± 5.6</td>
<td>0.118</td>
<td></td>
</tr>
<tr>
<td>Fat free mass (kg)</td>
<td>40.36 ± 13</td>
<td>51.2 ± 13.3</td>
<td>0.720</td>
<td></td>
</tr>
<tr>
<td>FFMI kg/m²</td>
<td>16.8 ± 4.2</td>
<td>18.02 ± 4.6</td>
<td>0.501</td>
<td></td>
</tr>
<tr>
<td>Hand grip (kg)</td>
<td>22.1 ± 6.17</td>
<td>23.3 ± 6.2</td>
<td>0.986</td>
<td></td>
</tr>
<tr>
<td><strong>Diet</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Energy requirement (kcal)</td>
<td>2289 ± 738</td>
<td>2358 ± 523</td>
<td>0.730</td>
<td></td>
</tr>
<tr>
<td>Protein requirement (g)</td>
<td>85.6 ± 5.7</td>
<td>83.8 ± 10.7</td>
<td>0.511</td>
<td></td>
</tr>
<tr>
<td>Energy intake (kcal)</td>
<td>598.8 ± 233</td>
<td>737.3 ± 278.4</td>
<td>0.643</td>
<td></td>
</tr>
<tr>
<td>Protein intake (g)</td>
<td>26.65 ± 4.2</td>
<td>20.3 ± 9.9</td>
<td>0.06 0.022</td>
<td></td>
</tr>
<tr>
<td><strong>Calorie deficit (kcal)</strong></td>
<td>2035 ± 214</td>
<td>1813 ± 508</td>
<td>0.05 0.045</td>
<td></td>
</tr>
<tr>
<td><strong>Protein deficit (g)</strong></td>
<td>70.7 ± 7.5</td>
<td>60.9 ± 19.2</td>
<td>0.02 0.051</td>
<td></td>
</tr>
</tbody>
</table>

Data expressed as mean ± SD, n (%). P value ≤0.05 is significant.

Conclusion: High calorie and protein diet with maintained body weight improves survival in SAH.

Results: In 60 patients with SAH [age 40 ± 7.37 yrs; ascites 47 (84%); BMI- 21.3 ± 3.8 kg/m²; mDF-62.4 ± 21.4, MELD 28 ± 9.3, CTP 10.6 ± 1.4, on steroids 14 (25%)] there was significantly low calorie intake despite >3 weeks of abstinence (Table 1). Those 16 (26.6%) patients who died at 2 mo had significantly lower BMI, higher P and C deficit and total bilirubin compared to survivors; that predicted mortality.
CHRONIC ALCOHOLIC LIVER DISEASE : PRESENTATION AND PATHOPHYSIOLOGY

Background and aims: Severe alcohol-related hepatitis (sAH) is a florid presentation of alcohol-related liver disease with very high short-term mortality. A genome-wide association study identified solute carrier family 38 member 4 (SLC38A4) as a potential risk locus for the development of sAH. SLC38A4 is characterised as an amino acid transporter and is predominantly hepatically expressed under the regulation of HNF4a. The aim of this project was to investigate how changes in SLC38A4 expression may contribute to the pathogenesis of sAH.

Method: SLC38A4 expression was determined by RNA-seq in whole liver biopsies obtained from patients with alcohol related liver disease, including sAH, from a published study. In vitro experiments were conducted to investigate the effects of known disease mediators on SLC38A4 expression in Huh7.5 cells. SLC38A4 knock-out lines (aliases P1.7 and C12 SLC38A4-KO) were generated by CRISPR/Cas9 editing in Huh7.5 cell lines; a control cell line (SCWT) was generated using a non-targeted scramble guide RNA. The functional impact of SLC38A4 knock-out was then characterised using gene expression analysis (RT-qPCR and RNA-seq) and protein expression by immunofluorescence (IF). Assays were performed to assess the impact of knock-out on cell morphology and proliferation in addition to CYP3A4 activity and ureagenesis.

Results: SLC38A4 expression was reduced in whole liver tissue from cohorts of patients with sAH compared to their early alcoholic steatohepatitis controls (p <0.0001). In vitro SLC38A4 expression was downregulated by mediators of alcoholic hepatitis i.e., IL-1b, TGFb1, TNFa and sAH patient plasma but upregulated by dexamethasone (Figure 1A). SLC38A4-KO lines demonstrated upregulation in the epithelial-mesenchymal transition markers, EPCAM and Vimentin (p <0.0001 and p <0.01 respectively) (Figure 1B). SLC38A4-KO resulted in reduced cell proliferation, ureagenesis, and downregulation of bile acid transporters, BSEP (p <0.0001) and MRP2 (p <0.01). The cell morphology of knock-out cells exhibited stemness like features and the upregulation of the foetal isoform of HNF4a, P2 (p <0.001). CYP3A4 expression and activity were reduced (p <0.001). RNA-seq confirmed the increase of EPCAM and Vimentin and the reduction of CYP3A4 across the SLC38A4-KO lines. Additionally, SLC38A4-KO resulted in differential expression of other SLC genes and cell growth/differentiation regulating genes (Figure 1C). Pathway analysis indicated changes in amino acid metabolism and cytokine signalling pathways.

Conclusion: AFD displays a specific gene signature differentiated from that of AH. Genetic functional pathways associated with lipid metabolism and mitochondrial function are upregulated in patients with AFD. In contrast, there is a downregulation of pathways associated with inflammation, fibrosis and senescence. Histological findings are consistent with genetic profile, with a predominant pattern of steatosis, with scarce fibrosis and steatohepatitis.

THU040
Loss of solute carrier family 38 member 4 (SLC38A4) as a driver for the pathogenesis of severe alcoholic hepatitis

Nchimunya Nelisa Tebeka1, Stephen Atkinson1, Luke D. Tyson1, Josepmaria Argemí2, Adam Syanda1, Ramon Bataller2, Tamir Rashid1, Mark Thursz1.
1Imperial College London, Department of Metabolism, Digestion and Reproduction, London, United Kingdom; 2University of Pittsburgh, Medical Center, Pittsburgh, United States

Email: n.tebeka@imperial.ac.uk

Background and aims: Severe alcohol-related hepatitis (sAH) is a florid presentation of alcohol-related liver disease with very high short-term mortality. A genome-wide association study identified solute carrier family 38 member 4 (SLC38A4) as a potential risk locus for the development of sAH. SLC38A4 is characterised as an amino acid transporter and is predominantly hepatically expressed under the regulation of HNF4a. The aim of this project was to investigate how changes in SLC38A4 expression may contribute to the pathogenesis of sAH.

Method: SLC38A4 expression was determined by RNA-seq in whole liver biopsies obtained from patients with alcohol related liver disease, including sAH, from a published study. In vitro experiments were conducted to investigate the effects of known disease mediators on SLC38A4 expression in Huh7.5 cells. SLC38A4 knock-out lines (aliases P1.7 and C12 SLC38A4-KO) were generated by CRISPR/Cas9 editing in Huh7.5 cell lines; a control cell line (SCWT) was generated using a non-targeted scramble guide RNA. The functional impact of SLC38A4 knock-out was then characterised using gene expression analysis (RT-qPCR and RNA-seq) and protein expression by immunofluorescence (IF). Assays were performed to assess the impact of knock-out on cell morphology and proliferation in addition to CYP3A4 activity and ureagenesis.

Results: SLC38A4 expression was reduced in whole liver tissue from cohorts of patients with sAH compared to their early alcoholic steatohepatitis controls (p <0.0001). In vitro SLC38A4 expression was downregulated by mediators of alcoholic hepatitis i.e., IL-1b, TGFb1, TNFa and sAH patient plasma but upregulated by dexamethasone (Figure 1A). SLC38A4-KO lines demonstrated upregulation in the epithelial-mesenchymal transition markers, EPCAM and Vimentin (p <0.0001 and p <0.01 respectively) (Figure 1B). SLC38A4-KO resulted in reduced cell proliferation, ureagenesis, and downregulation of bile acid transporters, BSEP (p <0.0001) and MRP2 (p <0.01). The cell morphology of knock-out cells exhibited stemness like features and the upregulation of the foetal isoform of HNF4a, P2 (p <0.001). CYP3A4 expression and activity were reduced (p <0.001). RNA-seq confirmed the increase of EPCAM and Vimentin and the reduction of CYP3A4 across the SLC38A4-KO lines. Additionally, SLC38A4-KO resulted in differential expression of other SLC genes and cell growth/differentiation regulating genes (Figure 1C). Pathway analysis indicated changes in amino acid metabolism and cytokine signalling pathways.

Conclusion: AFD displays a specific gene signature differentiated from that of AH. Genetic functional pathways associated with lipid metabolism and mitochondrial function are upregulated in patients with AFD. In contrast, there is a downregulation of pathways associated with inflammation, fibrosis and senescence. Histological findings are consistent with genetic profile, with a predominant pattern of steatosis, with scarce fibrosis and steatohepatitis.
Refining the natural history of alcohol related liver disease: a THU041 recapitulates several features considered important in disease.

**Method:** WALDO is an international, retrospective cohort of patients with biopsy-proven liver disease using competing risk analysis to accurately describe the risks of liver and non-liver related outcomes in ALD.

**Results:** The WALDO cohort includes 710 patients of whom 423 had cirrhosis. Alcoholic hepatitis was present in 184 patients at the time of biopsy, and 216 patients were not cirrhotic and without alcoholic hepatitis. During a median follow-up of 4.6 years (IQR 1.1–9.5 years, totalling over 4 thousand patient-years) there were 381 deaths (54% of the total cohort) and 47 patients (7%) underwent liver transplantation. Deaths were liver related in 144 cases (39% of all deaths). New LACE occurred in 87 patients during follow-up and new medical morbidity occurred in 133 patients (19%). When compared to patients without cirrhosis CIF for liver-related death was significantly higher in patients with cirrhosis (1.87, 1.56–2.18, p = 0.042), decompensated cirrhosis (5.88, 5.60–6.165, p < 0.001) and alcoholic hepatitis (6.40, 6.12–6.68, p < 0.001), whereas the CIF of non-liver related deaths was not significantly different. The strongest baseline predictors of outcomes were stage of disease, MELD or ALBI scores, and abstinence. The cumulative incidence of liver-related deaths at sample baseline MELD scores of 6, 12, and 20 was 8%, 18% and 49% respectively with significant differences between patients who were abstinent or non-abstinent.

**Conclusion:** Patients with ALD are at risk of multiple causes of ill health. Competing risk analysis takes these into account to give a more accurate analysis of the probability of outcomes. The risk of liver-related mortality increases significantly above that of non-liver related mortality only in decompensated cirrhosis and alcoholic hepatitis.

**THU042 Potential biomarkers for differentiating alcoholic hepatitis from decompensated cirrhosis by serum metabolomic analysis**

**Background and aims:** Alcohol-related liver disease (ALD) is common throughout the world and is a common cause of ill-health and death. Alcohol consumption affects multiple organs and systems, therefore, increasing the risk of a wide range of conditions. Previous systematic review demonstrated that both liver and non-liver related mortality increased depending on the stages of liver disease. We have analysed a cohort of patients with biopsy-proven liver disease using competing risk analysis to accurately describe the risks of liver and non-liver related outcomes in ALD.

**Method:** WALDO is an international, retrospective cohort of patients with biopsy-proven liver disease followed up through health records to capture outcome data regarding mortality and morbidity. Competing risk analysis was used to estimate cumulative incidence functions (CIF) of mortality (liver-related or non-liver related deaths), and morbidity. Morbidity was classed as liver-associated clinical events (LACE) and major adverse medical events included cancer, cardiovascular disease or diabetes. Subdistribution hazards were calculated with univariable and multivariable analyses to understand factors affecting outcomes. These analyses were used to describe the cumulative incidence of liver-specific mortality for given MELD scores.

**Results:** The WALDO cohort includes 710 patients of whom 423 had cirrhosis. Alcoholic hepatitis was present in 184 patients at the time of biopsy, and 216 patients were not cirrhotic and without alcoholic hepatitis. During a median follow-up of 4.6 years (IQR 1.1–9.5 years, totalling over 4 thousand patient-years) there were 381 deaths (54% of the total cohort) and 47 patients (7%) underwent liver transplantation. Deaths were liver related in 144 cases (39% of all deaths). New LACE occurred in 87 patients during follow-up and new medical morbidity occurred in 133 patients (19%). When compared to patients without cirrhosis CIF for liver-related death was significantly higher in patients with cirrhosis (1.87, 1.56–2.18, p = 0.042), decompensated cirrhosis (5.88, 5.60–6.165, p < 0.001) and alcoholic hepatitis (6.40, 6.12–6.68, p < 0.001), whereas the CIF of non-liver related deaths was not significantly different. The strongest baseline predictors of outcomes were stage of disease, MELD or ALBI scores, and abstinence. The cumulative incidence of liver-related deaths at sample baseline MELD scores of 6, 12, and 20 was 8%, 18% and 49% respectively with significant differences between patients who were abstinent or non-abstinent.

**Conclusion:** Patients with ALD are at risk of multiple causes of ill health. Competing risk analysis takes these into account to give a more accurate analysis of the probability of outcomes. The risk of liver-related mortality increases significantly above that of non-liver related mortality only in decompensated cirrhosis and alcoholic hepatitis.
three molecules were selected for further analysis and the most significant biomolecules were selected to discriminate the AH versus ArDC phenotype and infection status.

Results: Seventy-two percent of patients were male and 97% of them had cirrhosis. The main molecules that showed increased levels in AH group comparative to ArDC group were C16 Sphinganine-1-phosphate (S1P), Prostaglandin F1a/b (PGF1a/b), Cerotic acid and arachid acid while Prostaglandin D2/E2 (PGD2/E2), Prostaglandin E2-ethanolamide (PGE2-EA), dinor cholic acid, 12-ketodeoxycholic acid 2-hydroxy stearic acid, D-Sphingosine decreased (1a).

In the multivariate analysis, PLSDA score plot showed a co-variance of 19.4%, with a good discrimination between AH and ArDC groups (Figure 1b).

In the subgroup analysis, (infected AH and ArDC and non-infected AH and ArDC), a good discrimination was showed by S1P, with a p value = 1.49E-15, Mean Decrease Accuracy (MDA) >0.035 and an area value under ROC curve (AUC) of 0.984 (0.943–1) and PGD2/E2, which had a decreased level (p = 2.56E-1, MDA >0.025 and AUC 0.958 (0.898-0.994)) (Figure 1c, d). The semiquantitative analysis of the combination between S1P and PG2E2 showed increased (95%) diagnostic accuracy to discriminate AH from ArDC, with 100% NPV and 100% Se.

Conclusion: Sphingolipids are now known to regulate important physiological cellular processes (1). Especially, S1P has an anti-necrotic and anti-inflammatory effects via TNF-a signaling pathway; In an ischemia/reperfusion (I/R) model, plasma S1P levels were noted to be decreased after hepatic I/R injury (2). Prostaglandins have protective effects by inhibiting the generation of reactive oxygen species and regulating the production of inflammatory cytokines. In this study, the prostaglandin levels were decreased in patients with AH showing that beta-oxidation could be a valuable target pathway.

THU043
A phase II, multicenter, open-label, randomized trial of pegfilgrastim for patients with alcohol-associated hepatitis
Timothy Morgan1, Aliya Asghar1, John Tayek2, Danh Nguyen3, M. Wayne Fleischman2, John Donovan4, Joseph Alcorn5, Daniel Chao6, Andrew Stolz7, 1VA Medical Healthcare System, Medicine, Long Beach, United States; 2Harbor-UCLA Medical Center, Torrance, United States; 3University of California-Irvine, Irvine, United States; 4LAC-USC Medical Center, Los Angeles, United States; 5VA Healthcare System, Albuquerque, United States; 6VA Healthcare System, Loma Linda, United States
Email: timothy.morgan@va.gov

Background and aims: In trials conducted in India, recombinant granulocyte colony stimulating factor (GCSF) improved survival in alcohol-associated hepatitis (AH). The aim of this trial was to determine the safety and efficacy of pegfilgrastim, a long-acting recombinant GCSF, in patients with AH in the United States.

Method: This prospective, open label trial randomized patients with a clinical diagnosis of AH and a Maddrey discriminant function score ≥32 to standard of care (SOC) or SOC+pegfilgrastim (0.6 mg subcutaneously) on Day 1 and Day 8. SOC was 28 days of either pentoxifylline or prednisolone, as determined by the patient’s primary physician. The second injection of pegfilgrastim was not administered if the white blood cell count exceeded 30,000/mm³ on Day 8. Primary outcome was survival at Day 90. Secondary outcomes included the incidence of acute kidney injury (AKI), hepatorenal syndrome (HRS), hepatic encephalopathy, or infections.

Results: The study was terminated early due to COVID19 pandemic. Eighteen patients were randomized to SOC and 16 to SOC+pegfilgrastim. All patients received prednisolone as SOC. Nine patients failed to receive a second dose of pegfilgrastim due to WBC>30,000/mm³ on Day 8. Survival at 90 days was similar in both groups (SOC: 0.83 [95% confidence interval (CI): 0.57–0.94] vs. pegfilgrastim: 0.73 [95% CI: 0.44–0.89]; p > 0.05). The incidences of AKI, HRS, hepatic encephalopathy, and infections were similar in both treatment arms and there were no serious adverse events attributed to pegfilgrastim.

Conclusion: This phase II trial found no survival benefit at 90 days among subjects with AH who received pegfilgrastim+prednisolone compared with subjects receiving prednisolone alone.

THU044
Trends of alcohol-related liver disease hospitalisation during the COVID-19 pandemic
Oyekoya Ayanrinde1,2,3, Richard Goodheart1, 1Fiona Stanley Hospital, Gastroenterology and Hepatology, Murdoch, Australia; 2The University of Western Australia, Medical School, Crawley, Australia; 3Curtin University, Faculty of Health Sciences, Bentley, Australia
Email: oyekoya.ayanrinde@uwa.edu.au

Background and aims: Alcohol-related liver disease (ALD) is a common and potentially serious liver disorder associated with substantial morbidity and mortality. Recent reports have described increased alcohol since the onset of the COVID-19 pandemic. Therefore, the primary aim of this study was to examine trends in ALD hospital admissions prior to and during the Covid-19 pandemic. The secondary aim was to assess patient demographic and clinical characteristics associated with short and medium-term mortality.

Method: We retrospectively analysed data on patients who were admitted with ALD to a quaternary care hospital in Australia. The study population comprised adults hospitalised with International Classification of Diseases, Tenth Revision (ICD-10) principal diagnosis code K70.1 (alcoholic hepatitis), 70.3 (alcoholic cirrhosis), and 70.4 (alcoholic hepatic failure) between January 2018 and December 2021.

Data recorded included patient demographics, alcohol history, clinical and laboratory characteristics. The Model for End Stage Liver Disease (MELD) score was calculated.
Results: Amongst 345 hospitalisations with ALD, there was a non-statistically significant rise in cases comparing the two years preceding and during the first two years of the COVID-19 pandemic (Figure 1). There were 104 (30.1%) ARH and 69.9% with decompensated ARC or alcoholic liver failure (ALF). Those with ARH, compared with those with ARC and ALF, had a higher mean [standard deviation] MELD score (22.6 [9.3] vs. 20.3 [7.8], p = 0.02), were younger (47.6 [11.7] vs 54.6 [10.6] years, p < 0.001), had longer median [interquartile range] length of hospital stays (7.7 [4.0–13.0] vs. 6.0 [2.0–9.0] days, p = 0.008), and were predominantly male (58.7%). The in-hospital mortality was 12.8% overall, comprising 17.3% with ARH, 10.8% with ARC/ALF, and 5/47 (10.6%) aged under 40 years. Patients aged <40 years, compared with those ≥40 years had a similar 30-day mortality (14.9% vs. 20.5%, p = 0.37) but lower one-year mortality (25.5% vs. 43.0%, p = 0.02). Using multivariable logistic regression analysis, predictors of 30-day mortality were male sex (odds ratio [OR] 2.89, 95% confidence interval [CI] 1.29–6.46, p = 0.02), age (OR 1.06, 95% CI 1.02–1.10, p = 0.004), serum bilirubin (OR 1.006, 95% CI 1.003–1.008, p < 0.001), respiratory failure (OR 3.64, 95% CI 1.62–8.21, p = 0.002), hepatic encephalopathy (OR 6.43, 95% CI 2.91–14.21, p < 0.001), and type 2 hepatorenal syndrome (OR 3.27, 95% CI 1.55–6.87, p = 0.002).

Conclusion: Admissions with ALD have risen during the COVID-19 period. Young adults with severe ALD requiring hospitalisation, have a high mortality that is identical to mortality after a fractured neck of femur in older people. Multi-organ involvement and male sex predict mortality.

THU045
Increased hospital admissions for alcohol-associated hepatitis during the COVID-19 pandemic in Alberta, Canada: a retrospective cohort study
Alexandra Frolkis1, Meredith Borman1, Matthew Sadler1, Stephen Congly1, Henry Nguyen1, Samuel Lee1, Mark G Swain1, Kelly Burak1, Carla Coffin1, Alexander Aspinall1, Laura Stanton1, Abdel Aziz Shaheen1.1University of Calgary, Calgary Liver Unit Email: adfrolki@ucalgary.ca

Background and aims: Alcohol-associated hepatitis (AH) is the most severe and fulminant form of alcohol-related liver disease with females at greater risk of liver injury from alcohol use. Alcohol consumption increased during the COVID pandemic. The aim of our study was to assess the changing epidemiology of hospitalizations for AH by sex before and during the COVID-19 pandemic.

Method: We identified all hospitalizations for adults >18-years-old in Alberta, Canada using a validated algorithm of international classification of disease-10 codes and lab values for AH between March 2018 and September 2020. Severe AH was defined as Model for End-Stage Liver Disease (MELD) >20. Onset of the pandemic was defined as March 2020. Logistic regression was used to identify factors associated with AH severity, and separately mortality, adjusted for age, sex, and pandemic onset. Binomial regression was used to assess changes in frequency of admission for AH with the denominator as all cirrhosis-related admissions over the same time-period.

Results: There were 991 hospitalizations for AH prior to the pandemic (n = 381, 38.5% female) and 417 during the pandemic (n = 144, 34.5% female). Hospitalizations for AH significantly increased during the pandemic (p = 0.04) (Figure 1). Overall, a higher percentage of females (34.5%) had severe AH compared to males (31.0%) however this difference was not statistically significant (p = 0.25) (Figure 1). Though the total number of hospitalizations for AH increased during the pandemic, the odds of severe AH was higher pre-pandemic (odds ratio [OR] 0.73; 95% confidence interval [CI] 0.55–0.98) after adjusting for age and sex. For every year increase in age, the adjusted odds of severe AH increased by 1.02 (95% CI 1.01–1.03). Prior to the pandemic, more females (38.6%) than males (32.2%) had severe AH; during the pandemic, more males (28.4%) than females (24.0%) had severe AH though these differences were not statistically significant (p = 0.1). Median age at admission was significantly lower for both male and female during the pandemic (age 44 and 41, respectively) as compared to prior (age 47 and 45, respectively) p < 0.05. There was no significant difference in mortality between sexes before (10.4% in female, 11.5% in male, p = 0.22) and after the pandemic (9.2% in female, 9.9% in male, p = 0.67).

Conclusion: Hospitalizations for AH rose during the pandemic and occurred at younger ages in both sexes with less severe presentations.
There was no significant difference in mortality by sex before and during the first wave of the pandemic. Advanced age was associated with more severe AH. Public health efforts should continue to educate about the harms of alcohol excess and offer community support.

**THU046**  
**The lysosomal enzyme cathepsin D as a new marker for alcoholic liver disease**  
Mengying Li1, Tom Houben1, Mads Israelsen2, Maria Kjaergaard2, Marit Westerterp3, Aleksander Krag2, Maja Thiele2, Ronit Shiri-Sverdlov1, Schalk van der Merwe3, Jef Verbeek1

**Background and aims:** Alcohol is the seventh leading cause of premature death worldwide, many of whom die from alcohol-related liver disease (ALD). However, the underlying pathological mechanisms that cause the early stages of ALD are currently under-investigated. Lysosomal cathepsin D (CTSD) was previously shown to be useful in detecting NASH, and circulating CTSD is elevated in advanced liver disease. We therefore investigated plasma CTSD in relation to different histological stages of early ALD.

**Method:** We conducted a cross-sectional study of 305 asymptomatic ALD patients with a liver biopsy scored according to the NAS CRN system, and compared their plasma CTSD levels with 40 healthy controls, matched for age, gender and BMI. We excluded patients with decompensation at baseline. Next, we determined the correlations between plasma CTSD levels and histology scored for fibrosis, ballooning, lobular inflammation and steatosis. Areas under the receiver operating characteristic curve (AUC) were generated to investigate the accuracy of plasma CTSD levels alone or in combination with known non-invasive markers of fibrosis to predict ALD.

**Results:** Plasma CTSD levels were significantly higher in ALD patients compared to matched healthy controls (37.7 vs 22.9 ng/ml; AUC 0.84). The highest CTSD levels was measured in ALD patients with no ballooning and lobular inflammation, and a slightly lower CTSD levels were observed in patients with more severe inflammatory activity. Further, plasma CTSD levels exhibited a weak negative correlation with the ELF test and transient elastography, and did not correlate with fibrosis stage. Moreover, transient elastography, ELF, GGT, AST/ALT, and AST independently correlated with plasma CTSD levels. Furthermore, combining plasma CTSD levels with transient elastography and AST/ALT resulted in a high diagnostic accuracy (ROC-AUC: 0.908) for predicting ALD.

**Conclusion:** Lysosomal leakage of CTSD into the circulation may be a sensitive marker of early stages of ALD.

**THU047**  
**Ductular bilirubinostasis is a diagnostic biomarker for acute-on-chronic liver failure: results from a well-defined cohort of patients with alcoholic steatohepatitis**  
Annelot Broekhoven1, Tessa Ostyn2, Lukas Van Melkebeke3, H.W. Verspaget1, Schalk van der Merwe1, Jef Verbeek1, Minneke Coenraad1, Tania Roskams2, Frederik Nevens3,1 Leiden University Medical Center, Gastroenterology and Hepatology, Leiden, Netherlands; 2 Translational Cell and Tissue Research, KU Leuven, Imaging and Pathology, Leuven, Belgium; 3 University Hospitals KU Leuven, Gastroenterology and Hepatology, Leuven, Belgium

**Background and aims:** Ductular bilirubinostasis (DB) is identified as a marker of ACLF in alcoholic cirrhosis, but overall, the histological features of ACLF are not well characterized. We assessed the diagnostic and prognostic value of DB and other histological features in addition to clinical features for the presence and development of ACLF in a well-defined cohort of ASH patients.

**Method:** Prospective study in consecutive patients admitted with a diagnosis of ASH to a tertiary referral center between 03–2008 and 04-2021. Diagnosis of ASH was based on clinical presentation and confirmed by transjugular liver biopsy. All biopsies were assessed by a dedicated liver pathologist who was blinded for clinical data and outcome. Clinical and histological data were collected from time of biopsy until 1 year follow-up. Diagnosis of ACLF was based on EASL-CLIF criteria. Differences between patients with and without ACLF at baseline were assessed using chi-square test. Predictors for development of ACLF within 28 days were assessed using Cox regression.

**Results:** 184 patients with biopsy-confirmed ASH were enrolled, with a median follow-up time of 365 days (IQR 83.5–365). At baseline, ACLF was present in 73 patients (39.7%). Another 30 (16.3%) patients developed ACLF within 28 days (median 7.5 days, IQR 2–20). At baseline, DB was significantly more present in patients with ACLF compared to patients without ACLF (50.7% vs. 30.6%, p = 0.007). Presence of DB was not correlated with level of c-reactive protein, level of white blood cell count, presence of infection or positive blood culture (all p > 0.05). None of the other histological features, including the histological severity of ASH, was associated with presence of ACLF. The CLIF-C AD score predicted the development of ACLF at 28-days (HRα, 1.09, p <0.001). However, no association between histological features and development of ACLF could be found.

**Conclusion:** In this well-defined cohort of patients with biopsy-proven ASH, we show that DB is a histological feature of the presence of ACLF. Presence of DB was independent of presence of clinical features of sepsis within this group. The CLIF-C AD score had a high performance in predicting the development of ACLF, while the additional role of histology seems limited.

**NAFLD: Clinical aspects except therapy**

**THU048**  
**The most recent and in-depth meta-analytic assessment of the global epidemiology of non-alcoholic fatty liver disease (NAFLD)**  
Zobair Younossi1,2,3, Pegah Golabi1,2,3, James Paik1,2,3, Austin Henry1,2, Catherine Van Dongen2, Linda Henry2,4,1 Inova Fairfax Medical Campus, Center for Liver Disease, Department of Medicine, Falls Church, United States; 2Inova Health System, Betty and Guy Beatty Center for Integrated Research, Falls Church, United States; 3Inova Medicine, Falls Church, United States; 4Center for Outcomes Research in Liver Disease, Washington, DC, United States

**Background and aims:** NAFLD is a leading cause of liver-related morbidity and mortality. We assessed the global and regional prevalence and incidence of NAFLD using an in-depth meta-analytic approach.

**Method:** We systematically searched PubMed and Ovid MEDLINE® for population-based studies of NAFLD published 2015–2021 (data collected: 1988–2020). Two reviewers extracted data according to age, sex, race, diagnostic methods, sample size, data collection year, comorbidities, and other study characteristics. Adjustments were applied using prevalence of viral hepatitis and ALD from the Global Burden of Disease study 2019 to approximate prevalence and incidence of NAFLD in general population. The meta-analysis was conducted using a random-effects model. Assessment of bias risk used the Joanna Briggs Institute Critical Appraisal Instrument for studies reporting prevalence data.
Results: Of 1,857 studies included, 132 studies (N = 9,945,423) met the eligibility criteria [106 NAFLD prevalence and 26 NAFLD incidence, high-income North America (H-NA, 19.8%), high-income Asia Pacific (27.4%), East Asia (23.6%), and Western Europe (WE, 11.3%)]. The pooled global prevalence of NAFLD based on a random-effects model was 29.1% (95% confidence interval: 26.8–31.5%). The highest prevalence was reported in Latin America (n = 3, 44.4% [30.7–59.0%]), followed by Middle East and North Africa (MENA) (n = 9, 39.9% [32.6–47.6%]), H-NA (n = 21, 32.9% [27.4–38.9%]) and WE (n = 12, 24.6% [19.1–31.0%]). The prevalence of NAFLD increased over time: 1991–2006 (n = 10, 24.4% [19.6–30.0%]), 2007–2010 (n = 28, 25.7% [22.1–29.7%]), 2011–2015 (n = 38, 27.9% [24.1–32.0%]) and 2016–2020 (n = 30, 36.0% [31.6–40.7%]). The global prevalence rate of NAFLD varied between 11.2%–48.6% depending on the diagnostic modality (Table). The incidence of NAFLD ranged from 19.0–99.0 per 1,000 person-years. Meta-regression showed that diagnostic method/criteria (p < 0.001), data collection year (p = 0.004) and geographic location (p = 0.015) jointly accounted for 72.1% of the heterogeneity between studies.

<table>
<thead>
<tr>
<th>Diagnostic Modality</th>
<th>N. of study</th>
<th>Prevalence % (95% CI)</th>
<th>I²</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ultrasound: mild to severe steatosis</td>
<td>54</td>
<td>32.61 (30.30 to 35.01)</td>
<td>99.74</td>
</tr>
<tr>
<td>Ultrasound: moderate to severe steatosis</td>
<td>14</td>
<td>15.36 (13.33 to 17.63)</td>
<td>99.07</td>
</tr>
<tr>
<td>Controlled Attenuation</td>
<td>9</td>
<td>40.78 (32.22 to 49.93)</td>
<td>99.47</td>
</tr>
<tr>
<td>Parameter</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CAP of ≥248 dB/m</td>
<td>3</td>
<td>46.76 (37.12 to 56.65)</td>
<td>98.50</td>
</tr>
<tr>
<td>CAP of ≥260 dB/m</td>
<td>3</td>
<td>48.61 (43.16 to 54.08)</td>
<td>95.29</td>
</tr>
<tr>
<td>CAP of ≥274 dB/m</td>
<td>3</td>
<td>27.71 (16.41 to 42.80)</td>
<td>99.20</td>
</tr>
<tr>
<td>Computerized Tomography</td>
<td>3</td>
<td>11.23 (8.37 to 14.89)</td>
<td>93.43</td>
</tr>
<tr>
<td>Non-invasive Biomarkers (FLI, US-FLI, HIS)</td>
<td>22</td>
<td>31.11 (26.37 to 36.28)</td>
<td>99.95</td>
</tr>
<tr>
<td>Other (KD-9 or 10)</td>
<td>4</td>
<td>25.23 (23.37 to 27.18)</td>
<td>81.36</td>
</tr>
</tbody>
</table>

Conclusion: The global prevalence of NAFLD is high and growing. Given its impact on the heterogeneity of the reported studies, it is critical to use standardized diagnostic criteria to provide accurate and consistent epidemiologic data across the world.

THU049
Comorbidities and malignancy among NAFLD patients compared to general population
Naim Abu-Freha1, Bracha Cohen2, Michal Gordon3, Alexander Fich2, Danella Munteanu4, David Yardeni5, Ohad Etzion3. 1Soroka University Medical Center, Department of Gastroenterology and liver diseases, Beer Sheva, Israel; 2Soroka University Medical Center, Beer-Sheva, Israel; 3Soroka University Medical Center, Beer-Sheva, Israel; 4Soroka University Medical Center, Beer Sheva, Israel; 5Soroka University Medical Center, Beer Sheva, Israel
Email: abufreha@yahoo.de

Background and aims: Non-alcoholic fatty liver disease (NAFLD) is a common liver disease; we aimed to investigate the frequency of comorbidities and malignancy among NAFLD patients compared to general population.

Method: Retrospective study included all patients older than 18 years with NAFLD diagnosis. A control group was matched in gender and age. The data were extracted using the MDClone platform of the largest health maintenance organization “Clalit” in Israel. Demographics, comorbidities, malignancy and mortality were collected and compared.

Results: 211, 955 NAFLD patients (mean age 42.2 ± 15 years, 47.2% males) were analyzed in comparison to 452, 012 matched general population controls (mean age 42.4 ± 14.8 years, 48.5% males). Significant higher rate of diabetes mellitus (23.2% vs 13.3%), obesity (58.8% vs 27.8%), Hypertension (57.2% vs 39.9%), chronic ischemic heart disease (24.7% vs 17.3%), CVA (3.2% vs 2.8%) and chronic obstructive lung disease (10.1% vs 8.3%) was found among NAFLD patients. Patients with NAFLD have significant higher rate of the following malignancy: prostate (1.6% vs 1.2%) breast cancer (2.6% vs 1.9%), colorectal cancer (1.8% vs 1.4%), uterus (0.4 vs 0.2%) kidney (0.8% vs 0.5%), melanoma (1.6% vs 1.2%), basal cell carcinoma (11.6% vs 8.6%) thyroid (0.7% vs 0.5%) cancer, non-Hodgkin lymphoma (0.7% vs 0.6%) and lower rate of lung cancer (0.9% vs 1.2%), stomach (0.3% vs 0.4%). The all-cause mortality among NAFLD patients was significantly lower in comparison to general population (10.8% vs 14.7%, p < 0.001)

Conclusion: Higher rate of comorbidities and malignancy among NAFLD patients was observed, but lower rate of all-cause mortality was found.

Keywords: Fatty liver, comorbidities, malignancy, Israel

THU050
The prevalence of non-alcoholic fatty liver disease in the United Kingdom: a systematic review and meta-analysis
Yusef Alenazi1, Timothy Card1,2, Joanne Morling1,2, Rebecca Harris2, 1University of Nottingham, Lifespan and Population Health, Nottingham, United Kingdom; 2University of Nottingham, NIHR Nottingham Biomedical Research Centre (BRC), United Kingdom
Email: msxya10@nottingham.ac.uk

Background and aims: Non-alcoholic fatty liver disease (NAFLD) is a growing cause of cirrhosis and indication for a liver transplant. Since this growth is putting pressure on hepatology services and healthcare systems, up-to-date measures of the size of the problem are needed to plan future services. We have therefore conducted a systematic review of studies in the UK to estimate the prevalence of NAFLD.

Method: We identified studies that investigate NAFLD prevalence among the UK population through a systematic search of electronic databases (PubMed, EMBASE via OVID, CINAHL, Web of Science, and Google). A random-effects meta-analysis was performed on subsets of studies limited to populations with specific conditions and those not so restricted.

Results: Our study included a total of 25, 439 participants from 9 studies. Our results indicate a pooled prevalence of 23.7% in non-disease restricted populations (95% CI: 20.6%-26.8%). Of the disease restricted populations, a single study of HIV patients reported a prevalence of 71.2% (CI: 59.7%-82.7%). Two studies of liver-related hospital referral yielded a prevalence of 37.90% (CI: 15.3%-60.5%), a single study of BMI ≥25 (29.6%) (CI: 27.9%-31.3%), and type-1 diabetic patients (1.8%) (CI: 0.0%-3.6%). Our results also included three studies of type-2 diabetic patients with an overall prevalence of 38.6% (CI: 25.5%-51.7%).

Conclusion: Our major finding is that the prevalence of NAFLD within the UK general population is similar to the average global estimate. There is good evidence that adults with T2DM have a higher risk of NAFLD. NAFLD has been linked to impaired health-related quality of life and so updates to this data will be essential to allow ongoing appropriate service planning.

THU051
Health-related quality of life is impaired in people living with HIV and hepatic steatosis
Maurice Michel1,2, Christian Laborz2,3, Malena Anders1,2, Alisha Wahl1,2, Lisann Girolstein1,2, Leonard Kaps1, Wolfgang Maximilian Kremer1,2, Yvonne Huber1,2, Peter Galle1,2, Martin Sprinzl1,2, Jörn Schattenberg1,2. 1Metabolic Liver Disease Research Program, I. Department of Medicine, University Medicine Centre Mainz, Mainz, Germany; 2Department of Medicine, University Medicine Centre Mainz, Mainz, Germany
Email: joern.schattenberg@unimedizin-mainz.de

Background and aims: People living with HIV (PLWH) show a high prevalence of hepatic steatosis and non-alcoholic fatty liver disease (NAFLD). NAFLD has been linked to impaired health-related quality of
life (HRQL) and therefore could be an aggravating factor in PLWH. The aim of this study was to determine differences in HRQL between PLWH presenting with and without hepatic steatosis and to identify predictors associated with impaired HRQL.

Method: A total of 245 PLWH were prospectively enrolled at an outpatient clinic. Hepatic steatosis was assessed using vibration controlled transient elastography (VCTE) and defined as a controlled attenuation parameter (CAP) of >275 dB/m. The cohort was then divided into two groups: no steatosis and steatosis. The generic EQ-5D-5L questionnaire was used to determine differences in the HRQL. It consists of an overall value (UI-value) and five dimensions, each addressing different aspects of an individual HRQL. Univariable and multivariable linear regression models were applied to identify predictors with impaired HRQL in both groups.

Results: In this cohort of PLWH, the prevalence of hepatic steatosis was 35% (n = 85) of whom 76.5% (n = 65) had NAFLD and 16.5% (n = 14) alcoholic liver disease. The median age was 52 years (IQR 42; 58) and the majority of PLWH were male (n = 174, 71%). Metabolic risk factors were more prevalent in the steatosis group. The mean UI-value in the total cohort was 0.90 ± 0.15. The HRQL (UI-value) was significantly lower in PLWH and steatosis in comparison to no steatosis (p = 0.013). The most strongly affected dimensions were mobility (p = 0.016) and pain/discomfort (p = 0.012) in the steatosis group, and the dimension anxiety/depression was equally impaired in both groups (p = 0.062) (Figure 1). Unemployment (β = −0.270, p = 0.025) and waist circumference (β = −0.289, p = 0.017) remained independent predictors of a poor HRQL in the steatosis subgroup. In turn, age (β = −0.168, p = 0.045), female sex (β = −0.173, p = 0.030), BMI (β = −0.214, p = 0.010) and arterial hypertension (β = −0.194, p = 0.025) were independent predictors of a low HRQL in the subgroup without steatosis.

Conclusion: Hepatic steatosis and metabolic comorbidities negatively affect HRQL. Addressing these factors may improve patient reported and liver related outcomes in PLWH.

Funding: This analysis was in parts supported by a research grant from Gilead Sciences.

THU052
Moderate alcohol consumption is associated with significant fibrosis progression in non-alcoholic fatty liver disease-a cohort study with over 17 years of follow-up
Julia Blomdahl1, Patrik Nasr1, Mattias Ekstedt2, Stergios Kechagias1. 1Linköping University, Department of Gastroenterology and Hepatology, Department of Health, Medicine, and Caring Sciences, Linköping, Sweden
Email: julia.blomdahl@liu.se

Background and aims: Non-alcoholic fatty liver disease (NAFLD) affects approximately 25% of the adult population worldwide. The effect of moderate alcohol consumption on NAFLD histology is disputed. Assessment of alcohol consumption is commonly performed with interview or questionnaires. A highly sensitive and specific alcohol biomarker is phosphatidylethanol in blood (PEth), which only forms in the presence of ethanol. PEth has hitherto not been evaluated in longitudinal NAFLD studies. This study aimed to examine the impact of moderate alcohol consumption on histologic progression and to evaluate the utility of PEth in NAFLD.

Method: A cohort of NAFLD patients with serial biopsies were reviewed for inclusion in the study. Baseline alcohol consumption was <140 g/week in all patients. Anthropometric and biochemical measurements were performed at baseline and follow-up. Alcohol consumption was measured at follow-up, using three different methods (clinical interview, Alcohol Use Disorder Identification Test-Concise [AUDIT-C], and analysis of PEth). Patients were reviewed for progression of steatosis, ballooning, lobular inflammation, and significant fibrosis progression, defined as progression of fibrosis stage ≥2 stages or development of end-stage liver disease (ESLD).

Results: Eighty-two patients were included. Mean follow-up time was 17.2 years (SD ± 6.0). Twenty-two patients were considered to have fibrosis progression or developed ESLD. Patients with significant fibrosis progression reported higher alcohol consumption and had significantly higher PEth. Progression of other histological parameters (i.e., steatosis, ballooning and lobular inflammation) was unaffected during follow-up and showed no significant associations with alcohol consumption. Consumption >66–96 grams per week (i.e., moderate alcohol consumption) was associated with increased risk for significant fibrosis progression compared with no or low consumption. PEth ≥50 ng/ml and binge drinking showed the highest risk for significant fibrosis progression (aOR 5.2 [95% CI 1.4–19.6], p <0.05, and aOR 5.1 [95% CI 1.4–18.1], p <0.05, respectively).

Conclusion: NAFLD patients consuming moderate amounts of alcohol are at increased risk for significant fibrosis progression and development of ESLD. PEth can be used as a reliable biochemical alcohol marker in NAFLD. Patients reporting moderate consumption or exhibiting PEth ≥50 ng/ml should be advised to reduce alcohol consumption.

THU053
Prevalence trends of non-alcoholic fatty liver disease among young men in Korea: korean military population-based cross-sectional study
Jaejun Lee1,2, Hyun Yang1, Si Hyun Bae1. 1Eunpyeong St. Mary hospital, Department of Internal Medicine, Seoul, Korea, Rep. of South; 2College of Medicine, Eunpyeong St. Mary's Hospital, The Catholic University of Korea, Department of Internal Medicine, Seoul, Korea, Rep. of South Email: baeshi@catholic.ac.kr

Background and aims: Non-alcoholic fatty liver disease (NAFLD) has become a major concern in Korea since its emergence as a dominant cause of chronic liver disease. However, no study has explored its prevalence in adults under 30 years of age. Therefore, we performed a cross-sectional study to investigate the prevalence of NAFLD in Korean men in their early twenties.

Method: We collected data on 596, 359 Korean soldiers who participated in a health examination between January 2015 and July 2021. A total of 571, 872 individuals were analyzed after excluding those with missing data and hepatitis B antigen positivity. Hepatic steatosis was determined using the hepatic steatosis index (HSI). Participants with an HSI >36 were considered to have NAFLD. The BARD score was used to determine the presence of advanced fibrosis.

Results: All participants were men, and the mean age was 20.9 ± 1.3 years. Of the 571, 872 participants screened, 77, 020 (13.47%) were classified as having NAFLD. The prevalence of NAFLD consistently increased from 2015 to 2021 (10.66% vs. 16.44%, P < 0.001). Increases from 2015 to 2021 were also noted in the prevalence of hypercholesterolemia (1.78% vs. 2.56%, P < 0.001), dysglycemia (10.17% vs. 11.68%, P < 0.001), and hypertension (2.87% vs. 3.51%, P < 0.001). The mean body mass index (BMI) also increased from 23.3 ± 3.0 kg/m² to
Conclusion: The prevalence of NAFLD and of other metabolic dysfunctions (hypercholesterolemia, dysglycemia, and hypertension) in Korean men in their early twenties increased from 2015 to 2021. The Korean society should be alert for an increase in the disease prevalence and continue making efforts to reduce the associated complications.

THU054
Hepatocellular and extrahepatic cancers in non-alcoholic fatty liver disease: a systematic review and meta-analysis

James Thomas1,2, Bradley Kendall1,2, Christine Dalais3, Graeme Macdonald1,2, Aaron Thrift1, 1Princess Alexandra Hospital, Woolloongabba, Australia; 2The University of Queensland, Saint Lucia, Australia; 3Baylor College of Medicine, Houston, United States
Email: aaron.thrift@bcm.edu

Background and aims: Non-alcoholic fatty liver disease (NAFLD) affects approximately one-quarter of the global adult population. Its prevalence is expected to continue to increase with rising rates of obesity and its associated metabolic disorders. Hepatocellular (HCC) and extrahepatic cancers have been associated with NAFLD however the extent and nature of this relationship remain to be clarified. We aimed to estimate the absolute incidence rates of these cancers in adults with NAFLD with respect to key clinical factors.

Method: This systematic review and meta-analysis of published studies reporting the incidence rates of any cancer in adults with NAFLD was registered with PROSPERO (CRD42020164725). The literature search of 4 databases (PubMed, Embase, Cochrane Library and Web of Science) was from inception to 31 August 2020. Teams of independent reviewers assessed each record for inclusion with subsequent extraction of reported data. The main outcomes were pooled incidences of cancers in NAFLD using a random-effects model with subgroup analyses to examine the effects of NAFLD disease stage.

Results: The systematic review returned 10, 042 unique records from which 64 studies including 625, 984 and 41, 027 patients were eligible for analysis of HCC and extrahepatic cancer incidence respectively. The pooled HCC incidence rate was 1.25 per 1000 person-years (95%CI:0.58–1.99) in fully adjusted models. Interestingly, NAFLD was associated with a significantly decreased risk for incident dementia until five years after FLI-assessment (HR:0.48; 95%CI:0.24–0.94). Moreover, NAFLD was not associated with worse cognitive function (G-factor, mean difference:0.032; 95% CI:–0.029–0.092).

Table 1: Risk of incident dementia for NAFLD and liver stiffness

<table>
<thead>
<tr>
<th>cases</th>
<th>FU (year)</th>
<th>HR</th>
<th>95% CI</th>
</tr>
</thead>
<tbody>
<tr>
<td>NAFLD (FLI ≥60)</td>
<td>753/3975</td>
<td>15.5</td>
<td>0.92</td>
</tr>
<tr>
<td>NAFLD (Ultrasound)</td>
<td>262/4557</td>
<td>5.7</td>
<td>0.84</td>
</tr>
<tr>
<td>Fibrosis</td>
<td>127/3300</td>
<td>5.6</td>
<td>1.07</td>
</tr>
<tr>
<td>Liver stiffness (kPa)</td>
<td>127/3300</td>
<td>5.6</td>
<td>1.01</td>
</tr>
</tbody>
</table>

Results are given as HR and 95% CI for incident dementia as outcome. NAFLD was either based on FLI ≥60 or on hepatic steatosis assessed with abdominal ultrasound and was compared to participants with FLI <30 or participants without hepatic steatosis. The pooled incidence rate of extrahepatic cancers in NAFLD is over eight-fold higher than HCC. Extrahepatic cancer rates are not related to liver fibrosis stage thereby implicating the metabolic dysfunction associated with NAFLD as a risk factor for these malignancies. Given the high and increasing prevalence of NAFLD, these findings support a public health focus on its prevention and the early detection of cancer in adults with NAFLD.

THU055
Association of non-alcoholic fatty liver disease and fibrosis with incident dementia and cognitive function: the Rotterdam Study

Tian Xiao1,2, Laurens van Kleef2, Kamran Ikram1, Robert De Knegt2, Arfan Ikram1, 1Princess Alexandra Hospital, Woolloongabba, Australia; 2The University of Queensland, Saint Lucia, Australia; 3Baylor College of Medicine, Houston, United States
Email: lvankleefer@erasmusmc.nl

Background and aims: Non-alcoholic fatty liver disease (NAFLD) might affect brain health, via the so-called liver-brain axis. Whether this results in increased risk for dementia remains unclear. Therefore, we investigated the association of NAFLD and fibrosis with incident dementia and cognition among the elderly.

Method: We performed longitudinal and cross-sectional analyses within The Rotterdam Study, an ongoing prospective cohort. Participants visiting between 1997 and 2002 with available fatty liver index (FLI) (set 1; n = 3, 975; FU = 15.5 years) or participants visiting between 2009 and 2014 with abdominal ultrasound (set 2; n = 4, 577; FU = 5.7 years) and liver stiffness (set 3, n = 3, 300; FLI ≥5.6 years) were included. Exclusion criteria were secondary causes for steatosis, prevalent dementia and missing alcohol data. NAFLD was defined as FLI≥60 or steatosis on ultrasound as liver stiffness ≥8.0 kPa. Dementia was defined according to the DSM-III-R. Cox-regression was used to quantify associations for NAFLD, fibrosis, or liver stiffness with incident-dementia and logistic regression for NAFLD and cognitive function.

Results: NAFLD and fibrosis were consistently not associated with increased risk for dementia (NAFLD based on ultrasound, HR:0.84, 95%CI:0.61–1.16; NAFLD based on FLI, HR:0.92, 95%CI:0.69–1.22; fibrosis, HR:1.07, 95%CI:0.58–1.99) in fully adjusted models. Interestingly, NAFLD was associated with a significantly decreased risk for incident dementia until five years after FLI-assessment (HR:0.48; 95%CI:0.24–0.94). Moreover, NAFLD was not associated with worse cognitive function (G-factor, mean difference:0.032; 95% CI:–0.029–0.092).

Conclusion: In conclusion, individuals with NAFLD were not at increased risk of dementia among this general elderly population, nor could an association with fibrosis and dementia be demonstrated. Moreover, NAFLD was associated with a reduced risk of dementia for the first five years after the assessment, suggesting that NAFLD regression is likely before dementia onset, which could be driven by weight loss before dementia onset. As yet, NAFLD may have no clinical implications for dementia awareness. Further studies should focus on NAFLD exposure duration and risk of dementia with longer follow-up durations.
THU056
High meat consumption is prospectively associated with non-alcoholic fatty liver disease and liver fibrosis markers
Dana Ivanovska Wajcman1, Naomi Fliss-Isakov2, Laura Sol Grinshpan, Muriel Webb2, Oren Shibolet2, Revital Kariv2, Shira Zelber-Sagi1,2, 1University of Haifa, School of Public Health, Haifa, Israel; 2Tel Aviv Medical center, Gastroenterology, Tel Aviv, Israel Email: danaivane@gmail.com

Background and aims: Non-alcoholic fatty liver disease (NAFLD) is a chronic disease related to lifestyle. The association of meat consumption with NAFLD has been tested. However, the prospective association between meat consumption and steatosis incidence and remission and liver fibrosis is yet to be tested. Therefore, this study aims to prospectively test the association of meat types consumption with incidence and remission of NAFLD and liver fibrosis markers.

Method: A prospective cohort study among subjects 40–70 years old, participating in two screening days, at least five years apart. NAFLD was determined by ultrasonography or CAP≥294 dB/m. Liver fibrosis was evaluated by Fibrotest (significant fibrosis ≥F2 was defined as a result of ≥0.48) or Fibroscan (significant fibrosis ≥F2 was defined as a result of ≥8.2 Kp). Meat consumption was assessed by a detailed food frequency questionnaire (FFQ), the trajectories of consumption were calculated as the percent of change from baseline (gr/d).

Results: A total of 320 subjects had completed two screening days and had valid FFQ. Mean follow-up of 6.65 ± 0.73 years. In multivariate-adjusted analyses, high consumption of red and/or processed meat (gr/d above the baseline consumption median) was associated with higher risk for NAFLD with elevated ALT incidence (OR = 5.97, 1.84–19.37, P = 0.003). Unprocessed red meat consumption was associated with NAFLD with elevated ALT incidence, lower odds for NAFLD remission, and greater odds for new or persistent liver fibrosis (≥F2) was defined as a result of ≥294 dB/m. Liver fibrosis was evaluated by Fibrotest (significant fibrosis ≥F2 was defined as a result of ≥0.48) or Fibroscan (significant fibrosis ≥F2 was defined as a result of ≥8.2 Kp). Meat consumption was assessed by a detailed food frequency questionnaire (FFQ), the trajectories of consumption were calculated as the percent of change from baseline (gr/d).

Conclusion: High consumption of red meat or processed meat is associated with NAFLD and significant fibrosis in a prospective study

THU057
Relevance of diabetes medication on recruitment criteria for clinical studies in patients with non-alcoholic fatty disease and type 2 diabetes mellitus
Michael Holzhey1, David Petroff2, Valentin Blank1, Florian Gerhardt2, Albrecht Boehler1, Toni Herta1, Florian van Bömmel3, Thomas Berg3, Kamal Kant Mangla3, Zobair Younossi4, 1University of Leipzig, Division of Gastroenterology, Germany; 2University of Leipzig, Clinical Trial Center, Germany; 3University of Leipzig, Division of Hepatology, Leipzig, Germany Email: johannes.wiegand@medizin.uni-leipzig.de

Background and aims: Guidelines for patients with diabetes mellitus increasingly recommend the use of sodium-glucose cotransporter 2 (SGLT-2) inhibitors and glucagon-like peptide 1 (GLP-1) agonists to prevent cardiovascular end points. Both drugs are promising candidates for treatment of non-alcoholic fatty liver disease (NAFLD). However, pre-existing therapies with SGLT-2 inhibitors or GLP-1 agonists are often an exclusion criterion for clinical trials. Thus, we analyzed use of diabetes medications and their adjustment.

Method: Patients with type 2 diabetes mellitus and NAFLD were prospectively recruited from 2011 to 2018 and followed up in 2021. They were characterized non-invasively by transient elastography (TE) including liver stiffness measurement (LSM), controlled attenuation parameter (CAP) and Fibroscan-AST-score (FAST). Diabetes medication was recorded from patient charts. Data were compared to the time point of the first available TE measurement.

Results: 90 patients were recruited (57% female, age 63.9 ± 9.6 years, BMI 31.3 ± 5.0 kg/m², LSM 7.4 kPa [5.3, 14.1], CAP 315 ± 57 dB/m, FAST 0.38 [0.18, 0.65]). After 4.2 [3.7, 7.9] years, follow-up data were available from 78 cases, the remaining 12 individuals had died. At follow-up, patients received the following diabetes medication:

SGLT-2 inhibitors: 17/78 (22%)
GLP-1 agonists: 13/78 (17%)
Metformin: 42/78 (54%)
Dipeptidyl-Pepptide-4 (DPP-4) inhibitors: 15/78 (19%)
Insulin: 42/78 (54%).

From these five drug classes, patients took a mean of 1.38 substances at baseline compared to 1.65 at follow-up (difference 0.27, 95% CI 0.01 to 0.53, p = 0.046).

Conclusion: A relevant and increasing proportion of NAFLD patients with diabetes mellitus is treated with SGLT-2 inhibitors and GLP-1 agonists in clinical routine. These treatments affect recruitment for clinical studies and should be considered as confounders in case they are continued during the study period.

THU058
Comorbidity severity scores and cardiovascular comorbidities in patients with non-alcoholic steatohepatitis (NASH), with and without cirrhosis, in a real-world setting
Jeffrey Lazarus1, Abhishek Shankar Chandramouli2, Kamal Kant Mangla3, Zobair Younossi4, 1University of Haifa, School of Public Health, Haifa, Israel; 2Tel Aviv Medical center, Gastroenterology, Tel Aviv, Israel Email: johannes.wiegand@medizin.uni-leipzig.de

Background and aims: NASH is estimated to be present in 3–6% of the US population and has been linked to end-stage liver disease, type 2 diabetes (T2D), and cardiovascular disease (CVD). The AWARE study aimed to describe the association of NASH with comorbidity severity scores and CVD comorbidities, which has not been well studied previously.

Method: Data were collected from a large US healthcare dataset covering 1 October 2015 to 31 December 2020. Records were included for adult patients diagnosed with NASH (using ICD-10 CM), with no evidence of hepatitis B or C, excessive alcohol use, or liver transplant prior to NASH diagnosis, and with no evidence of pregnancy or cancer in the study period. ICD CM coding was used to identify all diagnoses. Statistical significance of differences in comorbidities and severity scores between cirrhotic patients (CPs) and non-cirrhotic patients (NCPs) was assessed.

Results: Of 4, 989 patients identified, 489 had evidence of cirrhosis prior to NASH diagnosis. CPs were older and more progressed in terms of NASH-relevant biomarkers, glycated haemoglobin (HbA1c), and comorbidities (Table). CVD comorbidities were significantly higher in CPs at baseline, including atherosclerotic CVD, as were severity scores for T2D and comorbidities overall.
Table: Selected baseline characteristics

<table>
<thead>
<tr>
<th></th>
<th>NCPs (n = 4,500)</th>
<th>CPs (n = 489)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age, years</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>52.2 (11.0)</td>
<td>59.6 (9.4)</td>
</tr>
<tr>
<td>Female, %</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>55.2</td>
<td>62.4</td>
</tr>
<tr>
<td>NAFLD, %</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>56.5</td>
<td>67.4</td>
</tr>
<tr>
<td>Provider</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>20: 17: 16</td>
<td>28: 11: 7</td>
</tr>
<tr>
<td>Gastroenterologist:</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Internalist: GP, %</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>49.3</td>
<td>62.4</td>
</tr>
<tr>
<td>Aspartate transaminase</td>
<td></td>
<td></td>
</tr>
<tr>
<td>platelet ratio index*</td>
<td>586: 0.62 (0.96)</td>
<td>86: 1.09 (1.57)</td>
</tr>
<tr>
<td>Fib-4*</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>454: 1.56 (1.42)</td>
<td>71: 4.68 (5.28)</td>
</tr>
<tr>
<td>Quan-Charlson</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>1.9</td>
<td>4.4</td>
</tr>
<tr>
<td>Comorbidity Index*</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>0.1</td>
<td>0.4</td>
</tr>
<tr>
<td>Hypertensive disease %</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>64.8</td>
<td>73.0</td>
</tr>
</tbody>
</table>

Data are mean (SD) or n; mean (SD) unless stated

*Assessed by univariate analysis for statistical significance: p < 0.001 for NCPs vs CPs.
†Multivariable logistic regression analysis for atherosclerotic CVD, adjusted for demographic factors: odds ratio 1.34 (1.02, 1.78); p < 0.005 for CPs vs NCPs.

Conclusion: This study found that patients with NASH are often not diagnosed until an advanced stage, suggesting the need for greater disease awareness to avoid diagnostic inertia and to better assess the burden associated with NASH. These data also suggest that NASH correlates with a higher risk of developing comorbidities, especially CVD, and that patients progress to cirrhosis.

THU059
NAFLD association with renal impairment in type 2 diabetes patients

Jesús Rivera1, Monica Pons1, Alejandra Planas2, Rafael Simo Canonge2, Jordi Bañeres1, Ignacio Ferreira3, María José Soler4, Daniel Serró4, Joan Genesca5, Juan Manuel Pericàs5. 1Vall d’Hebron Hospital Universitari, Liver Unit, Spain; 2Vall d’Hebron Hospital Universitari, Diabetes and Metabolism Research Unit, Spain; 3Vall d’Hebron Hospital Universitari, Cardiology Department, Spain; 4Vall d’Hebron Hospital Universitari, Nephrology Department.

Email: jesusriveraest@gmail.com

Background and aims: Non-alcoholic fatty liver disease (NAFLD) and type 2 diabetes (T2DM) frequently coexist in high-risk metabolic patients. NAFLD and T2DM share a multisystemic involvement and the coexistence of both may increase the organ damage, worsening the patient prognosis. The aim of this study was to evaluate the role of NAFLD in the development and severity of extrahepatic conditions in a well-characterized T2DM cohort.

Method: Prospective cohort with case-control analysis comprising 290 T2DM subjects with 60 non-diabetic subjects matched by age with available transient elastography data. Patients were selected from the Outpatient Diabetes Clinic of Vall d’Hebron Hospital and the Primary Healthcare centres within its catchment area. Diabetic nephropathy (DN) was defined as the presence of microalbuminuria >30 mg/dl. According KDIGO guidelines, we defined renal impairment (RI) as a urine albumin:creatinine ratio >30 mg/g and chronic kidney disease (CKD) as an estimated glomerular filtration rate (eGFR) <60 ml/min per 1.73m². NAFLD was defined as Controlled Attenuation Parameter (CAP) ≥275 dB/m and/or Fatty liver index (FLI) ≥60 after exclusion of the other liver diseases and alcohol consumption over 30 gr/day in males and over 20 gr/day in females. Multivariable regression analysis was performed to identify predictors of extrahepatic diseases.

Results: Patients with T2DM with NAFLD (n = 134) presented higher rates of arterial hypertension (76.1% vs 61.5%, p = 0.004) and obesity-BMI ≥30 kg/m² (61.2% vs 23.1%, p < 0.001) than T2DM-nonNAFLD (n = 52). Distribution for gender, age and presence of dyslipidemia were similar between groups. Respect to T2DM complications, 38.6% of T2DM-NAFLD patients showed DN compared to 19.6% T2DM-nonNAFLD subjects (p = 0.014). No statistical differences were found for diabetic retinopathy (25.4% vs 30.8%, p = 0.45) or peripheral neuropathy (19.4% vs 17.3%, p = 0.74). Of note, T2DM-NAFLD patients showed worse median creatinine and eGFR values (0.85 ± 0.26 vs 0.74 ± 0.14, p = 0.001 and 80.1 ± 17.4 vs 86.1 ± 10.1, p = 0.004, respectively), and also presented a higher proportion of RI (71.6% vs 49.0%, p = 0.004) and CKD (14.2% vs 3.9%, p = 0.049) respect to T2DM subjects without NAFLD. Median liver stiffness did not differ among patients with and without RI or CKD. In multivariate analysis the presence of NAFLD (HR = 2.48; 95%CI 1.61–3.52, p = 0.019) was associated with the development of RI, independently of well-known risk factors, such as arterial hypertension (HR = 3.23; 95%CI 1.58–6.58, p = 0.001) or advanced age (HR = 2.79; 95%CI 1.40–5.56, p = 0.003).

Conclusion: Our results suggest that NAFLD poses an increased risk of extrahepatic diseases in T2DM patients, including other metabolic conditions and specially kidney disease. Renal function in diabetic patients with NAFLD should be screened and monitored closely, since NAFLD may lead to further worsening of kidney disease.

THU060
The impact of liver fibrosis on the immune response to SARS-CoV-2 vaccination in metabolic associated fatty liver disease patients

Marta Freitas1,2,3, Tiago Capela1,2,3, Vítor Macedo Silva1,2,3, Sofia Xavier1,2,3, Joana Teixeira Magalhães1,2,3, Carla Maria Moura Marinho1,2,3, Márcio Cotter1,2,3, Joana Teixeira Magalhães1,2,3. 1Vall d’Hebron Hospital Universitari, Liver Unit, Spain; 2Vall d’Hebron Hospital Universitari, Nephrology Department; 3School of Medicine, University of Minho, Braga, Portugal, Life and Health Sciences Research Institute (ICVS); 4PT Government Associate Laboratory, Braga/Guiarrães, Portugal, ICVS/3B.

Email: martasfreitas@gmail.com

Background and aims: There has been growing concern about the response to severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) vaccination in patients with chronic liver disease, as it may confer an immunosuppression state, potentially being associated with a lower response to vaccination. However, this issue in metabolic associated fatty liver disease (MAFLD) patients remains unestablished. We aimed to assess the impact of liver fibrosis on the immune response to SARS-CoV-2 vaccination in patients with MAFLD.

Method: Prospective cohort study that included MAFLD patients with complete SARS-CoV-2 vaccination. Patients with previous SARS-CoV-2 infection were excluded. Serum SARS-CoV-2 immunoglobulins (Ig), laboratory and transient elastography (TE) data were assessed 1 month after complete vaccination. Significant fibrosis was defined as 

<table>
<thead>
<tr>
<th></th>
<th></th>
<th>p</th>
</tr>
</thead>
<tbody>
<tr>
<td>NAFLD</td>
<td>2.48</td>
<td>1.61-5.32</td>
</tr>
<tr>
<td>Age ≥ 65y</td>
<td>2.79</td>
<td>1.40-5.56</td>
</tr>
<tr>
<td>Arterial hypertension</td>
<td>3.23</td>
<td>1.58-6.58</td>
</tr>
<tr>
<td>Obesity (BMI ≥ 30 kg/m²)</td>
<td>1.37</td>
<td>0.66-2.73</td>
</tr>
</tbody>
</table>

Conclusion: Patients with MAFLD presented higher rates of arterial hypertension (76.1% vs 61.5%, p = 0.004) and obesity-BMI ≥30 kg/m² (61.2% vs 23.1%, p < 0.001) than T2DM-nonNAFLD (n = 52). Distribution for gender, age and presence of dyslipidemia were similar between groups. Respect to T2DM complications, 38.6% of T2DM-NAFLD patients showed DN compared to 19.6% T2DM-nonNAFLD subjects (p = 0.014). No statistical differences were found for diabetic retinopathy (25.4% vs 30.8%, p = 0.45) or peripheral neuropathy (19.4% vs 17.3%, p = 0.74). Of note, T2DM-NAFLD patients showed worse median creatinine and eGFR values (0.85 ± 0.26 vs 0.74 ± 0.14, p = 0.001 and 80.1 ± 17.4 vs 86.1 ± 10.1, p = 0.004, respectively), and also presented a higher proportion of RI (71.6% vs 49.0%, p = 0.004) and CKD (14.2% vs 3.9%, p = 0.049) respect to T2DM subjects without NAFLD. Median liver stiffness did not differ among patients with and without RI or CKD. In multivariate analysis the presence of NAFLD (HR = 2.48; 95%CI 1.61–3.52, p = 0.019) was associated with the development of RI, independently of well-known risk factors, such as arterial hypertension (HR = 3.23; 95%CI 1.58–6.58, p = 0.001) or advanced age (HR = 2.79; 95%CI 1.40–5.56, p = 0.003).

Conclusion: Our results suggest that NAFLD poses an increased risk of extrahepatic diseases in T2DM patients, including other metabolic conditions and specially kidney disease. Renal function in diabetic patients with NAFLD should be screened and monitored closely, since NAFLD may lead to further worsening of kidney disease. 
liver stiffness measurement (LSM) ≥ 8.2 kPa, NAFLD fibrosis score ≥ 1.455, FIB-4 score ≥ 1.45, or FAST score ≥ 0.35.

Results: Thirty-seven patients were included, 62.2% of male gender, with a mean age of 55 ± 9 years. The mean LSM was 6.9 ± 2.9 kPa and 32.4% of patients had significant fibrosis in TE. The mean SARS-CoV-2 IgG levels were 10048 ± 9395 U/ml and all patients had response to vaccination (IgG ≥ 50 U/ml). There were no differences in SARS-CoV-2 IgG levels regarding gender (p = 0.93), presence of obesity (p = 0.20), metabolic syndrome (p = 0.26), diabetes (p = 0.70), hypertension (p = 0.52), dyslipidemia (p = 0.96), and tobacco use (p = 0.99). There were no differences in SARS-CoV-2 IgG levels between patients with or without significant fibrosis (p = 0.13) in TE, NAFLD fibrosis score (p = 0.18), FIB-4 score (p = 0.56), or FAST score (p = 0.24).

Conclusion: In our cohort, all MAFLD patients had IgG response to vaccination. Significant liver fibrosis did not compromise response of MAFLD patients to SARS-CoV-2 vaccination. SARS-CoV-2 vaccination is serologically effective in MAFLD patients, regardless of fibrosis.

THU061
Non-alcoholic steatohepatitis is also becoming a major liver transplant indication in Spain, a historically low risk area
Laura Martínez-Arenas1, Angela Carvalho-Gomes2, Fernando Díaz Fontela3, Sara Lorente Perez4, Marta Guerrero5, Jose Ignacio Herrero6, Marina Berenguer7, Instituto de Investigación Sanitaria La Fe, Department of Hepatology, Valencia, Spain; 1Instituto de Investigación Sanitaria La Fe, Department of Hepatology, Valencia, Spain; 2Instituto de Investigación Sanitaria La Fe, Department of Hepatology, Valencia, Spain; 3Hospital General Universitario Gregorio Marañón, Department of Clinical and Transplantation, Madrid, Spain; 4Hospital Clínico Universidad de Navarra, CIBERehd, Hepatology and Liver Transplantation Unit, Pamplona, Spain; 5Hospital Universitario Reina Sofia, CIBERehd, Hepatology and Liver Transplantation Unit, Zaragoza, Spain; 6Hospital Universitario Reina Sofia, Instituto Maimónides de Investigación Biomédica de Córdoba, CIBERehd, Department of Hepatology and Liver Transplantation, Córdoba, Spain; 7Clinica Universidad de Navarra, Instituto de Investigación Sanitaria de Navarra, CIBERehd, Department of Internal Medicine, Pamplona, Spain; 8Hospital Universitario y Politécnico La Fe, Instituto de Investigación Sanitaria La Fe, Universidad de Valencia, CIBERehd, Hepatology and Liver Transplantation Unit, Valencia, Spain
Email: laura.munera15@hotmail.com

Background and aims: Non-alcoholic fatty liver disease (NAFLD) is becoming one of the most common chronic liver diseases in Spain, particularly in individuals with features of metabolic syndrome, yet its exact prevalence and incidence are not completely known. In fact, non-alcoholic steatohepatitis (NASH) is a growing indication for liver transplantation (LT) in our setting. Our aim was to describe NAFLD evolution as a LT indication and the most frequently found features associated with this indication.

Method: Patients undergoing LT for NASH-related cirrhosis from 2010 to 2020 in five reference LT centers in Spain were included. The medical records of all these patients were reviewed for determining NASH-associated comorbidities. Survival analyses were performed with SPSS to determine survival rates at different follow-up points after LT.

Results: NASH-related cirrhosis was the LT indication in 118 patients (n = 10), none of them related to primary liver disease. The greatest number of deaths occurred within the first year after transplantation (n = 10), 1- and 5-year post-LT and only 2 cases of graft loss due to recurrence of primary disease. The mean age of 55 ± 9 years. The mean LSM was 6.9 ± 2.9 kPa and 32.4% of patients had significant fibrosis in TE. The mean SARS-CoV-2 IgG levels were 10048 ± 9395 U/ml and all patients had response to vaccination (IgG ≥ 50 U/ml). There were no differences in SARS-CoV-2 IgG levels regarding gender (p = 0.93), presence of obesity (p = 0.20), metabolic syndrome (p = 0.26), diabetes (p = 0.70), hypertension (p = 0.52), dyslipidemia (p = 0.96), and tobacco use (p = 0.99). There were no differences in SARS-CoV-2 IgG levels between patients with or without significant fibrosis (p = 0.13) in TE, NAFLD fibrosis score (p = 0.18), FIB-4 score (p = 0.56), or FAST score (p = 0.24).

Conclusion: In our cohort, all MAFLD patients had IgG response to vaccination. Significant liver fibrosis did not compromise response of MAFLD patients to SARS-CoV-2 vaccination. SARS-CoV-2 vaccination is serologically effective in MAFLD patients, regardless of fibrosis.
Cardiovascular (CV) drug classes (8%) and anti-diabetes medication classes (12%), and presence (vs absence) of CV disease (71%) and osteoarthritis (51%) at baseline. Female (vs male) patients had higher follow-up costs and a larger change in costs.

Figure: Annualised follow-up total healthcare cost (US$) for patients with NASH

Conclusion: NASH correlates with noticeable total healthcare cost and increases in costs following onset of NASH for all patients. The costs reported here are reflective of short-term burden. This analysis did not include indirect costs or costs associated with loss of work productivity. Due to the unavailability of approved treatments for patients with NASH, the cost burden is expected to increase with the presence and increasing severity of comorbidities. Therefore, the aim of managing NASH through pharmacotherapy should be to stop progression to cirrhosis and to manage NASH-related comorbidities.

Background and aims: NAFLD and NASH contribute to the global burden of liver disease. Previous studies suggest an association between NAFLD/NASH and the severity of COVID-19 illness. This analysis aimed to characterise the impact of NAFLD/NASH on hospitalisation-related outcomes for patients with COVID-19 using hospital administrative data from the United States (US) Premier Healthcare Database Special Release (PHD-SR).

Method: Adults with COVID-19 (primary or secondary International Classification of Diseases [ICD]-10 diagnosis code U07.1) hospitalised for the first time (index event) and discharged between 1 Apr 2020 and 31 Mar 2021 were examined. Pregnant patients and those with human immunodeficiency virus, alcohol dependence/abuse, viral hepatitis, biliary cirrhosis or sclerosing cholangitis were excluded. Cases with NAFLD/NASH (ICD-10: K75.81, K76.0) at index or 3 months before (in- or outpatient) hospitalisation were matched to controls without NAFLD/NASH using exact matching for age; propensity scores were calculated for sex, race and other variables.

Results: The PHD-SR dataset included 513,623 eligible patients; 14,672 (2.9%) with a NAFLD/NASH diagnosis. Among 29,334 patients analysed (14,667 cases with NAFLD/NASH and 14,667 matched controls), mean (standard deviation) age was 57.5 (15.0) years, 51.0% were female and 43.8% were white non-Hispanic. Baseline characteristics (eg, age, sex, race) were similar (standard difference <0.10) in cases and controls, except for cirrhosis (9.7% cases vs 0.5% controls) and malignancy (13.6% cases vs 10.2% controls). Regression analysis with IPTW adjusted for cirrhosis and malignancy revealed that patients without NAFLD/NASH had a significantly shorter mean LOS and reduced odds of IMV use with no difference in in-hospital mortality and readmission vs patients with NAFLD/NASH (Table), controlled for age, sex, race and other NAFLD-related comorbidities (eg, diabetes, obesity).

Background and aims: Previous estimates of the prevalence of advanced fibrosis (AF) due to NAFLD in the general US population utilized non-invasive tests that have relatively low positive predictive value leading to potentially overestimating the true prevalence. The AGILE3+ score was developed by combining routine clinical variables and vibration-controlled transient elastography parameters to specifically increase the PPV of predicting AF. Our aim was to estimate the prevalence of AF due to NAFLD using the AGILE3+ score in the general US adult population.

Method: Our study population included participants aged ≥18 years old who had a complete VCTE exam in the national health and nutrition examination survey (NHANES) 2017–2018 cycle. We excluded pregnant women, patients with excessive alcohol consumption defined as ≥2 drinks/day for males and ≥1 drink/day for females, hepatitis B or C, and ALT >50 IU/L. NHANES used FibroScan model 502 V2 Touch equipped with medium and extra-large probes. The presence of NAFLD was based on having a CAP score ≥248 dB/m. NAFLD subjects with AGILE3+ score of ≥0.68 were considered to have AF (rule-in), 0.45–0.67 were to be the grey zone, and <0.45 were considered low risk for AF (rule-out).

Results: Our cohort consisted of 1244 subjects with evidence of NAFLD and complete data to calculate the AGILE3+ score. The median age was 52.5 (50.7–54.2) years, 54.5% were male, median BMI was 32.7 kg/m2 and 36.2% had type 2 diabetes. Based on AGILE3+ score <0.45, 80.3% (95% CI: 77.1–83.2) of the NAFLD population were at low risk for AF 11.5 (9.2–14.5) of patients were in the grey zone and would have needed another test to determine the presence of AF. The overall prevalence of AF due to NAFLD was 8.1 (6.2–10.6) corresponding to 4.5 million Americans. Patients with AF were older, more likely to be obese and have type 2 diabetes.

Conclusion: Using NHANES 2017–2018, our results suggest that approximately 4.5 million people in the US have AF due to NAFLD based on the AGILE3+ score. Evaluating the cost-effectiveness of using AGILE3+ as a screening tool in high-risk populations is needed before implementing in clinical practice.
Non-alcoholic fatty liver disease associated liver fibrosis is linked with the severity of coronary artery disease mediated by systemic inflammation

Xianbin Cai1, Lingzi Chen1. 1The First Affiliated Hospital of Shantou University Medical College, Department of Gastroenterology, Shantou, China

Email: cxbin1@qq.com

Background and aims: Non-alcoholic fatty liver disease (NAFLD) is an independent risk factor of cardiovascular disease. Hepatic fibrosis is the most significant determinant of all cause- and liver-related mortality in NAFLD. However, the relationship between NAFLD fibrosis and severe coronary artery disease (CAD) remains unclear.

Method: We conducted a retrospective study of 531 patients with ultrasonogram-confirmed NAFLD who underwent percutaneous coronary intervention (PCI). Then all patients were separated into four categories by Gensini score (0, 0–9, 9–48, ≥48) for use in ordinal logistic regression analysis to determine whether NAFLD fibrosis was associated with increased Gensini scores. Mediation analysis were used to investigate whether systemic inflammation is a mediating factor in the association between NAFLD fibrosis and CAD severity.

Results: FIB-4 >2.67 (OR = 5.67, 95%CI 2.59–12.38) and APRI >1.5 (OR = 14.8, 95%CI 3.24–67.60) remained to be independent risk factors for the severity of CAD after adjusting for conventional risk factors, whereas among the inflammation markers, only neutrophils and neutrophil-to-lymphocyte ratio (NLR) were independently associated with CAD. Multivariable ordinal regression analysis suggested that increasing Gensini score (0, 0–9, 9–48, ≥48) was associated with advanced NAFLD fibrosis. ROC curve showed that either fibrosis markers or inflammation markers, integrating with traditional risk factors, could increase the predictive capacity for determining CAD (Figure 1). Inflammation markers, especially neutrophils and NLR, were mediators of the relationship between NAFLD fibrosis and CAD severity (Figure 2).

Conclusion: NAFLD patients with advanced fibrosis are at a high risk of severe coronary artery stenosis, and inflammation might mediate the association between NAFLD fibrosis and CAD severity.

Prevalence of portal vein thrombosis in non-alcoholic fatty liver disease related cirrhosis: a meta-analysis of observational studies

Roberta Stupia1, Filippo Cattazzo1, Alessandro Mantovani2, David Sacerdoti1, Andrea Dalbeni1. 1Azienda Ospedaliera Universitaria Integrata Verona, General Medicine, Hypertension and Liver Unit, Verona, Italy; 2Azienda Ospedaliera Universitaria Integrata Verona, Endocrinology, Diabetes and Metabolism, Verona, Italy

Email: robertastupia1@gmail.com

Background and aims: Portal vein thrombosis (PVT) is a common complication of cirrhosis because of modification in hemodynamics and hemostatic balance, especially in decompensated stage. Furthermore, patients with non-alcoholic fatty liver disease...
(NAFLD) related cirrhosis seem to be at higher risk of PVT development than patients with cirrhosis due to other causes. Nevertheless, definitive data in favor of an increased rate of PVT in NAFLD are missing. This meta-analysis attempted to estimate the prevalence of PVT in patients with NAFLD related cirrhosis.

**Method:** We systematically searched PubMed, Scopus and Web of Science databases from the inception date to November 1st 2021 using predefined keywords to identify observational cohort studies. Meta-analysis was performed using random-effects modelling.

**Results:** We included seven articles published over the past 10-year period reporting a total of 231,399 cirrhotic patients from five different countries. NAFLD-cirrhosis patients were 268,531 (11, 6%), with a PVT incidence of 6.5% (n = 17,481). Meta-analysis demonstrated a significant positive association between NAFLD and PVT (OR 1.37, 95% CI 1.06-1.78 p < 0, 001). The between-study heterogeneity was substantial (I² = 92, 73%).

After stratifying the eligible cohort studies by country, we observed that, compared to other regions, in European patients the incidence of PVT in NAFLD-cirrhosis was higher (OR: 1.42, 95% CI 1.05-1.88) and Arabian (OR: 1.91). The between-study heterogeneity was substantial (I² = 92, 73%).

By a meta regression analysis, neither age nor diabetes seemed to impact on the relationship between NAFLD and PVT.

**Conclusion:** This meta-analysis suggests that NAFLD-cirrhosis is associated with an increased risk of developing PVT. Further research is required to understand the complex link between NAFLD and PVT.

**References**


**THU067**
Real-world prevalence of metabolic associated fatty liver disease (MAFLD) and fibrotic-non-alcoholic steatohepatitis (NASH) in patients with obesity (PwO) in an outpatient specialist clinic in Italy

Federico Ravaioli1, Maria Letizia Petroni1, Francesca Marchignoli1, Laura Leonì1, Giulia Bocedi1, Federica Sacilotto1, Valentino Osti1, Dorina Mità1, Francesca Barbanti1, Lucia Brodosi1, Giulio Marchesini Reggiani1, Loris Pironi1. 1IRCCS Azienda Ospedaliero-Universitaria di Bologna, Dipartimento di Scienze Mediche e Chirurgiche (DIMEC)
Email: f.ravaioli@unibo.it

**Background and aims:** Obesity is a major player of "metabolic dysfunction associated fatty liver disease" (MAFLD); however, scanty data is available on the prevalence of MAFLD and non-alcoholic steatohepatitis (NASH) in patients presenting with obesity to a specialist outpatient clinic; to date, data being available from bariatric surgery patient series only. For this purpose, we aimed to evaluate the prevalence of MAFLD and the applicability of non-invasive tests (NITs) for fatty liver and liver fibrosis identification in an outpatient specialist clinic in Italy.

**Method:** We consecutively screened patients with obesity (PwO) who attended our outpatient obesity clinic from January 2020 to June 2021. Diagnosis of MAFLD was based on results from abdominal ultrasound (US); the anthropometric and laboratory data of the patients were collected, and the Fatty Liver Index (FLI), Fibrosis-4 (FIB4) and NAFLD (NFS) scores were calculated. Liver fibrosis was assessed within one month of the first visit using liver stiffness measurements (LSM) by transient elastography (FibroScan); Probe-specific LSM cut-offs were used to detect significant (F≥2) and advanced (F≥3) fibrosis and NASH cirrhosis. In a subgroup, hepatic fat was also evaluated through controlled attenuation parameter (CAP) with the FibroScan Expert 630 apparatus; all patients underwent oral glucose tolerance test (OGTT).

**Results:** Among 249 PwO, according to the WHO obesity classification, obesity I°, II°, III° was classified in 144 (57.8%), 56 (22.5%), 49 (19.6%), respectively. In addition, about half of the PwO had type 2 diabetes (T2DM) or impaired glucose tolerance (IGT) with a median HOMA index of 3.6 (IQR 2.44-4.94). According to US or FLI definitions, the prevalence of MAFLD was 90.4% and 91.6% and did not differ significantly in the different WHO categories of obesity (p value 0.264). The distribution of hepatic steatosis classification on ultrasound was 25.8%, 38.7%, 35.6% for mild, moderate, and severe steatosis, respectively. The median CAP values were 287 dB/m (IQR 262-337). According to LSM values, 29%, 18% and 9.8% had significant fibrosis, advanced fibrosis, and NASH cirrhosis, respectively. The median LSM value was 5.4 kPa (IQR 4.3-7.5). The liver fibrosis prevalence significantly increased according to WHO categories of obesity (p value <0.001). Applying the screening with NITs, 10% and 9% of patients are wrongly classified, and this leads to misclassify about 50% and 11.4% of patients with advanced fibrosis using FIB-4 or NFS, respectively; moreover, 34.1% and 54.5% of patients with advanced fibrosis result in the grey area of the two tests respectively.

**Conclusion:** The results from the present study in a real-world setting strongly advocate for routine screening for MAFLD and NASH by LSM in PwO, regardless of WHO category, attending the outpatient specialist clinic for obesity.
Background and aims: Fatty liver disease has been associated with metabolic disturbances. NAFLD is defined as hepatic steatosis with either overweight, type 2 diabetes (T2D), or at least two metabolic comorbidities. We hypothesized that metabolic disturbances associated with liver disease are pronounced in the postprandial phase and may be identified by a standardized meal. We therefore aimed to study the fasting and postprandial state in biopsy-proven healthy, overweight/obese patients with MAFLD and cirrhosis.

Method: We included 29 participants, 10 healthy controls (age 23 ± 0 years, BMI 25 ± 1 kg/m²), 9 patients with non-alcoholic fatty liver disease (NAFLD) (age 50 ± 5 years, BMI 35 ± 2 kg/m², no/mild fibrosis) and 10 patients with cirrhosis (age 62 ± 3 years, BMI 32 ± 2 kg/m², Child A/B). None of the included participants had T2D. The participants were randomized 1:1 to “fasting” or “postprandial” (Nutridrink, Nutricia, 300 kcal). Blood samples were obtained at baseline and 15, 45, 60, 90 and 120 minutes. At time point 60, blood from the liver vein was collected and a transjugular liver biopsy was performed. Levels of glucose, insulin, C-peptide, glucagon, and fibroblast growth factor 21 (FGF21) were measured in peripheral and liver vein blood. Results are presented as ± SEM. Peak concentrations were calculated as mean ± SEM of individual peaks. The analyses compared controls versus NAFLD and cirrhosis.

Results: 8/9 patients with NAFLD and 9/10 patients with cirrhosis were classified as NAFLD. Postprandial increase in glucose and C-peptide was significantly greater in NAFLD and cirrhosis compared to controls, with peak glucose of 7 and 10 mmol/L (p = .006), and peak C-peptide of 2675 ± 273 and 3340 ± 1048 pm versus 1689 ± 190 pm. Postprandial iAUC for insulin was greatest in patients with NAFLD (p = .037). Patients with NAFLD and cirrhosis had hyperglucagonemia, a phenotype causally related to prediabetes. FGF21 was significantly increased in NAFLD and cirrhosis and correlated to age (r = .61, p = .001) and fasting glucose (r = .54, p = .006). Glucagon was higher in liver vein compared to peripheral blood while FGF21 levels were similar in liver and peripheral blood.

Conclusion: We found significant metabolic dysfunction after a test meal in patients with NAFLD without diabetes compared to healthy controls and that finding that was pronounced in cirrhosis. Patients with MAFLD had impaired glucose tolerance, hyperinsulinemia and hyperglucagonemia, suggesting NAFLD to be a condition of prediabetes.
Background and aims: Non-alcoholic fatty liver disease (NAFLD) is the leading cause of chronic liver disease with increasing rates globally. Patients with a higher degree of liver fibrosis in NAFLD are at an increased risk for liver-related mortality but get missed easily during the referral process, based on our and other prior data. Our project aims to improve early detection and linkage-to-care of fibrotic NAFLD patients using a combination of automated electronic health record (EHR)-based FIB-4 score and directed provider education within our tertiary care center, serving a large population of Northern California.

Method: We implemented a health-system wide FIB-4 score calculator, embedded in the EHR that providers can easily add to their workflow for NAFLD patient triaging. Subsequently we provided targeted education to all relevant providers taking care of NAFLD patients. All referrals for NAFLD (defined by specific ICD 9/10 codes), NAFLD patients using a combination of automated electronic health record (EHR)-based FIB-4 score and directed provider education within our tertiary care center, serving a large population of Northern California.

Results: A total of 303 referrals were placed for NAFLD, of which 62% (n = 188) patients had FIB-4 score at the time of referral. Of the 188 patients, 62 patients with diabetes mellitus and 44% of them had FIB-4 ≥1.3. Compared to prior referrals of 49% with FIB-4 score<1.3, in current referrals after a 6-month post-FIB-4 triage implementation, 37% had FIB-4 <1.3 (Fig 1). This suggested a decrease in unnecessary referrals to hepatology. Primary care doctors referred 73% while endocrinology referred 1% of all patients. We noted higher rates of fibrotic NAFLD patients with FIB-4 ≥1.3 in current referrals compared to prior (63% vs 41%). Furthermore, 32% of current referrals were with severe fibrotic disease defined by FIB-4 ≥2.67 vs 11% previously (Fig 1). This suggested an increase in appropriate referrals for specialty care. Secondary fibrotic testing using imaging modalities such as ultrasound or magnetic resonance elastography was done in 36% of those with FIB-4 ≥1.3, suggesting room for further refinement.

Conclusion: Automated FIB-4 score in EHR can improve appropriate linkage-to-care for at-risk fibrotic NAFLD, especially when coupled with targeted provider education. The durability of such improvement is essential to study along with the need to increase broad acceptance across health systems.

References
Leung et al., PMID: 3227318
Srivastava et al., PMID: 30965069

THU071
Long term outcomes of non-alcoholic fatty liver disease (NAFLD) and metabolic associated fatty liver disease (MAFLD)
Zobair Younossi1,2,3, James Paik2,3, Issah Younossi4, Pegah Golabi1,2,3, Michael Harring1, Linda Henry1,2,4, 1Inova Health System, Inova Medicine; 2Beatty Liver and Obesity Research Program, Inova Health System; 3Center for Liver Disease, Inova Medicine; 4Center for Outcomes Research in Liver Disease
Email: zobair.younossi@inova.org

Background and aims: NAFLD and MAFLD are part of the spectrum of fatty liver disease (FLD). Our aim was to compare the outcomes of patients with NAFLD or MAFLD.

Method: Using data from NHANES III and NHANES 2017–2018, FLD was defined as moderate to severe hepatic steatosis by ultrasound (NHANES III) or controlled attenuation parameter (CAP) of ≥285 dB/m (NHANES 2017–2018). Death data were obtained from National Death Index (NDI). NAFLD was defined as FLD without other liver diseases and excessive alcohol consumption (EAC). MAFLD was defined as FLD with metabolic dysfunction—one of the following three criteria, overweight/obesity, presence of type 2 diabetes mellitus or metabolic dysregulation (at least two metabolic risk abnormalities).

Conclusion: FLD was defined as moderate to severe hepatic steatosis by ultrasound (NHANES III) or controlled attenuation parameter (CAP) of ≥285 dB/m (NHANES 2017–2018). Death data were obtained from National Death Index (NDI). NAFLD was defined as FLD without other liver diseases and excessive alcohol consumption (EAC). MAFLD was defined as FLD with metabolic dysfunction—one of the following three criteria, overweight/obesity, presence of type 2 diabetes mellitus or metabolic dysregulation (at least two metabolic risk abnormalities).

References
Leung et al., PMID: 3227318
Srivastava et al., PMID: 30965069
Background and aims: Hepatic steatosis is modulated by genetic variants like PNPLA3 (p.L148M), TM6SF2, MBOAT7, MARC1 and HSD17B3 polymorphisms were shown to have protective effects in patients with chronic liver diseases. Here, we analyse these fatty liver-related genes in patients undergoing bariatric surgery.

Method: The study cohort was composed of 165 prospectively recruited obese individuals (BMI 43.8 ± 5.7 kg/m², 66% women, 48 with diabetes mellitus) who underwent laparoscopic sleeve gastrectomy. The PNPLA3, TM6SF2, MBOAT7, MARC1 and HSD17B3 polymorphisms were genotyped performed using TaqMan assays. Liver biopsies were performed intraoperatively in all patients.

Results: In total, 70.3% of operated patients presented with hepatic steatosis, whereas NASH was detected in 28.5% of them; none had cirrhosis. Patients carrying the MARC1 minor allele displayed a lower risk of developing fibrosis stage 1a (OR = 0.54, p = 0.03), 1b (OR = 0.47, p = 0.01), 1c (OR = 0.46, p = 0.01), and 2 (OR = 0.42, p = 0.03). The PNPLA3 risk allele was associated with increased odds of hepatic steatosis (S2 and S3), fibrosis (1b to 2), and NASH (OR = 2.22, p = 0.04 in multivariate model). This variant was also significantly (p < 0.01) associated with increased fasting glucose (p = 0.03) and glycated haemoglobin (HbA1c) levels. Analysis restricted to 48 carriers of the PNPLA3 risk alleles (29.1%) showed that the MARC1 polymorphism decreases the odds of developing fibrosis. Furthermore, MARC1 was an independent protective factor against fibrosis in multivariate analysis (OR = 0.51, 95% CI 0.28–0.92, p = 0.04). Carriers of the HSD17B3 variant presented, in turn, with lower serum ALT (p = 0.03) and AST (p = 0.04) activities. The TM6SF2 polymorphism was associated with the risk for S3 steatosis (OR = 17.52, p < 0.01) and increased ALT (p = 0.04).

Conclusion: Fatty liver is a frequent condition in patients scheduled for bariatric surgery, but the MARC1 and HSD17B3 gene variants diminish hepatic injury in these individuals. Variant MARC1 might reduce the harmful effects of the major genetic risk factor for fatty liver, namely, PNPLA3 p.I148M.

THU073 The impact of fatigue on mortality of patients with non-alcoholic fatty liver disease (NAFLD): data from national health and nutrition examination survey (NHANES) 2005–2018 Zobair Younossi1,2,3, James Pafi1,2,3, Pegah Golabi1,2,3, Youssef Younossi2, Linda Henry1,2,3, Fatema Nader4, Inova Health System, Medicine Service Line; 2Center for Liver Disease, Inova Medicine; 3Betty and Guy Beatty Center for Liver and Obesity, Inova Health System; 4Center for Outcomes Research in Liver Disease Email: zobair.younossi@inova.org

Background and aims: Fatigue is common among patients with NAFLD. Fatigue can negatively impact patient reported outcomes and clinical outcomes.

Aim: To determine the prevalence of fatigue and its association with all-cause mortality for patients with NAFLD.

Method: Data for adults (≥18 years) collected as part of the National Health and Nutrition Examination Survey (NHANES 2005–2010 and 2017–2018) with mortality data via linkage to the National Death Index (through 2015) were used for this study. For NHANES 2005–2010, NAFLD was defined by Fatty Liver Index adjusted for the multiethnic U.S. population (US-FLI). Additionally, transient elastography (TE) with a controlled attenuation parameter (CAP) of ≥285 dB/m was used to define NAFLD for NHANES 2017–2018.

Excluded were patients with other liver diseases and excessive alcohol use. Fatigue was assessed through the Patient Health Questionnaire (PHQ-9) question, “Over the last 2 weeks, how often have you been bothered by feeling tired or having little energy?” Significant fatigue was defined as a response of “nearly every day” to the question.

Results: In the NHANES 2005–2010 study cohort (n = 5, 429, mean age 47.1 years, 49.7% male, 69.5% white), 37.6% had NAFLD. Compared to non-NAFLD group, fatigue was more common in individuals with NAFLD (8.35% vs 6.0%, p = 0.002). Among the NHANES 2017–2018 study cohort (n = 3, 830, mean age 48.3 years, 48.6% male, 62.3% white), 36.9% had NAFLD and 7.2% had fatigue. Compared to non-

Background presentations

Table 1. Hazard ratios of risk factors for All-Cause Mortality among Adults with NAFLD and MAFLD: NHANES III

<table>
<thead>
<tr>
<th>Risk factors</th>
<th>NAFLD</th>
<th>MAFLD</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hepatic steatosis</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>High Triglycerides</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Low HDL</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Low Insulin resistance</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>T2DM</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>History of Cancer</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>History of CVD</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Risk for fibrosis***</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Excess Alcohol Use</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ALD</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
NAFLD subjects, those with NAFLD were older (51.4 vs 46.4 years), more likely to be male (55.6% vs 44.6%), and more likely to report fatigue (8.7% vs 6.2%), sleep trouble (ST) (34.0% vs 26.7%), metabolic abnormalities (90.4% vs 58.4%), asthma (17.3% vs 12.7%), Chronic Obstructive Pulmonary Disease (COPD) (7.7% vs 6.1%), arthritis (34.3% vs 24.1%), thyroid disease (13.0% vs 9.9%), cardiovascular disease (CVD) (10.4% vs 6.3%), significant fibrosis (liver stiffness >8.0 kPa, 17.9% vs 3.5%), and advanced fibrosis (>13.1 kPa, 5.4% vs 0.9%) (all p < .003). Among NAFLD, multivariate logistic regression analysis showed that presence of depression (Odds Ratio = 16.2, 95% Confidence interval, 6.02–43.6), ST (3.34, 1.85–6.05), arthritis (2.25, 1.29–3.92), COPD (2.91, 1.47–5.77), CVD (3.64, 2.04–6.51) and sleep quantity (+7 hours) (0.52, 0.31–0.88) were associated with presence of fatigue. Multivariable Cox model demonstrated that NAFLD patients with fatigue had a 2.3-fold higher mortality than NAFLD without fatigue (HR: 2.31, 95%CI: 1.37–3.89, P = 0.0024).

Conclusion: Fatigue is more common among NAFLD and is driven mainly by depression, sleep trouble, and CVD. Among NAFLD, presence of fatigue is associated increased risk for mortality.

THU074

Metabolic dysfunction-associated fatty liver disease increases cardiovascular risk regardless of classical risk factors

Maria Del Barrio Azaceta, Paula Iruzubieta, Rocío Aller De La Fuente, Jesús María Banales, Álvaro Santos-Laso, José Luis Galleja Panero, Luis Ibáñez, María Teresa Arias Loste, Manuel Romero Gomez, Carmelo García-Monzón, Judith Gómez-Camareño, Pere Ginés, Rosa M Morillas, Juan Manuel Pericás, Patricia Aspichueta, Rosa Martín-Mateos, Rocío Gallego-Durán, Mercedes De La Torre Sanchez, Desamparados Escudero-García, Vanesa Bernal Monterde, Salvador Benlloch, Juan Turnes, Javier Crespo, Gastroenterology and Hepatology Department, Marqués de Valdecilla University Hospital, Clinical and Translational Digestive Research Group, IDIVAL, Santander, Spain; 2Center of Investigation of Endocrinology and Nutrition, School of Medicine, and Unit of Investigation, Hospital Clinico Universitario de Valladolid, Valladolid, Spain; 3Department of Liver and Gastrointestinal Diseases, Biodonostia Health Research Institute-Donostia University Hospital, University of the Basque Country (UPV/EHU), San Sebastian, Spain; 4Gastroenterology Department. Hepatology Unit, Hospital Universitario Puerta de Hierro, IDIPHISA, Madrid, Spain; 5Gastroenterology and Hepatology Department Hospital Universitario Gregorio Marañón Instituto de Investigación Sanitaria Gregorio Marañón (ISCM) Universidad Complutense de Madrid, Madrid, Spain; 6UCM Digestive Diseases, Virgen del Rocio University Hospital, SeLiver group at the Institute of Biomedicine of Seville (IBIS), The University of Seville, Seville, Spain; 7Liver Research Unit, Hospital Universitario Santa Cristina Instituto de Investigación Sanitaria Princesa, Madrid, Spain; 8Department of Gastroenterology and Hepatology, Complejo Asistencial Universitario de Burgos, Burgos, Spain; 9Liver Unit, Hospital Clinic, IDIBAPS, University of Barcelona, Barcelona, Spain; 10Gastroenterology and Hepatology Department, Hospital Universitari Germans Trias i Pujol, Badalona, Spain; 11Liver Unit, Vall d’Hebron University Hospital, Vall d’Hebron Institute of Research (VHIR), Barcelona, Spain; 12Department of Physiology, Faculty of Medicine and Nursing, Biocruces Research Institute, University of the Basque Country UPV/EHU, Leioa, Spain; 13Department of Gastroenterology and Hepatology, Hospital Universitario Ramón y Cajal, Instituto Ramón y Cajal de Investigación Sanitaria (IRYCYC), Madrid, Spain; 14Unit for the Clinical Management of Digestive Diseases, Hospital Universitario de Valme, Sevilla, Spain; 15Hepatology Unit, Consorcio Hospital General Universitario de Valencia, Valencia, Spain; 16Hospital Clinico Universitario de Valencia, Universitat de Valencia, Valencia, Spain; 17Hospital Universitario Miguel Servet, Zaragoza, Spain; 18Department of Hepatology, Hospital Universitario y Politécnico La Fe, Valencia, Spain; 19Service of Digestive Diseases, Complejo Hospitalario Universitario de Pontevedra, IES Galicia Sur, Pontevedra, Spain

Email: javiercrespo1991@gmail.com

Background and aims: Cardiovascular disease (CVD) is the main cause of mortality among patients with Metabolic dysfunction-Associated Fatty Liver Disease (MAFLD). Currently, clinical evidence shows that MAFLD could be a precursor for future development of metabolic syndrome (MS) components, linked to higher cardiovascular risk (CVR), regardless of classical risk factors. For this reason, our main aim was to determine if patients with MAFLD have a higher CVR as a consequence of liver disease activity.

Method: Cross-sectional study that includes 1, 587 patients with MAFLD, diagnosed by liver biopsy from the HEPAmet Registry, and 1, 587 from the general population (ETHON cohort), age- and sex-matched. The CVR was evaluated using the Systematic Coronary Risk Evaluation (SCORE) model. In addition, the presence of carotid plaques and carotid intima-media thickness were analysed by ultrasound, in a subgroup of MAFLD patients without previous CVD, to establish their use in reclassification of CVR determined by SCORE. Multivariate regression analysis, adjusted for classical CVR factors, was used to evaluate whether CVR is influenced by liver disease activity.

Results: An increased prevalence of cardiovascular events was observed among patients with MAFLD compared to general population (10.3% vs 7.9%; p = 0.02), finding significant differences (p < 0.001) in CVR regarding SCORE categories (low CVR: 32.5% vs 37.3%; very high CVR: 36.9% vs 14.6%). NASH presence (OR 1.490 [IC 95%: 1.001–2.076]) and advanced fibrosis (OR 1.442 [IC 95%: 1.001–2.076]) were independent risk factors associated with high/very high SCORE category, after adjusted by classical CVR factors. The Fibrosis-4 (FIB-4) index was associated with high/very high SCORE category, maintaining as an independent and significant risk factor after adjusting by classical factors (OR 1.423 [IC 95%: 1.238–1.634]; p < 0.001), and showing statistically significant discrimination of high/very high CVR category (AUC: 0.655 [IC 95%: 0.628–0.682]; p < 0.001). Using carotid ultrasound, it was observed that 20% of patients with low/moderate CVR were reclassified into high-risk category due to the presence of atheromatosis.

Conclusion: The presence of NASH, advanced fibrosis and a higher FIB-4 index were associated with a high/very high CVR in patients with MAFLD, even after considering classical risk factors. The ability of the SCORE model to predict CVD in MAFLD patients may not be as powerful as in the general population.
THU075
Changes in hepatic fat fraction as assessed by MRI-PDFF are correlated with changes in markers of hepatic inflammation, disease activity and fibrosis in biopsy-proven non-cirrhotic NASH with fibrosis
Samuel Daniels¹, Darren Robertson¹, Jose Sanchez², Janeli Sarv², Antonio Manzur², Lutz Jermutus³, Arun Sanyal⁴, Benjamin Challis⁵, Sudha Shankar⁶. ¹Early CVRM, Biopharmaceuticals RandD, Early Clinical Development, Cambridge, United Kingdom; ²Data Science and Artificial Intelligence, RandD, Early Biometrics and Statistical Innovation, Gothenburg, Sweden; ³Early CVRM, Biopharmaceuticals RandD, Cambridge, United Kingdom; ⁴Virginia Commonwealth University, Division of Gastroenterology, Hepatology and Nutrition, Richmond, United States; ⁵Early CVRM, Biopharmaceuticals RandD, Translational Science and Experimental Medicine, Research and Early Development, Cambridge, United Kingdom; ⁶Early CVRM, Biopharmaceuticals RandD, Early Clinical Development, Gaithersburg, United States
Email: samuel.daniels@astrazeneca.com

Background and aims: MRI-PDFF is the gold standard for non-invasive assessment of hepatic fat fraction (HFF) in non-alcoholic steatohepatitis (NASH) and is commonly used within early clinical trials to determine treatment efficacy on steatosis. HFF reduction has been associated with an increased likelihood of NASH resolution. However it is unclear whether reductions in hepatic steatosis bear a relationship with changes in markers of hepatic inflammation, disease activity and fibrosis.

Method: PROXYMO was a 19 week multi-centre phase 2 trial to investigate the safety and efficacy of cotadutide in 74 participants with biopsy confirmed non-cirrhotic NASH with fibrosis (NCT04019561). Post-hoc analysis was performed to investigate whether changes in HFF in the study population were associated with changes in non-invasive markers of hepatic fibrosis, NASH disease activity and inflammation within participants who had baseline and week 19 values. Participants were pooled (active and placebo) and the relative changes in HFF after 19 weeks were assessed against percentage change in non-invasive markers.

Results: Within pooled participants, relative change in HFF was significantly correlated with markers of hepatic inflammation (ALT R = 0.52 (p < 0.0001)), NASH disease activity (NIS-4 R = 0.63 (p < 0.0001)) and hepatic fibrosis (PRO-C3 R = 0.44 (p = 0.0012)). Changes in fibrosis biomarkers were correlated with changes in liver enzymes. Change in body weight was significantly correlated with change in HFF. Relative HFF change was divided into quartiles; those in the quartile of greatest relative HFF reduction had significantly greater reductions in ALT, AST, NIS-4 and PRO-C3.

Conclusion: Reductions in HFF as assessed by MRI-PDFF were associated with reductions in non-invasive markers of hepatic inflammation, NASH disease activity and fibrosis. Furthermore, subjects with improvements in HFF had significantly greater reductions in ALT, AST, NIS-4 and PRO-C3.

THU076
The metabolic dysfunction-associated fatty liver disease definition, regardless of its clinical subclassification, identifies patients at high risk for liver disease progression
María Del Barrio Azaceta¹, Paula Iruzubieta¹, Roger Aller de la Fuente², Jesus María Banares³, Álvaro Santos-Laso¹, José Luis Calleja Panero⁴, Luis Ibañez⁵, María Teresa Arias Losete¹, Manuel Romero Gomez⁶, Carmelo García-Monzón⁷, Judith Gómez-Camarero⁸, Pere Ginés⁹, Rosa M Morillas¹⁰, Juan Manuel Pericàs¹¹, Patricia Aspichueta¹², Rosa Martín-Mateos¹³, Rocío Gallego-Durán¹⁴, Mercedes De La Torre Sanchez¹⁵, Desamparados Escudero-García¹⁶, Vanesa Bernal Monterde¹⁷, Salvador Benlloch¹⁸, Juan Turnes¹⁹, Javier Crespo¹, ¹Gastroenterology and Hepatology Department, Marqués de Valdecilla University Hospital, Santander, Spain; ²Center of Investigation of Endocrinology and Nutrition, School of Medicine, and Unit of Investigation, Hospital Clinico Universitario de Valladolid, Valladolid, Spain; ³Department of Liver and Gastrointestinal Diseases, Biodonostia Health Research Institute–Donostia University Hospital, University of the Basque Country (UPV/EHU), San Sebastian, Spain; ⁴Gastroenterology Department, Hepatology Unit, Hospital Universitario Puerta de Hierro, IDIPHISA, Madrid, Spain; ⁵Gastroenterology and Hepatology Department Hospital Universitario Gregorio Marañón Instituto de Investigacion Sanitaria Gregorio Maranon (ISCM) Universidad Complutense de Madrid, Madrid, Spain; ⁶UCM Digestive Diseases, Virgen del Rocio University Hospital, SeLever group at the Institute of Biomedicine of Seville (IBIS), The University of Seville, Seville, Spain; ⁷Liver Research Unit, Hospital Universitario Santa Cristina Instituto de Investigación Sanitaria Princesa, Madrid, Spain; ⁸Department of Gastroenterology and Hepatology, Complejo Asistencial Universitario de Burgos, Burgos, Spain; ⁹Liver Unit, Hospital Clinic, IDIBAPS, University of Barcelona, Barcelona, Spain; ¹⁰Gastroenterology and Hepatology Department, Hospital Universitari Germans Trias i Pujol, Badalona, Spain; ¹¹Liver Unit, Vall d’Hebron University Hospital, Vall d’Hebron Institute of Research (VHIR), Barcelona, Spain; ¹²Department of Physiology, Faculty of Medicine and Nursing, Biocruces Research Institute, University of the Basque Country UPV/EHU, Leioa, Spain; ¹³Department of Gastroenterology and Hepatology, Hospital Universitario Ramón y Cajal, Instituto Ramón y Cajal de Investigación Sanitaria (IRYCS), Madrid, Spain; ¹⁴Unit for the Clinical Management of Digestive Diseases, Hospital Universitario de Valme. Sevilla, Spain; ¹⁵Hepatology Unit, Consorcio Hospital General Universitario de Valencia, Valencia, Spain; ¹⁶Hospital Clinico Universitario de Valencia, Universitat de Valencia, Valencia, Spain; ¹⁷Hospital Universitario Miguel Servet, Zaragoza, Spain; ¹⁸Department of Hepatology, Hospital Universitario y Politécnico La Fe, Valencia, Valencia, Spain; ¹⁹Service of Digestive Diseases, Complejo Hospitalario Universitario de Pontevedra, IIS Galicia Sur, Pontevedra, Spain
Email: javiercrespo1991@gmail.com

Background and aims: Several population studies indicate that Metabolic dysfunction-Associated Fatty Liver Disease (MAFLD) diagnostic criteria better identify which patients are at high risk for liver disease progression. However, the impact of this new definition on specialized clinical practice is still unknown. Here, our aim was to compare MAFLD vs non-MAFLD patients, for a cohort of Non-Alcoholic Fatty Liver Disease (NAFLD) patients with liver biopsy.

Method: A cross-sectional multicenter study with 2, 148 NAFLD patients from the HEPAmet Registry with liver biopsy, with no other causes of chronic liver disease and with the necessary clinical data to reach MAFLD diagnosis. Clinical, analytical and elastographic data, close to liver biopsy date, were collected. The Non-Alcoholic Steatohepatitis (NASH) diagnosis was based on the presence at once of steatosis, ballooning and lobular inflammation.

Results: Only 1.5% of patients did not fulfill MAFLD diagnostic criteria. Compared to non-MAFLD, MAFLD patients showed a higher mean value of Fibroscan (12.5 ± 9 vs 6.5 ± 2.3; p = 0.002) and had more ballooning, lobular inflammation and significant/advanced fibrosis.
Conclusion: The metabolic dysfunction that defines MAFLD better identifies patients at risk for advanced liver disease, regardless of whether they are overweight/obese or diabetic.

**THU077**

Assessment of the prevalence of non-alcoholic fatty liver disease, its severity, and comorbidities in lean americans: national health and nutrition examination surveys (NHANES) with transient elastography assessment from 2017 to 2018

Emily Truong1, Galen Cook-Wiens2, Naim Alkhouri3, Mazen Noureddin4.

1Cedars Sinai Medical Center, Internal Medicine, Los Angeles, United States; 2Cedars Sinai Medical Center, Los Angeles, United States; 3Arizona Liver Health, Phoenix, United States; 4Cedars Sinai Medical Center, Los Angeles, United States

Email: emily.truong@cshs.org

**Background and aims:** Previous studies examined lean non-alcoholic fatty liver disease (NAFLD), which affects 10-20% of non-obese or lean Americans and is associated with lower rates of hyperlipidemia, hypertension, diabetes, and cirrhosis. We described characteristics and NAFLD prevalence and severity in the lean population in National Health and Nutrition Examination Surveys (NHANES) from 2017 to 2018 by using Fibroscan to directly assess steatosis and fibrosis.

**Method:** We analyzed NHANES data from 2017–2018. Inclusion criteria were age ≥ 18 years and completion of interview, laboratory testing, and FibroScanTM. Exclusion criteria were excessive alcohol use (≥7 or 14 drinks/week for females or males, respectively) or viral hepatitis. Non-lean NAFLD was defined as body mass index (BMI) ≥ 25 kg/m², and lean NAFLD was defined as BMI < 25 kg/m². NAFLD was defined as controlled attenuation parameter > 274 dB/m.

**Results:** Of 3893, 120 (3.1%) respondents were lean NAFLD, and 1453 (37.3%) respondents were non-lean NAFLD. Overall NAFLD prevalence was 40.34% (non-lean 37.27% vs lean 3.08%). Compared to non-lean NAFLD, lean NAFLD had significantly lower prevalence of prediabetes, though not significantly different prevalence of diabetes or hypertension. Lean NAFLD had lower mean CAP, FAST score, and median stiffness than that of non-lean NAFLD. Lean NAFLD had lower prevalence of fibrosis stage 2 or 3 and higher (≥F2 or ≥F3) and Fibroscan-AST (FAST) score compared to non-lean NAFLD. Neither fibrosis stage 4 (F4) nor FAST score ≥ 0.67 were significantly different between lean and non-lean NAFLD.

**Conclusion:** Compared with non-lean NAFLD, lean NAFLD had significantly higher prevalence of prediabetes and severity of hyperlipidemia. Although lean NAFLD had significantly decreased prevalence of ≥F2 and ≥F3 and lower FAST score compared to non-lean NAFLD, neither fibrotic non-alcoholic steatohepatitis nor cirrhosis prevalence were significantly different between lean and non-lean NAFLD. The largest to date to examine this subpopulation, this study highlights important implications for monitoring disease progression in the lean NAFLD population.

**THU078**

Coagulation imbalance is associated with hepatic fibrosis and vascular complications in patients with type 2 diabetes and NAFLD

Francesca Alleoto1,2, Paolo Francione1,2, Gabriele Maffi1,2, Giordano Sigon1,2, Annalisa Cespiati1,2, Daniela Bignamini1, Mariagrazia Clerici1, Veena Chantarangkul1, Armando Tripodi1, Flora Peyvandi2, Silvia Fargion1,2, Anna Ludovica Fracanzani1,2, Rosa Lombardi1,2, Fondazione Ca’ Granda IRCCS, Policlinico Hospital of Milan, Unit of Internal Medicine and Metabolic Diseases, Milan, Italy; 1University of Milan, Department of Pathophysiology and Transplantation, Milan, Italy; 2Fondazione Ca’ Granda IRCCS, Policlinico Hospital of Milan, Angelo Bianchi Bonomi Hemophilia and Thrombosis Center and Fondazione Luigi Villa, Milan, Italy; 3Fondazione Ca’ Granda IRCCS, Policlinico Hospital of Milan, Unit of Internal Medicine Hemostasis and Thrombosis, Milan, Italy

Email: rosa.lombardi@unimi.it

**Background and aims:** Both non-alcoholic fatty liver disease (NAFLD) and type 2 diabetes mellitus (T2DM) are characterized by a pro-coagulant state and expose patients to vascular complications. The interaction between pro-coagulant state, vascular complications and advanced liver disease has not been defined yet. Aim: to evaluate in a cohort of patients with T2DM and NAFLD if alterations in coagulation tests are associated with high prevalence of hepatic fibrosis and vascular complications.

**Method:** 96 consecutive outpatients with T2DM and ultrasound fatty liver and an age and sex matched control group of 156 healthy individuals were enrolled. For all subjects, determination of serum pro- (i.e factor II-FII, factor VIII-FVIII) and anti-coagulant factors (i.e protein C-PC, antithrombin-AT) and test of thrombin generation (ETP ratio, peak ratio, FVIII/PC) were obtained. In the T2DM cohort, significant liver fibrosis (≥F2) was diagnosed by Fibroscan (i.e liver stiffness measurement-LSM > 7.0/6.2 kPa M/XL probe). Evaluation of microvascular (i.e retinopathy, nephropathy and neuropathy) and macrovascular complications (i.e carotid plaques and history of cardiovascular (CV) events) was assessed.
**RESULTS**

The T2DM group mean age was 65±7 years, 66% male. Mean FII was 95.9±12.8, FVIII 130.3±33.2, PC 112.8±20.8, AT 106±14.4, ETP ratio 0.64±0.09, peak ratio 0.93±0.05, FVIII/PC 1.2±0.3. Despite only 5% of the cohort had increased transaminases, significant hepatic fibrosis was present in 14% by LSM. Microvascular complications were present in 29 (30%) patients (retinopathy in 8%, nephropathy in 23% and neuropathy in 4%) whereas plagues in 70 (73%) and CV events in 23 (24%). Compared to the control group, T2DM patients presented a pro-coagulant imbalance (ETP ratio 0.64±0.09 vs 0.59±0.18, p = 0.012; FVIII/PC 1.2±0.3 vs 1.02±0.3, p = 0.003). In the T2DM cohort, indexes of procoagulant imbalance as AT and FVIII/PC were independently associated with significant fibrosis by LSM>7.0/6.2 kPa with M/XL probe (multivariate analysis for AT corrected for age, sex, T2DM duration, HbA1C, overweight, hypertension: OR 0.89; CI 95% 0.88–0.98) and microvascular complications (multivariate analysis corrected for age, sex, smoking, T2DM duration, HbA1C, overweight, hypertension, use of statins, uric acid for AT: OR 0.93; CI 95% 0.88–0.98; and for FVIII/PC ratio: OR 8.0; CI 95% 1.00–65.8).

**Conclusion:** In patients with T2DM and NAFLD a pro-coagulant imbalance was found compared to healthy controls and it was associated with both hepatic and vascular complications, speculating on a possible common pathogenetic pattern. Further studies and a wider cohort are warranted to define the clinical application of these coagulation alterations. However, our results point on the need of a careful evaluation also of hepatic complications in diabetics.

**THU079**

**Presence of two or more metabolic risks regardless of fatty liver is a risk factor for significant hepatic fibrosis**

Huyu Park1, Daewon Jun2, Eileen Yoon3, Sang Bong Ahn4, Hye Young Lee4, Hyunwoo Oh4, Bo-Kyeong Kang4, Mi Mi Kim5, Chul-min Lee6, Joo Hyun Sohn7. 1Uijeongbu Eulji Medical Center, Department of Family Medicine, Gyeonggi-do, Korea, Rep. of South; 2Hanyang University College of Medicine, Department of Medicine, Seoul, Korea, Rep. of South; 3Nowon Eulji Medical Center, Eulji University School of Medicine, Department of Medicine, Seoul, Korea, Rep. of South; 4Uijeongbu Eulji Medical Center, Department of Medicine, Gyeonggi-do, Korea, Rep. of South; 5Hanyang University College of Medicine, Department of Radiology, Seoul, Korea, Rep. of South; 6Hanyang University Guri Hospital, Hanyang University College of Medicine, Department of Medicine, Gyeonggi-do, Korea, Rep. of South

**Email:** mseileen80@gmail.com

**Background and aims:** Metabolic syndrome and diabetes are well-known risk factors for hepatic fibrosis. However, hepatic fibrosis screening strategies for subjects with these risks have not yet been established. We aimed to identify the high-risk group for hepatic fibrosis screening, according to the type and number of metabolic risk factors.

**Method:** This was a retrospective cross-sectional cohort study using data from 13 nationwide centres. A total of 5,111 subjects who underwent both magnetic resonance elastography and abdominal ultrasound as part of their health check-up were included. Subjects with viral hepatitis and/or a history of significant alcohol consumption were excluded.

**Results:** The prevalence of significant hepatic fibrosis was 7.3%. Among subjects with significant hepatic fibrosis, 41.3% did not have fatty liver. Hepatic fibrosis burden increased according to the number of metabolic abnormalities. Nearly 70% of subjects with significant hepatic fibrosis also had two or more metabolic risks and/or diabetes. However, significant fibrosis prevalence did not differ between the groups with and without fatty liver among those with healthy metabolic conditions. The presence of two or more metabolic abnormalities was an independent risk factor for significant hepatic fibrosis, even when the presence of fatty liver was corrected.

**Conclusion:** Health check-up examinees who have two or more metabolic risks and/or diabetes are at risk of hepatic fibrosis, regardless of fatty liver status. Thus, active screening for hepatic fibrosis in the setting of health check-up centres should be extended to subjects with two or more metabolic risks and/or diabetes, beyond those with fatty liver.

**THU080**

**Pregnancy as a unique opportunity to identify NAFLD in women: a prospective assessment**

Tatyana Kushner1, Shaelyn O’Hara1, Marcia Lange1, Carin Carroll2, Emma Rosenbluth3, Pamela Argiriadi4, Rachel Meislin5, Joanne Stone1, Keith Sigel1, Rhoda Sperling1, Scott Friedman1, Norah Terrault1, 1Icahn School of Medicine at Mount Sinai; 2University of Miami School of Medicine; 3University of Southern California Keck School of Medicine

**Email:** tatyana.kushner@mssm.edu

**Background and aims:** Non-alcoholic fatty liver disease (NAFLD) in U.S. women of reproductive age is rising and recent administrative claims-based data suggest a significant association of NAFLD with adverse pregnancy outcomes. We evaluated the prevalence and associated risk factors of NAFLD at a high-volume obstetrics center.

**Method:** In this prospective study, a liver ultrasound at time of routine pregnancy anatomy scan at 18–22 weeks’ gestation was performed to assess for presence of NAFLD. Obstetric sonographers were trained to obtain liver images that were subsequently graded for hepatic steatosis by a radiologist blinded to clinical status. The proportion having elevated hepatic steatosis index (HSI) and meeting recently defined metabolic associated fatty liver disease (MAFLD) criteria was evaluated. A multivariable logistic regression model assessed independent predictors of NAFLD among pregnant women.

**Results:** Among 749 women approached for participation, satisfactory liver ultrasounds were obtained on 560 (75%) pregnant individuals; median age 28, 58% Hispanic ethnicity, 65% with pre-pregnancy BMI ≥25, 22% nulliparous. Seventy-eight (14.3%) had steatosis on ultrasound; 83% grade 1, 14% grade 2 and 3% grade 3. Overall, 36% had HSI ≥3; 11% satisfied MAFLD criteria. Only 4 out of 560 (0.71%) carried a previous diagnosis of NAFLD. Women with steatosis were more likely to be of Hispanic ethnicity, have diagnoses of chronic hypertension and diabetes and have a pregnancy history of gestational diabetes (p < 0.05; see Table). Women with grade 2/3 steatosis were more likely to have a history of preeclampsia (30% vs 10%, p = 0.05). In multivariable analyses, Hispanic ethnicity (OR 2.57; 95% CI 1.30–5.09) and BMI (OR 1.06; 95% CI 1.01–1.11) were independently associated with NAFLD.

**Conclusion:** In this first time U.S. based prospective study of pregnant women, integration of ultrasound into obstetric care was feasible and effective in identifying women with NAFLD. NAFLD prevalence was 14%, similar to reports in non-pregnant women of reproductive age with Hispanic and elevated pre-pregnancy BMI women being at highest risk of NAFLD. Most had no prior diagnosis of NAFLD, highlighting a unique opportunity to identify and link women to specialized care.
THU081
N-terminal propeptide of type III collagen (PRO-C3) based risk for liver fibrosis predict cardiovascular events in non-alcoholic fatty liver disease
Francesco Baratta1, Giulia Tozzi1, Daniele Pastori1, Alessandra Colamorti1, Nicholas Cocomello1, Stefano Cecchi2, Mattia Coronati1, Francesco Angelico1, Maria Del Ben1. 1Sapienza-University of Rome; 2Children’s Hospital Bambino Gesù Email: francesco.baratta@uniroma1.it

Background and aims: N-terminal propeptide of type III collagen (PRO-C3) is cleaved off during the process of collagen III deposition. Serum levels of PRO-C3 properly correlate to biopsy-proven liver fibrosis stage and PRO-C3 was included in some risk scores, namely ADAPT, FIB-C3 and ABC3D to predict advanced liver fibrosis. While the association between other liver fibrosis risk scores (FIB4 and NAFLD fibrosis score) and cardiovascular events (CVEs) has been demonstrated, the association between PRO-C3 derived scores and CVEs has never been investigated. Aim of the study was to investigate the association between scores including PRO-C3, and CVEs incidence in a large prospective cohort of NAFLD patients.

Method: The present study is a post hoc analysis of the Plinio Study (ClinicalTrials.gov: NCT04036357). PRO-C3 detection was performed in plasma using ELISA commercial kit (Novus Biological). ADAPT, FIBC3 and ABC3D were calculated. Data on CVEs were prospectively collected with periodical phone calls (every six months) and visits (every 12 months).

Results: The median follow-up was 47.8 [25.3–72.8] months yielding 2786.5 person-years of observation. During the follow-up, 41 patients (1.5% year) experienced CVEs. Patients who experienced CVEs were more frequently males (p = 0.010) and had higher prevalence of type 2 diabetes (p = 0.006), metabolic syndrome (p = 0.002) and of prior CVE event (p < 0.001). The prevalence of impaired ADAPT (p = 0.038), FIBC3 (p = 0.015) and ABC3D (p < 0.001) were higher in patients with CVEs. At multivariate Cox regression analyses, the association with CVEs was confirmed for ABC3D>3 (HR: 2.29 [1.17–4.47]) in the whole population and for FIBC3 (HR: 1.40 [1.06–1.85]) and ABCD3 (HR: 1.40 [1.06–1.84]) only in patients who did not experience a CV event before enrollment (in primary prevention) (Table 1). In all the analyses performed in the whole cohort, prior-CVE was the strongest predictor of new onset CVEs during the follow-up (data not shown).

Conclusion: This from the Plinio cohort study is the first evidence of an association between ADAPT, FIBC3, ABC3D and cardiovascular events in NAFLD. These scores detect high-risk patients for both liver and cardiovascular complications, may contribute to better identify a sub-population of NAFLD patients who deserve a more holistic approach.

THU082
Genetic risk of fatty liver disease and mortality in the general population
Helene Gellert-Kristensen1, Børge Nordestgaard2, Anne Tybjaerg Hansen1, Stefan Stender1. 1Rigshospitalet, Clinical Biochemistry, Copenhagen, Denmark; 2Herlev Hospital, Clinical Biochemistry, Herlev, Denmark Email: stefan.stender@regionh.dk

Background and aims: Fatty liver disease associates with increased mortality due to extrahepatic causes, as well as increased all-cause mortality. However, it remains unclear if these associations reflect a causal effect of fatty liver disease rather than confounding due to coexisting comorbidities. The aim of this study was to use genetic variants (which are less susceptible to confounding) to assess if fatty liver disease per se is likely to causally influence mortality.

Method: We included participants from two prospective studies of the general Danish population, the Copenhagen City Heart Study and the Copenhagen General Population Study, totaling 110, 913 persons. All participants were genotyped for six variants with known effects on fatty liver disease: PNPLA3 rs738409, TM6SF2 rs58542926, HSD17B13 rs72613567, MBOAT7 rs641738, MTARC1 rs2642438, and GCKR rs1260326.

Table 1. Multivariate Cox regression analysis in the whole population (Panel A) and in patients in primary prevention (Panel B).

<table>
<thead>
<tr>
<th>Gene</th>
<th>CVD</th>
<th>Age</th>
<th>Panel A</th>
<th>Panel B</th>
</tr>
</thead>
<tbody>
<tr>
<td>ADAPT</td>
<td>1.24 [1.03–1.48]</td>
<td>1.39 [1.05–1.86]</td>
<td></td>
<td></td>
</tr>
<tr>
<td>ADAPT+rs17609610</td>
<td>0.77 [0.69–0.87]</td>
<td>0.84 [0.72–0.97]</td>
<td></td>
<td></td>
</tr>
<tr>
<td>FIB4</td>
<td>1.22 [0.78–1.95]</td>
<td>1.15 [0.82–1.61]</td>
<td></td>
<td></td>
</tr>
<tr>
<td>FIB4+rs58542926</td>
<td>1.20 [1.06–1.36]</td>
<td>1.16 [1.03–1.30]</td>
<td></td>
<td></td>
</tr>
<tr>
<td>ABC3D</td>
<td>1.31 [1.08–1.60]</td>
<td>1.27 [1.06–1.51]</td>
<td></td>
<td></td>
</tr>
<tr>
<td>ABC3D+rs58542926</td>
<td>2.89 [1.46–5.78]</td>
<td>2.83 [1.43–5.60]</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Conclusion: This from the Plinio cohort study is the first evidence of an association between ADAPT, FIBC3, ABC3D and cardiovascular events in NAFLD. These scores detect high-risk patients for both liver and cardiovascular complications, may contribute to better identify a sub-population of NAFLD patients who deserve a more holistic approach.
Results: During a median of 9.5 years of follow-up, 16,119 individuals died, hereof 201 due to liver-related causes, 1,736 to ischemic heart disease, and 4,973 to extrahepatic cancer. The variants at PNPLA3, HSD17B13, TM6SF2, and MBOAT7 (but not those at MTAR1 and GCKR) were individually associated with liver-related mortality, with per-allele hazard ratios of 1.3 to 1.6 (p values <0.06). The strongest effect was seen for the PNPLA3 variant, for which homozygous carriers had a three-fold higher risk of liver-related death compared to non-carriers. A previously developed genetic risk score comprised of the variants at PNPLA3, TM6SF2 and HSD17B13 was robustly associated with stepwise increased liver-related mortality, with a maximum hazard ratio of 13 (95% CI: 3.8 to 48) for those with 5 or 6 versus 0 risk-increasing alleles (p for trend = 9 < 10E-7, see Figure, bottom panel). The fatty liver disease variants, individually or combined into risk scores, did not associate with ischemic heart disease-related, extrahepatic cancer-related, or all-cause mortality (Figure, top panel).

Conclusion: High genetic risk of fatty liver disease increased liver-related mortality and increased the risk of death due to ischemic heart disease or extrahepatic cancer, nor all-cause mortality in the general population. These data support that fatty liver disease is causally associated with liver-related mortality, but not with mortality due to other causes.

THU083 Role of NAFLD-associated genetic variants on renal function in patients with non-alcoholic fatty liver disease
Laura D’Eraso1, Francesco Baratta2, Alessia Di Costanzo1, Ilaria Umbro1, Alessandra Colantoni1, Nicholas Cocomello1, Daniele Pastori1, Marcello Arca1, Francesco Angelico1, Maria Del Ben1.1Sapienza, University of Rome
Email: laura.derasmo@uniroma1.it

Background and aims: Previous studies demonstrated the association between non-alcoholic fatty liver disease (NAFLD) and chronic kidney disease (CKD). Recent studies focused the attention on the role of Patatin-like Phospholipase domain-containing 3 (PNPLA3) rs738409 polymorphism in the association between NAFLD and CKD in non-metabolic adults and children, but the genetic impact on NAFLD-CKD association is still matter of debate. Aim of the study was to investigate the impact of PNPLA3, Transmembrane 6 Superfamily Member 2 (TM6SF2), Membrane Bound O-Acyltransferase Domain Containing 7 (MBOAT7) and Glucokinase Regulatory Protein (GCKR) genes on renal function in a large population of NAFLD patients.

Method: The present study is a post hoc analysis of the Plinio Study (ClinicalTrials.gov: NCT04036357). PNPLA3, TM6SF2, MBOAT7 and GCKR genes were analyzed by using Real Time PCR with TaqMan probes. Glomerular filtration rate (GFR) was estimated with CKD-epi formula. The effect of the NAFLD genetic background on eGFR was estimated both including each gene individually and considering the NAFLD genetic risk score (wGRS). The effect of NAFLD on renal function was assessed by analyzing two end points: 1) eGFR <90 ml/min (rGFR) or 2) eGFR <60 ml/min (moderate-to-severe CKD). The present study is a post hoc analysis of the Plinio Study.

Results: A total of 485 subjects (mean age 42.0 ± 11.4 years) were counted through analysis of variance (ANOVA) and multivariate logistic regression. The distribution of genotypes was superimposable if considering the entire group of patients with eGFR <90 ml/min or only those with eGFR <60 ml/min. At multivariate regression analyses (table 1), we did not observe any correlation between genotypes and renal function. Conversely, we found that metabolic syndrome was highly associated with rGFR (Odds ratio (OR): 1.52 (1.07–2.18)), whereas prior Atherosclerotic Cardiovascular Disease (ASCVD) with moderate-to-severe CKD (OR: 3.54 (1.22–10.24)). When introduced in the model, arterial hypertension emerged as the strongest risk factor for eGFR decline (OR: 1.45 (1.02–2.06) and OR: 2.85 (1.20–6.79) respectively for rGFR and moderate-to-severe CKD) (table 1).

Conclusion: In our cohort of adult patients with NAFLD, we found no association between CKD and PNPLA3, TM6SF2, MBOAT7 and GCKR gene variants. Hypertension was the stronger predictor of eGFR impairment. Based on these findings, the association between NAFLD and CKD might be due to the shared metabolic risk factors rather than the genetic NAFLD background.

THU084 The association between non-alcoholic fatty liver disease and insulin resistance within normal glucose level population
Chun-Yi Wang1, Kuan-Yu Lai1, Wen-Yuan Lin1, Tsung Po Chen1.1China Medical University Hospital, Department of Community and Family Medicine, Taichung, Taiwan
Email: tsungpo88@gmail.com

Background and aims: The study of non-alcoholic fatty liver disease (NAFLD) with association of type 2 diabetes (T2DM) reveals rapid growth of prevalence and incidence in recent years. The mechanism of NAFLD shows connection between insulin resistance (IR) and T2DM. The aim of this study was to investigate the association between NAFLD and IR in normal glucose level population.

Method: We recruited participants from community and outpatient department in a hospital from central and northern Taiwan. Those with impaired fasting glucose or with diagnosis of T2DM were excluded from our study. We screened the items of body mass index (BMI), systolic/diastolic blood pressure (SBP/DBP), body fat ratio (%) and social factors. We performed serum test after 8 hours overnight fasting. NAFLD was diagnosed based on an abdominal ultrasonography measurement. The calculation of IR used HOMA-IR formula and was shown by tertile (T1, T2, and T3). The method of statics counted through analysis of variance (ANOVA) and multivariate logistic regression.

Results: A total of 485 subjects (mean age 42.0 ± 11.4 years) were involved. The prevalence of NAFLD increased significantly among increasing level of IR (34.1%, 40.1%, 47.8%, p <0.001). Although fasting plasma glucose were within normal range among three groups, higher level of IR presented higher glucose value (81.9 ± 7.4 mg/dL, 85.1 ± 7.6 mg/dL, 87.3 ± 6.5 mg/dL, p < 0.0001). After adjusting for age, sex, BMI, exercise, alcohol consumption and cigarette smoking, the risk of NAFLD was increased with the increment of IR (T3 v.s. T1: Odd ratio [OR] 3.87, 95% confidence interval [CI], 2.08 to 7.21: T2 v.s. T1: OR 1.83, 95% CI, 1.11 to 3.00) after adjusting for confounding factors.
Conclusion: This study shows that in normal sugar level groups, there is only limited data on pruritus in hepatobiliary disorders in general. This study therefore aimed at further investigating the epidemiology, clinical features, and influence on quality of life (QoL) in a large cohort of patients with different liver diseases.

Method: We performed a prospective, cross-sectional study in a large Hepatology outpatient clinic from August 2020-May 2021. We collected extended clinical data including characteristics of pruritus (e.g. mean/worst itch intensity on a numeric rating scale, NRS) and questionnaires containing validated scores such as ItchyQoL and SF12. Statistical analyses were performed using Mann-Whitney-U-test and Spearman’s rank correlation. Data are given as mean ± SEM.

Results: In total, 609 patients participated in this study of whom 27.3% (N = 166) presented with liver cirrhosis. 24.1% (N = 147) of all patients reported on pruritus with 61.9% (N = 91) being female. In the pruritus group 52.7% (N = 79) of all patients suffered from non-cholestatic liver diseases such as (non)alcoholic fatty liver disease, (non)alcoholic steatohepatitis (NASH), viral hepatitis, and associated liver cirrhosis. Immune-mediated and cholestatic liver diseases such as primary biliary cholangitis, primary and secondary sclerosing cholangitis, and genetic disorders represented 46.3% (N = 68). The majority of all pruritic patients reported on chronic itch with a duration >6 weeks (80.9%; N = 119). Only 17.7% (N = 26) received oral anti-pruritic therapy with fibrates being most commonly prescribed (30.5%; N = 8). Mean and worst itch intensity during the last week were rated at moderate intensities of 3.7 ± 0.2 and 4.2 ± 0.3 on a NRS, respectively. The QoL of affected patients quantified by ItchyQoL and SF12. Statistical analyses were performed using Mann-Whitney-U-test and Spearman’s rank correlation. Data are given as mean ± SEM. Linkage of RNA-seq with EHR data identified DEGs associated with mortality including potential biomarkers such as growth/differentiation factor 15 (GDF15) and fibroblast growth factor 21 (FGF21). Deconvolution analysis revealed statistically significant correlations between histological fibrosis scores and expanded populations of scar-associated macrophages, myofibroblasts, endothelial cells and B- and T-cell subtypes across discrete NAFLD stages.

Results: RNA-seq identified 45 DEGs in early NAFLD (i.e., isolated steatosis) and 9826 DEGs in advanced NAFLD (i.e., fibrosis stage F4), compared with controls. KEGG analysis showed enrichment of inflammatory pathways in early-stage disease (e.g., cytokine-cytokine receptor interactions; q <0.01), whilst pathways linked to extracellular matrix were only enriched in advanced disease (q <0.001). Linkage of RNA-seq with EHR data identified DEGs associated with mortality including potential biomarkers such as growth/differentiation factor 15 (GDF15) and fibroblast growth factor 21 (FGF21). Deconvolution analysis revealed statistically significant correlations between histological fibrosis scores and expanded populations of scar-associated macrophages, myofibroblasts, endothelial cells and B-cells.

Conclusion: Using SteatoSITE, the world’s first data commons for NAFLD, we defined hepatic gene signatures across the full disease severity spectrum. Linkage to EHR-derived outcomes enables identification of liver transcriptional features associated with increased mortality. This work will underpin future studies aimed at developing a stratified medicine approach for NAFLD.

THU087 Different effects of low muscle mass on the risk of non-alcoholic fatty liver disease and liver cirrhosis in a prospective cohort Hun Jee Choe1,2, Hyunsuk Lee1,2, Dongho Lee1,2, Soo-Heon Kwak1,2, Bo Kyung Koo2,3.

Background and aims: Studies have correlated liver gene expression to pathological and clinical features of NAFLD cross-directionally, but there is a paucity of longitudinal data using molecular features to predict patient outcomes. Such data is critical for accurate risk stratification and identification of novel treatments for specific subphenotypes of NAFLD. Using SteatoSITE (https://steatosite.com/), a resource containing integrated genetic, clinical and pathological data, we studied hepatic RNA-sequencing (RNA-seq) and linked electronic health record (EHR) data to identify gene expression patterns across the full histological NAFLD spectrum and to determine transcriptomic signatures that are associated with adverse clinical outcomes. Bulk tissue cell-type deconvolution was also performed using published single-cell RNA-seq (scRNA-seq) data to elucidate changes in cellular composition to inform rational biomarker and drug development.

Method: Bulk RNA-seq data was analysed from 692 liver samples (normal liver controls (n = 28), isolated steatosis (n = 43), steatosis with inflammation and/or hepatocyte ballooning (n = 621), including samples from all fibrosis stages). Time until death or censoring was retrieved for each patient. Differentially expressed genes (DEGs) between alive and dead patients at 1, 2, 3 and 5 years were used to generate a transcriptional signature predictive of mortality. Multi-subject Single-cell Deconvolution (MuSiC) was used to compare counts from each bulk RNA-seq sample with scRNA-seq data from healthy and cirrhotic livers to estimate proportions of liver macrophage, mesenchymal, endothelial, B- and T-cell subtypes across discrete NAFLD stages.

Results: RNA-seq identified 45 DEGs in early NAFLD (i.e., isolated steatosis) and 9826 DEGs in advanced NAFLD (i.e., fibrosis stage F4), compared with controls. KEGG analysis showed enrichment of inflammatory pathways in early-stage disease (e.g., cytokine-cytokine receptor interactions; q <0.01), whilst pathways linked to extracellular matrix were only enriched in advanced disease (q <0.001). Linkage of RNA-seq with EHR data identified DEGs associated with mortality including potential biomarkers such as growth/differentiation factor 15 (GDF15) and fibroblast growth factor 21 (FGF21). Deconvolution analysis revealed statistically significant correlations between histological fibrosis scores and expanded populations of scar-associated macrophages, myofibroblasts, endothelial cells and B-cells.

Conclusion: Using SteatoSITE, the world’s first data commons for NAFLD, we defined hepatic gene signatures across the full disease severity spectrum. Linkage to EHR-derived outcomes enables identification of liver transcriptional features associated with increased mortality. This work will underpin future studies aimed at developing a stratified medicine approach for NAFLD.
to the development of NAFLD and NAFLD-related liver cirrhosis were investigated in the Korean population.

**Method:** This prospective community-based cohort study included 40–70-year-old adults, followed-up biennially from 2001–2002 to 2017–2018. NAFLD was defined as a hepatic steatosis index of 36 or higher, and liver cirrhosis was defined based on the fibrosis-4 index. Sex-specific quartiles of body mass index (BMI)-adjusted muscle mass were calculated, and low muscle mass was defined as the lowest quartile (Q1). Cox proportional hazard models for incident NAFLD or liver cirrhosis incorporating age, sex, BMI of 25 kg/m² or higher, metabolic syndrome, and PNPLA3 and TM6SF2 risk alleles were used to assess the independent determinants for incident NAFLD and liver cirrhosis among individuals with NAFLD at baseline.

**Results:** Among the 4,038 participants without NAFLD at baseline (mean age, 51.5 ± 8.8 years), 920 (22.8%) developed NAFLD during the follow-up period of 12 years. As muscle mass decreased, the risk of NAFLD increased even after adjustment for age, sex, obesity, metabolic syndrome, and PNPLA3 and TM6SF2 risk alleles (hazard ratio [HR] per quartile, 1.18, 95% confidence interval [CI], 1.11–1.27, p <0.001). TM6SF2 also affected the risk of NAFLD (HR 1.19, [95% CI, 1.00–1.40]).

Of the 1,176 patients with NAFLD but without hepatic fibrosis at baseline, incident liver cirrhosis was found in 51.8%, 44.7%, 42.6%, and 41.0% in Q1, Q2, Q3, and Q4 of BMI-adjusted muscle mass, respectively, during the follow-up period (p for trend = 0.006). However, this trend lost its statistical significance when adjusted for confounders. The PNPLA3 risk variant and not the TM6SF2 genotype, was an independent risk factor for developing liver cirrhosis among NAFLD patients (HR 1.17, 95% CI 1.04–1.32, p = 0.010).

**Conclusion:** Both lower muscle mass index and genetic risk variants are important contributors to the development of NAFLD. In patients already diagnosed with NAFLD, however, PNPLA3 conferred a greater risk for progression to liver cirrhosis than did lower muscle mass.

**THU088**

**Age and the relative importance of liver-related deaths in non-alcoholic fatty liver disease**

Huapeng Lin1, Terry Cheuk-Fung Yip1, Xinrong Zhang1, Guanlin Li1, Tee-Kit Tse1, Vicki Wing-Ki Hui1, Yan Liang1, Che To Lai1, Stephen Chan1, Henry LY Chan1, Grace Wong1, Vincent Wai-Sun Wong1. The Chinese University of Hong Kong, Hong Kong

Email: linhuapeng5@163.com

**Background and aims:** It is unclear if the leading causes of death in patients with non-alcoholic fatty liver disease (NAFLD) differ by age. In particular, we aim to investigate if the relative importance of liver-related deaths is lower in the elderly population such that screening is no longer meaningful.

**Method:** We conducted a territory-wide retrospective cohort study of adult NAFLD patients between 2000 and 2021 in Hong Kong. The outcomes of interest were all-cause and cause-specific mortality. Age at time of death were studied by subgroups of 10-year intervals.

**Results:** During 662,471 person-years of follow-up of 30,943 NAFLD patients, there were 2,097 deaths. The top 3 causes of death were pneumonia, extrahepatic cancer and cardiovascular diseases. Extrahepatic cancer was the leading cause of death, followed by pneumonia and cardiovascular diseases before the age of 80. Pneumonia became the leading cause of death after the age of 80. Liver disease was the sixth leading cause of death in patients aged 70–79 and 80–89 years, accounting for 5.1% and 5.9% of deaths, respectively, but only accounted for about 3% or less of the deaths in the other age groups. The incidence of liver-related death was higher in men before the age of 70 but higher in women afterwards. The incidence of liver-related death in women increased from 0.62 to 7.14 per 10,000 person-years from age 60–69 to 70–79 years.

**Conclusion:** The relative importance of liver-related death increases with age in NAFLD patients, especially among women. Thus, detection of NAFLD and advanced liver disease should be continued in the elderly population so far if they remain candidates for treatment.

**Key words:** non-alcoholic fatty liver disease, liver-related deaths, age
was associated with higher CAC score (p = 0.008), number of HRP features (p = 0.007) and presence of obstructive CAD (p = 0.01) and CAC (p = 0.02) as demonstrated in Figure 1. HS was associated with the presence of both HRP (odds ratio [OR]: 1.48; 95% confidence interval [CI]: 1.09–2.00; p = 0.01) and proximal HRP features (OR: 1.52; 95% CI: 1.18–1.96; p = 0.001). Associations persisted when controlling for cardiovascular risk factors, features of metabolic syndrome, lipid-lowering treatment use, presence of obstructive CAD and CAC score. HS was associated with a higher PV (Q4: 499 mm3 vs Q1: 414 mm3, p = 0.02), driven by low attenuation (p = 0.03) and non-calcified (p = 0.03) plaques. No differences in PCAT were observed.

Figure 1: Coronary Artery Disease Characteristics, Stratified by HU L-s Quartile

Conclusion: HS is associated with multiple indices of coronary atherosclerosis, particularly HRP features, in patients with FH. This appears to be independent of conventionally measured risk factors and may involve additional mechanisms related to HS.

THU090
Non-alcoholic fatty liver disease impact on cardiovascular disease death: a population-based study
Chaonan Jin1, Sheng Bi1, Mei Deng2-3,4, Jifang Sheng1, 7 The First Affiliated Hospital, College of Medicine, Zhejiang University; State Key Laboratory for Diagnosis and Treatment of Infectious Diseases, National Clinical Research Center for Infectious Diseases, Collaborative Innovation Center for Diagnosis and Treatment of Infectious Diseases, Hangzhou, Zhejiang Province, China; 2Guangxi Key Laboratory of Molecular Medicine in Liver Injury and Repair, Affiliated Hospital of Guilin Medical University, Guilin, Guangxi, China; 3Department of Radiation Oncology, Affiliated Hospital of Guilin Medical University, Guilin, Guangxi, China; 4Guangxi Health Commission Key Laboratory of Basic Research in Sphingolipid Metabolism Related Diseases, Affiliated Hospital of Guilin Medical University, Guilin, Guangxi, China
Email: jifang.sheng@zju.edu.cn

Background and aims: Non-alcoholic fatty liver disease (NAFLD) represents a common risk factor for cardiovascular disease (CVD). However, the impact of NAFLD on CVD mortality remains to be defined. We aimed to investigate whether NAFLD has a negative influence on CVD mortality.

Method: 11035 participants who were aged 20–74 years, completed both interview and examination in mobile examination centers, with ‘confident or absolute confident’ reports from clear and gradable ultrasound images, from US Third National Health and Nutrition Examination Survey (NHANES III: 1988–94) with follow-up of mortality to 2015 were included. NAFLD was defined as moderate or severe steatosis grade. Mortality and follow-up data were obtained from NHANES III public-use linked mortality file with underlying cause of death. NAFLD and MAFLD participants were compared. Weighted survival was analyzed using univariate and multivariate Cox proportional hazards model.

Results: A total of 2299 (weighted 2*107 subjects) NAFLD and 8736 (weighted 108 subjects) subjects without NAFLD were included. NAFLD individuals were older (age 20–39 years 34.8% (standard error [SE] (1.9) vs 52.5% (1.1), p <0.001), male dominant (54.0% (SE (1.5) vs 45.3% (0.7), p <0.001), had more often a lower education level (<9 years 15.6% (1.2) vs 9.6% (0.7), p <0.001), hypertension (33.0% (1.8) vs 18.3% (0.7), p <0.001), type 2 diabetes (10.8% (0.8) vs 3.4% (0.3), p <0.001) and CVD history (7.3% (0.7) vs 3.5% (0.3), p <0.001) comparing to no-NAFLD participants.

Multivariate analysis showed that after adjusting age and gender, NAFLD was not associated independently with CVD mortality (adjusted hazard ratio (aHR) 1.079, 95% confidence interval (CI) 0.911–1.279, p = 0.369). This did not differ (aHR 1.109 95% CI 0.892–1.378, p = 0.345) after adjustment for putative risk factors including age, gender, race, education, poverty income ratio, hypertension, diabetes, smoking status and CVD history.

Conclusion: This prospective cohort suggests that the presence of NAFLD is not associated with CVD mortality among US adults.

THU091
Sarcopenia is associated with the severity of metabolic associated fatty liver disease in elderly residents
Xiaohui Liu1, Jingjing Song1, Shuang Zhang1, Shan Liang1, Zhang Jing1, 7Beijing Youan Hospital, Capital Medical University, The Third Unit, The Department of Hepatology, Beijing, China
Email: 2jiyouan@ccmu.edu.cn

Background and aims: It has been proved that sarcopenia was associated with the metabolic associated fatty liver disease (MAFLD), but their relationship in elderly patients has not been studied in which sarcopenia is more prevalent.

Method: A cross-sectional survey was conducted among 1353 elderly residents over 65 years old in a community in Beijing. Demographic data, medical history, physical examination and laboratory examination results were collected for all subjects. Fatty liver was detected by B type ultrasound. Body composition was detected by Inbody720 (Bios pace, Korea). Liver fat content and liver stiffness was examined by Fibro Scan. Sarcopenia index (SI) was calculated as total ASM (kg)/BMI (kg/m²). Sarcopenia was defined as SI<0.789 for men and<0.521 for women.

Results: Among the 1353 elderly residents, the mean age is 70.5±5.0 years old and women account for 66.0%. There were 755 (55.8%) patients were diagnosed as MAFLD. The BMI, waist circumference, hip circumference, waist-to-hip ratio, upper arm circumference, body fat percentage and visceral fat area in MAFLD group were significantly higher than those in the non-MAFLD group (all p<0.05). The proportion of patients with sarcopenia (20.3%) was significantly higher than those in the non-MAFLD group (16.5%, p=0.026). MAFLD patients with sarcopenia had higher BMI, waist circumference, hip circumference, waist-to-hip ratio, upper arm circumference, body fat rate, visceral fat area, glucose and lipid metabolism indexes than those without sarcopenia (all p<0.05). They also had higher liver fat content [ (300.6 ± 43.5) vs. (295.1 ± 40.3), p<0.001] and liver stiffness scores [5.3 (4.3, 7.0) vs. 5.0 (4.1, 6.3), p<0.001] when compared to non-sarcopenia group. According to quartile stratification, Serum creatinine, HbA1c, HOMA-IR, hs-CRP, CAP and LSM increased significantly from subjects with non-MAFLD to subjects with sarcopenia in MAFLD group and subjects with sarcopenia in MAFLD group (all p for trend<0.001).
Effects of SARS-CoV2 pandemic in a cohort of Italian NAFLD patients
Bernardo Stefanini1,2, Simona Leoni1, Roberta Capelli1,2, Alice Secomandi1,2, Luca Muratori1,2, Fabio Piscaglia1,2, Silvia Ferri1.
1IRCCS Azienda Ospedaliero-Universitaria di Bologna, Division of Internal Medicine, Hepatobiliary and Immunological Diseases, Bologna, Italy; 2University of Bologna, Department of Medical and Surgical Sciences (DIMEC)
Email: silvia.ferri@aosp.bo.it

Background and aims: SARS-CoV2 wide and uncontrolled spread in Italy in winter 2020 forced the authorities to declare an emergency status characterized by a complete lock-down and a massive temporary conversion of medical resources into COVID-positive patients care. Some of the consequences were a great limitation to physical activity and a reduced possibility to regularly follow outpatients in hospital.

Aim of our study was to evaluate the effect of COVID pandemic on subjects with stable NAFLD followed in our outpatient liver clinic.

Method: we enrolled 43 patients (58% females, median age 59 years, mean BMI 29) with defined NAFLD in charge to our liver outpatient unit with these characteristics: a first visit in 2017–2018, a pre-pandemic visit in 2019, a programmed visit between March and June 2020 not performed due to the pandemic condition and a post-pandemic visit after September 2020.

At first visit all patients were given dietary advice following the Mediterranean approach and encouraged to increase physical activity up to 150 minutes/week of aerobic and/or anaerobic activity of moderate intensity. Medications were prescribed when needed. At the three time points a complete anamnestic, physical, laboratory and ultrasound evaluation was performed.

Patients with advanced disease (decompensated cirrhosis and/or hepatocellular carcinoma) were excluded from the study as they were seen in outpatient clinic also during the lock-down period.

Results: compared to first visit, post-pandemic evaluation in our cohort of patients revealed stable BMI, HOMA index, transaminases, lipid profile, NAFLD fibrosis score (NFS), FIB-4, B-mode hepatorenal ratio (BMHRR) and liver stiffness (2D:SWE:SSI), whereas a reduction in gammaGT levels (p = 0.02).

We then considered separately patients that at pre-pandemic visit had lost >5% of their basal weight (10 patients, mean weight loss 7.2%, mean BMI 27, 0) and those who had not (33 patients, mean weight loss +1.4%, mean BMI 29, 4). At post-pandemic control, patients in both groups maintained their weight trend (mean BMI 27, 3 and 29, 6 respectively; weight change compared to first visit −6.0% and +2, 1% respectively; weight change compared to first visit −6.0% and +2, 1% respectively; p < 0.0001). Weight variations were associated to NFS modifications (in weight losers: −19.4%, in weight maintainers +55.9%, p = 0.034).

Surprisingly, all patients, especially those in the latter group, reported an increase in their physical activity after the first visit that was maintained also during the pandemic phase (from scarce-moderate to moderate-good p = 0.004).

Conclusion: in patients with NAFLD, when the behavioral approach (in which physical activity may exert an independent protective role) had been well consolidated in the pre-pandemic phase, it was maintained also during COVID pandemic even without a strict medical follow-up, thus allowing a preservation of the results obtained.
THU094
A higher Fibrosis-4 (FIB-4) score is associated with higher healthcare costs and hospitalizations in patients with non-alcoholic steatohepatitis (NASH)
Elliot Tapper1, Jesse Fishman2, Stephen Dodge2, Keith Miller2, Ni Zeng3, Aliina Bogdanov4, Maachaon Bonafele3, 1University of Michigan, United States; 2Madrigal Pharmaceuticals, United States; 3Veradigm
Email: alina.bogdanov@gmail.com

Background and aims: The cost and complexity of care for patients with Non-alcoholic Steatohepatitis (NASH) increases with disease stage. We aimed to study the Fibrosis-4 (FIB-4) score as a proxy for disease severity and test its association with increased disease burden.

Method: The Veradigm Health Insights Electronic Health Record Database and linked Komodo administrative claims data were used to identify adult patients with coded NASH with aspartate aminotransferase (AST), alanine aminotransferase (ALT) and platelet results and age to compute a FIB-4. The index date was the first coded NASH encounter between 2016 and 2020 with at least 6 months of database activity pre- and post-encounter and a FIB-4 score. We excluded patients coded with viral hepatitis, alcoholism, or alcoholic liver disease. Inpatient hospital admissions and log-transformed costs for pharmacy, hospital inpatient, emergency department, and outpatient services were measured in the 12-month period surrounding index. Multivariate logistic regression for any hospitalization and linear regression for log total cost was performed, controlling for patient demographics (age, race, sex, and geography), smoking status, Charlson comorbidity index (CCI), and diabetes complications severity index (DCSI).

Results: 6,743 patients met the study criteria; mean age was 56.1 ± 13.3, patients were 62.9% female and 53.6% of patients were diagnosed with Type 2 Diabetes. Mean FIB-4 at index was 1.79 ± 1.88. A 1 unit increase FIB-4 at index was associated with a 4.2% increase in mean total annual cost (p < 0.0001 CI 2.2% to 6.3%) and with an odds ratio of 1.12 (p < 0.0001 CI 1.08 to 1.15) for hospitalization. CCI and DCSI were also significantly associated with higher odds ratios for hospitalization (OR 1.27, p < 0.001 CI 1.22 to 1.33).

Conclusion: Higher FIB-4 score across a variety of ranges is associated with increased costs and hospitalizations in the NASH population.

THU095
Comparison of hepatic and cardiovascular damage between HIV patients with steatosis and NAFLD: role of metabolic alterations and low visceral adiposity
Felice Cinque1,2, Rosa Lombardi1,2, Annalisa Cespiati1,2, Paolo Francione1, Erika Fatta2, Cristina Bertelli2, Giuseppe Pisano2, Giovanna Oberti1,2, Lucia Colavolpe1,2, Francesca Alletto1,2, Paola Dongiovanni2, Marica Meroni2, Giorgio Bozzi3, Alessandra Bandera1,2, Anna Ludovica Francanzeri2,1 University of Milan, Department of Pathophysiology and Transplantation, Milan, Italy; 2Fondazione Ca’ Granda IRCCS Ospedale Maggiore Policlinico, Unit of Internal Medicine and Metabolic Disease, Milan, Italy; 3Fondazione Ca’ Granda IRCCS Ospedale Maggiore Policlinico, Infectious Diseases Unit, Milan, Italy
Email: rosa.lombardi@unimi.it

Background and aims: People living with HIV (PLWH) develop metabolic alterations and hepatic steatosis (HS), exposing them to increased cardiovascular (CV) risk. However, if presentation of HS in this category of patients is different from that of non-alcoholic fatty liver disease (NAFLD) is unknown. Aim: to evaluate metabolic, hepatic and CV alterations in PLWH and to compare them with those observed in primary NAFLD subjects.

Method: Forty-two HIV mono-infected patients (mean age 46 ± 12 y, male 81%; 90% with viral suppression) were enrolled. The cohort of PLWH underwent hepatic ultrasound (US) and those with evidence of HS were compared to a sex and age matched NAFLD control group (1:2). For all enrolled subjects, anthropometric parameters (BMI, waist circumference-WC), metabolic comorbidities, CV damage by carotid ultrasound (plaques, arterial stiffness by radiofrequency as pulse wave velocity-pWv) and heart ultrasound (systolic and diastolic function and epicardial adipose tissue-EAT) were assessed. All patients underwent transaminases determination, Fibroscan to detect advanced fibrosis (LSM >8.9/7.2 kPa/ML probe) and bioimpedance (BIA) to quantify sarcopenia (SMI ≤10.5/7.5/6.5 kmg/m2 male/females) and fat mass. CV risk was assessed according to ESC guidelines. Genotyping for PNPLA3 was determined by Taqman assay.

Results: Thirty (63%) PLWH presenting HS were compared with 60 NAFLD patients. PLWH with HS presented no difference in the prevalence of metabolic alterations (type 2 diabetes 13% vs 13%, p = 1.0), hypertension 47% vs 42%, p = 0.82; dyslipidemia 83% vs 85%, p = 1.0; and sarcopenia (40% vs 52%, p = 0.81) compared to NAFLD, despite lower BMI (27.1 ± 4 vs 29.1 ± 4.3 kg/m2, p = 0.04), WC (98 ± 9 vs 103 ± 10.3 cm, p = 0.03) and trunk fat mass (9.8 ± 3.3 vs 12.4 ± 4.7 kg, p = 0.02). No difference in the prevalence of increased transaminases (17% vs 20%, p = 0.78) and advanced fibrosis (17% vs 12%, p = 0.53) was found, as well of high CV risk (84% vs 83%, p = 0.86), pWv (7.4 ± 2 vs 6.9 ± 1.4 m/s, p = 0.18), carotid plaques (39% vs 28%, p = 0.33), increased EAT (20% vs 17%, p = 0.77) and systolic (6% vs 5%, p = 1.0) and diastolic dysfunction (7% vs 6%, p = 1.0). PNPLA3 distribution was not significantly different between groups (p = 0.16).

Conclusion: Hepatic steatosis and fibrosis are highly prevalent in patients with HIV. Interestingly, in PLWH metabolic alterations, liver and cardiovascular damage are superimposable with those observed in a primary NAFLD cohort, although in presence of lower visceral adiposity. Therefore, screening for liver disease in HIV patients is mandatory independently of obesity, as the increased risk of metabolic and CV complications.
Impact of intermittent fasting on anthropometric and clinical outcomes in non-alcoholic fatty liver disease: systematic review and meta-analysis

Marcia Lange1, Devika Nadkarni1, Lily Martin1, Carolyn Newberry2, Sonal Kumar3, Tatyana Kushner1. 1Icahn School of Medicine at Mount Sinai, New York, United States; 2Weill Cornell Medicine, Division of Gastroenterology and Hepatology, New York, United States; 3Icahn School of Medicine at Mount Sinai, Division of Liver Medicine, New York, United States

Email: marcia.lange@icahn.mssm.edu

Background and aims: Currently, weight loss through caloric restriction is the cornerstone of initial non-alcoholic fatty liver disease (NAFLD) management. However, there remains a lack of evidence-based guidelines on the benefits of intermittent fasting (IF) for NAFLD. In this systematic review with meta-analysis, we evaluated the effect of IF on anthropometric and clinical markers of NAFLD.

Method: We conducted a comprehensive search of MEDLINE, EMBASE, and Cochrane Central databases as well as triall registries and conference abstracts up to January 31, 2022. The search strategy included all appropriate controlled vocabulary and keywords for NAFLD and fasting. No date, language, or article type restrictions were included in the search strategy. Studies of adults with NAFLD or non-alcoholic steatohepatitis (NASH) undergoing an intermittent fasting intervention reporting at least one anthropometric or clinical outcome were included in our review. A random effects model was used for meta-analysis to estimate mean differences between intervention and control group for various outcomes.

Results: Initial literature search yielded 16 294 studies, of which 10 772 were duplicates, leaving 5517 studies to screen for title/abstract. An additional 5367 studies were excluded after title/abstract review with moderate concordance (k = 0.53). The remaining 150 studies were assessed for full text review with fair concordance (k = 0.24). Twelve studies were included in the systemic review and meta-analysis, totaling 908 participants with NAFLD, combined mean age of 42.50 years (SD 14.54), 50% male. Meta-analysis of anthropometric outcomes showed that the effect of IF on BMI and body weight was statistically significant (Mean difference (MD) −0.69 kg/m², 95% CI −1.29 to −0.09, p < 0.05; MD −2.51 kg, 95% CI −4.44 to −0.58, p < 0.05) with moderate though statistically significant heterogeneity for both (I² = 47%, p = 0.07; I² = 62%, p = 0.02). Clinical outcome analysis showed that the effect of IF on liver steatosis (CAP, dB/m) and ALT levels was also statistically significant (MD −27.52 dB/m, 95% CI −42.26 to −12.77, p < 0.01; MD −10.35 IU/L, 95% CI −19.9 to −0.8, p < 0.05) with zero to low heterogeneity for both outcomes (I² = 16%, p < 0.01; I² = 0%, p < 0.05). IF did not have a significant effect on AST levels or liver stiffness (kPa).

Conclusion: Intermittent fasting interventions may improve BMI and body weight as well as reduce both liver steatosis and serum ALT levels in adults with NAFLD. Studies with varying types of IF interventions and varying intervention durations likely contributed to meta-analysis heterogeneity. This data suggests that IF likely provides a benefit in NAFLD, but future randomized controlled studies are needed to validate the use of IF for NAFLD treatment.
Results: A total of 2999 patients with BMI $\geq 30$ kg/m$^2$ were identified, of which 1082 patients had no documentation of CLD during the study period. Majority were female (66%), mean age 57 years (SD 13), and mean BMI 35 kg/m$^2$ (SD 4.9). One third were white and 17% Hispanic. Mean ALT and AST were 23 IU/L (3–671). Approximately 40% (385/1082) had a FIB-4 $\geq 1.3$, of which 80% had normal liver enzymes. The median BMI was 32.8 kg/m$^2$ with 68% ≥ 240 dB/m, or histology) were prospectively screened for OSA using STOP-BANG (SB) and Epworth Sleepiness Score (ESS) in an outpatient liver clinic. SB $\geq 3$ or ESS $\geq 10$ were characterized as ‘high risk’ for OSA and referred to Sleep Medicine for home sleep testing with a WatchPAT device. Patients confirmed with OSA were followed in Sleep Medicine and Hepatology. Baseline characteristics, demographics and severity of liver disease were collected and students t test as well as logistic regressions were used to assess differences. Patients with NAFLD and OSA were followed over time to determine the impact of OSA treatment on NAFLD.

Results: Sixty-eight patients with NAFLD from a tertiary hospital system were screened for OSA from; 41% were male, mean age 49 years, 21% were White Non-Hispanic, 32% Hispanic, 26% Other/Unknown. The median BMI was 32.8 kg/m$^2$ with 68% $\geq 30$ kg/m$^2$ consistent with obesity. At baseline, 53% had ALT above the upper limit of normal (ALT $\geq 30$U/L). Forty patients (59%) screened positive for OSA (mean SB = 5 and ESS = 7). There were no differences observed in BMI, ALT, AST, liver stiffness (LF), or CAP scores for patients that screened positive and negative for OSA, however, the group that screened negative for OSA, on average had higher high-density lipoprotein (HDL) (99.1 mg/dL vs 116.9 mg/dL, p = 0.03), low-density lipoprotein (LDL) (91.1 mg/dL vs 116.9 mg/dL, p = 0.03), and cholesterol (176.4 mg/dL vs 200.7 mg/dL, p = 0.01). Compared to patients with no diabetes (DM) (p = 0.015), preDM and DM showed statistically significant increased odds of screening OSA positive (OR = 5.3 [CI: 1.535–18.15]; OR = 4.6 [CI: 1.12–18.80]). Of those referred for formal OSA testing, n = 20 (55%) complied, and n = 17 (85%) patients were subsequently diagnosed with OSA and underwent treatment (mean AHI4 = 19.6/hr). Due to lack of OSA treatment acceptance/adherence, overall impact could not be assessed.

Conclusion: Screening for high risk OSA with a combination of STOP-BANG and ESS was reliable for identifying subjects with OSA confirmed by sleep test. Closer attention to lipid profile and insulin resistance (preDM and DM) were risk factors identified contributing to the diagnosis of OSA. Impact of treatment for OSA needs further evaluation.
Background and aims: Obesity is a leading risk factor for non-alcoholic fatty liver disease (NAFLD), with estimated prevalence rates as high as 50–90%. There is a strong correlation between obesity and hepatocellular carcinoma (HCC), cirrhosis and advanced liver disease. Despite the rising burden of NAFLD in obesity, no concrete guidance exists for screening in this high-risk population. Early detection can facilitate early intervention and development of pathways to specialty care. Herein, we describe the burden of NAFLD in an obese population and affirm the need to proactively assess patients that would otherwise be undiagnosed.

Method: Patients with a diagnosis of obesity (body mass index [BMI] >30 kg/m²) and no documented chronic liver diseases (CLD) were identified using electronic medical record (EMR) from a tertiary care clinic between 01/2019 to 01/2020. Patients who met the criteria for NAFLD (as per AASLD guidelines) were also identified from the same cohort with attention to those who had documentation of NAFLD diagnosis in EMR (ICD-10 codes and review of notes) and those who did not. Demographic information, markers of liver inflammation and synthetic function, medical conditions, imaging and histology were recorded. Fibrosis Index 4 (FIB4) was calculated to determine the stage of liver fibrosis. We reviewed the reason for referrals, differences in the two groups of patients with NAFLD who were and were not diagnosed.

Results: A total of 2999 patients with BMI >30 kg/m² were identified, 586 (20%) had a diagnosis of NAFLD (D-NAFLD) and 1350 had no diagnosis of CLD. One-fifth (268/1350, 20%) of patients without diagnosis of CLD met diagnostic criteria for NAFLD (UD-NAFLD). Baseline characteristics of D-NAFLD and UD-NAFLD were comparable. Majority of UD-NAFLD had normal (<30 IU/L) alanine transaminase (ALT) and aspartate transaminase (AST), 65% and 69% compared to 48% and 60% in D-NAFLD, respectively. Mean AST and ALT were higher in D-NAFLD (38 IU/L and 46 IU/L, respectively) versus UD-NAFLD (33 IU/L and 33 IU/L, respectively). Mean FIB4 was similar, 1.62 and 1.64. FIB4 in the UD-NAFLD group with normal ALT and AST was 1.17 compared to 1.34 in D-NAFLD. Hypertension (55%), coronary artery disease (15%) and diabetes mellitus (30%) were more common in patients in the undiagnosed cohort. Presence of CAD or DM in both groups was associated with a higher FIB4. Majority of patients in D-NAFLD were referred to the specialty clinic for either elevated liver tests (24%), radiographic evidence of steatosis (26%) or both (19%).

Conclusion: We have demonstrated that obesity continues to be an underrecognized risk factor for NAFLD. In our cohort, 20% of patients with obesity had missed diagnosis of NAFLD. Based on current guidelines, 70% of these patients would not have been worked up for NAFLD with normal liver enzymes. NAFLD should be considered as a comorbidity when evaluating patients with obesity.

THU100
Prevalence of non-alcoholic steatohepatitis in patients undergoing laparoscopic cholecystectomy for gallstone with non-alcoholic fatty liver disease
Utpal Anand1,1, Aaron John1, Ramesh Kumar1, Rajeev Priyadarshi2,1 All India Institute of Medical Sciences, Patna, Surgical Gastroenterology, Patna, India; 2All India Institute of Medical Sciences, Patna, Radiodiagnosis, Patna, India

Background and aims: Gallstone disease (GSD) and non-alcoholic fatty liver disease (NAFLD) share common risk factors. Non-alcoholic steatohepatitis (NASH) is a more progressive form of NAFLD and is among the most frequent causes of cirrhosis. There is a lack of prospective studies utilizing liver biopsy during laparoscopic cholecystectomy in patients of gallstones and NAFLD for assessing the prevalence of NASH and factors associated with it. The aim of the study was to assess the usefulness of liver biopsy for patients with gallstones and NAFLD who underwent laparoscopic cholecystectomy.

Method: Among the 250 patients with symptomatic GSD, 55 had associated NAFLD diagnosed by ultrasound. These patients underwent liver biopsy during laparoscopic cholecystectomy between June 2021 to Feb 2022.
Results: The mean age of patients was 41.6 ± 11.69 years and 60% of patients were female. The mean BMI of subjects was 26.43 ± 3.84 kg/m². Eight patients had hypothyroidism, 7 patients had diabetes mellitus, and 6 patients had hypertension as comorbidities. The histopathology of NAFLD patients revealed no significant steatosis in 7 patients. NAFLD in 38 patients and NASH in 10/55 (18.1%). Higher AST (44 ± 22.15 vs 31.5 ± 13.0; p = 0.02) and controlled attenuation parameter (CAP) (294 ± 58.5 vs 202.9 ± 69.6; p < 0.001) were significantly associated with NASH in GSD patients with NAFLD.

Table: Clinical characteristics of NASH and non-NASH patients

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Non-NASH</th>
<th>NASH</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age (years)</td>
<td>40.9 ± 10.6</td>
<td>44.8 ± 12.0</td>
<td>0.34</td>
</tr>
<tr>
<td>Female (%)</td>
<td>31 (68%)</td>
<td>8 (80%)</td>
<td>0.48</td>
</tr>
<tr>
<td>Body mass index (kg/m²)</td>
<td>26.46 ± 3.96</td>
<td>26.33 ± 3.46</td>
<td>0.92</td>
</tr>
<tr>
<td>Laboratory parameters</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>INR</td>
<td>0.97 ± 0.10</td>
<td>0.94 ± 0.07</td>
<td>0.49</td>
</tr>
<tr>
<td>ALT (U/L)</td>
<td>31.3 ± 17.9</td>
<td>40.8 ± 24.67</td>
<td>0.18</td>
</tr>
<tr>
<td>AST (U/L)</td>
<td>31.5 ± 13.0</td>
<td>44 ± 22.15</td>
<td>0.02*</td>
</tr>
<tr>
<td>ALP (U/L)</td>
<td>88 (72.5–102)</td>
<td>76.5 (74–84.5)</td>
<td>0.23</td>
</tr>
<tr>
<td>Total bilirubin (mg/dL)</td>
<td>0.61 (0.45–0.8)</td>
<td>0.75 (0.48–0.94)</td>
<td>0.23</td>
</tr>
<tr>
<td>Albumin (g/dL)</td>
<td>4.09 ± 0.37</td>
<td>4.10 ± 0.32</td>
<td>0.93</td>
</tr>
<tr>
<td>Cholesterol (mg/dL)</td>
<td>164.9 ± 36.64</td>
<td>169.22 ± 33.89</td>
<td>0.73</td>
</tr>
<tr>
<td>Triglyceride (mg/dL)</td>
<td>137.24 ± 60.9</td>
<td>146.8 ± 24.67</td>
<td>0.18</td>
</tr>
<tr>
<td>HDL (mg/dL)</td>
<td>39.08 ± 11.08</td>
<td>42.78 ± 6.53</td>
<td>0.31</td>
</tr>
<tr>
<td>CAP</td>
<td>202.9 ± 69.6</td>
<td>294 ± 58.5</td>
<td>&lt;0.001*</td>
</tr>
<tr>
<td>LSM (kPa)</td>
<td>5.3 ± 1.8</td>
<td>6.1 ± 1.8</td>
<td>0.19</td>
</tr>
</tbody>
</table>

Conclusion: The high prevalence of NASH in patients of GSD with NAFLD may justify the need of routine liver biopsy during laparoscopic cholecystectomy in these patients.

THU101

Lack of awareness of NAFLD pandemic in a high risk group. Is it time to act in primary care?

Maria Guerra Veloz1, Kosh Agarwal1, Marck Chamley2, Saima Ajaz1.
1Institute of Liver Studies. King’s College Hospital, London, United Kingdom; 2Partner, North Wood GP Practice, Lambeth Diabetes Intermediate Care Team, United Kingdom
Email: maria.guerraveloz@nhs.net

Background and aims: Non-alcoholic fatty liver disease (NAFLD) includes a wide spectrum of conditions and is currently the leading cause of chronic liver disease. NAFLD is intrinsically associated with obesity and is particularly common in people with type 2 diabetes (T2D) with a prevalence ranging from 70 to 80%. As NAFLD is mostly a silent disease, early diagnosis and the accurate staging of fibrosis is crucial for patients who are at risk. The complex relationship between NAFLD and T2D, the risk of cardiovascular disease, raises the question of the cost effectiveness of screening for NAFLD in the general population. With current guidelines discouraging screening in the general population, early recognition and intervention are important in high-risk groups in order to improve clinical outcomes. The aim of our project was to evaluate the awareness of NAFLD knowledge, the prevalence of NAFLD, and the prevalence of advanced fibrosis in patients with T2D who regularly attend a secondary diabetes clinic.

Method: Patients with T2D that have a regular follow-up at the Lambeth Diabetes Intermediate Care Centre were invited to participate in the NAFLD screening using a Fibroscan. A structured diet, exercise activity and NAFLD knowledge questionnaires were provided by a liver doctor to all patients that agreed to participate in this project. Anthropometric measures, medical history, LSM and CAP were recorded for each patient. The presence of steatosis was defined with a CAP cut off ≥ 275 dB/m and advanced fibrosis ≥ 8kpa.

Results: We screened 90, 47.3% were male with a median age of 59 years (IQR 52 – 66), most were of black African descent 55.6% (50) with a median BMI of 31.8 kg/m² (26 – 37). Comorbidities, such as hypertension, coexisted in 61.1% and 58.9% had dyslipidaemia. (Baseline characteristics Figure 1)

The Fibroscan data was valid in 96.7% (87), 56.3% (49/87) had steatosis and 27.6% (24/87) had advanced fibrosis. 14.4% (13) were aware of NAFLD/NASH, 33.3% were aware that they were overweight or obese and 88.9% stated that they had received guidance about having a healthy lifestyle. Of the patients who were not aware of NAFLD (85.6%), 58% of these had steatosis and those who were not aware of being overweight/obese (66.7%), 40.6% of these were overweight and 25% were obese. 38% of patients who had steatosis and 47.8% who had advanced fibrosis were on GLP-1 analogue (24.4% of all patients).

Conclusion: T2D patients are mostly unaware of this silent epidemic, and so do not recognise themselves as being overweight/obese, which is intrinsically linked with NAFLD. Preliminary data suggests that the screening of NAFLD in patients with T2D can yield important information regarding the prevalence of advanced fibrosis and factors affecting the progression of NAFLD in this multi-ethnic high-risk group. It is particularly important to screen the patients who are already in our healthcare system due to other pre-existing conditions.
Non-alcoholic fatty liver disease and type 2 diabetes: low referral rate of patients at increased risk of progressive liver disease

Lucy Gracen1,2, Kelly Hayward1,2, Melanie AIkebuse1,2, Anthony Russell3,4, James O’Beirne5, Katharine Irvine6, Suzanne Williams7, Patricia Valera8, Elizabeth Powell1,2, Princess Alexandra Hospital, Gastroenterology and Hepatology, Woolloongabba, Australia; 2Translational Research Institute, The University of Queensland, Centre for Liver Disease Research, Faculty of Medicine, Woolloongabba, Australia; 3Princess Alexandra Hospital, Department of Endocrinology, Woolloongabba, Australia; 4The University of Queensland, Centre for Health Services Research, Faculty of Medicine, Saint Lucia, Australia; 5Sunshine Coast University Hospital, Gastroenterology and Hepatology, Birtinya, Australia; 6Translational Research Institute, Mater Research, Woolloongabba, Australia; 7Inala Primary Care, Inala, Australia; 8QIMR Berghofer Medical Research Institute, Herston, Australia

Email: lucy.gracen@hotmail.com

Background and aims: Routine assessment of liver fibrosis in people with non-alcoholic fatty liver disease (NAFLD) is recommended. The aim of this study was to determine whether a community-based NAFLD diagnosis, risk-stratification and referral pathway for people with type 2 diabetes (T2D) provides targeted detection of advanced fibrosis and appropriate referral to liver clinics.

Method: People with T2D were screened for NAFLD when they attended a diabetes clinic appointment in the community, using FibroScan (VCTE) as a point-of-care test to assess steatosis (CAP score ≥248) and fibrosis (liver stiffness measurement, LSM). A letter to participants’ general practitioners (GPs) provided the LSM result and guidance on appropriate management/follow-up of their patients in primary care, as well as investigation of abnormal liver enzymes. Referral to a liver clinic was advised if LSM ≥8.0 kPa. Patients were advised to discuss their liver health and FibroScan result with their GP. A monthly audit of GP referrals to liver clinics was provided by the central referral hub to assess whether GPs pursued the recommended referral.

Results: To date, 129 people with T2D (61.9% male, 58.8 ± 9.7 years) were assessed and VCTE met quality criteria in 126 (97.7%). Referral to a liver clinic for further assessment was advised for 28 (22.2%) patients with LSM ≥8.0 kPa and 8 patients with other indications (Figure). 68 (54.0%) of 126 patients had abnormal liver function tests and 13 (10.3%) had LSM ≥12.0 kPa suggestive of advanced chronic liver disease (CLD). 34 (27.0%) of 126 patients had a prior ultrasound (US) of which two-thirds (n = 23) showed steatosis and 2 had clear signs of CLD. None of these patients had been referred for fibrosis assessment reflecting the need to embed this in routine clinical pathways. A greater proportion of people with LSM ≥8 kPa had a prior US compared to those with LSM ≤8 kPa (46.4% vs. 21.4%, p = 0.009), suggesting GPs are identifying patients that need investigation but not pursuing further management. A GP referral was received for 13 (36.1%) of the 36 patients with a recommendation for referral.

Conclusion: VCTE as a point-of-care test provides a well-validated real-time assessment of liver fibrosis as well as steatosis and allows for timely delivery of the diagnosis and fibrosis risk category (low or increased risk) to the patient’s healthcare team. The high detection rate of people requiring specialist assessment supports this screening approach. However the low GP referral rate in a cohort at increased risk of progressive liver disease calls attention to the need for improved education, guidelines and referral pathways for NAFLD to embed fibrosis assessment in the patient workflow.

Hypertension and diabetes mellitus are associated with high FIB-4 index in a health checkup examination cohort without known liver disease

Shunsuke Sato1, Hidehiko Kawai2, Sho Sato1, Hirohiko Iwasaki2, Yuji Kita1, Yuji Ikeda1, Ayato Murata1, Yuji Shimada1, Takuya Genda1, Juntendo University Shizuoka Hospital, Gastroenterology and Hepatology, Shizuoka, Japan; 2Fujiu Town Medical Center, Shizuoka, Japan

Email: syusato@juntendo.ac.jp

Background and aims: Non-alcoholic fatty liver disease (NAFLD) is usually asymptomatic and lacks a specific biomarker; therefore, many individuals might remain undiagnosed even with advanced liver fibrosis. The aim of this study was to clarify the prevalence and clinical features of subjects with a high risk of advanced liver fibrosis in the general population, using the FIB-4 index.

Method: We retrospectively investigated 6,183 subjects without known liver disease who had participated annual health checkup examination. We analyzed the factors associated with high FIB-4 index (≥2.67) using a logistic regression analysis.

Results: Among 6,183 subjects, 76 (1.2%) had high FIB-4 index. Multivariate analysis identified hypertension (odds ratio [OR] = 8.926; 95% confidence interval [CI] 4.031–19.768; P < 0.001) and diabetes mellitus (OR = 4.045; 95% CI 1.694–9.660; P = 0.002) as important risk factors for high FIB-4 index. The rates of hypertension and diabetes mellitus in subjects with high FIB-4 index were 78.9% and 23.7%, respectively. No significant association was observed between obesity or large waist circumference and a high FIB-4 index. A history of cardiovascular disease was significantly more common in subjects with high FIB-4 index. These results were also observed in the subjects with normal aminotransferase (ALT) levels.

Conclusion: The present study revealed that approximately 1% of the general Japanese population has a high risk of advanced liver fibrosis. Many of these patients had hypertension and/or diabetes mellitus. The findings suggest that there are many undiagnosed NAFLD patients with risk of advanced liver fibrosis in the general population.

Statins, but not aspirin, reduce the risk of hepatocellular carcinoma and mortality in Danish patients with cirrhosis due to alcohol-related liver disease: a nationwide causal study

Frederik Kraglund1, Diana Hedevang Christensen2, Peter Jeppsen1.

1Aarhus University Hospital, Department of Hepatology and Gastroenterology, Aarhus, N, Denmark; 2Aarhus University Hospital, Department of Clinical Epidemiology, Aarhus, N, Denmark

Email: frekra@clin.au.dk

Background and aims: Observational studies have shown a strong association between use of statins or aspirin and a lower risk of hepatocellular carcinoma (HCC). We emulated a trial assessing the causal link between statin and aspirin use and HCC development and mortality in Danish patients with cirrhosis due to alcohol-related liver disease (ALD cirrhosis).

Method: Using nationwide Danish healthcare registries, we identified all patients diagnosed with ALD cirrhosis, 2000-2018. We determined their statin and aspirin use through reimbursed prescriptions. A target trial was designed in which patients were randomised to initiate and adhere to statins (and, in a separate analysis, aspirin) or to not initiate treatment. The primary end point

Figure: Proportion of patients with type 2 diabetes recommended for referral to liver clinic following FibroScan assessment. Circles proportionate to group size; liver function tests (LFTs).
was HCC development, and the secondary end point was death without HCC. The target trial was emulated using inverse probability of treatment and censoring weights to create a marginal structural model adjusted for comorbid diseases, prescription drugs, procedures, hospital contacts, and prior use of statins among other covariates. Based on this model we estimated the average treatment effect (ATE) of statin use (and aspirin use) on the cumulative risk of HCC and of death without HCC.

Results: Of 16,811 patients with ALD cirrhosis, 4,540 used statins at some point during follow-up, 4,647 used aspirin, and 899 were diagnosed with HCC. The ATE of statin use was 0.74 (95% confidence interval [CI] 0.47 to 1.02) for HCC and 0.77 (95% CI 0.70 to 0.83) for death without HCC. The ATE of aspirin use was 1.08 (95% CI 0.73 to 1.44) for HCC and 1.10 (95% CI 1.02 to 1.19) for death without HCC. The cumulative HCC incidence functions and corresponding relative risk estimates reflected the ATEs (Figure).

Conclusion: Statin use reduces the risk of HCC and death without HCC in patients with ALD cirrhosis. Conversely, aspirin use does not reduce the risk of either HCC or death without HCC in patients with ALD cirrhosis. Thus, statins, but not aspirin, likely have a chemopreventive effect in patients with ALD cirrhosis. While we wait for truly randomized studies, studies such as ours provide the strongest possible evidence in favour of statins.

Figure: (abstract: THU104)

**Gut microbiota and liver disease**

**THU151**

Altered fecal microbiome and metabolome in hepatitis B related chronic liver diseases

Wei Jiang¹, Yue Shen¹, Wu ShengDi¹, Jian Wu²,²,². Zhongshan Hospital, Fudan University; Shanghai Institute of Liver Diseases, Department of Gastroenterology and Hepatology, Xuhui District, Shanghai, China; Fudan University Shanghai Medical College, Dept. of Medical Microbiology and Parasitology, MOE/NHC/CAMS Key Laboratory of Medical Molecular Virology, School of Basic Medical Sciences, Shanghai, China

Email: jiang.wei@zs-hospital.sh.cn

Background and aims: It is well accepted that microbiota is a major modulator of liver diseases and is associated with severe clinical outcomes. However, the influence of gut dysbiosis on chronic hepatitis B (CHB) progression as well as the interplay between microbiota shift and antiviral treatment remains to be clarified. The present study aims to provide a comprehensive profile of gut microbiome and metabolomics in CHB patients at different disease stages. Taking advantage of a cohort of CHB patients with entecavir
therapy for five years, influence of antiviral treatment on the characteristics of microbial composition and function in CHB patients was investigated.

**Method:** Fecal samples from subjects with CHB (n = 64) and healthy controls (n = 17) were sequenced with 16S rRNA analysis. Fecal metabolomics was measured via untargeted LC-MS in subgroups of 58 subjects (Fig. 1A).

**Results:** Compared to healthy controls, community richness, diversity and evenness of gut microbiota were decreased during CHB progression (Fig. 1B and 1C). Overall gut microbial community was shifted (Fig. 1D). Four genera: Faecalibacterium, Streptococcus, Sutterella and Ruminiclostridium were enriched in CHB patients. Eight genera including Blautia, Escherichia-Shigella, Klebsiella, Bifidobacterium, Parasutterella, Eubacterium hallii group,
Collinsella and Lactococcus were found to decrease, accompanying with 206 metabolites statistically different in abundance. Importantly, distinct patterns of microbiota composition and metabolic activity were identified in subgroup analysis based on disease stages and the presence of antiviral treatment (Fig. 2 and 3). It was demonstrated that there was a potential association between microbial or metabolic signatures and clinical characteristics (Fig. 4). Notably, disease-enriched genera Streptococcus and metabolite 20-hydroxy-leukotriene E4 were negatively correlated with albumin (ALB) and positively with direct bilirubin (DB). Concordant depletion of Turicibacter and Adlercreutzia accompanying with 4-hydroxyretinoic acid tended to correlate with elevated AST and DB in CHB patients. Potential links between clinical parameters and restored genera or metabolites in CHB patients receiving antiviral treatment were detected. In particular, concordant increase of Ruminococcaceae_UCG-013 and sebacic acid was positively correlated with ALB, suggesting that novel host-microbial interplay was involved in the antiviral treatment of CHB patients.

Figure 2:

Conclusion: Microbiome and metabolomics analysis was integrated to provide a comprehensive profile of gut dysbiosis characterized by microbial and metabolic alterations in CHB patients. CHB progression and antiviral treatment significantly contributed to the imbalance of gut microbial community and metabolomics profiles in this study.
Background and aims: Lactobacillus is considered a potential probiotic and has shown therapeutic potential for several liver diseases including non-alcoholic fatty liver disease (NAFLD). However, it is not known how dietary supplementation of L. plantarum has favoring effect on liver. Therefore, we investigated the therapeutic potential of L. plantarum supplementation on NAFLD in a mouse model and aimed to elucidate its mechanism.

Method: We used the choline-deficient high fat diet (CD-HFD)-induced murine model that recapitulates key features of human metabolic syndrome. To induce NASH status, C57BL/6N mice were fed a CD-HFD for 30 weeks. Then these mice were divided into three groups: vehicle, L. plantarum (10⁹ CFU/day), and empagliflozin, selective SGLT2 inhibitor (10 mg/kg/day). After 12 weeks of treatment, mice were sacrificed and subjected to blood measurements, and liver tissue for RNA isolation, lipid measurements, histology, and stool for microbiome analysis.

Results: L. plantarum and empagliflozin treatment significantly improved several metabolic phenotypes such as insulin tolerance, and hepatic lipid contents compared to vehicle group, respectively. However, the histological NAFLD activity score (NAS) was more improved in the L. plantarum group (3.0, p = 0.0286) than in the empagliflozin group (4.0, p = 0.0591) compared to vehicle group (5.5).

RNA-sequencing analysis revealed that administration of L. plantarum downregulated genes related to inflammation such as T cell differentiation and leukocyte activation in liver. In the microbiobial analysis of stool samples, the elevated Firmicutes-to-Bacteroidetes ratio in the vehicle group (21.97) was decreased in the L. plantarum group (0.86). Furthermore, disrupted intestinal epithelial barrier function was restored in L. plantarum group and elevated serum endotoxin level was significantly reduced in L. plantarum group compared to vehicle group.

Conclusion: Our data demonstrated that administration of L. plantarum can improve NAFLD associated phenotypes by altering gut microbiome composition and decreasing serum endotoxin levels.
Conclusion: Stool microbiota are more extensively linked with systemic metabolites than saliva microbiota, irrespective of cirrhosis severity and country. These changes are more prominent in Decomp and are centered around plasma lactate, which might be related to interaction of diet and lactulose therapy. Stool microbiota have a greater functional footprint associated with the systemic milieu compared to salivary microbiota.

THU154

The gut virome in non-alcoholic fatty liver disease: distinct changes in Phapecoctavirus composition in a human microbiota associated animal model

Hau-Tak Chau1, Hein Tun2, Saisai Zhang1, Dengwei Zhang2, Fung Yu Huang1, Lung Yi Loey Mak1, 3, Man-Fung Yuen1, 3, Wai-Kay Seto1,3, Hau-Tak Chau1, Hein Tun2, Saisai Zhang1, Dengwei Zhang2, Fung Yu Huang1, Lung Yi Loey Mak1, 3, Man-Fung Yuen1, 3, Wai-Kay Seto1,3, 1The University of Hong Kong, Hong Kong, Department of Medicine, Hong Kong; 2The University of Hong Kong, Hong Kong, School of Public Health, Hong Kong; 3The University of Hong Kong, Hong Kong, State Key Laboratory of Liver Research, Hong Kong

Email: wkseto@hku.hk

Background and aims: There is increasing knowledge on the role of the gut microbiome in the development of non-alcoholic fatty liver disease (NAFLD), but the role of the gut viral community in disease development remains poorly understood. We aimed to discover gut virome related to NAFLD development via a human-microbiota-associated (HMA) rodent model of NAFLD.

Method: Human fecal donors were recruited and classified into obese NAFLD, non-obese NAFLD and non-obese healthy controls. Liver steatosis was assessed by vibration-controlled transient elastography (Fibroscan, Echosens, Paris). The HMA-NAFLD rodent model was established by high-fat diet and transplantation of human fecal microbiota (FMT) for 12 weeks. The profile of the gut virome of both human donors and rodents was assessed by shotgun metagenomic sequencing (Illumina NovaSeq 6000, US).

Results: Human donors with NAFLD had a significantly higher controlled attenuation parameter measurement when compared to healthy controls (median 324 [IQR 305.5–355.75] vs. 182.5 [179.25–199.25] dB/m, p <0.001). Based on Bray-Curtis distance and PERMANOVA testing, human NAFLD donors had a distinct gut DNA virome compared with healthy controls (p = 0.04). Analysis via linear discriminant analysis (LDA) effect size method identified the Phapecoctavirus genus as a potential biomarker (LDA score 3.80), indicating a lower median relative abundance of Phapecoctavirus in NAFLD donors when compared to healthy donors (3.54% [IQR 2.93–3.98%] vs. 4.15% [3.94–4.94%], p = 0.038). As a putative host for Phapecoctavirus, the abundance of Escherichia coli was negatively associated with Phapecoctavirus (rho = −0.51, p = 0.012). In the animal model, mice receiving FMT from obese NAFLD (FMT-ON) displayed a more severe NAFLD phenotype than those receiving FMT from healthy control (FMT-NC) (liver triglyceride: median 65.35 [IQR 62.32–73.33] vs. 48.7 [38.61–54.44] mg/g liver tissue, p = 0.015; blood triglyceride: 207.89 [187.87–216.94] vs. 110.05 [102.16–120.76] mg/dL, p <0.001). Phapecoctavirus genus was similarly identified as a potential fecal biomarker when comparing FMT-ON vs. FMT-NC (LDA score 3.19). It was the only viral genus that distinguished NAFLD from control in both human donors and mouse recipients. FMT-ON mice with more severe NAFLD had a significantly lower level of fecal Phapecoctavirus than FMT-NC mice (median 2.47% [IQR 2.39–2.75%] vs. 2.82% [2.6%–3.14%], p = 0.038).

Conclusion: We reported the association of reduced fecal Phapecoctavirus with NAFLD in both human donors and HMA-mice recipients. Further interventional studies in animal and human are warranted to determine its potential causality and function in NAFLD.

THU155

Mitochondrial hyperactivation determines a transferable protective gut microbiota profile in metabolic-associated fatty liver disease development

María Juárez-Fernández1, Naroa Goikoetxea2, David Porras1, María-Victoria García-Mediavilla1,3, Héctor Rodríguez4, Esther Nistal1,3, Susana Martínez-Flórez1, Mercedes Rincón2, Marta Varela-Rey2, Javier González-Gállego1,3, Leticia Abejia1,5, Juan Anguita1,6, María Luz Martínez-Chantar1,3, Sonia Sánchez-Campos1,3, Instituto de Biomedicina (IBIOMED) University of León, Spain; 2Liver Disease laboratory, CIC bioGUNE, Centro de Investigación Biomédica en Red de Enfermedades Hepáticas y Digestivas (CIBERehd), Spain; 3Centro de Investigación Biomédica en Red de Enfermedades Hepáticas y Digestivas (CIBERehd), ISCIII, Spain; 4Inflammation and Macrophage Plasticity laboratory, CIC bioGUNE, Spain; 5University of Vermont, Department of Medicine and Immunobiology, College of Medicine, Burlington, United States; 6Ikerbasque, Spain

Email: ssanc@unileon.es

Background and aims: Mitochondrial dysfunction plays a key role in metabolic-associated fatty liver disease (MAFLD). Methylation-controlled J protein (MCJ) is a negative regulator of mitochondrial complex I. Its deletion increases mitochondrial activity and reduces diet or hepatotoxic drug-induced lipid accumulation and hepatic damage. The study aims to determine the microbiome signature associated to MCJ deficiency and its capacity to transfer its protective gut microbiota profile in metabolic-associated fatty liver disease development.

Method: Wild type (WT) and MCJ-KO C57BL/6J mice were fed with a diet or hepatotoxic drug-induced lipid accumulation and hepatic damage. Stool microbiota have a greater functional footprint associated with the systemic milieu compared to salivary microbiota.

Results: CDA-HFD during 6 weeks induced an inflammatory and fibrotic state compatible with steatohepatitis development. MCJ-KO mice showed a lower liver expression of inflammatory and fibrotic markers. This effect was reproduced in FGM colonized with caecal microbiota transplantation.

Conclusion: We reported the association of reduced fecal Phapecoctavirus with NAFLD in both human donors and HMA-mice recipients. Further interventional studies in animal and human are warranted to determine its potential causality and function in NAFLD.

THU155

Mitochondrial hyperactivation determines a transferable protective gut microbiota profile in metabolic-associated fatty liver disease development

María Juárez-Fernández1, Naroa Goikoetxea2, David Porras1, María-Victoria García-Mediavilla1,3, Héctor Rodríguez4, Esther Nistal1,3, Susana Martínez-Flórez1, Mercedes Rincón2, Marta Varela-Rey2, Javier González-Gállego1,3, Leticia Abejia1,5, Juan Anguita1,6, María Luz Martínez-Chantar1,3, Sonia Sánchez-Campos1,3, Instituto de Biomedicina (IBIOMED) University of León, Spain; 2Liver Disease laboratory, CIC bioGUNE, Centro de Investigación Biomédica en Red de Enfermedades Hepáticas y Digestivas (CIBERehd), Spain; 3Centro de Investigación Biomédica en Red de Enfermedades Hepáticas y Digestivas (CIBERehd), ISCIII, Spain; 4Inflammation and Macrophage Plasticity laboratory, CIC bioGUNE, Spain; 5University of Vermont, Department of Medicine and Immunobiology, College of Medicine, Burlington, United States; 6Ikerbasque, Spain

Email: ssanc@unileon.es

Background and aims: Mitochondrial dysfunction plays a key role in metabolic-associated fatty liver disease (MAFLD). Methylation-controlled J protein (MCJ) is a negative regulator of mitochondrial complex I. Its deletion increases mitochondrial activity and reduces diet or hepatotoxic drug-induced lipid accumulation and hepatic damage. The study aims to determine the microbiome signature associated to MCJ deficiency and its capacity to transfer its hepatoprotective phenotype to germ-free (GF) mice through caecal microbiota transplantation.

Method: Wild type (WT) and MCJ-KO C57BL/6J mice were fed with a control or a choline-deficient high fat diet (CDA-HFD) for 6 weeks. Then, a donor mouse from each experimental group was selected based on MAFLD development parameters. GFm were colonized with caecal microbiota from donors and subjected to dietary intervention (C or CDA-HFD) for 3 weeks. After that, samples were collected and processed for assessment of liver disease and gut microbiota composition.

Results: CDA-HFD during 6 weeks induced an inflammatory and fibrotic state compatible with steatohepatitis development. MCJ-KO mice showed a lower liver expression of inflammatory and fibrotic markers. This effect was reproduced in FGM colonized with microbiota from MCJ-KO donors and fed with CDA-HFD. Metagenomic analysis revealed a profound reshaping of gut microbiota due to the diet, but also changes in specific bacterial
taxa attributed to MCJ-KO genotype. *Dorea* and *Oscillospira* genera were increased, while *AF12*, *Allobaculum* and *Ruminococcus* were decreased. This microbiota profile was also observed in GFm following microbiota transplantation, highlighting an increase in the abundance of the genus *Dorea* in all groups colonized with microbiota of MCJ-KO mice. Finally, MCJ-KO mice fed with CDA-HFD showed a higher hepatic and intestinal production of nicotinamide-adenine dinucleotide (NAD), likewise a higher expression of its synthesis enzymes. These results were reproduced in GFm transplanted with MCJ-KO microbiota.

**Conclusion:** The protective effect of MCJ deficiency on MAFLD progression implies a mitochondrial hyperactivation mechanism associated to a higher NAD production capacity, that determines a gut microbiota profile, which is transferred by transplantation to GFm. Supported by BRFU2017–87960-R, PID2020–120363RB–10, GRS2126/A/2020, LE017–P20. CIBERehd is funded by ISCIII.

**THU156**

Fecal transplant-related reductions in Alcohol intake from human to mice are associated with alterations in the intestinal but not liver or prefrontal cortex transcriptome

Jennifer Wolstenholme1, Maren Smith1, Ryan Balfour Sartor2, Javier Maeso-Gonzalez1, Derrick Zhao1, Huiping Zhou1, Jason Kang1, Phillip Hylemon1, Jasmohan S Bajaj1. *Virginia Commonwealth University and Richmond VA Medical Center; *UNC Chapel Hill Email: jasmohan.bajaj@vcuhealth.org

**Background and aims:** In a recent randomized placebo-controlled trial in men with cirrhosis, we found that fecal microbiota transplant (FMT) reduced alcohol craving and consumption compared to placebo. We found that transmitting stool post-FMT but not pre-FMT to germ-free mice (GF) reduces alcohol drinking but the metabolic pathways associated with this reduction are unclear. Aim: determine the genes activated along the gut-liver-brain axis after stool transfer into mice.

**Method:** To test whether FMT can act as a therapy to reduce craving, mice were gavaged with fecal microbiota material from the same pts after FMT (post-FMT). Initial ethanol acceptance, intake and preference were measured using a 2-bottle choice ethanol drinking assay. A bottle of ethanol (20% v/v) and water were placed on each mouse’s cage and readings were taken at 2 (binge), 24 and 48 hours. Intestinal mucosa, liver and prefrontal cortex (PFC) were harvested 18 hours post-alcohol. RNASeq was run on 6 mice that drank the most in each group. 16S rRNA sequencing (V3-V4) and analyzed using QIIME2.

**Results:** DEGs were in the intestine (Fig D) with only 1/20th of genes upregulated in the liver (Fig E-G). Specifically, 500 genes were upregulated in the intestine post-FMT whereas only 25 were upregulated in the liver post-FMT. Overrepresented KEGG pathways were focused on TGFβ signaling and underlines the role of the gut in the modulation of behavior that is transmissible from humans.

**Conclusion:** FMT from humans, through a successful trial, leads to lower alcohol intake in GF mice colonized with post-FMT stools through significant changes in intestinal genes rather than liver or prefrontal cortex. Changes in gut immune-inflammatory response after FMT could strengthen the gut barrier and reduce gut-liver-brain signaling and underlines the role of the gut in the modulation of behavior that is transmissible from humans.

**THU157**

New insights from mapping of the mucosal gut microbiota in primary sclerosing cholangitis before and after liver transplantation

Mikal Jacob Hole1, Kristin Jorgensen1,2, Kristian Holm1, Malin Holm Meyer-Myklestad2, Asle Wilhelm Medhus1, Dag Henrik Reikvam1, Alexandra Götz3, Krzysztof Gryzb5, Kirsten Muri Boberg1, Tom Hemming Karlsen4, Martin Kumm1, Johannes R. Hov5. *1Oсло University Hospital and University of Oslo, Norwegian PSC Research Center, Department of Transplantation Medicine; 2Akershus University Hospital, Department of gastroenterology; 3Oсло University Hospital and University of Oslo, Department of infectious diseases; 4Oсло University Hospital, Department of gastroenterology; 5Oсло University Hospital, Division of pathology*

Email: m.j.hole@studmed.uio.no

**Background and aims:** The fecal microbiota in primary sclerosing cholangitis (PSC) is characterized by low diversity and increased relative abundance of Veillonella, while data on the mucosal microbiota are inconsistent. No particular microbiota features have been linked to the presence of PSC-LT, and little is known about the impact of recurrent PSC (rPSC-LT) after liver transplantation (LT). We aimed to investigate the mucosal microbiota in PSC and utilize rPSC-LT to define consistent microbiota features associated with PSC irrespective of transplantation.

**Method:** We included 84 PSC and 51 PSC-LT patients (of which 25/51 [49%] had or developed rPSC median 5.0 years after LT) with biopsies available from at least two ileocolonic segments. 19 healthy controls (HC) were included for comparison. Biopsy DNA was subjected to 16S rRNA sequencing (V3-V4) and analyzed using QIME2.

**Results:** Mucosal gut expansion of Proteobacteria was more pronounced in PSC-LT (up to 19%) than in HC (up to 11%), compared to only ∼5% in HC (QFDR <0.05). A limited set of genera was significantly associated with PSC both before (PSC compared with HC) and after LT (rPSC-LT compared with PSC-LT). This set consisted of *Bilophila*, *Eubacterium hallii* and two different *Lachnospiraceae*, which had reduced relative abundance in PSC, and *Enterococcus*, *Streptococcus*, *Eisenbergiella* and *Hungatella*, which had increased abundance in PSC.
Alpha diversity was reduced (p < 0.05) and Veillonella was significantly increased in PSC and PSC-LT compared to HCs, but did not separate rPSC-LT from PSC-LT. Concomitant IBD was associated with significantly reduced relative abundance of Akkermansia, irrespective of LT, ranging from 0.8–1.0% to 4.5–5.6% mean relative abundance. The potential pathobiont Klebsiella was detected in the mucosa in at least one segment in 18% of the patients before and 41% after LT (p < 0.05) and associated with significantly reduced transplantation- and recurrence-free survival.

**Conclusion:** Liver transplantation does not normalize potentially disease-related microbiota features. Multiple bacterial genera associated with both PSC and rPSC-LT, and Akkermansia associated with PSC-IBD irrespective of transplantation status. Furthermore, Klebsiella associated with poor outcome both before and after liver transplantation.

**THU158**

**Designing a polymetabolic risk score for non-alcoholic steatohepatitis patients by differentiating their metabolic profiles from healthy controls**

Nadeen Habboub1,1, Pinelopi Manousou1, Roberta Forlano1, Benjamin H. Mullish1, Gary Frost1, Benjamin Chalilis2, Mark Thrusz1, Marc-Emmanuel Dumas1,3, 1Imperial College London, Metabolism, Digestion and Reproduction, London, United Kingdom; 2AstraZeneca, Science and Experimental Medicine, Cambridge, United Kingdom; 3Imperial College London, Heart and Lung Institute, London, United Kingdom

**Background and aims:** The gut microbiome plays a role in the pathogenesis of non-alcoholic fatty liver disease (NAFLD) and its progression to non-alcoholic steatohepatitis (NASH). Studies have shown that changes in gut microbiota result in increased intestinal permeability, facilitating the translocation of bacteria and gut microbiome-modulated metabolites to the liver, inciting NASH. Our aim is to investigate the differences in metabolic profiles of NASH patients in comparison to healthy controls. We designed a metabolic profile scoring model based on plasma $^1$H-NMR metabolic data which could distinguish NASH/NAFLD patients from healthy individuals.

**Method:** Biopsy-proven NASH patients (n = 55) were recruited from St Mary’s Hospital and were compared to controls (n = 677), selected from the AIRWAVE population study by excluding the clinical characteristics of metabolic syndrome. Metabolic profiling of non-fasted plasma and urine samples were carried out by $^1$H-NMR spectroscopy and UPLC-MS using HILIC and C18 reverse-phase columns. Untargeted and targeted $^1$H-NMR metabolic profiles of plasma samples from both cohorts were examined by multivariate analysis for signature variation and scoring.

**Results:** We have demonstrated distinct differences in the plasma $^1$H-NMR metabolic profiles of NASH patients and healthy controls. Multivariate models of the $^1$H-NMR data showed a significant separation between the controls and NASH patients’ clusters ($R^2$ >0.6, $Q^2$ >0.6, pR$^2Y$ <0.001, pQ$^2$ <0.001). The polymetabolic risk score was computed using the O-PLS-DA model of the untreated $^1$H-NMR metabolic profiles of the controls and NASH patients.

**Conclusion:** We have shown that the $^1$H-NMR plasma metabolic profiles of NASH patients and healthy controls are significantly distinctive, which allowed for the construction of a polymetabolic risk-score to separate and distinguish these groups, demonstrating potential for interventions based on the metabolome.

**THU159**

**Intestinal hyperpermeability in cirrhosis is predictive for survival and associated with distinct microbiome changes**

Rosa Haller1, Benard Aliva1,2, Angela Horvath1, Vanessa Stadlbauer1,3, 1Medical University of Graz, Department of Gastroenterology and Hepatology, Graz, Austria; 2University of Nairobi, Department of Food Science, Nutrition and Technology, Nairobi, Kenya; 3Gumed Center of Biomarker Research in Medicine, Area Microbiome Research, Graz, Austria

**Email:** vanessa.stadlbauer@medunigraz.at

**Background and aims:** Liver cirrhosis, the 10th most common cause of death in the western world is associated with increased intestinal permeability and alterations of gut microbiome composition. It is however not fully understood how intestinal permeability and the microbiome are interrelated in cirrhosis. We aim to investigate the potential of gut permeability biomarkers to predict mortality and their relation to microbiome composition.

**Method:** Stool, serum and urine samples from 78 cirrhotic patients (56±9 years, 22 female) were obtained at baseline and after six months; survival was assessed after 24 months. Intestinal permeability was assessed by zonulin in stool and diamine oxidase (DAO) in serum. Kaplan-Mayer survival analysis, group comparisons and correlation analysis (Spearman) were performed. Gut microbiome 16s rRNA sequencing data were analyzed by diversity metrics, ANCOM and LEfSe.

**Results:** Neither DAO nor zonulin at baseline were able to predict mortality, but when assessing the dynamics over 6 months, patients whose zonulin levels worsened or did not change (ZWOR, n = 45) had a higher mortality than those whose zonulin levels improved (ZIMP, n = 33) (log rank Mantel-Cox p = 0.048). ZWOR patients did not differ in etiology from ZIMP patients but had significantly worse international normalized ratio (p = 0.021) levels, and MELD score at baseline (p = 0.032). Microbiome composition (alpha- and beta diversity) did not differ between ZWOR and ZIMP patients. The genus Phascolarctobacterium was more abundant in ZIMP patients with both ANCOM and LEfSe. The relative abundance of Phascolarctobacterium correlated negatively with calprotectin in stool and sCD14 in serum as biomarker for intestinal inflammation and bacterial translocation.

**Conclusion:** Worsening of zonulin levels in over 6 months predicted mortality in patients with liver cirrhosis, indicating that serial assessments of this biomarker improve predictive power in cirrhosis. The genus Phascolarctobacterium was more abundant in ZIMP patients and correlated negatively with markers for intestinal inflammation and bacterial translocation. Phascolarctobacterium can produce short-chain fatty acids and upregulate the miRNA expression of Claudin-1, a tight junction protein, indicating a possible link between the microbiome and intestinal hyperpermeability.

**THU160**

**Novel multi-technology meta-analysis identifies gut microbiome strains associated with clinical fibrosis in NAFLD patients**

Nicole Narayan1, Erica Rutherford2, Karim Dabbagh1, Arun Sanyal1, Todd Z. DeSantis1, 1Second Genome, Brisbane, United States; 2Virginia Commonwealth University, Richmond, United States

**Email:** nicole@secondgenome.com

**Background and aims:** While NAFLD consists of two subtypes (NAFL and NASH), patients within both subtypes lie on spectrums of multiple axes of disease severity including fibrosis. NASH diagnosis typically relies on liver biopsy. However, liver biopsies are not only invasive but carry substantial risk of complications rendering them
impractical for tracking disease progression in patients. Therefore, there is a substantial need for non-invasive diagnostic tools to identify patients with advancing stages of NASH, including clinical fibrosis (fibrosis scores 2–4). While many studies have associated members of the gut microbiota with NAFLD and NASH, these studies either do not discriminate by fibrosis score or they focus on advanced disease (fibrosis score 4). Here we integrated samples from multiple datasets to find strains specifically associated with clinical fibrosis compared to controls and low fibrotic score NAFLD patients using multi-technology meta-analysis (MTMA). We hypothesized that patients with clinical fibrosis would display a different microbial signature and this could constitute the basis of a diagnostic method to non-invasively diagnose clinical fibrosis.

**Method:** We incorporated data from 189 patients across three studies (two public datasets and one collaboration between Arun Sanjay and Second Genome). Across this meta-cohort, 42 patients had clinical fibrosis (fibrosis score 2–4) and 147 patients were either controls or NAFL with low fibrosis (fibrosis score 0–1). All studies were processed using Second Genome’s sg-4sight platform to harmonize 16S amplicon and shotgun metagenomic sequencing, mapping all data against our proprietary StrainSelect reference database. We developed a novel multi-technology meta-analysis (MTMA) procedure to identify the strains which are consistently associated with clinical fibrosis in NAFL patients.

**Results:** A total of 996 strains were found common across at least two of the three datasets used for analysis. After adjusting for false discovery, MTMA found seven strains from families Lachnospiraceae, Erysipelotrichiaceae, and Ruminococcaceae were associated with clinical fibrosis, with four reduced and three enriched in clinical fibrosis. Two of these strains are within provisionally-named taxa not identified with existing open access tools, and therefore would not have been found without leveraging Second Genome’s StrainSelect database. This demonstrates the utility of using reference databases which organize both well-documented and emerging taxa.

**Conclusion:** Second Genome’s proprietary technology (including sg-4sight, StranSelect, and MTMA) was able to leverage multiple datasets and find a robust signature of strains associated with clinical fibrosis.

**THU162 Duodenal permeability is associated with mucosal microbiota in compensated cirrhosis**

Patricia Bloom1, Krishna Rao1, Shi-Yi Zhou1, Christine Bassi1, Borko Nojov1, Chung Owyang1, Vincent B. Young1, Anna Lok2.

1University of Michigan, Ann Arbor, United States

Email: ppbloom@med.umich.edu

**Background and aims:** Several complications of cirrhosis result from the translocation of bacteria or their products across the intestinal epithelium. However, little is known regarding the precise relationship between mucosal bacteria and epithelial permeability in cirrhosis. We aimed to assess epithelial permeability and associations with mucosal bacteria in patients with compensated cirrhosis.

**Method:** We obtained duodenal tissue biopsies from patients with compensated cirrhosis and controls without liver disease. Patients were excluded if they used antibiotics or immunosuppression. The composition of the mucosal microbiota was determined via 16S RNA gene sequencing and epithelial permeability assessed by measuring transepithelial electrical resistance (TEER) and tight junction protein expression. Associations between microbiota relative abundance and markers of epithelial permeability were assessed in a beta binomial model.

**Results:** We studied 24 patients with compensated cirrhosis and 20 controls. Patients with cirrhosis were older than controls (61 vs. 51 years, p = 0.02), but had a similar number of extra-hepatic comorbidities (Charlson Comorbidity Index without points for liver disease: 2.2 vs. 1.4, p = 0.13). Patients with compensated cirrhosis had median MELD 7 (IQR 7, 10); 62% were male.

Patients with compensated cirrhosis had lower duodenal TEER (i.e. increased epithelial permeability; 13.3 Ω/cm² ± 3.4 vs. 18.9 Ω/cm² ± 7.1; p = 0.004) and trended towards diminished expression of tight junction proteins: claudin-1 (p = 0.18), occludin (p = 0.19), and zonulin-1 (p = 0.09).

Patients with compensated cirrhosis had lower microbial burden in the duodenal mucosa (median: 34, 962 copies vs. 20, 982 copies,
Conclusion: Compensated cirrhosis is characterized by increased duodenal epithelial permeability, with a distinct mucosal microbial community. Intriguingly, bacteria previously associated with health, Lactobacillus and Bifidobacterium, were protective of duodenal permeability. Future research will be required to extend and validate these findings in larger cohorts, to investigate if these microbes have a mechanistic role in epithelial barrier function, and to assess whether these trends persist or progress in decompensated cirrhosis.

THU163
Impact of phenylacetic acid, a microbiota derived-metabolite, on hepatic endoplasmic reticulum-mitochondria interactions and steatosis
Rémy Lefebvre1, Cyrielle Caussy1,2, Jennifer Rieusset1. 1CarMeN Laboratory, UMR INSERM U1060/INRA U1393, 69495 Pierre-Bénite, France; 2Hospices civils de Lyon, département endocrinologie, diabète et nutrition, 69495 Pierre-Bénite, France
Email: remy.lefebvre@univ-lyon1.fr

Background and aims: The gut-liver axis has emerged as an important factor in the development of non-alcoholic fatty liver diseases (NAFLD). Microbiota-derived metabolites such as phenylacetic acid (PAA) have been shown to trigger hepatic steatosis in human primary hepatocytes but the molecular mechanism involved is not elucidated. Moreover, mitochondrial dysfunction is also a key component of NAFLD and oxidative capacities of mitochondria are regulated by the communication of this organelle with endoplasmic reticulum at contact points named mitochondria-associated membranes (MAMs). Hence, MAMs are nutrient sensitive controlling mitochondrial oxidative metabolism and ER-mitochondria miscommunication was associated with hepatic insulin resistance and steatosis. We hypothesized that PAA may induce hepatic steatosis through a disruption of MAMs integrity (Figure 1).

Method: We investigated the impact of PAA (500 µM) on MAMs integrity and steatosis in Huh7 cell line and primary mouse hepatocytes (PMH) incubated for 16 hours in normal (BSA) and lipotoxic (palmitate 200 µM) conditions. Co-treatments with diazoxide (100 µM) or EGTA (10 mM) allowed to investigate the involvement of electrogenic effects of PAA in Huh7 cells. ER-mitochondria interactions were measured by in situ proximity ligation assay (PLA) targeting VDAC1 (mitochondrial protein) and IP3R1 (reticular protein) proximity and BODIPY labelling was used to evaluate hepatocyte lipid accumulation. Fixed cells were analyzed by fluorescent microscopy and images analyses were performed using either blobfinder (PLA) or ImageJ (BODIPY) to quantify mitochondria-endoplasmic reticulum contacts and lipid droplets size respectively. All experiments were performed in a single time triplicate.

Results: Treatment with PAA reduced MAMs in Huh7 (n = 30 photos, fold change = −72 ± 0.025%, p = 0.0001) and PMH (n = 30 photos, fold change = −23 ± 0.064%, p <0.0001), it also induced lipid accumulation in Huh7 (n = 30 photos, fold change = +20 ± 0.035%, p = 0.0001) and PMH (n = 20 photos, fold change = +35 ± 0.047%, p = 0.0001). The effect of PAA on MAM integrity is observed as soon as one hour of treatment (n = 30 photos, fold change = −39% ± 0.029, p <0.0001) in Huh7. This effect is fully prevented by diazoxide which inhibits membrane depolarization (n = 30 photos, fold change = +9% ± 0.066% with diazoxide versus −30 ± 0.042% without it, p <0.0001) and partially by EGTA treatment, a Ca2+ chelation agent, (n = 30 photos, fold change = −29 ± 0.044% with EGTA versus −50 ± 0.022% without it, p <0.0007). Altogether, these results suggest an electrogenic mechanism of PAA action on MAMs.
Fecal samples lengthways collected at 1, 4, 8 and 12 weeks after modeling were used for gut microbiota 16S rRNA sequencing. Bile acid profiles in feces and serum were measured by ultra-performance liquid chromatography-tandem mass spectrometry (UPLC-MS/MS). Intestinal barrier integrity was assessed by measuring ileal permeability to FITC-dextran 4 kDa and Lipopolysaccharide.

**Results:** Different fibrosis stages from inflammation, mild, moderate, to advanced fibrosis were successfully induced by CCL4 administration for 1, 4, 8, 12 weeks respectively. 16S rRNA sequencing revealed that gut dysbiosis mainly occurred in the early and advanced stages of fibrosis, while the composition of the gut microbiota was close to normal in the moderate stage of fibrosis. Only the relative abundances of Lactobacillus at different phylogenetic levels were underrepresented in the four fibrosis stages. As fibrosis progressed, total bile acids in feces gradually decreased, mainly manifested as a decrease in unconjugated bile acids such as lithocholic acid (LCA) and Deoxycholic acid (DCA). Conversely, serum total bile acids increased, with marked increase in conjugated bile acids such as glycocholic acid hydrate (GCA) and tauro-alpha-murocholic acid (T-alpha-MCA). The hepatic FXR-SHP and intestinal FXR-FGF15 pathways, the master regulators of BA biosynthesis in the enterohepatic circulation, were significantly inhibited with increasing fibrosis. Interestingly, in our experimental settings, ileal pathology and permeability tests showed that the intestinal barrier remained relatively intact even in the cirrhotic stage.

**Conclusion:** The advances in knowledge of the gut-liver axis of this model provide useful supplements for us to apply it for research and drug evaluation.

**THU165**

**Association between gut microbiome and variceal bleeding risk in compensated cirrhosis: a prospective multicenter study**

Hongwei Zhou1,2, Xiaojiao Chen1, Zewen Li1, Xiang Huiling3, Heping Street, Heping District, Shenyang, Liaoning 110006, P.R.China; 12Department of Gastroenterology, Guangyuan First People's Hospital, Guangyuan, Sichuan, China; 13The People's Hospital of Guangxi Zhuang Autonomous Region, 530021, Nanning, China; 14Gastroenterology clinic, The Sixth People's Hospital of Shenyang, No.85, South Heping Street, Heping District, Shenyang, Liaoning 110006, P.R.China; 15Department of Gastroenterology, The Sixth People's Hospital of Shenyang, No.85, South Heping Street, Heping District, Shenyang, Liaoning 110006, P.R.China; 16Department of Gastroenterology and Hepatology, Guangzhou First People's Hospital, Guangzhou, China; 17The People's Hospital of Lanzhou University, Lanzhou, China; 18Department of Infectious Diseases, The First Hospital of Lanzhou University, Lanzhou, China; 19Department of Gastroenterology, Hospital of Chengdu Office of People's Government of Tibetan autonomous Region, Chengdu, China; 20Department of Gastroenterology and Hepatology, Guangyuan First People's Hospital, Guangyuan, China; 21Department of Gastroenterology, Tianjin Second People's Hospital, Tianjin, China

**Background and aims:** Gut microbial dysbiosis is associated with the progression of cirrhosis, but the relationship to the risk of variceal bleeding (EVB) remain unkown. Our study aims to evaluate the diagnostic value of gut microbiome for EVB in compensated cirrhosis.

**Method:** A total of 270 compensated cirrhotic patients from 13 centers in China were prospectively recruited between July 2019 and April 2021. Stool samples and results of endoscopy was collected following a standard detailed protocol. The total bacterial DNA in each stool sample was extracted and profiled by sequencing the 16S rRNA gene v4 region. Then the role of gut microbiome in EVB was explored and compared with endoscopy, which was considered as the gold standard for evaluating the risk of EVB.

**Results:** In this prospective multicenter study (NCT03990753, CHESS1901), the median age was 53 years (range 20–75 years), and 69.6% (n = 188) were male. 95 patients were assessed as high risk of EVB, and 175 patients were estimated at low risk. Firstly, patients from Lanzhou (LZ, n = 30), Tianjin (TJ, n = 131), Xingtai (XT, n = 74) and Chengdu (CD, n = 20) were picked out to explored whether regional variation could affect the composition of gut microbiota. Although alpha diversity was similar in four regions (Fig. A), the relative abundances at the phylum and genus levels of all samples were quite different (Fig. B, C). At the phylum level, the relative abundance of Firmicutes was higher in XT than in other cities; conversely, Bacteroidetes were relatively less abundant in XT. Furthermore, the genus level further reflected the relative differences in the abundance of microbial composition. Principal coordinate analysis (PCoA) based on unweighted UniFrac distance showed that the spatial distributions of patients for four regions were significantly different from each other overall (p < 0.001, Fig. D). However, we did not observe significant differences between high risk and low risk of EVB groups for alpha diversity, beta diversity or the relative abundances of the predominant bacterial taxa (Fig. E-H). In addition, no significant difference was obtained between the groups of high and low risk of EVB for the single center in TJ and XT respectively (Fig. J, K).
Immunology

THU167
Increased expression of programmed cell death ligand 1 and galectin 9 in transplant recipients who achieved tolerance after immunosuppression withdrawal
Nguyen Hai Nam1, Kojiro Taura1, Yukinori Koyama1, Takahiro Nishio1, Gen Yamamoto2, Yusuke Uemoto1, Yusuke Kimura1, Li Xuefeng1, Daichi Nakamura3, Kenji Yoshino2, Eri Ogawa2, Tatsuya Okamoto2, Atsushi Yoshizawa4, Satoru Seo5, Keiko Iwaisako5, Tomoaki Yoh1, Koichiro Hata1, Toshihiko Masui1, Hideaki Okajima6, Hironori Haga7, Shinji Uemoto8, Etsuro Hatano1, 1Graduate School of Medicine, Kyoto University, Kyoto, Japan; 2Graduate School of Medicine, Osaka University, Osaka, Japan; 3Graduate School of Dentistry, Kobe University, Kobe, Japan; 4Graduate School of Medicine, Tokyo Medical and Dental University, Tokyo, Japan; 5Department of Surgery, Shiga University of Medical Science, Otsu, Shiga, Japan; 6Department of Immunology, Kanazawa Medical University, Kanazawa, Ishikawa, Japan; 7Department of Surgery, Osaka University Hospital, Osaka, Japan; 8Tokyo Medical and Dental University, Tokyo, Japan

Background and aims: Programmed cell death protein 1 (PD-1)/its ligand PD-L1, and domain-containing protein 3 (TIM-3)/its ligand galectin 9 (Gal-9) and the forkhead box protein P3 (Foxp3) might be involved in tolerance after liver transplantation (LT).

Method: Liver biopsies from 38 tolerant, 19 nontolerant (including 16 samples that triggered reintroduction of immunosuppression (IS) and 19 samples after IS reintroduction) and 38 control LT patients were studied. The expressions of PD-1, PD-L1, Gal-9, and Foxp3 were determined by immunohistochemical and immunofluorescence (IF) staining. The success period of IS withdrawal was calculated using Kaplan-Meier analysis.

Results: Tolerant and control patients exhibited higher PD-L1, higher Gal-9, and higher Foxp3 levels than nontolerant patients at the moment of triggering IS reintroduction. High expression of PD-L1 and Gal-9 was associated with prolonged success of tolerance (83.3% vs. 36.7%, p <0.01; 73.1% vs. 42.9%, p = 0.03). A strong correlation between PD-L1 and Gal-9 expression levels was detected (Spearman r = 0.73, p <0.0001) and IF demonstrated colocalization of PD-L1 and Gal-9 in the cytoplasm of hepatocytes.

Conclusion: The present study demonstrated that an increased expression of PD-L1 and Gal-9 was associated with sustained tolerance after IS withdrawal in pediatric liver transplantation.

THU168
Acidic microenvironment aggravates the severity of hepatic ischemia/reperfusion injury by modulating PPAR-γ signal
Wei Ding1, Yunfei Duan1, Zhen Qu1, Donglin Sun1, Yunjie Lu1, 1The Third Affiliated Hospital of Soochow University, Hepatopancreatobiliary Surgery Department, Changzhou, China

Background and aims: Hepatic injury induced by ischemia and reperfusion (HIRI) is a major clinical problem after liver resection or transplantation. The polarization of macrophages plays an important role in regulating the severity of hepatic ischemia/reperfusion injury. Recent evidence had indicated that the ischemia induces an acidic microenvironment by causing increased anaerobic glycolysis and accumulation of lactic acid.

Method: We hypothesize that the acidic microenvironment might cause the imbalance of intrahepatic immunity which aggravated HIRI. The hepatic ischemia/reperfusion injury model was established to investigate the effect of the acidic microenvironment to liver injury. Liposomes were used to deplete macrophages in vivo. Macrophages were cultured under low pH conditions to analyze the polarization of macrophages in vitro. Activation of the PPAR-γ signal was determined by Western Blot. PPAR-γ agonist GW1929 was administrated to functionally test the role of PPAR-γ in regulating macrophage-mediated effects in the acidic microenvironment during HIRI.

Results: We demonstrate that acidic microenvironment aggravated HIRI while NaHCO3 reduced liver injury through neutralizing the acid, besides, liposome abolished the protective ability of NaHCO3 through depleting the macrophages. In vivo and vitro experiment showed that acidic microenvironment markedly promoted M1 polarization but inhibited M2 polarization of macrophage. Furthermore, the
mechanistic study proved that the PPAR-γ signal was suppressed during the polarization of macrophages under pH = 6.5 culture media. The addition of PPAR-γ agonist GW1929 inhibited M1 polarization under acidic environment and reduced HIRI.

**Conclusion:** Our results indicate that acidic microenvironment is a key regulator in HIRI which promoted M1 polarization of macrophages through regulating PPAR-γ. Conversely, PPAR-γ activation reduced liver injury, which provides a novel therapeutic concept to prevent HIRI.

**THU160**

**Toll-like receptor 3 polymorphisms rs5743305 and rs3775291 affect innate immune responses in whole blood analyses**

Sophia Barkow¹, Madlen Matz-Soja¹, Thomas Berg¹, Janett Fischer¹.

¹Division of Hepatology, Department of Medicine II, Leipzig University Medical Center, Laboratory for Clinical and Experimental Hepatology, Leipzig, Germany

Email: janett.fischer@medizin.uni-leipzig.de

**Background and aims:** As a part of the innate immunity, the Toll-like receptors (TLR) 3 signaling has been linked to the outcome of hepatitis B virus (HBV) infection. Polymorphisms (SNPs) in the TLR3 gene were associated with an increased risk of developing chronic hepatitis B. This research aimed to assess the impact of the two TLR3 SNPs rs5743305 and rs3775291 on the immune responses in a whole blood assay.

**Method:** The study included 30 healthy volunteers matched according to the two functionally relevant TLR3 SNPs (10 TT/10 TA/10 AA for rs5743305 and 11 CC/12 CT/7 TT for rs3775291), and in age and gender. Heparinized whole blood was treated with 5 µg/ml polyinosinic-polycytidylic acid (PolyI:C) for 3 and 6 hours. The relative gene expression (rGE) of TLR3, IL-1β, IL-6, IL-10, IL-12, IFNγ, IFNα and TNFα was analyzed by quantitative real-time polymerase chain reaction. Normalization (2ΔΔCt) was performed in relation to the housekeeping gene TBP and untreated blood. The plasma protein levels (PPL) of all cytokines were measured after 6 h of stimulation by performing a bead-based sandwich-immunoassay.

**Results:** The rs5743305 minor allele A showed significantly lower rGE of IFN-α (A: 8.97, TT: 14.82, p = 0.022) and absolute PPL (A: 6.99 pg/ml, TT: 15.6 pg/ml, p = 0.025) after 6 h compared to the wild type (WT) TT. Additionally, IL-1β PPLs were reduced for the minor allele A compared to the WT (A: 43.5 pg/ml, TT: 75.95 pg/ml, p = 0.011) as depicted in figure A. The rs3775291 risk allele T showed increased rGE of IFNβ after 6 h (T: 4.32, CC: 2.08, p = 0.017). Interestingly, the relative PPL of IFNβ was significantly lower for the T allele than for the WT CC (T: 2.6, CC: 8.52, p = 0.014). Furthermore, the risk allele significantly reduced the relative PPL of IFNα (T: 1.4, CC: 1.9, p = 0.004) (figure B).

**Conclusion:** This study showed significant effects of the two TLR3 SNPs on cytokine expression in the complex whole blood system. The minor allele A of rs5743305 decreased pro- and anti-inflammatory cytokine expression. As expected, the rs3775291 risk allele T reduced the synthesis of inflammatory type 1 interferons. This may lead to a dysbalanced immune system and therefore to a less functional defense against virus infections. Further research in larger cohorts and in cell culture systems is required to enlighten the impact of the SNPs on immune responses, especially during HBV infection.

**THU170**

**IL-15 boots HBV-specific CD8⁺ cell response by activated progenitor pool mitochondrial remodelling in on treatment e-Ag negative chronic hepatitis B**

Julia Peña Asensio¹,², Henar Calvo¹, Joaquin Miquel¹, Eduardo Sanz de Villalobos³, Alejandro González-Praetorius³, Miguel Torralba¹,³, Juan Ramón Larrubia¹,³, ¹Guadalajara University Hospital, Translational Hepatology Unit, Guadalajara, Spain; ²University of Alcala, Department of Biology of Systems, Alcalá de Henares, Spain; ³University of Alcala, Department of Medicine and clinical specialties, Alcalá de Henares, Spain.

Email: hlnd.julia@gmail.com

**Background and aims:** In the HBV-specific-CD8⁺ progenitor pool (PP), mitochondrial remodelling could re-establish the functionality of the effector proliferative progeny (EPP) in nucleos (t)ide analogue (NUC) treated eAg (-) chronic hepatitis B (CHBe (-)). We analysed the role of IL-15 in the metabolic profile of the HBV-specific CD8⁺ PP after Ag encounter in CHBe (-) with low probability of T cell restoration during NUC treatment.

**Method:** According to clinical variables, level of HBV-specific-CD8⁺ cell exhaustion was estimated in NUC treated CHBe (-) HBV-specific-CD8⁺ cells were visualized by pentameric technology. After Ag- encounter in CHBe (-), quiescent PP expresses a memory-like phenotype (PD-1+/CD127+). After Ag-encounter, APP gives rise to the effector proliferative progeny (EPP) were tested by proliferation ability, interferon- (IFN)gamma, Tumour necrosis factor (TNF)alpha and FSC level. Metabolic profile, memory-like phenotype and IFNβ was analyzed by quantitative real-time polymerase chain reaction.

**Results:** During CHBe (-), quiescent PP expresses a memory-like phenotype (PD-1+/CD127+). After Ag-encounter, APP gives rise to the EPP. In comparison with IL2, IL-15 decreases the initial boost of mTORC1 in APP, but maintains its activation longer, which translates into an inflation of EPP, and improvement in metabolic profile (Glut-1low, PGC1αhigh, CPT1high). IL-15 induced metabolic changes correlate with an enhancement in EPP effector abilities (IFN gamma high, TNF alpha high, CD107α high). In those cases with low probability of HBV-specific-CD8⁺ cell restoration during NUC treatment, IL-15 plus anti-PD-L1 restored the proliferation ability of these cells after Ag-specific-in-vitro challenge.
Conclusion: IL-15 induces an intermediate but sustained mTORC1 activation in HBV-specific CD8<sup>+</sup> APP that translates into a catabolic mitochondrial phenotype and enhancement in EPP of effector abilities. In those CHBe (••) cases with low probability of achieving a functional response during NUC treatment, IL-15+anti-PD-L1 in-vitro treatment restores their reactivity.

THU171
Mucosal-associated invariant T cells are rendered functionally exhausted within the tumour microenvironment in HCC in a cell-contact dependent manner
Junika Pohl1, Alexandra Georgieva1, Anna-Marie Pedde2, Anna Hirschberger2, Sebastian Deschler1, Melanie Laschinger3, Daniel Hartmann3, Jan Boettcher2, Norbert Hüsler1, Roland M. Schmid1, Percy A. Knolle2, Katrin Böttcher1. 1University Hospital Rechts der Isar, School of Medicine, Technical University of Munich (TUM), Department of Internal Medicine II, München, Germany; 2University Hospital Rechts der Isar, School of Medicine, Technical University of Munich (TUM), Institute of Molecular Immunology and Experimental Oncology; 3University Hospital Rechts der Isar, School of Medicine, Technical University of Munich (TUM), Department of Surgery

Background and aims: Hepatocellular carcinoma (HCC) is still one of the major causes of cancer death worldwide. Immunotherapy has recently become the first-line treatment for advanced HCC, although response rates remain low. MAIT cells, innate-like T cells particularly enriched in the liver, express pro-inflammatory cytokines as well as cytolytic molecules and have therefore been attributed anti-tumour properties. In this study, we aim to decipher direct interactions between MAIT cells and HCC cells in order to unravel mechanisms of immune cell exhaustion within the tumour microenvironment in HCC.

Method: MAIT cells were isolated from tumour tissue, adjacent liver tissue and peripheral blood of human patients with HCC or other liver tumours and healthy controls. Primary MAIT cells were co-cultured with various HCC cell lines in vitro and MAIT cell phenotype and function was analysed by multi-colour flow cytometry.

Results: We show that MAIT cells frequency is significantly reduced in peripheral blood of HCC patients compared to healthy controls, as well as in HCC tumour tissue compared to the adjacent liver tissue. Such MAIT cell loss was specific, since frequency of conventional T cell subsets was unaffected in HCC and MAIT cell frequency was unchanged in other liver tumours. Whereas MAIT cells from peripheral blood of HCC patients retained functional, tumour-educated liver-derived MAIT cells showed increased exhaustion marker expression and significantly impaired effector function, suggesting MAIT cell exhaustion within the tumour microenvironment in HCC. Interestingly, such MAIT cell dysfunction could be induced by co-culture of MAIT cells with different HCC cell lines, while the hepatocyte-like cell line HepG2 was unable to induce MAIT cell exhaustion. Mechanistically, induction of MAIT cell exhaustion by HCC cells was dependent on direct cell-cell contact.

Conclusion: Taken together, we show that MAIT cells, innate-like T cells with anti-cancer potential, are rendered dysfunctional within the HCC microenvironment, suggesting MAIT cells as a potential target for anti-cancer therapy in HCC. Understanding mechanisms of local MAIT cell exhaustion in HCC may facilitate the development of novel immunotherapeutic strategies against HCC.

THU172
Preclinical model for the study of immune responses specific for a hepatic-self-antigen
Anaïs Cardon1,2, Jean-Paul Judor1,2, Arnaud Nicot1,3, Sophie Conchon1,3, Amédee Renand3,1 INSERM UMR 1064 Centre de Recherche en Transplantation et Immunologie, Nantes, France; 2Université de Nantes, Nantes, France; 3INSERM, France

Background and aims: Despite a bias toward immune tolerance in the liver, autoimmune liver diseases such as autoimmune hepatitis (AIH) can occur. The etiology of this disease is still not well characterized, and little is known about the emergence process and dynamics of self-antigen-specific immune responses. Thus, to better understand AIH initiation mechanisms, we developed preclinical murine models allowing the study of specific immune responses (CD4<sup>+</sup> and CD8<sup>+</sup> T cells and antibody) against a liver antigen.

Method: The expression of the antigen hemagglutinin (HA) was induced with a CRE/LoxP system (cross-breeding of ROSA HA floxed mice with TTR-CREind mice). An adenovirus encoding for the CRE recombinase (AdCRE) was injected intramuscularly (i.m.) to induce a peripheral immunization or intravenously (i.v.) to induce hepatic HA expression and inflammation. Feeding mice with tamoxifen dry food induced HA expression only in the liver. In the different settings, HA-specific CD4<sup>+</sup> and CD8<sup>+</sup> T cells in the spleen and the liver were detected and characterized using tetramers, and antibody class switch was assessed by ELISA tests.

Results: Peripheral HA immunization (AdCRE i.m.) leads to a strong HA immune response, marked by the emergence of anti-HA responses (CD4<sup>+</sup> T cells and antibodies) and linked to HA expression in the muscle (but not in the liver). When HA expression is specifically induced in the liver (tamoxifen), no HA-specific adaptive response is detected, confirming the tolerogenic environment of the liver. However, after a peripheral immunization (AdCRE i.m.), tamoxifen-induced liver-specific HA expression leads to a massive recruitment of HA-specific PD-1<sup>+</sup> CD25<sup>-</sup> T cells in the liver. Finally, AdCRE i.v. causes concomitant hepatic HA expression and inflammation leading to the generation of HA-specific PD-1<sup>+</sup> CD25<sup>-</sup> CD4<sup>+</sup> T cells in the spleen and liver for over 12 weeks, and anti-HA IgG1 antibodies reflecting a chronic reaction against HA.

Conclusion: Our study shows that the conditions of expression of the antigen in the liver (e.g. inflammatory environment, peripheral immunisation) modulate hepatic self-antigen-specific responses. Taken together, this could depict a key element in the initiation of autoreactive responses toward a hepatic antigen. A long-term analysis of antigen-specific responses (CD4<sup>+</sup> T cells and antibody) in our models will provide a better understanding of responses dynamics during AIH development.

THU173
Proximity labelling reveals potential cis interactions of CD52 glycoprotein counter-receptors on circulating CD4+HLA-G<sup>+</sup> regulatory T cells in acute decompensation of cirrhosis
Tong Liu1, Gang Wu2, Cathrin Gudde2, Thomas Barbera2, Rooshi Nathwani1, Francesca Trovato3, Ian Liu1, Mark J W McPhail2, Mark Thrurs2, Wafa Kharmi3. 1Imperial College London, Department of Metabolism, Digestion and Reproduction, London, United Kingdom; 2Imperial College London, Department of Life Sciences, London, United Kingdom; 3King’s College London, Institute of Liver Studies, London, United Kingdom

Email: tong.liu15@imperial.ac.uk

Background and aims: We have recently described the expansion of a non-classical regulatory CD4<sup>+</sup>HLA-G<sup>+</sup> T cell population and its
Hevar Hamah Saed, First, we examined the cell surface protein expression of CD52 and Siglec-10 in CD4+HLA-G+ versus CD4+HLA-G+ T cells from patients with AD. Moreover, the results indicated a potential contribution to defective peripheral immune responses in patients with acute decompensation (AD) of cirrhosis. Gene profiling of this cell subset revealed an up-regulation of gene encoding for CD52: a sialylated glycosylphosphatidylinositol-anchored glycoprotein known to be involved in lymphocyte functions by ligating its released soluble form and the sialic acid-binding immunoglobulin-like lectin 10 (Siglec-10) receptor. However, the impact of cell surface CD52 is not fully understood. In this study, we aim to investigate the role of membrane-bound CD52 in CD4+HLA-G+ T cells.

**Method:** First, we examined the cell surface protein expression of CD52 and Siglec-10 in CD4+HLA-G+ versus CD4+HLA-G+ T cells of AD patients (n = 17) using flow cytometry. Endogenous CD52 N-glycan was digested with sialidase and binding affinity of CD52 to Siglec-10 was measured by flow cytometry using fluorochrome-labelled recombinant Siglec-10. Proximity labelling was used to identify potential membrane counter-receptors of CD52 on CD4+HLA-G+ T cells. Cells were probed with horseradish peroxidase (HRP)-conjugated anti-CD52 antibody, biotinyl tyramide was used to biotinylate membrane proteins within 100 nm radius of the HRP complex. Biotinylated proteins in proximity of CD52 were then enriched by streptavidin beads and identified via mass spectrometry.

**Results:** CD52 cell surface expression was significantly increased in CD4+HLA-G+ compared to HLA-G− cells (mean fluorescence intensity (MFI) median 25052 IQR [22989–26755] vs. 11529 [9459–14081], p < 0.0001). Siglec-10 expression was also significantly increased in the same subset (MFI 26987 [23892–28533] vs. 16765 [14534–17983], p < 0.0001). The membrane CD52 on CD4+ T cells showed high binding affinity towards Siglec-10, and this affinity could be reversed by digestion of the sialylated N-glycan of CD52. Proximity labelling revealed the T cell receptor (TCR) complex at CD3 epsilon, CD3 gamma, and TCR beta were in the immediate vicinity of CD52+HLA-G+ T cells from patients with AD. Moreover, the results imply that Siglec-10 interacting with CD52 could depend on TCR stimulation.

**Conclusion:** CD52 and its counter-receptor Siglec-10 are co-expressed on the CD4+HLA-G+ T cells of AD patients. Proximity labelling identified potential cis-ligands recruited to the proximity of the membrane-bound CD52 likely to have implications on CD4+HLA-G+ T cells responsiveness to TCR stimulation.

**Results:** 64 patients with CLD and 39 healthy volunteers were included. Both serological and T-cell responses were significantly lower in patients with CLD compared to healthy volunteers after the 1st and 2nd vaccine dose. 79% and 15% of CLD patients had inadequate antibody response after the 1st and 2nd vaccine dose respectively. Additionally, 79% and 38% of CLD patients had inadequate interferon-γ production after the 1st and 2nd vaccine dose, respectively. The potency of immune response did not correlate to liver fibrosis grade. Nevertheless, patients with higher Child-Pugh (CP) scores had a worse response to the vaccine. There were no differences in the occurrence of side effects to the vaccine between the groups.

**Conclusion:** Patients with CLD have a poorer response to vaccination compared to SARS-CoV-2 compared to healthy volunteers regardless of their fibrosis stage and many continue to be inadequately protected despite full vaccination.

**Background and aims:** Cirrhosis-associated immune dysfunction (CAID) has been proposed as one of the significant complications in cirrhotic patients, demonstrated by an impairment of innate immunity. Previous studies showed that reduction of phagocytic activity, as a part of innate immunity, might predict infection occurrence and 90-day survival in cirrhosis. However, there are still limited data on immunotherapeutic approaches to modulate the dysfunctional immune response. Our study aims to determine the effect of branched-chain amino acid (BCAA) granules on phagocytic activity in cirrhotic patients.

**Method:** A double-blinded, randomized-controlled trial was conducted at a single-centre tertiary care hospital. Thirty-seven cirrhotic patients were randomly assigned in a 1:1 ratio stratified by Child-Pugh status to receive either BCAA granules at a dose of 4.15 grams thrice daily or placebo. All patients received a multidisciplinary approach from hepatology and nutrition specialists. They were also assigned to record the adherence to study drug, seven-day food recall, and side effects, if occurred, in an interventional diary. At baseline, the 3rd and 6th months of the study, the phagocytic activity was assessed by a biochemist using pHrodo Red E. coli BioParticles Phagocytosis Kit and Image Stream II Imaging Flow Cytometer. The primary end point was the restoration of innate immunity at the sixth month, define by phagocytic activity ≥ 75%. Key secondary end points were the accretion of phagocytic activity and number of hospitalizations due to infection.

**Results:** Of all 37 eligible patients, the patients in Child-Pugh A/B/C were 26/8/3, respectively. Eighteen patients were in placebo, and nineteen were in BCAA group. The baseline characteristics and phagocytic activity were comparable between groups. At 6th month, a significantly higher phagocytic activity restoration was demonstrated in the BCAA group compared with placebo (68.4 vs. 5.6%, p <0.001). The mean phagocytic activity in the BCAA and placebo group were 75.4% and 63.4%, respectively (p <0.001). The progressive accretion of phagocytic activity was observed during the 3rd and 6th months, as shown in Figure. There were no differences in serum albumin and other inflammatory markers. Despite a higher phagocytic restoration rate in the BCAA group, there was no difference in hospitalization due to infectious events in comparison to the placebo group (2 VS 3 events, p = 0.487).
Figure: Phagocytic activity change from baseline at the 3rd month and 6th month of the study.

**Conclusion:** BCAA can significantly improve phagocytic activity in cirrhotic patients across all Child-Pugh stages. This may be an option for immunotherapeutic intervention of CAID. However, whether the improvement in phagocytic activity would correlate with a better outcome especially infectious complications may need longer follow-up studies.

**Background and aims:** Sarcopenia and phagocytic dysfunction were demonstrated to be associated with poorer clinical outcomes in cirrhotic patients. Branched-chain amino acid (BCAA) is a pivotal factor that activates the mammalian target of rapamycin (mTOR) complex, a central node that controls immunity and muscle synthesis. In cirrhosis with sarcopenia, the BCAA is depleted, which may associate with phagocytic dysfunction. However, there is a paucity of studies that established the effect of sarcopenia on phagocytic activity. Therefore, our study aims to determine the correlation between sarcopenia and the phagocytic activity in cirrhotic patients.

**Method:** We conducted a randomized controlled trial (RCT) evaluating the role of BCAA on phagocytic activity. In this study, we used the baseline data in patients enrolled in the RCT to study the correlation and factor affecting phagocytic activity. Thirty-seven cirrhotic patients with sarcopenia were included in this study (defined with skeletal muscle index [SMI] according to the JSH criteria). The SMI was measured at L3 vertebra by a cross-sectional CT scan and calculated by DICOM software. The phagocytic activity assessment was performed by a biochemist, using the pHrodo Red E. coli BioParticles Phagocytosis Kit for flow cytometry and Image Stream Mk II Imaging Flow Cytometer. The correlations between SMI and phagocytic activity was analysed using spearman test and adjusted with other covariates by multivariable linear regression

**Results:** Thirty-seven patients were included, the patients in Child-Turcotte-Pugh (CTP) A/B/C were 26/8/3, respectively. The baseline characteristics were difference as cirrhotic stage progressed from CTP-A to C. Our study demonstrated a trend towards lower phagocytic activity in the more severity of cirrhosis, but not statistically significant, as 62.3%, 60.5%, and 54.3% in CTP A, B, C, respectively (p = 0.12). In a multivariable linear regression analysis, CTP-C and SMI (cm²/m²) are independent factors associated with the prediction of phagocytic activity, with adjusted beta-coefficients of -14.4% (p = 0.001), and +0.75% (p <0.001), respectively. The strong correlation between SMI and phagocytic activity was demonstrated in the CTP-A cirrhosis, r = 0.84 (p <0.001) whereas there was no significant correlation in CTP-B/C cirrhosis, r = −0.068 (p = 0.84) as shown in the figure.

**Conclusion:** In cirrhosis with sarcopenia, our study demonstrated that both CTP-C and lower SMI were associated with phagocytic dysfunction. Emerging data had shown a strong correlation between sarcopenic status and phagocytic dysfunction, especially in CTP-A. Therefore, sarcopenic assessment is essential for all stages of cirrhosis despite compensated CTP-A status, to initiate the treatment and prevent further decompensation.

Figure: (abstract: THU176): The correlation between phagocytic activity and muscle mass in various stages of cirrhosis.
Background and aims: To control the COVID-19 pandemic, vaccination is the principal for general population globally. In patients suffered from SARS-CoV-2 infection, having cirrhosis has been associated with a higher risk of poor outcomes, and those with cirrhosis were strongly advised affirmatively by international hepatology societies to receive the SARS-CoV-2 vaccine. However, cirrhosis-associated immune dysfunction might contribute to hyporesponsive to the vaccine. Moreover, data of immune responses in those who received the different types of vaccines, especially heterologous vaccines are lacking. We studied whether different regimens of COVID-19 vaccines affect the humoral immune response in patients with cirrhosis.

Method: We conducted a prospective observational study, collecting blood samples from patients with cirrhosis who were regularly followed up at our centre, a tertiary care hospital in Thailand, and received 2 doses of SARS-CoV-2 vaccine. This is a preliminary report of patients enrolled between June and October 2021. Those who were on immunosuppressive agent were excluded. The SARS-CoV-2 vaccination in Thailand is provided by the government; there were 3 major vaccination regimens: inactivated vaccine (CoronaVac; SV/SV), viral vector vaccine (ChAdOx1 nCoV-19 vaccine; AZ/AZ), and heterologous vaccination regimens: inactivated vaccine followed by viral vector vaccine had a significant humoral immune response while all patients in SV/SV and AZ/AZ, respectively (p < 0.001). Two patients in AZ/AZ had inadequate immune response while all patients in SV/SV and AZ/AZ had Ab level >7.15 BAU/ml. Among 3 different vaccine regimens, the heterologous SV/AZ had the highest anti-spike RBD IgG level at the median level of 801.8 (IQR: 615.1, 1195.6) BAU/ml, significantly higher than SV/SV (median 95.8 (IQR: 27.3, 427.6) BAU/ml, p = 0.01) and AZ/AZ (median 238.3 (IQR: 57.7, 387.2) BAU/ml).

Conclusion: Heterologous COVID-19 vaccine with the inactivated vaccine followed by viral vector vaccine had a significant humoral immune response among patients with cirrhosis. This result highlighted the prime-boost effect of the vaccine to alleviate the shortage of vaccines in the situation of COVID-19 pandemic.

Results: A total of 61 patients completed their 2nd dose vaccine and had Ab level data available, 61% were male, the major cause of cirrhosis was chronic hepatitis B (42%), and 51/9/1 patients were in child A/B/C, respectively. Of those, 8 (13.1%) received SV/SV, 28 (45.9%) got heterologous SV/AZ, and 25 (40.9%) received AZ/AZ. The mean age was 53, 62, and 69 years in SV/SV, SV/AZ, and AZ/AZ, respectively (p = 0.09). Two patients in AZ/AZ had inadequate immune response, whereas all patients in SV/SV and AZ/AZ had Ab level >7.15 BAU/ml. Among 3 different vaccine regimens, the heterologous SV/AZ had the highest anti-spike RBD IgG level at the median level of 801.8 (IQR: 615.1, 1195.6) BAU/ml, significantly higher than SV/SV (median 95.8 (IQR: 27.3, 427.6) BAU/ml, p = 0.01) and AZ/AZ (median 238.3 (IQR: 57.7, 387.2) BAU/ml).

Background and aims: Discontinuation of long-term nucleos(t)ides analogue treatment can lead to clinical relapse and increased risk of hepatic decompensation in patients with HBeAg negative chronic hepatitis B. In others, NA cessation can result in functional cure. It is widely believed that restoration of antiviral immunity underpins this favourable outcome.

Method: Patients virally suppressed for >3 years were randomised to either stop-NA or discontinue NA for 4 weeks followed by 16 weeks of PEG-IFN-alpha before stopping both treatments (NA/IFN) (see Figure). Patients with exaggerated flares (ALT>20xULN) were retreated with NAs (RTx). Longitudinal peripheral blood mononuclear cells (PBMCs) were collected from 23 Stop-NA and 18 NA/IFN patients during a 3-year follow-up. Additional samples were collected during moderate (ALT>2xULN) and exaggerated flares. PBMCs were stimulated with 15 overlapping genotype-specific peptide pools (OPP), HBV core, surface (HBCag/HBsAg) and recall antigens. Ex-vivo frequency of HBV-specific IFN-gamma (IFN-g) producing T-cells was assessed by ELISpot assays, validated and standardised at GCLP. Virological and clinical parameters were correlated with immunological assessments.

Results: At week 130, 74% Stop-NA and 94% NA/IFN patients remained off treatment while 26% and 6% needed RTx respectively. A lower frequency of IFN-g-specific T-cells at BL, which persisted remained off treatment while 26% and 6% needed RTx respectively. A lower frequency of IFN-g-specific T-cells at BL, which persisted during follow-up, was associated with RTx (p < 0.04). Conversely, one HBeAg OPP-specific T-cell subset was associated with RTx and detected at higher frequency at BL (p = 0.019). PEG-IFN treatment was associated with a broad loss of T-cell response and epitope recognition contraction. Whilst this T-cell response recovered after PEG-IFN cessation, a high proportion of patients experienced viral rebound (>2000 IU/ml) (63% vs 18%). In the Stop-NA group, NA withdrawal was associated with moderate flares (52%), accompanied by a peak in T-cell response in sharp contrast to NA/IFN group with flares (62%) occurring when T-cell response was diminished. Finally, the frequency of 3 OPP-specific T-cells subsets at BL was associated with flares in both groups (p = 0.007; p = 0.005; p = 0.035).
Background and aims: Bacterial infection is a common and serious complication in patients with liver cirrhosis. Previous research has found that mucosa-associated invariant T cells (MAIT cells), antibacterial T cells, are reduced in numbers in patients with cirrhosis, both in liver and in peripheral blood. Little is known if MAIT cell levels might predict clinically relevant outcomes including infections. The aim of this study was to evaluate if MAIT cell levels in both in liver and peripheral blood can serve as a novel biomarker to cirrhotic patients with a higher risk for adverse outcomes.

Method: Patients with liver cirrhosis attending the Hepatology department at the Karolinska University Hospital between 2016 and 2019 were included. Levels of peripheral MAIT cells in blood were determined using flow cytometry. Baseline characteristics and incident outcomes (bacterial infections, hepatic decompensation and death) were ascertained by manual chart review during a mean follow-up of 2.6 years. A competing risk regression was performed to assess the risk of bacterial infection and hepatic decompensation, with death and liver transplant as competing events. Cox regression analysis was performed to evaluate mortality rates. Both models were adjusted for age, sex and severity of liver disease.

Results: We included 106 patients with cirrhosis, median age was 63 years and 64% were men. Median MAIT-cell percentage was 0.8% in peripheral blood while 1% were found in patients or healthy controls and re-stimulated in vitro in presence of free fatty acids. MAIT cell phenotype and function was analysed by multi-colour flow cytometry. MAIT cell metabolism was investigated by metabolic flux analysis.

Conclusion: We show that MAIT cell frequency is significantly decreased in peripheral blood of NAFLD patients and that NAFLD MAIT cells express significantly higher levels of activation markers and effector cytokines ex vivo, suggesting MAIT cell activation in NAFLD in vivo. However, upon in vitro stimulation, these activated MAIT cells are dysfunctional and fail to produce effector cytokines, such as IFN gamma, Granzyyme B and TNF alpha. Metabolically, MAIT cell effector function was dependent on glycolysis and oxidative phosphorylation, which was unaffected in NAFLD MAIT cells. Culture with distinct fatty acid species characteristic of the NAFLD microenvironment, however, impaired expression of effector cytokines by MAIT cells and induced MAIT cell death. Mechanistically, these effects were mediated by corrupted mitochondrial function and aberrant lipid metabolism.

Background and aims: Non-alcoholic fatty liver disease (NAFLD) driven by lipotoxicity and inflammation is becoming the most common chronic liver disease worldwide. Besides promoting pathogenesis, the unique liver microenvironment allows for the development of hepatocellular carcinoma in NAFLD. Here, we aim to decipher novel mechanisms of hepatic immune regulation in NAFLD that could be exploited for therapy. To this end, we analysed how metabolic changes in NAFLD affect the phenotype and effector function of mucosa-associated invariant T (MAIT) cells, innate-like T cells with antimicrobial and anti-cancer potential enriched in the liver.

Method: MAIT cells were isolated from peripheral blood of NAFLD patients or healthy controls and re-stimulated in vitro in presence of free fatty acids. MAIT cell phenotype and function was analysed by multi-colour flow cytometry. MAIT cell metabolism was investigated by metabolic flux analysis.

Results: We show that MAIT cell frequency is significantly decreased in peripheral blood of NAFLD patients and that NAFLD MAIT cells express significantly higher levels of activation markers and effector cytokines ex vivo, suggesting MAIT cell activation in NAFLD in vivo. However, upon in vitro stimulation, these activated MAIT cells are dysfunctional and fail to produce effector cytokines, such as IFN gamma, Granzyyme B and TNF alpha. Metabolically, MAIT cell effector function was dependent on glycolysis and oxidative phosphorylation, which was unaffected in NAFLD MAIT cells. Culture with distinct fatty acid species characteristic of the NAFLD microenvironment, however, impaired expression of effector cytokines by MAIT cells and induced MAIT cell death. Mechanistically, these effects were mediated by corrupted mitochondrial function and aberrant lipid metabolism.

Conclusion: These results show that MAIT cells are highly activated but dysfunctional in NAFLD and suggest that impairment of MAIT cell effector function is mediated by metabolic signals in the NAFLD microenvironment. Our data unravel a connection between lipotoxicity and immune cell dysfunction in NAFLD which may facilitate the development of therapeutic strategies.
they play an important role in maintaining homeostasis. However, Treg cells are phenotypically and functionally heterogeneous. In this study, we used multimodal single-cell profiling to delineate the mechanistic basis for the effects of butyrate on Treg cell heterogeneity.  

**Method:** We studied the whole transcriptome and several surface protein markers of approximately 6000 Treg cells. This was combined with experimental studies for biological validation.  

**Results:** We found that butyrate polarised naïve Treg cells into heterogeneous subpopulations with both immunosuppressive and pro-inflammatory subsets. Upon reconstructing the gene regulatory networks, we found an upregulation of the hypoxia, NFκB, JAK-STAT, TNFα, and MAPK signalling pathways. We also identified the individual reguons driving them. These findings were subsequently validated experimentally. Strikingly, butyrate increased the secretion of TNFα, IL-2, and IL-17A from the activated Treg cells whilst maintaining their immunosuppressive capacity. We also uncovered the novel capacity of butyrate to acutely inhibit STAT5 and p38. Mechanistically, we found that butyrate promotes diverse regulatory and effector cell subpopulations. These mechanisms could be therapeutically targeted to modulate the effects of SCFAs on Treg cells in the gut and liver.

**THU182 COVID-19 vaccination in liver cirrhosis: safety and immune and clinical responses**

Maria Ines Canha1, Mario Jorge Silva1, Maria Azevedo Silva2, Leiria, Gastroenterology; 3Centro Hospitalar Universitário de Coimbra, Gastroenterology; 4Hospital de Vila Franca de Xira, Gastroenterology; 5Centro Hospitalar de Lisboa Ocidental, Gastroenterology; 6Hospital Beatriz Ângelo, Gastroenterology; Email: m.inescanha@gmail.com

**Background and aims:** Available data regarding safety and efficacy of COVID-19 vaccination in liver cirrhosis patients is lacking. Their dysregulated immune system makes them susceptible to serious disease and to an attenuated response to certain vaccines. Our goal was to study safety, immunological and clinical responses of cirrhotic patients to COVID-19 vaccination and assess their relation to demographic, clinical and vaccine-related factors.  

**Method:** Interim analysis of an ongoing multicentric prospective study in patients with liver cirrhosis eligible for COVID-19 vaccination without prior infection. Demographic data, liver disease severity, comorbidities, medication and adverse events were registered. Patients were requested to assess IgG antibody titers (AbT) for SARS-CoV-2 at 2 weeks (W2), 3 months (M3) and 6 months after completing vaccination. During follow-up, post-vaccination infection and severity were registered. We analyzed the patients who completed the M3 assessment, using Stata 15 and a p < 0.05.  

**Results:** We included 121 patients, 82% males, mean aged 61 years. Alcohol is the most common (61%) cause of cirrhosis. Twenty percent have a Child Pugh score (CPS) of B/C; 42% had at least one decompensation and 68% have portal hypertension (PHT) signs. Seventeen percent of the patients reported adverse reactions after vaccination, none of them serious. Median [Q1; Q3] AbT were 1115 [291; 2080] BAU/ml at W2 and 293 [88; 1190] BAU/ml at M3. Group differences in AbT (using 33.8 and 200 BAU/ml as cut-offs) were assessed in a multivariable logistic regression considering the patients’ age, gender, cause of cirrhosis, immunosuppressant drugs, severity of cirrhosis (Table 1), type of vaccine and adverse reactions. Only older age and type of vaccine proved to be associated with lower AbT at W2 and M3. None of the patients was diagnosed with COVID-19 infection during a mean follow-up of 137 days.

**Conclusion:** COVID-19 vaccines in cirrhotics were safe and their clinical and humoral response seem not different from the observed in the general population assessed in clinical trials.

**THU183 Building a case for pancreas and liver targeted interleukin-22 therapy in fatty liver disease**

Haressh Saji1, Kuan Yau Wong1, Alexandra Mueller1, Sahar Keshtvari2, Ran Wang1, Percival Waid3, Grant Rams1, Graeme Macdonald4, John Prins4, Michael McGuckin5, Sumaira Hasnain1,6, 1Mater Research Institute-The University of Queensland, Immunopathology group, Brisbane, Australia; 2Mater Research Institute-The University of Queensland, Brisbane, Australia; 3QMIR Berghofer Medical Research Institute, Brisbane, Australia; 4Princess Alexandra Hospital, Brisbane, Australia; 5The University of Melbourne, Melbourne, Australia; 6Australian Infectious Diseases Research Centre, Brisbane, Australia; Email: sumaira.hasnain@mater.uq.edu.au

**Background and aims:** We discovered that the cytokine interleukin-22 (IL-22) is an efficient natural inhibitor of cellular stress and improved insulin quality in pancreatic beta-cells in preclinical models of Type 2 diabetes. Importantly, IL-22 completely restored glucose tolerance, suppressed fasting hyperinsulinaemia/hyperproinsulinaemia, and restored insulin sensitivity in obese animals. Treatment of obese animals with IL-22 also showed significant improvements in circulating triglycerides, liver function (AST:A1F ratio) and a reduction in hepatic lipid accumulation. IL-22 has also been shown to be protective in other models of liver disease including alcoholic hepatitis, acute-on-chronic liver failure, hepatic fibrosis and para-cetamol induced liver injury, and there are 3 versions of IL-22 based therapeutics in clinical trials for such pathologies. Interestingly, the IL-22 receptor, IL-22Ra1 is highly expressed in the pancreas and liver. Our study aimed to define the role of endogenous IL-22 in the liver and pancreas to provide additional support for IL-22-therapy in non-alcoholic fatty liver disease (NAFLD).

**Method:** To study the role of endogenous IL-22 in the pancreas and liver, we generated tissue specific IL-22Ra1 knockout mice lacking the IL-22 receptor, IL-22Ra1 is highly expressed in the pancreas and liver. We found that IL-22Ra1Hep−/− animals had a worsened phenotype which worsened on a high-fat diet. We also found that whilst female animals did not gain as much weight as male animals on a high-fat diet, female IL-22Ra1b-cell−/− mice had a worsened phenotype compared to males.
**Conclusion:** We confirmed the role of endogenous IL-22 in maintaining insulin quality control and healthy hepatic function. We also discovered a novel role for endogenous IL-22 in the pancreatic-beta cell-liver axis and demonstrated the importance of targeting IL-22 to both pancreatic beta-cells and hepatocytes to treat NAFLD.

**Background and aims:** Coronavirus disease-2019 (COVID-19) vaccination is recommended for all patients with chronic liver disease (CLD) and liver transplant recipients (LTR). However, the immunogenicity of COVID-19 vaccines such as ChAdOx1 (vector-based) and BBV152 (inactivated virus) in these immunocompromised patients is unknown. Therefore, we aimed to compare the humoral and cellular immune responses of CLD patients, LTR, and healthy individuals against the available COVID-19 vaccines.

**Method:** Completely vaccinated (either with ChAdOx1 or BBV152) non-cirrhotic CLD patients (NCCLD), cirrhotic patients, and LTR were compared against age-matched healthy controls (HC) for anti-spike antibody response (by chemiluminescence immunoassay [CLIA] method) and immune profiling of the T and B cells (by flow cytometry). Also, we assessed the number of patients developing breakthrough infections post-vaccination. We excluded patients with renal failure, active sepsis, patients <2 weeks from the last vaccination dose. An individual with antibody levels <15 AU/ml was considered as a non-responder.

**Results:** Fifty NCCLD patients, 63 compensated cirrhosis (CC), 50 decompensated cirrhosis (DC) patients, 60 HC, and 17 LTR consented for the study (Fig. A). A similar proportion of patients in NCCLD (16%) and HC (8.3%) were non-responders (p = 0.21). CD4 central memory

![Figure: HandE sections of animal livers at 20 weeks of age](image)

- **Groups** | **Responders**
- Healthy controls (n = 60) | 91.7%
- Non-cirrhotic CLD (n = 50) | 84%
- Compensated cirrhosis (n = 63) | 82.5%
- Decompensated Cirrhosis (n = 50) | 66%
- LT recipients (n = 17) | 41.2%

![Figure: (abstract: THU184)](image)

**THU184**

**Patients with decompensated cirrhosis and liver transplant recipients demonstrate poor humoral and cellular immune response against COVID-19 vaccine**

Anand Kulkarni¹, Sasikala Mitnala¹, Sowmya Iyengar¹, Shashidhar Jaggaiahgari¹, Baqar Gora¹, Hardik Rugwani¹, Mithun Sharma¹, Nagaraja Rao Padaki¹, Nageshwar Reddy¹. ¹AIG Hospitals, Hyderabad, India

**Email:** anandvk90@gmail.com

**Background and aims:** Coronavirus disease-2019 (COVID-19) vaccination is recommended for all patients with chronic liver disease (CLD) and liver transplant recipients (LTR). However, the immunogenicity of COVID-19 vaccines such as ChAdOx1 (vector-based) and BBV152 (inactivated virus) in these immunocompromised patients is unknown. Therefore, we aimed to compare the humoral and cellular immune responses of CLD patients, LTR, and healthy individuals against the available COVID-19 vaccines.

**Method:** Completely vaccinated (either with ChAdOx1 or BBV152) non-cirrhotic CLD patients (NCCLD), cirrhotic patients, and LTR were compared against age-matched healthy controls (HC) for anti-spike antibody response (by chemiluminescence immunoassay [CLIA] method) and immune profiling of the T and B cells (by flow cytometry). Also, we assessed the number of patients developing breakthrough infections post-vaccination. We excluded patients with renal failure, active sepsis, patients <2 weeks from the last vaccination dose. An individual with antibody levels <15 AU/ml was considered as a non-responder.

**Results:** Fifty NCCLD patients, 63 compensated cirrhosis (CC), 50 decompensated cirrhosis (DC) patients, 60 HC, and 17 LTR consented for the study (Fig. A). A similar proportion of patients in NCCLD (16%) and HC (8.3%) were non-responders (p = 0.21). CD4 central memory

![Figure: (abstract: THU184)](image)

![Figure: (abstract: THU184)](image)

![Figure: (abstract: THU184)](image)

- **P < 0.05**
POSTER PRESENTATIONS

cells and CD4 effector cells were lower in the NCCLD patients, while the other immune cells were similar in both groups (Fig. B). Non-response was similar between CC (17.5%) and healthy individuals (8.3%; p = 0.18). Only CD4 effector cells were lower in CC patients than healthy individuals, while the other immune cells were similar in both groups. A higher proportion of patients in DC group (34%) were non-responders than CC (17.5%; p = 0.04) and HC group (8.3%; p < 0.001). CD4 naïve cells, CD4 effector cells, B cells, and B memory cells were lower in the DC group. Though the central memory cells were higher in the DC group, they could not differentiate into effector cells (Fig. C). Fifty-nine percent in LT group were non-responders compared to 8.3% in HC group (p < 0.001). On immune profiling, CD4 and CD8 naïve cells were higher in the marrow in the LT group, while the CD4 effector memory cells and CD4 and CD8 effector cells were lower in the LT group. Furthermore, B cells were lower in the LT group, suggesting poor antibody response (Fig. D). Breakthrough infections were slightly higher in CC and DC group but non-significant (healthy-3.3%; NCCLD-2%; CC-8%; DC-8%; ITR-5.88%). Except for two patients in the DC group, all breakthrough infections were mild.

Conclusion: Patients with decompensated cirrhosis and liver transplant recipients demonstrate poor humoral and cellular immune response against COVID-19 vaccines. Therefore, decompensated cirrhosis patients and liver transplant recipients require a booster dose of COVID-19 vaccination.

THU185

Presence of cirrhosis in chronic liver disease patients associates with a lower immune response to COVID-19 vaccines—a multicenter European study

André L. Simão1, Carolina Santos Palma1, Laura Izquierdo-Sánchez2, Antonella Putignano3, Ángela Carvalho-Gomes4, Andreas Posch5, Paola Zanaga6, Irina Girleanu7, Carlos Araújo1, Degré Delphine8, Thierry Gostout4, Iván Sahuco4, Sofia Carvalhã9, Miguel Mourã9, Mariana Moura Henriques1, Diogo A. E. Fernandes1, Francisco Marques1, Jesús Maria Banales9,10,11,12, Manuel Romero Gomez13, Anca Trifan7, Francesco Paolo Russo6, Rudolf E. Stauber5, Marina Berenguer4, Andreas Posch5, Thierry Gustot8, Iván Sahuco4, Elia Spagnolo6, Sofia Carvalhã9, Paola Zanaga6, Irina Girleanu7, Carlos Araújo1, Degré Delphine8, Thierry Gostout4, Iván Sahuco4, Sofia Carvalhã9, Miguel Mourã9, Mariana Moura Henriques1, Diogo A. E. Fernandes1, Francisco Marques1, Jesús Maria Banales9,10,11,12, Manuel Romero Gomez13, Anca Trifan7, Francesco Paolo Russo6, Rudolf E. Stauber5, Marina Berenguer4, Christophe Moreno4, João Gonçalves1, Helena Cortez-Pinto1,14, Rui Castro1,1 Research Institute for Medicines (iMed.ULisboa), Faculty of Pharmacy, Universidade de Lisboa, Lisbon, Portugal; 2Department of Liver and Gastrointestinal Diseases, Biodonostia Health Research Institute, Universidad de Navarra, Pamplona, Spain; 3Department of Internal Medicine, Medical University of Graz, Graz, Austria; 4Gastroenterology and Hepatology, Basel, Switzerland; 5Cantonal Hospital St. Gallen, Division Gastroenterology and Hepatology, Basel, Switzerland; 6Division of Gastroenterology and Hepatology, Cantonal Hospital St. Gallen, Liver Biology Laboratory, St. Gallen, Switzerland; 7Cantonal Hospital St. Gallen, Institute of Immunobiology, St. Gallen, Switzerland; 8University Hospital Basel, Department of Biomedicine, Bioinformatics Core Facility, Basel, Switzerland; 9Cantonal Hospital St. Gallen, Division Gastroenterology and Hepatology, St. Gallen, Switzerland; 10University Hospital of Basel, Department of Biomedicine, Translational Hepatology, Basel, Switzerland; 11Department of Liver and Gastrointestinal Diseases, CIBERehd, Instituto de Salud Carlos III (ISCIII), Madrid, Spain; 12National Institute for the Study of Liver and Gastrointestinal Diseases, CIBERehd, Instituto de Salud Carlos III (ISCIII), Madrid, Spain; 13University of Basel, Department of Biomedicine and Genetics, School of Sciences, University of Navarra, Pamplona, Spain; 14Department of Internal Medicine, Università di Padova, Padova, Italy; 15Division of Gastroenterology and Hepatology, Iasi, Romania; 16Institute for Medical Immunology, Erasmus Campus, Brussels, Belgium; 17Department of Gastroenterology, Centro Hospitalar Universitário Lisboa Norte, Lisbon, Portugal; 18National Institute for the Study of Liver and Gastrointestinal Diseases, CIBERehd, Instituto de Salud Carlos III (ISCIII), Madrid, Spain; 19Department of Biochemistry and Genetics, School of Sciences, University of Navarra, Pamplona, Spain; 20Biogen pA, Basque Foundation for Science, Bilbao, Spain; 21Digestive Diseases Department, Virgen del Rocio University Hospital, Institute of Biomedicine of Seville, University of Seville, Seville, Spain; 22Clinica Universitaria de Gastroenterologia, Facultad de Medicina, Universidad de Lisboa, Lisbon, Portugal

Email: adlsimao@ff.ulisboa.pt

Background and aims: Vaccines in the European Union (EU) to prevent COVID-19 have been shown to be safe and effective in immunocompetent subjects. Nonetheless, studies in patients with chronic liver disease (CLD) are lacking. Our aim was to assess the humoral immune response of two-dose COVID-19 vaccines among CLD patients of different etiologies and identify predictors of “low” versus “high” humoral response.

Method: Patients were recruited from clinical centers in 6 EU countries, as part of a large consortium study. Serum levels of IgG, IgM (nM) and neutralizing antibodies (NA, %) against the SARS-CoV-2 spike S1 protein were determined in samples collected prior to vaccination (T0) and at least 14 days after the second vaccination dose (T2). Patients (n = 195) were divided into “low” (51.4%) or “high” (48.6%) responders according to their IgG antibodies at T2, using 419 nM (median) as the cut-off value. Logistic regression analysis was used to explore features associated with the vaccine-induced IgG levels.

Results: All patients were fully vaccinated with either BNT162b2 (68%), mRNA-1273 (21.5%) or ChAdOx1 (10.5%). Their median age was 58 (range 21–85); 57.4% were male. Underlying liver disease etiology included alcohol (28.7%), NAFLD (21%), HCV (29.2%) and HBV (16.9%), among others. 61.5% presented with cirrhosis. At T0, spike S1 IgG, IgM and NA levels were 0.76 (95% confidence interval (CI), 0.42–1.10), 0.37 (95% CI, 0.30–0.45) and 22.99 (95% CI, 21.39–24.58), respectively, increasing to 446.07 (95% CI, 400.60–491.53), 3.91 (95% CI, 2.20–5.62) and 78.88 (95% CI, 74.91–82.85) at T2 (p < 0.0001 for all). In addition, IgG and NA levels showed a high positive correlation. Age [odds ratio (OR) 1.06 (1.03–1.10)], alcohol [OR 2.25 (1.15–4.41)], metabolic drugs [OR 2.30 (1.20–4.43)], hepatocellular carcinoma [OR 5.41 (1.15–25.52)] and evidence of cirrhosis [OR 3.85 (1.95–7.61)], as well as type of vaccine, predicted “low” response. In multivariable analysis, cirrhosis and type of vaccine (ChAdOx1 >BNT162b2 >mRNA-1273) remained the only independent predictors of “low” response.

Conclusion: CLD patients with cirrhosis exhibit lower immune responses to COVID-19 vaccination, irrespective of disease etiology. Further, the type of administered vaccine appears to predict levels of humoral response, although this needs validation in larger cohorts with a more balanced representation of all vaccines.

THU186

Heterogeneity of peripheral blood monocytes in patients with cirrhosis

Anne Geng1, Robert G Brenig1,2, Mechthild Lütge2, Julien Roux4, Hung-Wen Cheng1, Patrizia Kuenzler2, David Semela2, Markus Heim1,3, Burkhard Ludewig3, Christine Bemsmiejer1,7,8

1University Hospital of Basel, Department of Biomedicine, Translational Hepatology, Basel, Switzerland; 2Division of Gastroenterology and Hepatology, Cantonal Hospital St. Gallen, Liver Biology Laboratory, St. Gallen, Switzerland; 3Cantonal Hospital St. Gallen, Institute of Immunobiology, St. Gallen, Switzerland; 4University Hospital Basel, Department of Biomedicine, Bioinformatics Core Facility, Basel, Switzerland; 5Cantonal Hospital St. Gallen, Division Gastroenterology and Hepatology, St. Gallen, Switzerland; 6University Hospital of Basel, Department of Biomedicine, Translational Hepatology, Basel, Switzerland; 7Clarinis, University Center for Gastrointestinal and Liver Disease, Basel, Switzerland

Email: anne.geng@unibas.ch

Background and aims: In patients with cirrhosis, we recently discovered dysfunctional monocytes (M-MDSC, CD14HI-LA-DR’AXL’, CD14’MERTK’) prevailing over regular monocytes, which were associated with reduced capacity to repel microbial challenge and infection susceptibility. Transcriptome wide single cell RNA sequencing (scRNA-seq) is expected to further enhance the understanding of the plasticity of immune cell differentiation processes in disease conditions. We aimed to systematically dissect the stage specific heterogeneity of circulating monocytes using scRNA-seq in cirrhosis with the intension to identify potential future immunotherapeutic targets.
Method: Monocytes (20,000 cells/sample) from compensated (CC, n = 5), decompensated (DC, n = 5) cirrhosis patients and healthy controls (HC, n = 5) were prepared for scRNA-seq (10X Genomics) and analysed (>4000 cells/sample) using R/Bioconductor. Flow cytometric analyses were used to confirm transcriptional findings on a translational level and to further evaluate the function of distinct monocytes.

Results: Our scRNA-seq data was grouped into eight monocyte clusters, based on the expression of specific genes, where five clusters were annotated to classical (CD14+CD16+), one cluster to intermediate (CD14+CD16+) and one cluster to non-classical (CD14−CD16−) monocyte subsets. One cluster showed a M-MDSC-like gene expression. CD14+CD16+–like monocytes were reduced in CC and DC patients, while M-MDSC-like monocytes were increased and gene expression of MHC class II members was downregulated compared to healthy controls. Differentially expressed (DE) gene analysis revealed upregulation of CD52, a T cell suppressor and inhibitor of TLR-signaling, in monocytes from CC/DC compared to HC. Upregulation of CD52 on monocytes was confirmed on translational level in CC/DC patients, but not detected on monocytes of patients with acute decompensation (AD) or acute-on-chronic liver failure (ACLF). CD52-expressing monocytes exhibited higher levels of CD16, HLA-DR, AXL and CD206, showed higher phagocytosis capacity and increased cytokine production (TNF-alpha, IL-6 and IL-10) upon microbial challenge (TLR4/TLR2 agonism). T cells co-cultured with monocytes with high proportion of CD52 expression (>60%) from cirrhosis patients showed reduced proliferation activity compared to T cells co-cultured with monocytes from healthy donors with lower CD52 expression (<40% of monocytes).

Conclusion: Using scRNA Seq we have identified eight circulating monocyte clusters with distinct prevalence between HC and CC/DC. DE gene analysis highlighted plasticity of CD52 expression on monocytes during disease evolution of cirrhosis.

THU187
JAM-A is a multifaceted regulator in hepatic fibrogenesis, supporting LSEC integrity and stellate cell quiescence

Jonathan Frederik Brozat1, Elisa Brandt1, Myriam Stark1, Petra Fischer1, Theresa Hildegard Wirtz1, Alexander Flaßhove1, Aaron Nikolai Rodenhausen1, Tanja Vajen2, Samira Abu Jhaisha1, Anjali A. Röth4, Rory R. Koenen3, Hacer Sahin1, Jonathan Frederik Brozat1, Elisa Brandt1, Myriam Stark1, Petra Fischer1, Theresa Hildegard Wirtz1, Alexander Flaßhove1, Aaron Nikolai Rodenhausen1, Tanja Vajen2, Samira Abu Jhaisha1, Anjali A. Röth4, Rory R. Koenen3, Hacer Sahin1.

Background and aims: Leukocyte extravasation is a hallmark of hepatic inflammation. Reduced shear stress within hepatic sinusoids and the specific phenotype of liver sinusoidal endothelial cells (LSEC) cumulate in differing adhesion characteristics during liver fibrosis. The Junctional Adhesion Molecule A (JAM-A) is a crucial regulator of leukocyte extravasation and upregulated in human viral fibrosis. The aim of this study was to define the functional role of cell-specific surface JAM-A during hepatic fibrogenesis, applying distinct knock-out strategies in a murine model.

Method: Complete, conditional intestinal epithelial, conditional endothelial and bone marrow chimeric jam-a knockout animals (C57Bl/6) were treated with carbon tetrachloride (CCl4, 6 weeks). Livers were investigated by qRT-PCR, Western blotting, immunohistochemistry, immunofluorescent stainings and flow cytometry. The functional relevance of JAM-A was assessed using co-culture models and flow-based adhesion assays.

Results: Complete and bone-marrow derived jam-a knockout animals showed aggravated fibrosis with increased non-sinusoidal, perivascular accumulation of CD1B+F4/80+ monocyte-derived macrophages in contrast to wild type mice. Despite being associated with disturbed endothelial barrier function, an intestinal epithelial jam-a knockout did not affect fibrogenesis. In endothelial-specific jam-a knockout animals, liver fibrosis was aggravated alongside CD31-sinusoid capillarization and hepatic stellate cell (HSC) activation. Here, leukocyte infiltration and adhesion to LSECs remained unaffected.

Conclusion: Our models decipher cell-specific JAM-A to exert crucial functions during hepatic fibrogenesis. JAM-A on bone marrow-derived cells regulates non-sinusoidal vascular immune cell adhesion and recruitment, while endothelial JAM-A controls liver sinusoid capillarization and LSEC-linked HSC quiescence.

THU188
Diminished function of cytotoxic T- and NK-cells in severe alcohol-associated hepatitis

Adam Kim1, Christina Cajigas-Du Ross2, David Streem2, Nicole Welch1, Adam Kim1, Christina Cajigas-Du Ross2, Nicole Welch1, Javidiya Dasarathy3, Srinivasan Dasarathy1, Laura Nagy4, 1Cleveland Clinic, Inflammation and Immunity, Cleveland, United States; 2Cleveland Clinic, Lutheran Hospital, United States; 3MetroHealth; 4Cleveland Clinic, Inflammation and Immunity, Cleveland, United States.

Background and aims: Severe Alcohol-associated Hepatitis (sAH) is characterized by inflammation and infiltration of immune cells into the liver. Peripheral monocytes are a major infiltrating cell type that can exacerbate inflammation and damage to the liver. sAH patients have a higher peripheral leukocyte count and an increased proportion of inflammatory monocytes. Even though there are more monocytes, sAH patients are often extremely susceptible to infections. Cytotoxic NK-cells and CD8 T-cells play an important immunological role in triggering apoptosis in infected cells, particularly monocytes. Cytotoxic cells secrete cytotoxic granules containing granzymes, perforin, and in humans, granulysin, to kill cells. We hypothesize that in sAH, cytotoxic cells are dysfunctional and unable to trigger cell death in target cells.

Method: We performed single-cell RNA-seq (scRNA-seq) in PBMCs collected from patients with sAH (n = 4) and healthy controls (HC, n = 4). Multi-panel intracellular flow cytometry was conducted to understand changes in cell proportion, correlated gene expression, and cytotoxic granule contents in NK-cells and CD8 T-cells in PBMCs from patients with sAH (n = 9) and HC (n = 7), as well as patients with moderate AH (mAH, n = 6), heavy drinkers (HD, n = 8), alcohol-associated cirrhosis (AC, n = 8), and non-alcohol-associated steatohepatitis (NASH, n = 8).

Results: scRNA-seq revealed receptors required for cytotoxic cell recognition of activated monocytes were downregulated in all
THU100
Liver cirrhosis and cirrhosis etiology impacts the circulating immune mediators of early stage hepatocellular carcinoma
Boris Beudeker1, Anthony Groooshuismink1, Annemie Van der Eijk2, Jose Debes1, Andre Boonstra1, Erasmus MC, Gastroenterology and hepatology, Rotterdam, Netherlands; 2Erasmus MC, Viroscience, Rotterdam, Netherlands
Email: borisbeudeker@live.nl

Background and aims: Novel blood biomarkers to predict and detect curable, early stage hepatocellular carcinoma (HCC) is the most effective strategy to improve survival of HCC patients. Others and we have previously published on the applicability of serum immune proteins as early HCC biomarkers, but these studies had limited reproducibility. We now study in detail the contribution of the cirrhotic stage and disease etiology on the circulating immune response, in order to increase the diagnostic robustness of an early HCC immune signature.

Method: A retrospective cohort of 1585 patients with pathology- or radiology-proven HCC was established at patients diagnosed at our large tertiary HCC referral center, among them were 522 (33%) with BCLC 0/A stage HCC. Immune profiles of a balanced cohort of 188 cirrhotic patients, and 195 early HCC patients with hepatitis B (HBV), hepatitis C (HCV), ALD alcoholic liver disease (ALD) or non-alcoholic liver disease (NAFLD) were determined through serum multiplex profiling.

Results: We show that liver cirrhosis had a profound effect on the levels of circulating immune proteins with significant dysregulation of 24 out of 59 serum immune mediators. Stratification of cirrhosis patients in groups with distinct etiologies identified 45 significant immune mediators and heat map revealed obviously distinct immune profiles in each etiology. HBV-cirrhosis was characterized by high levels of circulating TRAIL and IFN-gamma, HCV-cirrhosis by high levels of IP-10 and the immune profiles of ALD-cirrhosis; NAFLD-cirrhosis were more comparable with higher levels of IL-8, IL-6, CCL25 and LIF.

Eight immunological mediators were significant independent predictors of early stage HCC and displayed specificity for one of the four cirrhosis etiologies. These immune mediators improved existing tumors marker efficacy and when combined with AFP detected early stage HCC with an AUC of 0.80.

Conclusion: HCC develops in an inflammatory heterogeneous background. In our search for predictive HCC markers, we found that liver cirrhosis and cirrhosis etiology had a profound impact on the circulating immune response and associated with a wide repertoire of pro-inflammatory and HCC promoting immune mediators. Moreover, we identified Immunological markers that differentiated early stage HCC from cirrhosis. Strict stratification resulted in a set of immune mediators with good sensitivity for early stage HCC of different etiologies.

THU198
Multi-omics analysis of human livers reveals variation in intrahepatic inflammation across chronic hepatitis B infection phases
Noé Axel Montanari1, Ricardo Ramirez2, Abhishek Aggarwal2, Nicholas Van Buuren3, Michael Doukas1, Christina Moon2, Scott Turner3, Lauri Dieih3, Li Li4, Jose Debes1, Becket Feierbach2, Andre Boonstra1, Erasmus MC, Gilead Sciences
Email: boonstra.andre@gmail.com

Background and aims: Chronic HBV is clinically defined in 4 phases by a combination of serum HBV DNA levels, HBeAg status and ALT: immunotolerant (IT), immune-active (IA), inactive carrier (IC) and HBeAg-negatve hepatitis (ENEG). Immune and virological differences between phases, as detected in blood, have proven useful but do not fully explain the interrelation between the clinical phenotype and the immunological mechanism in the liver. We aimed to study the intrahepatic immune profile across the clinical phases in order to better understand the immunological mechanism of HBV.

Method: Immunological composition and transcriptional profiles of FFPE core needle liver biopsies in chronic HBV phases vs healthy were evaluated by multiplex immunofluorescence and RNA-Seq (n = 37 and 78, respectively).

Results: Irrespective of the phase-specific serological profiles, increased intrahepatic immune-gene expression and frequency were observed in chronic HBV compared to healthy control livers. A greater transcriptomic de-regulation was seen in IA and ENEG (172 vs 243 DEGs) than in IT and IC (13 vs 35 DEGs) livers. ISG, immune-activation and exhaustion genes (ICOS, CTLA4, PDCD1) together with chemokine genes (CXCL10, CXCL9) were significantly induced in IA and ENEG livers. Moreover, distinct immune profiles associated with ALT elevation, and a more accentuated immune-exhaustion profile (CTLA4, TOX, SLAMFS, FOXP3) found in ENEG and set it apart from IA phase (LGALS9, PDCD1). Interestingly, all HBV phases showed downregulation of metabolic pathways vs healthy livers (fatty and bile acid metabolism). Finally, we found increased leukocyte infiltration correlated with serum ALT, but not with HBV DNA or viral proteins.

Conclusion: Our comprehensive multi-omics analysis of human liver revealed distinct inflammatory profiles and pronounced differences in intrahepatic gene profiles across all chronic HBV phases in comparison to healthy liver.
Plasmalemma vesicle-associated protein expression is driven by senescent cell-endothelial crosstalk and shapes the immune landscape in chronic liver disease

Alex Wilkinson¹, Daniel Patten¹, Sam Hulme¹, Matthew Hoare², Shishir Shetty³, University of Birmingham, Institute of Immunology and Immunotherapy, United Kingdom; ²University of Cambridge, Department of Medicine, United Kingdom

Email: axw717@student.bham.ac.uk

Background and aims: Chronic liver diseases (CLDs) are driven by leukocyte recruitment and persistent inflammation. Cellular senescence is a key feature of CLD, yet its contribution to liver inflammation is poorly understood. Senescent cells release a secretome (senescence-associated secretory phenotype or SASP) which facilitates their clearance through leukocyte recruitment. This process is mediated by hepatic sinusoidal endothelial cells (HSEC) which undergo phenotypic and functional changes in response to SASP treatment. Plasmalemma vesicle-associated protein (PIVAP) is highly expressed by foetal liver endothelium, playing an important developmental role, yet human single-cell studies have highlighted its re-emergence in liver cirrhosis and hepatocellular carcinoma (HCC). Whilst PIVAP has previously been proposed as a leukocyte trafficking molecule, its specific role in hepatic leukocyte recruitment is not known. We hypothesised that PIVAP expression is driven by the senescent tissue microenvironment in CLD and sought to investigate its potential role in SASP-mediated leukocyte recruitment.

Method: PIVAP expression was characterised, in human liver samples by qPCR and immunohistochemistry, and in primary human HSEC by immunocytochemistry. SASP was obtained using a model of oncogene-induced senescence (conditioned media from RAS-senescent IMR90 fibroblasts–RAS-CM), and the effects of SASP treatment on primary HSEC were determined by qPCR and confocal microscopy. To investigate the molecular mechanisms of SASP-mediated leukocyte recruitment, flow-adhesion assays were performed with SASP-stimulated HSEC (following siRNA or antibody treatment) and peripheral blood lymphocytes or monocytes.

Results: PIVAP was significantly upregulated in liver endothelium of CLD and HCC patients compared to healthy controls, correlating with increased expression of senescent markers, p21 and p16. Treatment of primary HSEC with RAS-CM significantly increased PIVAP expression and stimulated recruitment of both lymphocytes and monocytes under physiologically low shear stress. However, these processes were morphologically and molecularly distinct. Lymphocytes predominantly (~60%) transmigrate via the transcellular pathway which was selectively inhibited by ICAM-1 blockade. In contrast, >90% monocytes transmigrate paracellularly in a CD31-dependent manner. Furthermore, genetic or antibody-mediated inhibition of PIVAP selectively impaired SASP-mediated monocyte transmigration whilst having no effect on lymphocyte recruitment.

Conclusion: These data highlight a previously unreported link between PIVAP and senescence, in which PIVAP expression is driven in HSEC by the senescent secretome to facilitate monocyte recruitment. PIVAP could therefore be a novel target for perturbing aberrant monocyte recruitment in liver disease.

THU193

Dysfunctional liver-resident CCR6+ CD8 T cells during persistent viral liver infection

Miriam Bosch¹, Nina Kallin¹, Donakonda Sainitin¹, Hannah Winterstellers¹, Ulrike Potzker², Dirk Wohlebër¹, Percy A. Knolle¹,¹ Institute of Molecular Immunology, Technical University of Munich, Munich, Germany; ²Institute of Virology, Technical University of Munich; ¹Institute of Virology, Helmholtz Center for Environment and Health; ²German Center for Infection Research, Munich

Email: percy.knolle@tum.de

Background and aims: CD8 T cell-mediated immunity is key for the clearance of hepatitis B virus infection and other hepatotropic viral infections. Persistent viral liver infections, however, are characterized by a lack of a robust anti-viral CD8 T cell response. We aimed at determining the mechanism causing the lack of CD8 T cell functionality during persistent viral liver infection.

Method: We used Adenovirus-based models (coding for ovalbumin or the HBV genome) to investigate persistent or acute-resolved infection. For virus-specific T cell analysis, we transferred naïve (CD44hiCD62Lhi) virus-specific CD8 T cells bearing a congenic marker before infection. T cells were analysed at different time points for phenotypic and functional characterization and RNAseq.

Results: After acute-resolved viral infection, we identified two distinct virus-specific CD8 T cell populations in the liver, i.e. CXCR3+ and CXCR6+CD69+ CD8 T cells. Contrasting, virus-specific CD8 T cells during persistent infection were mainly CXCR6+CD69+ liver-resident CD8 T cells. Independent of infection outcome, liver CXCR6+CD69+ CD8 T cells expressed a tissue-residency gene signature. However, virus-specific CXCR6+CD69+ CD8 T cells during persistent infection did not produce cytokines, lacked cytotoxicity, and were hence termed dysfunctional liver-resident T cells. Transcriptome analysis enabled us to define a single pathway marking these dysfunctional CXCR6+CD69+ T cells in persistent infection when compared to cytotoxic liver-resident memory T cells after resolved infection.

Conclusion: The identification of a single transcription factor distinguishing effector liver-resident memory T cells from dysfunctional liver-resident virus-specific liver-resident CD8 T cells in preclinical models of persistent expression of ovalbumin and HBV points towards a liver-specific mechanism mediating immune tolerance during persistent hepatocyte infection.
Background and aims: The viral entry-inhibitor bulevertide (BLV) leads to a decline of HDV viremia in chronic HDV infection, however, treatment for several years is likely required to prevent relapse. Sustained treatment response may be fostered by therapy-induced restoration of HDV-specific CD8+ T cell responses that are exhausted due to high viremia and antigen loads during chronic HDV infection. We thus studied the effect of BLV monotherapy on HDV-specific CD8+ T cell repertoire, phenotype, and functionality.

Method: HDV-specific CD8+ T cell responses were studied in 35 HDV infected patients, of whom 14 cirrhotic patients started treatment with BLV. Samples were collected from baseline up to 40 weeks on-treatment. HDV-specific CD8+ T cells were analyzed either upon stimulation with overlapping peptides (olp), spanning the entire L- and the S-protein, or upon stimulation with optimal epitopes in HLA-matched patients, following 14 days of in vitro culture. Ex vivo high-dimensional flow cytometry analysis of peptide-loaded MHC class I-specific CD8+ T cells in selected patients throughout therapy is currently ongoing.

Results: In two-thirds of patients, an HDV-specific CD8+ T cell response was detectable at baseline. This was characterized with high levels of apoptosis in CD56dimCD16+NK cells and tumor necrosis factor (TNF) co-secretion, without additional interleukin (IL)-2 production in response to optimal epitope stimulation in HLA matched patients. Targeted epitopes were restricted by HLA-B alleles only, predominantly by HLA-B*35 and HLA-B*18. Direct comparison of patient samples from an early time point during therapy (week 4) with a later time point during treatment (week 36–40) did not indicate a restoration or boosting of HDV-specific CD8+ T cell functionality coinciding with decreasing HDV viremia. Using the comprehensive olp approach, half of the patients displayed an HDV-specific CD8+ T cell response at the late time point during treatment (median of 2 olps recognized per patient), which is comparable with the response-rate in untreated patients.

Conclusion: During the first 40 weeks of BLV treatment, no obvious increase in HDV-specific CD8+ T cell response breadth and magnitude was observed. This might be due to the slow decline of HDV viremia, the fact that all patients treated with BLV had liver cirrhosis, and mostly unchanged HBsAg levels during BLV monotherapy that may continue to mediate HDV-specific CD8+ T cell exhaustion. In addition, some of the HDV-specific CD8+ T cell responses target epitopes affected by viral escape mutations and these responses are unlikely to benefit from reduction of viremia. Longer follow-up during continued BLV therapy, high-dimensional analysis of CD8+ T cell phenotype and function, as well as analysis of patients with BLV/pegIFN combination therapy will expand our understanding of HDV-specific CD8+ T cell restoration during BLV therapy.

Conclusion: Our findings imply that high ILT2 expression would facilitate HBV viral persistence by tempering NK cells into silence and blockade of ILT2 can enhance NK cell function as an alternative approach to treat CHB.
THU196
Elevated serum bilirubin levels and aminotransferases are associated with immuno-modulatory and suppressive subsets in pregnant females with intrahepatic cholestasis and hepatitis E virus infection

Anoushka Saxena1, Minal Kashyap2, Prabhjyoti Pahwa1, Fatima Ali1, Hamda Siddiqui1, E. Preedia Babu1, Y.M. Mala2, Shakun Tyagi2, Nirupma Trehanpati1, 1Institute of Liver and Biliary Sciences, New Delhi, India, Department of Molecular and Cellular Medicine, New Delhi, India; 2Maulana Azad Medical College, New Delhi, India, Department of Obstetrics and Gynaecology, New Delhi, India
Email: trehanpati@gmail.com

Background and aims: Elevated serum bilirubin levels and liver functions are well-recognized markers of hepatic damage and inflammation. Viral hepatitis, intrahepatic cholestasis of pregnancy, gallstones and pre-eclampsia are the most common causes of jaundice in pregnant women, inducing significant morbidity and mortality in both pregnant women and their infants. Therefore, we aimed to investigate the relationship between deranged liver function, high bilirubin and the immune dysfunction during pregnancy.

Method: An observational prospective study was carried out at a tertiary care hospital on antenatal patients with clinical and biochemical jaundice over a period of one year. Peripheral immune cell subsets were analyzed in pregnant women with serum bilirubin >2.0 mg/dl (Gr.1, n = 20, 25.8 ± 2), positive for IgM/IgG Hepatitis E virus (A VH-E) (Gr.2, n = 5, 24 ± 2) and healthy pregnant women (Gr.3, n = 7, 24.5 ± 2) by flow cytometry.

Results: Females with high bilirubin levels; 2–5 mg/dl (64%), 5–10 mg/dl (16%), >10 mg/dl (12%) had deranged LFT (28%), asymptomatic (12%), jaundice (31%), k/c/o liver disease (3%), k/c/o hepatitis-E (3%) and 6% presented with other complaints. Pregnant females with high bilirubin levels showed an overall increased percentage of Monocytes (p = 0.0012), CD4+ (p = 0.0009) and CD8+ T-cells (p <0.0001), compared to healthy (Fig. A). However, an increased expression of inhibitory markers (Fig. B); PD-1 (p <0.0001), CTLA-4 (p <0.0001), BTLA (p <0.0001), BLIMP-1 (p = 0.0008), SLAM-1 (p <0.0001), LAG-3 (p <0.0001), TIGIT (p <0.0001), TIM-3 (p <0.0001) on Transitional memory subset and PD-1 (p <0.0001), CTLA-4 (p <0.0001), BTLA (p <0.0001), BLIMP-1 (p = 0.0006), SLAM-1 (p <0.0001), LAG-3 (p <0.0001), TIGIT (p <0.0001), TIM-3 (p <0.0001) on effector memory subset of T-cells was evident. Compared to healthy, myeloid dendritic cell population was significantly higher (Fig. C) in females with high bilirubin (p <0.0001) and infected with HEV (p = 0.0095), as compared to healthy females, indicating immune suppression. An elevated frequency of B-cell subsets (p <0.0001) was observed in all females with high bilirubin. Yet, a defect in activation and proliferation as suggested by diminished expression of BAFF-R (p = 0.04) and APRIL (p = 0.02) and rise in PDL1 (p = 0.0025) was determined (Fig. D).

Conclusion: Our results clearly indicate that pregnant females with high bilirubin, including those infected with HEV exhibit increased suppressive T and B cells with diminished BAFF/APRIL expressing B cells.

THU197
Classification of HCV-specific CD8+ T cells by the differential expression pattern of Slamf6 and CD69 predicts that the majority of cells are rather preterminally versus terminally exhausted regardless of disease stage

Maximilian Knapp1, Christin Ackermann1, Claudia Beisel1, Vanessa Dittrich2, Melanie Wittner1, Julian Schulze Zur Wiesch1.
1University Medical Center Hamburg-Eppendorf, I. Department of Medicine, Infectious Diseases Unit, Hamburg, Germany; 2University Medical Center Hamburg-Eppendorf, Center for Diagnostics, Institute of Transfusion Medicine, Hamburg, Germany
Email: julianszw@googlemail.com

Background and aims: Exhausted T effector cells, commonly described in chronic viral infections and cancer, are phenotypically and functionally heterogeneous cell populations whose development, maintenance, and response to immunotherapies are incompletely understood. Today, many differentiations into progenitors, intermediates and terminal stages of exhausted T cells are already known based on numerous markers. A better description regarding different subsets of exhausted T cells will allow a better understanding for future cancer therapy and viral cure approaches. Acute and chronic hepatitis C (HCV) infection are ideal models to examine the development of T-cell exhaustion and its potential reversibility at cellular and molecular levels. To assess the molecular fingerprint of potential populations, we aimed to investigate the interaction of different immunomodulatory targets.

Method: HCV-specific CD8+ T cells from HLA-A*01:01, HLA-A*02:01 and HLA-A*24:02 positive patients were analyzed with a 21-color
FACS-panel evaluating the surface expression of lineage markers (CD3, CD4, CD8), ectoenzymes (CD38, CD39, CD73), markers of differentiation (CD62L, CD127), and markers of exhaustion and activation (CD96, TIGIT, PD-1, CD69, Slamf6, CD28) and transcription factors (T-bet, TCF1, NR2F6, TOX, IRF4).

**Results:** Analyzing the TIGIT-CD96-axis, the majority of HCV-specific Tet+ CD8+ T cells of all patient groups was TIGIT+ and CD96+. The frequencies of CD96+ cells in the Tet+ T cells were significantly higher than in bulk CD8+ T cells for acute, resolved and chronic infection. Furthermore, HCV-specific CD8+ T cells were stratified into four novel subsets of exhausted T cells based on expression of the transmembrane protein Slamf6 and the early activation antigen CD69 as currently described by Beltra et al. (2020, Immunity 52, 825–841) in the LCMV mouse model describing progenitor 1 (Tex prog1: Slamf6+ CD69−), progenitor 2 (Tex prog2: Slamf6+ CD69+), intermediate (Tex int: Slamf6− CD69−) and terminally exhausted (Tex term: Slamf6− CD69−) T cells. The majority of HCV-specific Tet+ cells in peripheral blood are in the Tex prog1 state and less than 6% of the Tet+ T cells were at the Tex term state.

**Conclusion:** We identified four exhausted T cell subsets defined by Slamf6 and CD69 in patients with different clinical status of HCV infection. The frequencies detected in PBMC of our patients are similar to those described in the LCMV mouse model by Beltra et al. They could also show that the majority of the Tex term subset is localized in the liver. To investigate the Tex term population in human, analyses from liver biopsies are required. In this context, it will be of interest whether the responsiveness of the Tex int subset to PD-1 blockade described in mice can also be confirmed in humans. Co-inhibitory receptors like CD96 in the TIGIT-CD155 signaling pathway also shaped the HCV-specific T cells.

**THU198**

**TAPBPR shapes the hepatitis B immunopeptidome presented on HLA class I molecules**

Ricky Sinharay*,1,2, Andreas Neerinck1, Arwen Altenburg1, Jens Bauer1,2,3,4,5, Mark R. Wills6, Juliane S. Walz3,4,5,7, Will Gelson8, Louise H. Boyle1,1 University of Cambridge, Department of Pathology, Cambridge, United Kingdom; 2Cambridge University Hospitals NHS Foundation Trust, Cambridge Liver Unit, Addenbrooke’s Hospital, Cambridge, United Kingdom; 3University Hospital Tübingen, Clinical Collaboration Unit Translational Immunology, German Cancer Consortium (DKTK), Department of Internal Medicine, Tübingen, Germany; 4University of Tübingen, Institute for Cell Biology, Department of Immunology, Tübingen, Germany; 5University of Tübingen, Cluster of Excellence iFit (EXC2180) “Image-Guided and Functionally Instructed Tumor Therapies”, Tübingen, Germany; 6University of Cambridge, Department of Medicine, Addenbrookes Hospital, Cambridge, United Kingdom; 7Margarete Fischer-Bosch Institute of Clinical Pharmacology and Robert Bosch Center for Tumor Diseases (RBCT), Stuttgart, Germany; 8Cambridge University Hospitals NHS Foundation Trust, Cambridge Liver Unit, Addenbrooke’s Hospital, Cambridge, United Kingdom

Email: rickysinharay@doctors.org.uk

**Background and aims:** The presentation of virus derived peptides on HLA class I molecules is crucial for mounting antiviral immune responses. TAPBPR is a recently identified peptide editor involved in optimizing antigen selection on MHC class I molecules. Here, we present novel data on the impact of TAPBPR on the hepatitis B (HBV) immunopeptidome presented on HLA class I by using a mass spectrometry approach.

**Method:** HeLa cells (HLA-A*68:02, -B*15:03 and -Cw12) and TAPBPR knock-out HeLa cells (TAPBPRKO) overexpressing individual HBV proteins HBsAg, Pol, HBeAg and HBx were generated. These cells were expanded to 5×10^6 cells, lysed and peptides were eluted using a pan HLA class I antibody (W6/32). Analysis was performed by liquid
chromatography coupled to tandem mass spectrometry (LC-MS/MS). Mass spectra data were then searched against a database of possible peptides that could be derived from the host and/or pathogen proteomes, to identify HBV derived peptides presented on HLA class I. The HBV immunopeptidome in TAPBPR depleted cells was compared to HeLa cells expressing wild type TAPBPR and individual HBV proteins.

**Results:** A greater number of HBV peptides were presented in TAPBPRKO cell lines compared to wild type cell lines, which was consistently observed between cells expressing different HBV proteins. This was despite the fact that no substantial change in the total cellular peptide count was observed between wild type and TAPBPRKO cells. Amino acids positions 2 and 9 were clearly preferred for binding in both wild type and TAPBPRKO cells, and a greater number of peptides were assigned to HLA-B*15:03 than HLA-A*02:01. Furthermore, semi quantitative analysis revealed that depletion of TAPBPR resulted in up-modulation of almost all HBV-derived peptides identified. In addition, changes in the hierarchy of the abundance of HBV peptides presented were observed in TAPBPRKO cells. Of the up-modulated peptides, only four have been identified previously and are catalogued on IEDB. A total of 26 HBV-derived peptides were identified, 22 (84.62%) of which were novel. Of the novel peptides 7 were only identified in the TAPBPRKO cell lines.

**Conclusion:** These findings strongly support a role of TAPBPR in HBV-derived peptide selection for presentation on HLA class I. However, it is still unclear whether this is advantageous for individuals with HBV expressing HLA alleles where TAPBPR mediates peptide exchange.

**THU199**

**Phenotypes of NK cells and the activation profile of T cells in the early stages of alcohol liver diseases**

Coral Zurera1,2, Anna Hernandez2, Aina Teniente1, Daniel Fuster3, Eva Martínez-Cáceres1, Robert Muga3, Paola Zuluaga1,2,3. *Investigation institute germans trias i pujol, immunology, badalona, Spain; 2Universitat Autònoma de Barcelona, Bellaterra, Spain; 3university hospital germans trias i pujol, internal medicine, badalona, Spain*

**Background and aims:** The role of cellular immunity in alcohol-related liver diseases (ARLD) is currently being characterized. While CD8 T cell activation is known to be detrimental, enhancing liver damage, the decrease of naïve T cells is associated with advanced liver fibrosis (ALF) in patients with alcohol use disorder (AUD). Natural Killer (NK) cells and NKT cells play an important role in the development of ARLD having subsets with opposing roles in the development of liver fibrosis. We aimed to evaluate the phenotype of NK and NKT cells and the activation profile of T cells in patients with AUD according to the presence of ALF.

**Method:** Patients were admitted to treatment of AUD between 2019 and 2021 in Germans Trias I Pujol Hospital, Spain. ALF was defined if the FIB-4 score was >2.67 (n = 19) or Forns score was >6.9 (n = 21). Patients with HCV infection, HIV infection and history of liver cirrhosis were excluded. Immunophenotyping of NK cells (CD3-CD56+, CD3-CD16+), NKT cells (CD3+CD56+), and the activation status of CD4+, CD8+ and regulatory T cells (Tregs) was evaluated according to the presence of HLA-DR.

**Results:** 79 patients (51 years, 71% males) were included. Patients had a mean AUD duration of 18 ± 11 years with a daily alcohol consumption of 155 ± 77 gr/day. Regarding the immunophenotype in peripheral blood, the mean ± SD absolute values were: 2.1 ± 0.9 cells/L for total lymphocytes, 1054.5 ± 501.7 cells/µL for CD4+, 540 ± 335.7 cells/µL for CD8+, 49.3 ± 24.8 cells/µL for Tregs, 150.3 ± 97.5 cells/µL for NK cells and 69.8 ± 78.3 cells/µL for NKT cells. The percentage of CD3-CD56+ NK cells of patients with ALF was significantly lower (4.8 ± 3.3 and 4.9 ± 3.4) than in patients without ALF (7.6 ± 6.2 and 7.7 ± 6.2), respectively. The percentage of CD3-CD16+CD56+ NK cells was significantly higher in patients with ALF (87 ± 11) compared to patients without ALF (80 ± 16) according to Forns. No significant differences were observed in the percentage of CD3-CD16+ NK cells and NKT cells among groups. ALF patients also presented an increased percentage of HLA-DR+ expressing Tregs (38 ± 11.6 and 39.2 ± 11.5) and CD8+ (16 ± 8.3 and 15.6 ± 8.8) compared to Tregs (32.7 ± 9.4 and 32.5 ± 9.3) and CD8+ (12 ± 9.1 and 12.2 ± 9) in patients without ALF according to Forns and FIB-4, respectively. The percentage of HLA-DR+ CD4+ was higher in patients with ALF (5.1 ± 3.1) than in patients without ALF (3.9 ± 3) according to FIB-4. Figure 1 depicts the aforementioned significant differences (p <0.05).

**THU200**

**A spatio-temporal map of malaria infected mouse liver**

Franziska Hildebrandt1, Johan Ankarklev1. *Stockholm University, Department of Molecular Biosciences, Stockholm, Sweden*

**Background and aims:** The liver is crucial for malaria parasite development in the vertebrate host. Once transmitted by a female mosquito, the malaria parasites start their development in the liver, before entering the symptomatic blood stage. Since the liver has high potential for an effective immune response towards invading parasites and other intruders, choosing the liver as a developmental niche is paradoxical. Thus, we aim to delineate host-pathogen interactions during the time course of an ongoing liver infection in vivo, with the main aim of studying the host’s response in a spatial context.

**Method:** To this end we are using Spatial Transcriptomics to describe the spatial organization of transcriptomic response in the mouse liver to an ongoing infection, using mosquito salivary gland lysate as a control.

**Results:** Our preliminary data suggests a differential onset of inflammation between infected and control mice, due to the presence of parasites in the tissue. We further investigated gene expression as a function of the distance to the site of infection for multiple time points and cell type compositions in specific areas of infection but also in the larger tissue context.
Conclusion: Our data indicates patterns of differential expression due to the influence of malaria parasites both locally and across tissues in challenged mice. Our preliminary data further suggests that the immune response towards a *Plasmodium* infection shows spatio-temporal patterns on the transcriptional level, providing a promising outlook for more detailed studies on the influence of the parasite on the surrounding liver environment.

**Public Health**

**THU217**

Reducing the risk of liver cirrhosis and hepatocellular carcinoma after treatment for smoking cessation in patients with chronic hepatitis B or C infection: a 12-year follow-up study

Ruey-Chang Lin¹, Chun Hsiang Wang¹,², Kuo-Kuan Chang¹, Lien-Juei Mou¹, Yuan Tsung Tseng¹, ¹Tainan Municipal Hospital (Managed by Show Chwan Medical Care Corporation), Tainan, Taiwan, ²Department of Hepatogastroenterology, ³Chung Hwa Medical University, Tainan, Taiwan, ⁴Department of Optometry; ⁵Tainan Municipal Hospital (Managed by Show Chwan Medical Care Corporation), Tainan, Taiwan, Committee of Medical Research

Email: b891040733@yahoo.com.tw

**Background and aims:** The possible hepatotoxic effect of cigarette smoking in patients with chronic hepatitis B virus (CHB) or chronic hepatitis C (CHC) virus infection has been proposed in numerous epidemiological and experimental studies. Varenicline and nicotine replacement therapy (NRT) are the current first-line treatment for smoking cessation. The present study compared the effects of different standard treatments for smoking cessation and of receiving no treatment for smoking cessation on the risk of liver cirrhosis and hepatocellular carcinoma (HCC) among patients with CHB or CHC infection.

**Method:** We identified patients with CHB or CHC infection who smoked regularly and whose data were input into Taiwan’s National Health Insurance Research Database between January 1, 2007, and December 31, 2018. The patients’ demographic data, medical history (including smoking habits), and paraclinical information were collected. The patients were classified into 4 groups—the no smoking cessation treatment, NRT only, varenicline only, and varenicline + NRT groups—according to the smoking cessation treatment they had received. Cox proportional hazards models were used to analyze the patients’ risks of liver cirrhosis and HCC, with adjustment for age, sex, comorbidities, and Charlson Comorbidity Index.

**Results:** A total of 4210 patients with CHB or CHC infection were recruited: 2535, 568, 427, and 680 were assigned to the NRT only, varenicline only, varenicline + NRT, and comparison (no treatment) groups, respectively. The mean follow-up duration was 7.2 ± 4.8 years. The outcomes were significantly different among the four groups. The NRT only, varenicline only, and varenicline + NRT groups had a lower prevalence of liver cirrhosis (p = .06) and HCC (p = .03) than did the no-treatment group in the cumulative incidence analysis (liver cirrhosis: prevalence = 8.5%, 3.9%, and 2.1% vs 11.3%, respectively; HR = 0.74[95%CI: 0.33–1.63], 0.63[0.34–1.15], and 0.40[0.19–0.84], respectively; HCC: prevalence = 15.0%, 11.6%, and 11.5% vs 23.1%, respectively; HR = 0.62[0.31–1.25], 0.32[0.10–1.00], and 0.26[0.10–0.69], respectively).

**Conclusion:** This study evaluated the effect of one month of NRT, varenicline, both, or no treatment on the risk of liver cirrhosis and HCC in smokers with CBC or CHC infection undergoing a smoking cessation program. All 3 smoking cessation treatments appeared to be effective in minimizing the risk of liver cirrhosis and HCC; a low prevalence of both conditions was observed in each of the 3 treatment groups. Cumulative incidence rates of liver cirrhosis and HCC over time among patients with CHB or CHC infection in the no smoking cessation treatment, NRT only, varenicline only, and varenicline + NRT groups.

**THU218**

Testing coverage and strategy required to sustain Hepatitis C elimination in an injecting network of people who inject drugs: a network-based model

Chloe Siegele-Brown¹, Martin Siegele-Brown², Charlotte Cook³, Mark Wright¹, Julie Parkers⁴, Salim Khakoo⁵, Ryan Buchanan⁶, ¹University Hospital Southampton NHS Foundation Trust, United Kingdom; ²University of Sussex, United Kingdom; ³University of Southampton, United Kingdom

Email: chloe.brown@doctors.org.uk

**Background and aims:** The World Health Organisation has set a target for the global elimination of Hepatitis B (HBV) and C (HCV) by 2030. To achieve the elimination target, a widespread scale-up of testing and treatment services is required. However, little is known about the level of testing required to sustain the low-prevalence state of elimination. In this study we model the testing coverage required to maintain HCV elimination in an injecting network of people who inject drugs (PWID). We also test the hypothesis that a ‘bring your friends’ testing strategy will be more efficient.

**Method:** We create a dynamic injecting network structure connecting 689 PWID based on empirical data. A burn-in period, where PWID are randomly treated according to empirical parameters until the elimination target is achieved, is followed by the 5-year simulation period. The primary outcome is the testing coverage required per month to maintain prevalence at the elimination threshold over 5 years. We compare two treatment scenarios: 1) random testing, and 2) ‘bring your friends’ testing, where 50% of tests are random and 50% of tests in injecting partners of randomly selected individuals.
**Results:** After 5 years, without any testing or treatment provision, the prevalence of HCV increased from the elimination threshold (11.68%) to a mean of 25.0% (SD 3.0%). To maintain elimination with random testing, on average 4.92% (SD 0.84%) of the injecting network needs to be tested per month. However, with a ‘bring your friends’ strategy, 3.69% (SD 0.63%) of the network needs to be tested per month ($p < 0.000001$).

The superiority of the ‘bring your friends’ approach was maintained in a sensitivity analysis that adjusted for changes in needle and syringe provision and the rate of engagement with treatment following a positive test.

**Conclusion:** If HCV testing and treatment does not continue after elimination targets are met, the prevalence of HCV in an actively injecting network of PWID will increase. A ‘bring your friends’ approach to treatment is a more efficient approach to maintaining elimination.

**Results:** Among the 7,739 individuals in the cohort, 56.9% were male, 75.2% lived in an urban area, and the mean age was 53 years. Most individuals had NAFLD/cryptogenic aetiology (43.4%), followed by alcohol-related liver disease (25.1%), hepatitis C virus (21.4%), autoimmune hepatitis (8.5%), and hepatitis B virus (1.6%). Nearly half of individuals had decompensated cirrhosis (47%). Most individuals (68.9%) received care from a gastroenterologist/hepatologist during their follow-up time, while 22.4% received care from a general practitioner alone.

The 1-year and 2-year cumulative incidences were 43.5% and 49.8%, respectively, for receiving screening by abdominal ultrasound. The 1- and 2-year cumulative incidences were 53.0% and 60.0%, respectively, for receiving any HCC screening. Individuals with hepatitis B virus had the highest 2-year cumulative incidence (73.2%) while those with NAFLD/cryptogenic aetiology had the lowest 2-year cumulative incidence (50.6%).

The 2-year cumulative incidence was 66.1% for hepatitis C virus, 63.7% for autoimmune hepatitis, and 68.4% for alcohol-related liver disease aetiologies. The 2-year cumulative incidence of HCC screening by calendar year of cirrhosis diagnosis ranged from 52.5% in 2012 to 63.4% in 2016.

**Conclusion:** We observed that HCC screening was underutilized among privately insured individuals with cirrhosis in North Carolina, indicating a need for targeted interventions to increase HCC screening rates.
**THU220**

**Cost- effectiveness evaluation of the hepatitis C elimination strategy in Cyprus in the era of affordable direct-acting antivirals**

Ilias Gountas1, Petros Katsioloudes2, Ioanna Yiasemi3, Evi Kyprianou4, Christos Mina4, Chrysanthos Georgiou4, Antri Kouroufexi5, Anna Demetriou6, Eleni Xenofontos7, Georgios Nikolopoulos1.

1University of Cyprus, Medical School; 2Evangelistria Medical Centre; 3Cyprus National Addictions Authority, Cyprus Monitoring Centre; 4Nicosia General Hospital; 5Pharmaceutical Services, Ministry of Health; 6Health Monitoring Unit, Ministry of Health; 7Limassol General Hospital, Department of Internal Medicine

Email: eliagoun@gmail.com

**Background and aims:** In the Republic of Cyprus, the prevalence of chronic Hepatitis C virus (CHC) among the general population is estimated at 0.6%, while the CHC prevalence among people who inject drugs (PWID) is estimated at 43%. A previous mathematical modeling study highlighted that to achieve Hepatitis C virus (HCV) elimination, 3080 (95% Credible intervals (CrI): 3000, 3200) patients need to be diagnosed and treated by 2034 (2680 from the general population and 400 from PWID)1. For the optimal use of available resources, it is essential to evaluate the cost-effectiveness of any proposed strategy. This study aims to undertake a cost-effectiveness analysis of the proposed HCV elimination strategy in Cyprus.

**Method:** A previously published, dynamic, stochastic, individual-based model of HCV transmission, disease progression, and cascade of care was calibrated to data from Cyprus (1). The model stratifies the population into the infected general population and the PWID population. We assumed that the ongoing HCV transmission is limited to the PWID group. The incremental cost-effectiveness ratio (ICER) per disability-adjusted life year (DALY) averted for HCV elimination versus the status quo scenario was computed. Cost-effectiveness was determined using Cyprus’ willingness-to-pay (WTP) threshold of €26623 per DALYs averted.

**Results:** Compared to the status quo, the elimination strategy would prevent 195 (95% CrI: 115, 220) and 2070 (95% CrI: 1600, 2640) new infections and DALYs by 2034, respectively. The additional required investment to meet the HCV elimination goals would be €20.4M (95% CrI: €19.4M, €21.4M)). The cost per averted DALY is estimated at €9915 (95% CrI: €7600, €13100) indicating that the elimination strategy is very cost-effective. In the probabilistic sensitivity analysis, 100% of simulations were below the WTP threshold (Figure).

![Cyprus WTP threshold](image)

**Conclusion:** Scaling-up HCV testing and treatment in Cyprus to reach the elimination targets is estimated to generate significant health and economic benefits.

**Reference:** Gountas et al. WJG 2021.

---

**THU221**

**Rethinking the management of chronic hepatitis B in the context of rural sub-saharan Africa: results from a social justice mixed methods study in rural Senegal (the AmBASS-PeCSen study)**

Marion Coste1-2, Cilor Ndong3, Aldiouma Diallo4, Assane Diouf5, Sylvie Boyer6, Jennifer Prah7, 1Aix Marseille University, CNRS, AMSE, Aix-Marseille School of Economics, Marseille, France; 2Aix Marseille Univ, INSERM, IRD, SESTSIM, Sciences Économiques et Sociales de la Santé et Traitement de l’Information Médicale, Marseille, France; 3Cheikh Anta Diop University, Anthropology, Dakar, Senegal; 4Campus International IRD-UCAD de FIRD, UMR VITROME, IRD-Université Aix Marseille, AP-HM, SSA, IHU-Méditerranée Infection, Dakar, Senegal; 5University of Pennsylvania, School of Social Policy and Practice and Perelman School of Medicine, Philadelphia, United States

Email: marion.coste@univ-amu.fr

**Background and aims:** Worldwide, the burden of chronic hepatitis B (CHB) infection is estimated to reach 800, 000 deaths annually, with highest CHB prevalence found in Western Pacific and Africa. In Senegal, where up to 10% of the adult population lives with CHB, the government aims to treat 30,000 patients by 2023. In this context, the Ministry of Health is piloting the decentralization of CHB care to rural populations in the Fatick region drawing from the 2017 EASL Clinical Practice Guidelines on the management of CHB. This study documents the CHB cascade of care in rural Senegal after community-based testing.

**Method:** All residents of households randomly selected in the rural area of Niakhar (Senegal) were offered at-home hepatitis B testing using dried blood sampling and administered socio-economic questionnaires (ANRS12356 AmBASS survey). Following a free CHB initial check-up, patients were referred to local healthcare facilities or invited to join a cohort in Dakar if eligible-for CHB management as per the Senegalese national recommendations adapted from the 2017 EASL guidelines. A few months after referral, purposeful sampling of one-on-one qualitative interviews based on an adaptation of the health capability profile were conducted to document perceptions, obstacles and levers in CHB participants linked to care and those who were not (A’Midex PeCSen study).

**Results:** In 2018–2019, 3, 118 participants representative of the Niakhar area’s population undertook hepatitis B testing. 206 participants tested positive, and among them, 163 patients (79%) performed the initial CHB check-up. By September 30 2021, 48 patients had gone to at least one visit for CHB management—a 23% linkage to care. Interviews (n = 34) revealed complex CHB-related health capability profiles, stalling high health-related motivation, skills, and self-efficacy despite low CHB-related knowledge. Gendered social norms, shared decision-making, reluctance towards blood sampling in the absence of treatment prescription, and limited ability to pay are among the main obstacles to linkage to care, and retention in CHB follow-up.
Conclusion: As the first mixed-methods study of the cascade of CHB care in rural Sub-Saharan Africa, our results call for action in rethinking CHB management to make it acceptable, accessible, and affordable to rural populations.

**THU222**

Global survey of healthcare workers’ attitudes to treatment of chronic hepatitis C infection in children and adolescents

Farah Malik1, Philippa Easterbrook2, Giuseppe Indolfi3, Claire Thorne1, 1UCL Great Ormond Street Institute of Child Health, London, United Kingdom; 2World Health Organization, Geneva, Switzerland; 3University Hospital Meyer, Firenze, Italy

Email: farah.malik.18@ucl.ac.uk

**Background and aims:** Direct acting antivirals (DAAs) are now approved for treatment of adolescents and children >3 years living with chronic hepatitis C (HCV) however, there is limited understanding of the attitudes of healthcare workers (HCWs) on expanding treatment, especially to younger age groups. We undertook the first global survey of HCWs managing HCV infection regarding treatment of children and adolescents, and on key challenges to implementation, to inform updated World Health Organization (WHO) HCV guidelines.

**Method:** A cross-sectional online survey was conducted during September 2021, distributed to networks providing care to children and adolescents living with HCV infection, and other key stakeholders. Survey questions were developed to reflect two key questions: which age groups to treat and prioritise, and which DAA regimens to use.

**Results:** There were 142 survey respondents, of whom 94 (66%) had cared for children or adolescents with HCV over the past 3 years. Every WHO region was represented, with highest proportion of respondents from the Western Pacific (43%) and the Americas (19%). There was a trend towards higher preference for treating older age groups: 60% of respondents reported a strong preference for treating (i.e., stating they were very likely or likely to treat) children aged 3 to <6 years, increasing to 81% and 94% for those aged 6 to <12 years and 12 to 18 years respectively. The main reasons reported for preferring not treating younger age groups were the chance of spontaneous clearance, lack of drug approvals and registration for treatment of younger age groups, slow disease progression and asymptomatic nature of disease in early childhood, difficulties with administering medication to young children and lack of clinical trial data.

The most commonly preferred and used DAA regimens for treatment across all paediatric age groups were: sofosbuvir/velpatasvir, sofosbuvir/ledipasvir and glecaprevir/pibrentasvir. The most frequent reasons for these regimen preferences were safety, guideline recommendations, drug availability, suitability to treat prevalent HCV genotypes (including pangenotypic) and efficacy.

**Conclusion:** This survey demonstrates strong HCW support for treatment of children and adolescents with HCV infection, especially those 6 years or older. Future priorities include updating national policies to incorporate case-finding strategies and treatment for children and adolescents, and access to paediatric DAA formulations.

**THU223**

Impact of community-based campaign in United States to increase hepatitis B virus screening and linkage to care among Asian immigrants from high endemic countries

Sung Kwon1,2, Aziza Win3, Gregory Wu4, 1Holy Name Medical Center, Teaneck, United States; 2Columbia University Irving Medical Center, New York, United States; 3Ross University School of Medicine-Academic Campus, Bridgetown, Barbados; 4Gesinger Commonwealth School of Medicine, Scranton, United States

Email: steve-kwonmd@holyname.org

**Background and aims:** With the ongoing population movements of migrants from high (>8%) to low (<2%) endemic regions, the prevalence and incidence of chronic Hepatitis B virus surface antigen (HBsAg) carriers are changing in low endemic countries like the United States. To address this, in the efforts for hepatitis B virus (HBV) eradication, the American Association for the Study of Liver Disease has established guidelines pushing for HBV screening in immigrants from high endemic regions including many Asian countries. Yet, many Asian immigrants remain unscreened and those with chronic hepatitis B (CHB) are often not linked to care citing multiple barriers. We sought to determine the impact of community-based HBV campaigns on screening and linkage to care (LTC) efforts through a large-scale community screening initiative.

**Method:** Asian immigrants from the New Jersey and New York metropolitan areas were screened for HBV using surveys and serological testing from 2009 to 2019. Those participants found to be positive were followed up by telephone, mail or email. We started to collect LTC data starting in 2015. In 2017, because of low LTC rates, nurse navigators whose role was to help participants navigate through individual barriers to care were hired to aid in the LTC process. Those excluded from the LTC data included those who were already linked to care, those who declined to be linked to care and those who had moved or passed away.

**Results:** 13, 566 participants were screened from 2009 to 2019, of which, the results for 13, 466 were available. Of these, 372 (2.7%) were found to have positive HBV status. Approximately 49.3% were female and 50.1% male, and the rest were of unknown gender. A total of 1, 191 (10.0%) participants were found to be HBV negative but required vaccination. When we started to track LTC, we found 195 participants that were eligible for LTC between 2015 through 2017 after the exclusion criteria were applied. It was found that only 33.8% were successfully linked to care in that time period. After hiring nurse navigators, we saw LTC rates increase to 85.7% in 2018 and to 89.7% in 2019.

**Number of HBV Infected Percentage (%)**

<table>
<thead>
<tr>
<th>Year</th>
<th>Number of LTC</th>
<th>Percentage</th>
</tr>
</thead>
<tbody>
<tr>
<td>2017</td>
<td>56 (out of 195)</td>
<td>33.8%</td>
</tr>
<tr>
<td>2018</td>
<td>12 (out of 14)</td>
<td>85.7%</td>
</tr>
<tr>
<td>2019</td>
<td>26 (out of 29)</td>
<td>89.7%</td>
</tr>
</tbody>
</table>

Figure: Successful linkage to care rates 2009 to 2019. A nurse navigator was hired in 2017 to focus on linkage to care.

**Conclusion:** HBV community screening initiatives are imperative to increase screening rates in the Asian immigrant population. We were also able to demonstrate that nurse navigators can successfully help increase LTC rates. Our HBV community screening model can address issues with barriers to care including lack of access in comparable populations.

**THU224**

The prognostic implications of liver function test abnormalities in patients admitted to hospital with COVID-19

Jason Cohen1, David Uihwan Lee2, Gregory Fan1, David Hastie1, Aakaash Mittal1, Khanh Le1, Yeun Jang1, Saraf Daid1, Raffi Karagozian1, Raza Malik1, 1Tufts Medical Center, Gastroenterology/Hepatology, Boston, United States; 2University of Maryland Medical Center, Gastroenterology/Hepatology, Baltimore, United States

Email: jcohen1353@gmail.com

**Background and aims:** Prior studies have indicated the presence of hepatic inflammation (as signified by elevated liver function test (LFT) values), as conferring an escalated risk toward adverse outcomes in patients admitted with COVID-19. In line with this hypothesis, we study the various thresholds of LFTs and its associated prognostic risks toward COVID-19 related hospital deaths.

**Method:** This was a single-center retrospective study involving patients admitted with COVID-19. Univariate Cox regression analysis identified the LFT variables significantly associated with our primary end point, in-hospital death. Subsequently, 500 iterations of thresholds were generated for each biomarker to estimate the prognostic
Conclusion: The delineated cutoffs for AST, ALT, and bilirubin levels can serve as clinical benchmarks to help determine when a COVID-19 infection poses significant risk. Given this finding, the cutoffs can be used as part of a risk assessment for patients to support early preventative therapies and medical management.

THU225
A novel prognostic model including liver function parameters accurately predicts 30-day mortality in patients admitted with COVID-19

David Uhiwan Lee1, Jason Cohen2, Gregory Fan3, David Hastie3, Akaash Mittal3, Khanh Le1, Yeun Jang3, Sarav Daid3, Raffi Karagozian1, Raza Malik2.

Background and aims: While the relationship between elevated liver enzymes and COVID-19 related adverse events is well-established, a liver-dependent prognostic model that predicts the risk of death is helpful to accurately stratify admitted patients. In this study, we use a bootstrapping-enhanced method of regression modeling to predict COVID-19 related deaths in admitted patients.

Method: This was a single-center, retrospective study. Univariate and multivariate Cox regression analyses were performed using 30-day mortality as the primary end point to establish associated hepatic risk factors. Regression-based prediction models were constructed using body mass index (BMI), age, diabetes, cancer, solid organ transplantation, hypertension, heart failure, chronic kidney disease (CKD), chronic obstructive pulmonary disease (COPD), hematologic malignancy, input from an expert panel.

Results: A total of 858 patients with COVID-19 were included with a median follow-up time of 5 days from admission. From the total, 90 patients passed away during admission (10.5%). Upon univariate Cox analysis, the following LFT parameters were associated with in-hospital death: Bilirubin (p < 0.001), AST (p < 0.001), ALT (p < 0.001). However, alkaline phosphatase (p = 0.449) was not associated with the primary end point. The iterations of event regression analyses using 500 sequences of LFT thresholds showed the following cutoffs to be significantly associated with in-hospital death (minimally significant values): ALT (281.71 IU/L), AST (120.94 IU/L), bilirubin (2.615 mg/dL). On the multivariate analysis, while controlling for demographics and cardiopulmonary/medical comorbidities, the following AUC for the respective models: model 1: 0.82 95%CI 0.776–0.82, model 2 (core + demographics): 0.828 95%CI 0.785–0.828, model 3 (prior terms + additional biomarkers): 0.842 95%CI 0.799–0.842, model 4 (prior terms + comorbidities): 0.851 95%CI 0.809–0.851, model 5 (prior terms + life-sustaining therapies): 0.933 95%CI 0.91–0.933, model 6 (prior terms + COVID-19 medications): 0.934 95%CI 0.91–0.934. Model 1 demonstrated the following parameters at 0.91 TPR: 0.54 specificity, 0.17 PPV, 0.98 NPV. Bootstrapped iterations showed the following AUC for the respective models: model 1: 0.82 95%CI 0.765–0.882, model 2 0.828 95%CI 0.764–0.885, model 3 0.842 95%CI 0.779–0.883, model 4: 0.851 95%CI 0.808–0.914, model 5: 0.933 95%CI 0.901–0.957, model 6: 0.934 95%CI 0.901–0.961.

Conclusion: Model 1 displays high prediction performance (AUC > 0.8) in both regression-based and bootstrapping-enhanced modeling iterations. Therefore, this model can be adopted for clinical use as a calculator to evaluate the risk of 30-day mortality in patients admitted with COVID-19.

THU226
Low health literacy is associated with higher healthcare service utilisation and costs among patients with cirrhosis

Patricia Valery1, Christina Bernardes1, Kelly Hayward2,3, Gunter Hartel1, Katerin Haynes4, Louisa Gordon1, Amy Johnson2,3, Elizabeth Powell2,3,1QIMR Berghofer Medical Research Institute, Herston, Australia; 2Princess Alexandra Hospital, Woolloongabba, Australia; 3The University of Queensland, Centre for Liver Disease Research, Faculty of Medicine, Woolloongabba, Australia; 4Hepatitis Queensland, Coorparoo, Australia

Background and aims: Optimal management of cirrhosis is complex, and patients often lack knowledge and skills which can affect self-management. We assessed patient knowledge about cirrhosis and examined whether knowledge was associated with clinical outcomes, healthcare service utilisation, and healthcare costs.

Method: A cross-sectional ‘knowledge survey’ was conducted between Jun-2018 and Aug-2020 with 123 cirrhosis patients with cirrhosis (44.4% of 277 invited and eligible). The ‘knowledge survey’ questions were derived from prior studies, and an expert panel
unanimously deemed eight items to be “key knowledge” about cirrhosis. The proportion of correct answers was calculated ("key knowledge" score) and patients were categorized as having ‘good knowledge’ vs ‘poor knowledge’ (cut-off based on median score). Detailed clinical data (extracted from medical records and through linkage to hospital admissions, emergency department presentations), healthcare costs, and self-reported health-related quality of life (SF-36) were available. Cumulative overall survival (Kaplan-Meier), rates of hospital admissions, emergency presentations and costs were assessed according to “key knowledge.” Incidence rate ratios (IRR; Poisson regression) were reported.

Results: Patients were aged 60.7 ± 10.8 years, 65.9% were male, 47.2% had formal education to Junior High School level or less, 43.9% lived in ‘most disadvantaged’ areas, alcohol was a cofactor for 65.9%, NAPFL was a cofactor for 50.4%, and 29.3% had decompensated cirrhosis. 58.5% of patients had ‘good knowledge’ about cirrhosis. In multivariable analysis, higher level of education was associated with over 5-fold odds of having ‘good knowledge’ about liver disease (adj-OR = 5.61, 95% CI 2.47–12.75). Patients with ‘good knowledge’ had a higher health status in the SF-36 domain related to physical functioning (p = 0.036) compared to those with ‘poor knowledge’. Patients with ‘good knowledge’ had 73% fewer all-cause admissions (IRR = 0.27, 95% CI 0.23–0.33), 57% fewer emergency presentations for cirrhosis (IRR = 0.43, 95% CI 0.21–0.89), and more planned one-day cirrhosis admissions (IRR = 4.47, 95% CI 1.61–12.37; see Table). The total cost of cirrhosis admissions was 45% lower for patients with ‘good knowledge’ (IRR = 0.55, 95% CI 0.54–0.56) during the follow-up period.

Table: Incidence rate ratios and cost ratios by knowledge score

<table>
<thead>
<tr>
<th>Knowledge Score</th>
<th>All-cause admission</th>
<th>Cirrhosis admission</th>
<th>Planned emergency admission (cirrhosis admission)</th>
<th>Emergency presentation</th>
<th>Emergency presentation (any reason)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Good</td>
<td>0.27 (0.23–0.31)</td>
<td>0.27 (0.23–0.31)</td>
<td>0.47 (0.91–1.37)</td>
<td>0.01</td>
<td></td>
</tr>
<tr>
<td>Poor</td>
<td>0.72 (0.64–1.19)</td>
<td>0.72 (0.64–1.19)</td>
<td>0.72 (0.91–1.37)</td>
<td>0.01</td>
<td></td>
</tr>
</tbody>
</table>

Conclusion: Low health literacy is associated with increased use of healthcare services and increased total cost of health care. This may reflect poorer health status and quality of life. Improving the health literacy of patients with cirrhosis may be an effective strategy to promote a more cost-effective use of healthcare services with fewer preventable emergency department visits and greater use of planned admissions.

THU227
A modelling approach to estimate alcohol-related liver morbidity and mortality in France
Claire Delacôte¹, Line Carole Ntandja Wandji¹ ², Alexandre Louvet¹ ², Pierre Bauvin¹, Guillaume Lasailly¹ ², Massih Ningarhari¹ ², Sebastien Dharancy¹ ², Guillaume Clement³, Amelie Brunet¹, Xavier Lenne¹, Philippe Mathurin¹ ², Sylvie Deuffic-Burban¹ ², ¹INSERM U1286-INFINITE, Lille, France; ²CHU de Lille, Service des maladies de l’appareil digestif, Lille, France; ³Lille University Hospital, Medical Information Department, Lille, France; ⁴INSERM U1137-IAIME, Paris, France
Email: claire.delacote@inserm.fr

Background and aims: Harmful alcohol use leads to the development of alcohol-related liver disease (ALD). In-depth knowledge of the natural history of ALD according to patterns of alcohol consumption is required to predict the future burden of ALD morbidity and mortality. This would allow to implement health policies targeting at-risk drinkers. Our aim was to integrate the relevant natural history data of ALD in a mathematical model. This model includes estimates of the incidence of at-risk drinking in order to predict morbidity and mortality related to ALD in France.

Method: First, we developed a Markov model simulating the trajectory of cohorts starting at-risk alcohol consumption until they die. It integrates the common risk factors associated with the progression of ALD (sex, age, amount of alcohol, genetic polymorphism). Unknown parameters of progression were back-calculated on the 2010–2018 alcohol-related decompensated cirrhosis and HCC mortality data provided by the French National Hospital Discharge database. Second, morbidity and mortality were predicted up to 2026.

Results: The developed model fits the observed mortality data: 63, 016 deaths were predicted over 2010–2018 for 62, 934 observed in database (Fig. A). Prediction of deaths fits the observed mortality according to cause of death and sex (Fig. B), as well as age. Between 2010 and 2021, annual ALD deaths decreased by 4%, from 7, 100 to 6, 700. However, while deaths by decompensation decreased from 4800 to 4, 300 (−10%), deaths by HCC rose from 2, 300 to 2, 400 (+4%) (Fig. B). Most of the ALD deaths occurred in men: 3 out 4 deaths by decompensation and 9 out 10 deaths by HCC.

In addition, the model estimated that, in 2021, 80, 000 French individuals have alcohol-related cirrhosis with 7, 900 incident cases. Decompensated cirrhosis and HCC are observed in around 33, 000 and 6, 000 cases, respectively. Women represent 30% of the cirrhotic individuals. The decline of French per capita consumption would lead in 2026 to decrease in cirrhosis (−70, 000) and liver related deaths (6, 400) compared to currently (Fig. B).

Conclusion: The present model predicts future burden of ALD in the general French population, based on robust epidemiological data. This model allows to predict not only liver-related mortality but also burdens of cirrhosis and liver-related complications. It may help to propose new health policies targeting patients most at-risk in order to obtain further reductions in the burden of ALD.

THU228
A model to predict drinking population at-risk of liver disease in France: a tool for decision-making public health policies
Claire Delacôte¹, Line Carole Ntandja Wandji¹ ², Alexandre Louvet¹ ², Pierre Bauvin¹, Guillaume Lasailly¹ ², Massih Ningarhari¹ ², Sebastien Dharancy¹ ², Philippe Mathurin¹ ², Sylvie Deuffic-Burban¹ ², ¹INSERM U1286-INFINITE, Lille, France; ²CHU de Lille, Service des maladies de l’appareil digestif, Lille, France; ³INSERM U1137-IAIME, Paris, France
Email: claire.delacote@inserm.fr

Background and aims: In France, daily alcohol intake is decreasing among 15–64 y-o whereas consumption of ≥2 drinks per occasion (binge drinking) is becoming more common, especially among 15–35 y-o. Estimating the proportions of individuals with alcohol use with intermediate (20–50 g/d) or high (≥50 g/d) risks of alcohol-related liver disease (ALD) would allow to predict the incident cases of cirrhosis and provide new tool for decision-making public health policies. Our aim was to predict the incidence of French people having an alcohol intake ≥20 g/d.

Method: Daily alcohol intake was calculated from individual data from national surveys (ESPS), conducted on a representative sample
of 15–64 y-o French people. A Markov model was fitted to this data to estimate entry into risky drinking, according to the history of binge drinking or not. Incidences were back-calculated by sex, age and annual per capita consumption from ESPS 2002 to 2014 (n = 45,054). The adequacy of the model was assessed by comparing the predicted alcohol patterns and prevalence to those estimated from ESPS. Entries into at liver-risk drinking were simulated between 1910 and 2014 considering competitive mortality. At liver-risk drinking incidences and prevalence were predicted until 2026 under 2 scenarios. Annual distributions of predicted and observed prevalence were closed according to daily alcohol intake (Fig. A), sex and age.

Results: While per capita consumption dropped from 26l to 12l (-54%) over 1960–2014, prevalence of at liver-risk drinking among 15–64 y-o decreased from 8.8% to 5.1% (-42%) (Fig. A). The number of new intermediate and high at liver-risk drinkers had respectively decreased by 35% and 65%. In 2021, ~5% of French people have an alcohol intake ≥20 g/d (8/10 are men). This prevalence increases with age (Fig. B). Each year, 60,000 individuals become intermediate at liver-risk drinkers and 9,500 switch from intermediate to high at-risk consumption. If the current decrease in per capita consumption continues (scenario 1), it will be 10.6l in 2026 (-4.5% over 5 years) and there will be 350,000 new at liver-risk drinkers over 2021–2026. If the per capita consumption significantly drops to 10l in 2026 (-10%, scenario 2), 7,400 intermediate at liver-risk drinkers would be avoided and ~1,200 intermediate at liver-risk drinkers will not switch into high at liver-risk drinking (Fig. C).

Conclusion: Although these 2 scenarios will allow differences in terms of incident cases, the expected prevalence will be little changed and 4.5% of the 15–64 y-o would be at liver-risk drinkers. 1/1000 French initiates an alcohol intake ≥20 g/d each year. In 2021, 1.9 million of French people have an alcohol consumption associated with a risk of cirrhosis and 310,000 of them have a high risk (≥50 g/d). By quantifying for the 1st time the incidence of French people and meta-analysis to HEV than in North America: results from a systematic review and anti-HEV IgG and/or HEV-RNA incidence rates among blood donors worldwide were identified via predefined search terms ("Hepatitis e" OR "HEV") AND ("blood donors" OR "transfusion" OR "blood donation" OR "blood testing") in Pubmed and Scopus. Data were stratified by year of publication, country/continent, diagnostic assay and methodological quality (according to PRISMA). Estimates were calculated by pooling study data (separately for each country/continent) via multivariable linear mixed effects meta regression analysis.

Results: Out of 1,103 studies, 151 (14%) were included in the final analysis. Estimated HEV viremia rate ranged from 0.01% to 0.14% worldwide (56 studies, 3,438,276 blood donors). Highest estimated HEV viremia rates were seen in Asia (0.14%), followed by South America (0.10%), Europe (0.09%), Africa (0.08%), Australia and North America (each 0.01%). In Europe highest rates could be found in Serbia (0.31%), closely followed by Germany (0.28%) and France (0.18%). Rate of HEV viremia as well as anti HEV seroprevalence were significantly lower in North America in comparison to Europe (OR = 0.14 [95% CI 0.03–0.58]; OR = 0.62 [95% CI 0.35–1.10]), independently of year of publication and methodological quality.

Conclusion: Our data demonstrate large regional differences regarding the risk of exposure to HEV. Considering the cost–benefit ratio, this supports blood-product screening programs in areas of high endemicity, such as Europe or Asia, in contrast to low-endemic regions, such as the U.S.

THU230
A population based-study of rates and trends of hepatitis C in immigrants and the Canadian-born in Quebec, Canada, 1998–2018
Ana Maria Passos-Castillo1,2, Marina B. Klein1,2, Julie Brunecue4,5, Dimitra Fanagiotoglou2, Karine Blouin7, Donald Murphy6, Christina Greenaway1,2,9, 1Lady Davis Institute, Jewish General Hospital, Centre for Clinical Epidemiology, Montreal, Canada; 2McGill University, Department of Medicine, Montreal, Canada; 3McGill University Health Center, Division of Infectious Diseases, Montreal, Canada; 4Centre Hospitalier de l’Université de Montréal, CHUM Research Centre, Montreal, Canada; 5Université de Montréal, Department of Family and Emergency Medicine, Faculty of Medicine, Montreal, Canada; 6McGill University, Department of Epidemiology, Biostatistics and Occupational Health, Montreal, Canada; 7Institut National de Santé Publique du Québec, Unité des infections transmissibles sexuellement et par le sang, Québec, Canada; 8Institut National de Santé Publique du Québec,
Background and aims: Immigrants bear a disproportionate hepatitis C (HCV) burden in Canada. They account for 30% of HCV cases and are at increased risk of end stage liver disease and liver cancer at the time of diagnosis. Determining sub-groups of immigrants at highest HCV risk will be essential to supporting micro-elimination efforts in this population. We estimated annual reported rates and trends of HCV over a 20-year period in Quebec.

Method: A population-based cohort of all HCV cases in Quebec from 1998 to 2018 reported to public health and the provincial reference laboratory were linked to the provincial health registry and the landed immigrant database. Immigrant status and country of birth were assigned through linkage to the immigrant database. Region of birth was classified by World Bank regions; East Asia/Pacific (SEA), South Asia (SA), Middle East/North Africa (MENA), Sub-Saharan Africa (SSA), Latin America/Caribbean (LAC), Western Europe (EUS), Other Europe/Central Asia (OECA) and North America/Australia/New Zealand (NAANZ). Annual reported crude cumulative incidence rates (%) of HCV among immigrants and the Canadian-born were estimated using Quebec population census data during the study period. Comparative rate ratios (RR) with 95% confidence intervals (CI) and the trend of HCV rates over the study period stratified by immigrant status were estimated using Poisson regression.

Results: Among 34,881 HCV cases identified, 13.5% (n = 4,720) were immigrants. Immigrants were older (median 46.8 vs. 44.1 years; p < 0.001) and diagnosed a median of 9.3 (IQR 2.8–17.2) years after arrival in Quebec. Comparing immigrants with Canadian-born: the HCV average annual rate/100,000 population was 33.1 vs. 30.8 and 18.4 vs. 12.3 during the periods 1998–2008 and 2009–2018, respectively; and the RR was 1.08 (1.03–1.12) in 1998–2008, and 1.50 (1.42–1.57) in 2009–2018. Between 2009 and 2018, subgroups of immigrants with higher HCV rates compared to the Canadian-born were those from OECA [rate; RR (95% CI); 45.6; 3.7 (2.0–7.0)], SSA [44.7; 3.6 (1.9–6.8)], and SA [28.8; 2.3 (1.2–4.6)]. Rates decreased more slowly over the study period among immigrants vs. Canadian-born [-4.84% (-6.17–3.45%) vs. –7.74% (-9.22–6.24%)] per year.

Conclusion: High rates of HCV among immigrants and long delays to HCV diagnosis after arrival in Canada highlight important gaps in HCV screening among immigrants. These data can be used to inform micro elimination efforts among the immigrant population in Quebec and Canada.
Conclusion: Despite the COVID-19 pandemic, by employing a community-based model of care utilizing novel simplified diagnostic tools, the HBV-COMSA VA study demonstrated the possibility to screen and vaccinate African migrants who may otherwise not have received care, reducing the possible pool of new infections among this high-risk group.

THU232
Community-based HBV testing among west African migrants in greater Barcelona, Spain increases linkage to specialist care and vaccination: the HBV-COMSA VA model
Camila Picchio1, Daniel Kwakye Nomah2, Ariadna Rando-Segura3, Silvia Gómez Araujo1, Emma Fernandez1, Omar Diatta1,4, Maria Buti5,6, Sergio Rodríguez-Tajes4,7, Sabela Lens6,7, Xavier Forns5,7, Nélida López1, Francisco Rodríguez-Frías1,2,4, Jeffrey Lazarus1.
1Barcelona Institute for Global Health (ISGlobal), Hospital Clínic, University of Barcelona, Barcelona, Spain; 2Center for Epidemiological Studies on HIV/AIDS and STIs in Catalonia (CEEISCAT), Badalona, Spain; 3Liver Pathology Unit, Biochemistry and Microbiology Service, Hospital Universitari Vall d’Hebrón, Barcelona, Spain; 4Community and Public Health Unit, Department of International Health Drassanes-Hospital Universitari Vall d’Hebrón, Barcelona, Spain; 5Liver Unit, Hospital Universitari Vall d’Hebrón, Barcelona, Spain; 6CIBER Hepatic and Digestive Diseases (CIBERHepD), Instituto Carlos III, Madrid, Spain; 7Liver Unit, Hospital Clínic, IDIBAPS, University of Barcelona, Barcelona, Spain
Email: camila.picchio@isglobal.org

Background and aims: Hepatitis B virus (HBV) infection affects an estimated 250 million people worldwide. Sub-Saharan Africa is disproportionately affected, particularly west and central African countries. Migrants arriving to Europe from these high-endemic areas may be unaware of their HBV status due to the unreliable testing and vaccination strategies in their home countries and underutilization of the host country health services, delaying timely diagnosis and linkage to care. The HBV-COMSA VA study aims to use point-of-care testing with simplified diagnostic tools in community settings to identify and link to care or vaccinate west African migrants in the greater Barcelona area. We report the HBV prevalence, associated risk factors, and the continuum of care.

Method: From 21/11/20–13/11/21, 397 people were offered HBV testing in community settings in greater Barcelona. Participants were first tested with an HBsAg rapid detection test (DETERMINE® HBsAg 2, Abbott Inc.). Then a whole blood sample (140 µl per spot) was collected utilizing a plasma separation card (PSC) (cobas® PSC, Roche Diagnostics) which was air-dried and transported to the laboratory. Those who tested positive for HBsAg were provided an instant referral to one of two collaborating tertiary hospitals where a full work-up was done, including liver function tests and liver fibrosis assessment (Fibroscan®). The proportion of participants with different HBV-serological status analyzed as of November 16, 2021 are reported using descriptive stats (STATA 16.0).

Results: 379 participants are included; 314 (82.8%) were Ghanaian with a mean age of 41.1 years (SD = 10.0), and 41.9% (n = 159) were female. The overall HBsAg prevalence was 9.0% (n = 34) of which 14 (41.2%) had detectable HBV-DNA and two (5.9%) had anti-HDV antibodies, none were HBeAg+. The mean HBV-DNA and HBsAg levels among patients attending a first specialist visit (n = 17) was 125, 834 UI/ml and 8, 190 UI/ml, respectively. Evidence of past resolved infection (anti-HBc+) was seen in 35.6% (n = 135) of those who were HBsAg− (Table 1).

Table 1. Description of participants who were HBsAg+, HBsAg+/anti-HBc+, and HBsAg/-anti-HBc−.

<table>
<thead>
<tr>
<th>HBsAg+ (n=34)</th>
<th>HBsAg+/anti-HBc+ (n=35)</th>
<th>HBsAg−/anti-HBc− (n=204)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age, SD</td>
<td>39.9 (9.0)</td>
<td>30.8 (10.5)</td>
</tr>
<tr>
<td>Female, n (%)</td>
<td>10 (29.4)</td>
<td>19 (54.3)</td>
</tr>
<tr>
<td>Years in Spain</td>
<td></td>
<td></td>
</tr>
<tr>
<td>0-5</td>
<td>7 (20.6)</td>
<td>34 (25.2)</td>
</tr>
<tr>
<td>6-12</td>
<td>11 (32.3)</td>
<td>28 (20.7)</td>
</tr>
<tr>
<td>13-20</td>
<td>12 (35.1)</td>
<td>41 (30.2)</td>
</tr>
<tr>
<td>≥21</td>
<td>2 (5.9)</td>
<td>10 (7.4)</td>
</tr>
<tr>
<td>Missing values</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Education level</td>
<td></td>
<td></td>
</tr>
<tr>
<td>No education</td>
<td>3 (8.8)</td>
<td>13 (36.1)</td>
</tr>
<tr>
<td>Primary school completed</td>
<td>9 (25.6)</td>
<td>22 (63.6)</td>
</tr>
<tr>
<td>Secondary school completed</td>
<td>17 (50.0)</td>
<td>91 (67.4)</td>
</tr>
<tr>
<td>Undergraduate/college school of greater completed</td>
<td>5 (14.6)</td>
<td>9 (6.7)</td>
</tr>
<tr>
<td>Country of origin</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ghana</td>
<td>30 (88.2)</td>
<td>115 (85.2)</td>
</tr>
<tr>
<td>Senegal</td>
<td>3 (8.8)</td>
<td>19 (14.1)</td>
</tr>
<tr>
<td>Liberia</td>
<td>1 (2.9)</td>
<td>1 (0.5)</td>
</tr>
<tr>
<td>Mali</td>
<td>0 (0)</td>
<td>0 (0)</td>
</tr>
<tr>
<td>Nigeria</td>
<td>0 (0)</td>
<td>0 (0)</td>
</tr>
<tr>
<td>Cameroon</td>
<td>0 (0)</td>
<td>0 (0)</td>
</tr>
<tr>
<td>Benin</td>
<td>0 (0)</td>
<td>1 (0.5)</td>
</tr>
<tr>
<td>Traditional tattoo or scarving</td>
<td>0 (0)</td>
<td>5 (3.7)</td>
</tr>
<tr>
<td>HIV or STI diagnosis</td>
<td>1 (2.9)</td>
<td>2 (1.5)</td>
</tr>
<tr>
<td>Ever been in jail</td>
<td>0 (0)</td>
<td>2 (1.5)</td>
</tr>
<tr>
<td>Ever received surgery outside of Spain</td>
<td>3 (8.8)</td>
<td>16 (11.8)</td>
</tr>
<tr>
<td>Family member living with HIV</td>
<td>4 (11.8)</td>
<td>14 (10.4)</td>
</tr>
<tr>
<td>Self-reported HBV vaccination status</td>
<td>Complete</td>
<td>4 (11.8)</td>
</tr>
<tr>
<td>1 or 2 doses</td>
<td>0 (0)</td>
<td>3 (2.2)</td>
</tr>
<tr>
<td>Don’t know/Not sure</td>
<td>3 (8.8)</td>
<td>26 (17.3)</td>
</tr>
<tr>
<td>HBV-DNA (mean, UI/ml)*</td>
<td>125,834</td>
<td>-</td>
</tr>
<tr>
<td>qTHBILag (mean, UI/ml)*</td>
<td>8,190</td>
<td>-</td>
</tr>
<tr>
<td>HBsAg−/anti-HBc− (n=204)</td>
<td>0 (0)</td>
<td>-</td>
</tr>
</tbody>
</table>

*Only patients who had a first documented visit with one of the participating hospitals are included here (n = 17) b Fibrosis stage determined by Fibroscan®. Missing values are not reported

Conclusion: This ongoing community-based HBV screening program provides an effective model of identifying and providing care to migrant populations at high risk of HBV infection in the greater

S208 Journal of Hepatology 2022 vol. 77(S1) | S119–S388
Barcelona area, who otherwise may not have been previously engaged in care. Community screening initiatives can increase testing, vaccination, and linkage to care, helping to reach the 2030 WHO HBV elimination targets.

**THU233**

The impact of COVID-19 pandemic control measures on HCV treatment initiation in British Columbia, Canada

Naveed Janjua1,2, Stanley Wong3, Dahn Jeong1,2, Mawuenu Binka1, Terri Buller-Tylor1, Sofia Bartlett1, Prince Adu1, Hector Velasquez1, Makuza Jean Damascene2, Amanda Yu1, Maria Alvarez1, Jason Wong1, Mel Krajen1, BC Centre for Disease Control, Vancouver, Canada; 2The University of British Columbia, School of Population and Public Health, Vancouver, Canada

Email: naveed.janjua@bccdc.ca

**Background and aims:** Coronavirus disease 2019 (COVID-19) and measures taken to limit the transmission of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) have directly and indirectly restricted access to healthcare services worldwide. We assessed the impact of these measures, first introduced in British Columbia (BC), Canada in March 2020, on hepatitis C (HCV) treatment initiation.

**Method:** We used data from the BC Hepatitis Testers Cohort, a large population-based cohort integrating data on HCV testing, primary care visits, hospitalizations, and medication dispensations. We compared the monthly HCV treatment initiations during 2020 with those in 2018 and 2019. We compared the sociodemographic and clinical characteristics of people initiating HCV treatment during pre-pandemic time period (Jan 2018-Feb 2020) to those initiating treatment during pandemic time period (Apr-Aug 2020).

**Results:** There was a declining trend in HCV treatment initiations pre-pandemic from 3, 172 in 2018 to 2, 331 in 2019 (26% reduction). However, there was a higher decline in 2020 to 1, 475 treatment initiations (37% reduction from 2019). HCV treatment initiations decreased immediately following the imposition of pandemic control measures; monthly pre-pandemic average treatment initiations fell from 172 to 106 during the pandemic (38% change). There were slight decreases in treatment initiations for the 1945–64 birth cohort (36% to 45%) and for people with HIV coinfection (5.9% to 4.3%) or HBV co-infection (5% to 4.3%). However, there was a slight increase in treatment initiation among the ≥1975 birth cohort (19% to 29%), people whoinject drugs (44% to 49%), and people with problematic alcohol use (32% to 37%) between pre-pandemic and pandemic time periods, respectively.

**Conclusion:** Similar to other healthcare services and HCV testing, there was a reduction in HCV treatment initiation following the introduction of control measures. Pandemic-related disruptions and the overall decline of treatment initiations could have a negative impact on progress towards HCV elimination goals.

**Figure:** Monthly HCV treatment initiations 2018–2020, British Columbia, Canada

**THU234**

Negative impact of COVID-19 infection related to life disruption events and health scores on patients with chronic liver disease

Zobair Younossi1,2, Yusuf Yilmaz3, Mohamed El Kassas5, Ajay Kumar Duseja6, Saeed Sadiq Hamid7, Gamal Elsmair4, Nahum Méndez-Sánchez9, Wah-Kheong Chan10, Ashwani Singal11, Janus Ong12, Brian Lam1,2, Sean Felix1, Elena Younossi1, Manisha Verma1,2, Jillian Price1, Fatema Nader13, Issah Younossi13, Andrei Racila1,2,3, Maria Stepanova2, Betty and Guy Beatty Center for Integrated Research, IHS; Center for Liver Disease, Inova Medicine; Inova Health System, Medicine Service Line; Department of Gastroenterology, Marmara University, Turkey; Helwan University; Postgraduate Institute of Medical Education and Research; Department of Medicine, Aga Khan University; Endemic Medicine and Hepatogastroenterology Department, Cairo University; Medica Sur Clinic and Foundation; University of Malaysia, Gastroenterology and Hepatology Unit; University of South Dakota and Avera Transplant Institute; University of the Philippines, College of Medicine; Center for Outcomes Research in Liver Disease

Email: zobair.younossi@inova.org

**Background and aims:** Patients with chronic liver disease (CLD) may experience a substantial burden from COVID-19 infection as well as disruption of life and routine healthcare associated with the pandemic. We assessed the impact of COVID-19 pandemic on patients with CLD.

**Method:** Patients with CLD enrolled in our Global Liver Registry since 2018 completed a specifically designed 23-item COVID-19 survey between March 2020–November 2021. Questions included patients’ COVID-19 infection status and, if infected, characteristics of the illness, along with various aspects of pandemic-related life disruptions for everyone regardless of the infection.

**Results:** As of November 2021, from 11, 200 historic enrollees, 2635 from 7 countries completed the survey: 21% chronic hepatitis B, 14% chronic hepatitis C, and 66% non-alcoholic fatty liver disease; mean (SD) age 49 ± 13 years, 53% male. Of all survey completers, 10.3% reported having had COVID-19. Of those infected, 87% reported being diagnosed by a laboratory test, 94% had least one symptom, and 73% received treatment for their symptoms. The mean (SD) duration of their illness was 12.5 ± 10.7 days, 66% reported receiving antiviral treatment, 15% were hospitalized, 13% needed oxygen support but no one was put on mechanical ventilation. Of all included CLD patients regardless of COVID-19 infection, 11.4% reported that the pandemic had an impact on their liver disease (p = 0.45 between those who were and were not infected); the majority of those (75%) reported delays in follow-up care. The Life Disruption Event Perception (LDEP) questionnaire confirmed that 80% of COVID-19-infected patients vs. 69% patients without history of COVID-19 infection (p = 0.0001) experienced worsening in at least one aspect of their life (food/nutrition, exercise, social life, vocation/education, financial situation, housing, or healthcare). The most substantial worsening was observed for social life (73% in infected vs. 61% in not infected), exercise (49% vs. 42%), and financial situation (36% vs. 30%) (all p < 0.05). Self-assessed health scores were lower in patients with history of COVID-19 than in those not infected: 6.8 ± 2.1 vs. 7.4 ± 2.2 (on a 0–10 scale with 10 indicating perfect health) (p < 0.0001) despite similar scores reported before the pandemic (8.5 ± 1.4 vs. 8.4 ± 1.6, p = 0.77). In multivariate regression analysis, after adjustment for country of enrollment, liver disease etiology and severity (assessed by FIB-4 score), age, sex, BMI, diabetes, and history of psychiatric comorbidities, having had COVID was found to be independently associated with lower self-assessed health scores (β = −0.62 ± 0.13, p < 0.0001).

**Conclusion:** Patients with CLD experienced a substantial burden of COVID-19 pandemic on their daily lives regardless of actual infection history. Self-reported health scores were lower in patients with history of COVID-19 infection.
THU235
Associations of food insecurity and fast-food consumption with diet quality in adults with non-alcoholic fatty liver disease in a large population-based U.S. cohort
Ani Kardasian1, Jennifer Dodge2,3, Norah Terrault1
1University of Southern California, Division of Gastrointestinal and Liver Diseases, Los Angeles, United States; 2University of Southern California, Department of Population and Public Health Sciences, Los Angeles
Email: ani.kardasian@med.usc.edu

Background and aims: Food insecurity (FIS) impacts the quality of foods consumed and is associated with greater risk of non-alcoholic fatty liver disease (NAFLD). While racial-ethnic disparities in NAFLD have not been explored, the interplay between FIS, diet quality (DQ) and fast food (FF) consumption in different racial-ethnic groups with risk have been reported, the interplay between FIS, diet quality (DQ) and its individual components.

Results: In total, 1,420 adults had NAFLD, of whom 520 (37%) were food insecure. Food insecure compared to food secure adults were more likely to be non-Hispanic (NH) black (11% vs 7%), Hispanic (33% vs 13%), foreign born (28% vs 15%), live in poverty (31% vs 4%), or have public/no insurance (59% vs 27%). Mean (standard error) DQ score was 49.1 (0.9) and 46.7 (1.2) for food secure and insecure groups, respectively. Controlling for age, gender, race/ethnicity, poverty, education, and alcohol use, FIS was associated with a 2.5-unit lower DQ score (per additional FF meal consumed weekly; 95%CI:-1.0 to -0.7). However, FF consumption was associated with a 0.4-unit lower DQ score, though did not reach statistical significance (95%CI:-0.7 to 0.0). NH blacks (+2.9 units, 95%CI[0.3 – 5.4]), NH Asians (+9.3[5.1 – 13.6]), and Hispanics (+5.2[1.1 – 9.2]) all had significantly better overall mean DQ than NW whites. Odds ratios of poor DQ for individual components are shown in the table. NH blacks, Asians, and Hispanics had lower odds of saturated fat consumption compared to NH whites, but differences between groups were also seen for total vegetables, whole fruits, whole grains, and total protein. The largest differences in individual DQ components by FS were seen among NH whites; in this group, food insecure (vs secure) adults had a greater proportion of poorer scores for seafood/plant proteins (60% vs 46%) and added sugars (29% vs 11%).

Conclusion: There was a trend towards worse DQ in food insecure adults with NAFLD. Fast-food consumption was also associated with lower DQ in NAFLD. NH whites had the lowest DQ with food insecurity potentiating poor DQ. Exploration of the sociocultural factors contributing to the observed differences in DQ by race/ethnicity may offer the potential opportunity to mitigate NAFLD disparities and reduce disease burden.

Table: Multivariable logistic regression evaluating the association of race/ethnicity with odds of poorer diet quality components compared to NH Whites

<table>
<thead>
<tr>
<th>Race/ethnicity</th>
<th>Total vegetables</th>
<th>Whole fruits</th>
<th>Whole grains</th>
<th>Total protein</th>
<th>Saturated fats</th>
<th>Added sugars</th>
</tr>
</thead>
<tbody>
<tr>
<td>NH white</td>
<td>DR (65%)</td>
<td>DR (65%)</td>
<td>DR (65%)</td>
<td>DR (65%)</td>
<td>DR (65%)</td>
<td>DR (65%)</td>
</tr>
<tr>
<td>NH black</td>
<td>1.06 (0.76 – 1.48)</td>
<td>0.10 (0.05 – 0.21)</td>
<td>1.04 (0.65 – 1.60)</td>
<td>1.07 (0.66 – 1.72)</td>
<td>0.37 (0.25 – 0.56)</td>
<td>1.13 (0.66 – 1.90)</td>
</tr>
<tr>
<td>NH Asian</td>
<td>0.59 (0.39 – 0.89)</td>
<td>0.34 (0.23 – 0.52)</td>
<td>0.50 (0.37 – 0.71)</td>
<td>0.27 (0.13 – 0.52)</td>
<td>0.61 (0.40 – 0.91)</td>
<td>0.56 (0.33 – 0.93)</td>
</tr>
<tr>
<td>Hispanic</td>
<td>0.59 (0.39 – 0.89)</td>
<td>0.34 (0.23 – 0.52)</td>
<td>0.50 (0.37 – 0.71)</td>
<td>0.27 (0.13 – 0.52)</td>
<td>0.61 (0.40 – 0.91)</td>
<td>0.56 (0.33 – 0.93)</td>
</tr>
</tbody>
</table>

*model also controlled for food insecurity status, poverty, age, gender, education level, alcohol use

THU236
Roberta D’Ambroso1, Giuliano Rizzardini2, Massimo Puoti3, Stefano Raguglione4, Maria Rosaria Aniol1, Claudia Gabiani1, Federico D’Amico5, Luisa Pascolo6, Massimo Colombo6, Pietro Lampertico1,7, Foundation IRCCS Ca’ Granda Ospedale Maggiore Policlinico, Gastroenterology and Hepatology, Milan, Italy; 2ASST Fatebenefratelli-Sacco, First Division of Infectious Diseases, Milan, Italy; 3ASST Grande Ospedale Metropolitano Niguarda, Division of Infectious Diseases, Milan, Italy; 4ASST Papa Giovanni XXIII, Gastroenterology, Hepatology and Transplantation, Bergamo, Italy; 5ASST Fatebenefratelli-Sacco, Internal Medicine, Italy; 6Ospedale San Raffaele, Liver Center, Milan, Italy; 7University of Milan, CRC “A. M. and A. Migliavacca” Center for Liver Disease, Department of Pathophysiology and Transplantation Email: roberta.dambroso@policlinico.mi.it

Background and aims: The World Health Organization (WHO) goal of hepatitis C virus (HCV) elimination by 2030 relies on the scaling-up of policies of both identification and treatment of the infected population, worldwide. In Italy, it has been estimated that at least 200,000 people are unaware of their HCV infection thus reinforcing the need for broadening population access to effective screening programs.

Method: A pivotal screening program targeting subjects born between 1969 and 1989 has been conducted in Lombardy, Northern Italy, where point-of-care (POC) testing was offered for free concomitantly to COVID-19 vaccination.

Result: Overall, 7,219 subjects underwent HCV screening in 4 vaccination hubs. Characteristics of the screened cohort and pivotal strategies are reported in Table. Seven (0.1%) subjects tested anti-HCV positive and 5 (0.07%) were HCV-RNA positive by standard confirmatory tests. Patients with HCV infection were all males, aged 41–46 years; only one of them came from Italy. Clinical data were available for 3 patients: all of them have altered transaminases, without HBV or HIV co-infection; HCV genotypes were 1b, 3a and 4, and liver stiffness ranged between 4.5 and 10.3 kPa. All patients underwent DAA therapies.

Table: Pivotal screening strategies according to each participating Center

<table>
<thead>
<tr>
<th>Milan Policlinico (N = 4,000)</th>
<th>Milan FBB-Sacco (N = 1,222)</th>
<th>Milan Niguarda (N = 1,000)</th>
<th>Bergamo (N = 997)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Time spent for screening program, hours</td>
<td>53</td>
<td>25</td>
<td>128</td>
</tr>
<tr>
<td>Daily vaccinations5</td>
<td>Any birth-cohort</td>
<td>7,081 (5, 833–9, 440)</td>
<td>766 (264–894)</td>
</tr>
<tr>
<td>Proposed anti-HCV POC</td>
<td>4,721</td>
<td>1, 629</td>
<td>NA</td>
</tr>
<tr>
<td>Accepted anti-HCV POC</td>
<td>4,000</td>
<td>1, 222</td>
<td>1, 000 (NA)</td>
</tr>
<tr>
<td>Age, years</td>
<td>(85%)</td>
<td>(75%)</td>
<td>(71%)</td>
</tr>
<tr>
<td>Males</td>
<td>42 (32–52)</td>
<td>44 (32–52)</td>
<td>44 (32–52)</td>
</tr>
<tr>
<td>Screening Team (per day)</td>
<td>5–6</td>
<td>2–3</td>
<td>9–11</td>
</tr>
<tr>
<td>Physicians</td>
<td>3–4</td>
<td>2</td>
<td>1</td>
</tr>
<tr>
<td>Nurses</td>
<td>3–4</td>
<td>2–3</td>
<td>1–3</td>
</tr>
<tr>
<td>Research Assistants</td>
<td>1 Auxiliary</td>
<td>Research Nurse</td>
<td>Research Assistant</td>
</tr>
<tr>
<td>Anti-HCV positive by POC test</td>
<td>0</td>
<td>0</td>
<td>1 (0.1%)</td>
</tr>
<tr>
<td>Lost to follow-up after POC test</td>
<td>1 (0.01%)</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Anti-HCV positive by confirmatory test</td>
<td>4 (0.10%)</td>
<td>–</td>
<td>1 (0.10%)</td>
</tr>
<tr>
<td>HCV-RNA positive</td>
<td>3 (0.08%)</td>
<td>–</td>
<td>1 (0.10%)</td>
</tr>
</tbody>
</table>

Results are reported as number (n) and percentages (%) or median (range). HCV: Hepatitis C Virus; POC: Point-of-Care; NA: Not Available.

Conclusion: This pivotal study demonstrated the feasibility of a POC-based anti-HCV screening program in young adults undergoing COVID-19 vaccination.
COVID-19 vaccination. The prevalence of HCV infection in subjects born in the 1969–1989 cohort in Italy seems to be lower than previously estimated, thus raising the question whether more HCV carriers can be identified if screening is moved up to embrace subjects born before 1969.

THU237
Real life pooling of plasma samples for hepatitis C RNA detection as a screening strategy of hepatitis C active chronic infection
A. Aguillera1,2,3, M. Cea1,2,1, A. Fuentes1,2, S. Pereira1,2,3, L. Vinuela1,2,3, Federico García García1,5,6, 1University Hospital of Santiago de Compostela, Microbiology, Santiago de Compostela, Spain; 2University of Santiago de Compostela, Microbiology, Santiago de Compostela, Spain; 3Instituto de Investigación Sanitaria de Santiago, Santiago de Compostela, Spain; 4University Hospital Clinic San Cecilio, Microbiology, Granada, Spain; 5Instituto de Investigación Biosanitario Ibs. Granada, Granada, Spain; 6Ciber Enfermedades Infecciosas ISCIII, Granada
Email: antonio.aguillera.guirao@sergas.es

Background and aims: The diagnosis of active hepatitis C virus (HCV) infection is the necessary first step for its elimination. In most countries, universal population screening and/or screening by age groups have not been adopted due to cost and cost-effectiveness considerations. Here we show a real-life sample pooling diagnosis strategy to overcome this challenge, and to contribute to increase the diagnostic capacity of clinical laboratories and expand access to massive screening of hepatitis C.

Method: We have analyzed consecutive samples submitted to microbiology services of CHUS (Santiago de Compostela, Spain) and HU CSC (Granada, Spain) for hepatitis C diagnosis during the first three weeks of November 2022. Samples were tested for HCV antibodies and, in parallel and in a blinded way, were pooled into 100 samples with the following strategy: first, 10 pools of 10 samples were built (a); second, two pools comprising five of the previous were made (b); finally, these two were pooled together and tested for HCV-RNA using Cobas® HCV 6800 (Roche Diagnostics) at CHUS and both Xpert HCV Viral load (Cepheid) and Cobas® HCV 6800 at HU CSC. When positive, the previous two pools (b) were tested and after, a strategy to unmask the positive (s) sample (s) that needed up to 15 total HCV-RNA tests was used.

Results: A total of 1700 samples (17 pools) were analyzed, 800 at CHUS and 900 at HU CSC. The overall anti HCV and HCV-RNA prevalence was 0.24% (4/1700). After our pooling strategy, we could detect all samples previously detected by standard diagnosis (anti-HCV followed by reflex HCV-RNA testing). While 13 master pools were negative, we needed to unmask 4 master pools, resulting in 60 total HCV-RNA tests to finally unmask the positive sample for each master pool. Specificity and sensitivity of the pooling strategy were 100%. Given median current prices on the market in Spain for anti-HCV (3€) and HCV-RNA (30€), testing with the pooling strategy would have resulted in 3420 € save (3220 € by traditional testing vs 1800 € by the pooling strategy), and a cost of 1,055 € per patient screened.

Conclusion: The strategy of pooling samples for the diagnosis of active HCV infection has advantages that should be exploited with the aim of eliminating HCV as a public health threat. Here we demonstrate that in settings with a low prevalence of chronic infection, by substantially improving cost-effectiveness, this strategy enables and provides the necessary sustainability for use in large-scale diagnosis of HCV.

THU238
Epidemiology of hepatocellular carcinoma in Portugal
Mario Jorge Silva1,2, Guillerme Simões1, Rita Catarina Saraiva1, Filipe Calinas1, Paulo Nogueira1,4,5,6, 1Centro Hospitalar Universitário Lisboa Central, Gastroenterology, Lisboa, Portugal; 2NOVA Medical School, Lisboa, Portugal; 3Faculdade de Medicina da Universidade de Lisboa, Instituto de Medicina Preventiva e Saúde Pública, Lisboa, Portugal; 4Faculdade de Medicina da Universidade de Lisboa, Instituto de Saúde Ambiental, Lisboa, Portugal; 5Faculdade de Medicina da Universidade de Lisboa, Área Disciplinar Autónoma de Bioestatística; 6Universidade NOVA de Lisboa, NOVA National School of Public Health, Comprehensive Health Research Center
Email: mariojorgesilva01@gmail.com

Background and aims: There is scarce data on the burden of hepatocellular carcinoma (HCC) in Portugal. We aim to characterize the recent epidemiology of HCC in Portugal.

Method: We evaluated HCC-related hospital admissions and mortality in Portugal between 2010 and 2017. We analyzed all hospital admissions from patients with HCC in public hospitals (data from Portuguese Health System’s Central Administration) and mortality due to HCC (data from National Statistics Institute)-coded with 155.0 (International Classification of Diseases-ICD-9-CM) or C22.0 (ICD-10). Additional analyses were performed to evaluate longitudinal trends and regional differences.

Results: Between 2010 and 2017, there were 20, 704 hospital admissions of patients with HCC, ranging annually from 2,086 in 2010 to 2,989 in 2015. In-hospital mortality rate during admission was 16.7%.

Annual number of admissions, admitted patients, mortality and potential years of life lost are detailed in the table.

<table>
<thead>
<tr>
<th>Year</th>
<th>Admissions (n)</th>
<th>Admitted patients (n)</th>
<th>Mortality (n)</th>
<th>Potential years of life lost (n)</th>
</tr>
</thead>
<tbody>
<tr>
<td>2010</td>
<td>2086</td>
<td>2600</td>
<td>2425</td>
<td>2641</td>
</tr>
<tr>
<td>2011</td>
<td>2694</td>
<td>2989</td>
<td>2739</td>
<td>2477</td>
</tr>
<tr>
<td>2012</td>
<td>2014</td>
<td>1205</td>
<td>1220</td>
<td>1560</td>
</tr>
<tr>
<td>2013</td>
<td>1371</td>
<td>1511</td>
<td>1376</td>
<td>1506</td>
</tr>
<tr>
<td>2014</td>
<td>1560</td>
<td>1640</td>
<td>1511</td>
<td>1410</td>
</tr>
<tr>
<td>2015</td>
<td>2477</td>
<td>3215</td>
<td>3340</td>
<td>2955</td>
</tr>
<tr>
<td>2016</td>
<td>3228</td>
<td>3005</td>
<td>3013</td>
<td>3838</td>
</tr>
<tr>
<td>2017</td>
<td>533</td>
<td>536</td>
<td>620</td>
<td>(p = 0.073)</td>
</tr>
</tbody>
</table>

Conclusion: The burden of HCC in Portugal is high and had an increasing trend between 2010 and 2017.
A high prevalence of active infection is observed in hospitalized patients at different divisions Valerio Rosato1, Loreta Kondili2, Riccardo Nevola1, Alessio Aghemo3, Pasquale Perillo1, Ruben Napolitano4, Antonio Sciambra5, Davide Mastrocinque1, Ernesto Claas1, 1Ospedale Evangelico Betania, Liver Unit, Naples, Italy; 2Istituto Superiore di Sanità, Center for Global Health, Roma, Italy; 3Humanitas Clinical and Research Center IRCCS, Division of Internal Medicine and Hepatology, Department of Gastroenterology, Rozzano, Italy; 4Ospedale Evangelico Betania, Laboratory Medicine Unit, Naples, Italy; 5Ospedale Evangelico Betania, Health Management, Naples, Italy

Email: valeriorosato@gmail.com

**Background and aims:** Chronic hepatitis C is a major public health problem in Southern Italy. Screening strategies in key populations and birth cohort 1969–1989 has been addressed for free of charge screening in Italy. However, larger birth population cohorts need to be screened due to expected high HCV prevalence. We conducted a hospital-based mass screening in order to assess the HCV active infection prevalence and address the feasibility of the opportunistic screening in the linkage to care of the infected patients.

**Method:** From January 2020 to May 2021 all consecutive in-patients were screened for HCV antibody (HCV Ab) at hospital admission throughout all divisions in the Evangelic Hospital Betania of Naples. HCV Ab positive patients were evaluated for previous HCV treatment. HCV RNA testing was required for those not previously treated. Patients with active infection the linkage to care and treatment start were planned within the hospital admission.

**Results:** Of 12,665 inpatients consecutively screened, 510 (4%) were HCV Ab positive. The HCV Ab positive patients were at least 20%–30% of those born before 1947 (9.4%). In each birth cohort, 20%–30% of patients have been previously treated whereas 30%–45% were discharged and not tested for HCV RNA. 194 (38% of HCV +) patients were tested for HCV RNA and 91 patients (46.2%) had active HCV infection. 87 patients were treated during hospital admission, while 4 were not evaluated for treatment due to severe comorbidities. All patients treated achieved sustained virological response at week 45% were discharged and not tested for HCV RNA. 194 (38% of HCV +) patients were screened for HCV antibody (HCV Ab) at hospital admission throughout all divisions in the Evangelic Hospital Betania of Naples. HCV Ab positive patients were evaluated for previous HCV treatment. HCV RNA testing was required for those not previously treated. Patients with active infection the linkage to care and treatment start were planned within the hospital admission.

**Conclusion:** A high prevalence of active infection is observed in patients with comorbidities in Southern Italy. The possibility of active infection testing in less than 50% of HCV Ab positive patients underline the importance of reflex testing for identifying active infection. HCV elimination requires increase of screening in patients who are unaware of the HCV status, but also of the screening and linkage to care in those with known liver damage yet unaddressed.
Conclusion: The link B strategy showed that more than one-third of known HBsAg-positive individuals had not been linked to care, and enabled the retrieval of a large number of patients.

THU241
Testing for liver disease in primary care: fibrosis first
Ian Rowe1,2, Richard Parker2, 1University of Leeds, Leeds Institute for Medical Research, United Kingdom; 2St James's Hospital, Leeds Liver Unit, United Kingdom
Email: i.a.c.rowe@leeds.ac.uk

Background and aims: The optimal method to identify persons with liver disease in primary care is unknown. Approaches to diagnose all persons with abnormal liver blood tests, e.g. intelligent liver function tests (iLFT), or screening all those with specific risk factors have been proposed but each incompletely identifies the population being tested in primary care. The aim of this study was to define testing strategies to identify persons with treatable liver disease and/or advanced fibrosis in primary care using unified pathways.

Method: A decision model was developed to assess 3 approaches to testing in comparison to the current practice of limited testing for liver disease and liver fibrosis in primary care. The outcomes considered were the incremental cost per diagnosis ratio and the net benefit of each pathway. Diagnosis was defined by treatable liver disease (viral hepatitis, metabolic liver disease, or autoimmune liver disease) and advanced fibrosis (in the case of alcohol-related liver disease) and advanced fibrosis (in the case of alcohol-related liver disease) and advanced fibrosis (in the case of alcohol-related liver disease) and advanced fibrosis (in the case of alcohol-related liver disease) and advanced fibrosis (in the case of alcohol-related liver disease) and advanced fibrosis (in the case of alcohol-related liver disease) and advanced fibrosis (in the case of alcohol-related liver disease). The tested approaches were: 1. “iLFT” (full aetiology testing of persons with abnormal LFTs); 2. “Comprehensive” (full aetiology testing for abnormal LFTs and non-invasive fibrosis tests for all persons tested); 3. “Fibrosis first” (abbreviated aetiology testing [HBV, HCV, iron studies] and non-invasive fibrosis testing for all). These approaches were compared with current practice patterns where 20% of persons with newly abnormal LFTs undergo downstream testing. Parameters were estimated from literature data and costs were derived from the UK NHS.

Results: All tested approaches identified more persons with treatable liver disease ± advanced liver fibrosis than the current standard of care. In the base case scenario, where 80% of the tested population had abnormal LFTs, the fibrosis first approach made a diagnosis of treatable disease/advanced fibrosis in 3.9% of the total population compared with 3.8% for iLFT and 4.3% in the comprehensive approach. Fibrosis first had the lowest incremental cost per diagnosis ratio: fibrosis first, £1349 (£1590); iLFT £3247 (£3828); and comprehensive, £2964 (£3494). The number of secondary care referrals was increased in all approaches above current testing, greatest in the comprehensive strategy. Considering these trade-offs the net benefit was greatest for the fibrosis first approach (Figure).

Conclusion: Current testing for liver disease is inadequate. Pathways that streamline testing, including testing of persons with normal liver blood tests but that are at risk of significant liver disease, will increase the yield of testing for liver disease in primary care. A “fibrosis first” pathway, taking a fast and frugal approach to identify persons with prognostically significant liver disease, warrants testing in comparison to comprehensive evaluation in primary care.

THU242
Hepatitis C care cascade analysis among adult women in Georgia
Ketevan Stvilia1, Shaun Shadaker2, Amiran Gamkrelidze3, Irma Khonelidze4, Maia Tsereteli5, Vladimir Getia6, Paige A Armstrong7. 1National Center for Disease Control and Public Health, Tbilisi, Georgia; 2Centers for Disease Control, Department of Viral Hepatitis, United States; 3National Center for Disease Control and Public Health, Tbilisi, Georgia
Email: stviliaak@gmail.com

Background and aims: According to the National HCV seroprevalence study of 2015, 3.8% of women in Georgia are positive for hepatitis C virus (HCV) antibodies; however, female-targeted interventions to promote HCV testing and treatment have been lacking. Further, women of reproductive age can transmit HCV during pregnancy, making outreach to this population particularly important. We constructed the HCV care cascade for women age ≥18 years, screened for anti-HCV within the National Hepatitis C Elimination Program during January 2015-October 2021 to compare progress in care and treatment and to assess gaps in the cascade of HCV care and treatment.

Method: The seven stages of HCV care recommended by WHO were assessed for women who tested positive for anti-HCV: (1) HCV antibody positive; (2) tested for viremia; (3) confirmed active infection; (4) initiated HCV treatment; (5) eligible for test for sustained virologic response (SVR), (6) tested for SVR and (7) achieved SVR. HCV care cascade results were assessed for women by age group to define gaps, and proportion retained at each step in the care cascade.

Results: As of October 2021, 2.1 million adults with known sex were screened for anti-HCV, including 1.1 million women. Among them, 38, 881 (3.4%) were positive for anti-HCV, and the majority (65.0%) were aged ≥50 years. In 2015, 3.8% of women in Georgia are positive for hepatitis C, ranging from 62.7% among those aged 18–29 years to 75.8% among those aged 40–49 years. Overall, 76.1% (16, 729) of women with HCV viremia initiated treatment, including 63.0% of women aged ≥60 years, and ≥84.0% of women in all other age groups. Of women treated, 95.6% (15, 986) completed the regimen, and 98.2% of those women were eligible for an SVR test. Women have demonstrated high uptake of SVR testing; 82.0% were tested for SVR across all age groups with an overall cure rate of 99.4%.

Conclusion: To reach elimination of hepatitis C by 2025 it is important to improve access to and support uptake of viremia testing and enrollment in treatment among anti-HCV positive women in Georgia, with special attention to ensuring the large proportion of anti-HCV positive women over 50 years complete viremia testing. Once enrolled in treatment, Georgian women with active HCV infection show high rates of compliance resulting in more than 99% of cases cured.
Progress in HCV screening in the national hepatitis C elimination program in Georgia during the COVID-19 pandemic, 2019–2021

Amiran Gamkrelidze1, Alexander Turdziladze1, Maia Tsetelhi1, Vladimir Getia1, Ana Aslanikashvili1, Tinatin Kuchuloria2, Irina Tskhomelidze2, Sophia Surguladze3, Lia Gvinjilia3, Senad Handanagic4, Shaun Shadaker4, Paige A Armstrong4.

Background and aims: Georgia, with a population of 3.7 million, had an estimated 150,000 adults living with chronic hepatitis C virus (HCV) infection based on a serosurvey conducted in 2015. The same year, the country initiated the world’s first national HCV elimination program, with free screening and treatment available to all citizens. Despite great progress, the COVID-19 pandemic has created new challenges for the program. This analysis describes the progress made in HCV screening since program initiation and the impact of the COVID-19 pandemic on HCV screening.

Method: The Hepatitis C Elimination Program tracks testing and treatment data using two databases, the national HCV Screening Registry, and the HCV treatment database. These databases are linked by the national ID. This analysis uses data from both databases and the 2014 general population census.

Results: As of September 30th, 2021, 2,081,548 adults have been screened for antibody to HCV (anti-HCV) (75% of the adult population), of whom 144,857 (6.9%) were anti-HCV positive. Overall, 118,398 (81.7%) anti-HCV positive individuals received follow-up viremia testing, and 94,315 (79.7%) were found to have active HCV infection. The number of anti-HCV tests performed among adult persons dropped as restrictions were imposed in March of 2020 from 74,815 tests in February 2020 to just 35,371 in April of the same year. Screening increased in the summer, with 106,212 tests performed in July, due in part to relaxed restrictions and intensified integrated screening programs (HCV, tuberculosis, and HIV). Compared to 2019, the number of tests performed in 2020 decreased by 24% (1,048,108 vs. 793,658). As the pandemic progresses, the number of tests performed for HCV during January – September 2021 remained lower than in the same period in 2020 (503,048 vs. 636,161).

Conclusion: Although the program has made significant progress towards HCV elimination, the ongoing pandemic has led to a decline in screening for HCV infection, with numbers continuing to decline in 2021. In response, Georgia intends to increase integrated screening, and seek active approaches to link patients to HCV care and treatment. The impact of the pandemic on the HCV elimination program demonstrates how a pandemic can be challenging for different public health programs and highlights the need to employ innovative strategies to avoid slowing of progress towards HCV elimination.

Could a multi-target blood test make hepatocellular carcinoma surveillance programs more effective? A modelling-based virtual trial

Jagpreet Chhatwal1,2,3, Sumeyye Samur4, Ju Dong Yang5, Lewis Roberts6, Mindie Nguyen7, A. Burak Ozbay8, Turgay Ayer9,10, Neelhar D. Parikh11, Amit Singal12, 1Harvard Medical School, Boston, United States; 2Mass General Hospital, Boston, United States; 3Harvard Medical School, Boston, United States; 4Division of Viral Hepatitis, Centers for Disease Control and Prevention, Atlanta, United States; 5Value Analytics Labs, Boston, United States; 6Mayo Clinic, Rochester, United States; 7Stanford University School of Medicine, Stanford, United States; 8Exact Sciences Corporation, Madison, United States; 9Georgia Institute of Technology, Atlanta, United States; 10Emory University-School of Medicine, Atlanta, United States; 11University of Michigan Medical School, Ann Arbor, United States; 12UT Southwestern, Dallas, United States.

Background and aims: Hepatocellular carcinoma (HCC) is among the fastest rising causes of cancer mortality in the Western world. Although guidelines recommend biannual ultrasound (U/S)-based HCC surveillance in at-risk patients, utilization in practice remains poor in practice. A recently validated, multi-target HCC blood test (mt-HBT), may potentially improve adherence to surveillance by forgoing the need for U/S. Our objective was to evaluate the comparative effectiveness of mt-HBT with the current surveillance strategy in cirrhosis patients.

Method: We simulated a virtual trial by developing a clinically valid microsimulation model of HCC natural history in compensated cirrhosis patients. Model parameters, including tumor progression, competing risks of mortality, and real-world adherence, were estimated from the literature. Test performance characteristics of U/S, AFP, and mt-HBT were informed from a network meta-analysis. We simulated the life course of cirrhosis patients and compared biannual surveillance using (1) AFP only, (2) U/S only, (3) U/S+AFP, and (4) mt-HBT only. We also simulated a scenario where mt-HBT would improve adherence by 10% (~4 absolute improvement) compared to current utilization.

Results: Per 10,000 cirrhosis patients simulated in each arm, mt-HBT detected 225 (+57%) more early-stage HCC cases compared with AFP, 108 (+21%) more early-stage HCC compared with U/S, and 20 (~3%) less early-stage HCC compared with U/S+AFP. In contrast, mt-HBT with improved adherence detected 21 (~3%) more early-stage HCC compared with U/S+AFP (Figure). The remaining HCC cases were either symptomatically identified or patients died from competing causes prior to detection. mt-HBT increased life years by 709 per 10,000 patients screened compared with AFP, 360 compared with U/S, but decreased life years by 19 compared with U/S+AFP. Of note, mt-HBT with improved adherence increased life years by 52 compared with U/S+AFP.
Conclusion: mt-HBT as a single blood test offers similar diagnostic efficacy for early HCC detection compared with the combination of U+AFP. Potential improved adherence with use of blood-based biomarkers, such as mt-HBT, would likely further increase real-world effectiveness of HCC surveillance.

THU245
Evaluation of immune response and disease flares in metabolic-associated fatty liver disease patients following SARS-CoV-2 vaccination: a prospective cohort study
Jumping Shi1, Qamaru Zhu2,3, Jin Gao4, Jiaping Gu5, Lu Shen5, Jing Liu6, Yu Song7, Xiying Gong7, Yutong Chen7, Jie Liao7, Yining He5, Siyi Zhang5, Junping Shi1, Geng He1, Li Shao3,5, Yee Hui Yeo8, Jie Li9,10.

Method:
In this prospective cohort, 50 participants with MAFLD and SARS-CoV-2 vaccination were recruited. Blood samples were collected before (day 0) and after (days 28, 57, and 180). Baseline vibration-controlled transient elastography and liver function tests were performed.

Results:
Repeated measures ANCOVA was used to estimate the magnitude of change of these markers throughout study period. On multivariable analysis, age and waist circumference were negatively associated with seropositivity of neutralizing antibody on day 57 while RBC and lymphocyte count were independent positive predictors on day 180 (Table).

Table: Factors associated with seropositive of neutralizing antibody on days 57 and 180, respectively.

<table>
<thead>
<tr>
<th>Characteristics</th>
<th>Univariable analysis</th>
<th>Multivariable analysis*</th>
<th>Univariable analysis</th>
<th>Multivariable analysis**</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age</td>
<td>OR 95% CI p</td>
<td>OR 95% CI p</td>
<td>OR 95% CI p</td>
<td>OR 95% CI p</td>
</tr>
<tr>
<td>Male (vs female)</td>
<td>1.054</td>
<td>0.997</td>
<td>1.054</td>
<td>0.997</td>
</tr>
<tr>
<td>Waist (cm)</td>
<td>0.940</td>
<td>0.564</td>
<td>2.045</td>
<td>0.564</td>
</tr>
<tr>
<td>BMI</td>
<td>1.286</td>
<td>0.589</td>
<td>1.028</td>
<td>0.760</td>
</tr>
<tr>
<td>CAP</td>
<td>0.989</td>
<td>0.589</td>
<td>1.006</td>
<td>0.474</td>
</tr>
<tr>
<td>LSM</td>
<td>1.082</td>
<td>0.634</td>
<td>1.299</td>
<td>0.103</td>
</tr>
<tr>
<td>BMI</td>
<td>1.087</td>
<td>0.701</td>
<td>0.981</td>
<td>0.703</td>
</tr>
<tr>
<td>ALT</td>
<td>1.010</td>
<td>0.577</td>
<td>1.024</td>
<td>0.275</td>
</tr>
<tr>
<td>ALP</td>
<td>1.009</td>
<td>0.952</td>
<td>1.051</td>
<td>0.002</td>
</tr>
<tr>
<td>OR</td>
<td>1.096</td>
<td>0.737</td>
<td>1.010</td>
<td>0.275</td>
</tr>
<tr>
<td>CRP</td>
<td>1.145</td>
<td>0.818</td>
<td>1.151</td>
<td>0.868</td>
</tr>
<tr>
<td>Fasting glucose</td>
<td>1.065</td>
<td>0.795</td>
<td>0.867</td>
<td>0.895</td>
</tr>
<tr>
<td>HOMA-IR</td>
<td>0.903</td>
<td>0.746</td>
<td>1.107</td>
<td>0.321</td>
</tr>
<tr>
<td>WBC</td>
<td>0.921</td>
<td>0.671</td>
<td>1.324</td>
<td>0.295</td>
</tr>
<tr>
<td>RBC</td>
<td>0.733</td>
<td>0.480</td>
<td>3.461</td>
<td>1.146</td>
</tr>
<tr>
<td>Lymphocyte</td>
<td>0.931</td>
<td>0.861</td>
<td>2.758</td>
<td>1.471</td>
</tr>
<tr>
<td>Hemoglobin</td>
<td>0.996</td>
<td>0.751</td>
<td>1.021</td>
<td>0.028</td>
</tr>
</tbody>
</table>

*Adjusted for age, sex, waist, CAP, LSM, WBC, ALP, and HOMA-IR.
**Adjusted for age, sex, CAP, LSM, WBC, RBC, lymphocyte, and hemoglobin.

Conclusion: CoronaVac vaccination in MAFLD patients was safe and well tolerated. MAFLD patients showed a similar immune response to health controls.

THU246
A model, screen test and treat hepatitis C elimination project among underserved communities in Islamabad-the federal capital of Pakistan
Huma Qureshi1, Hassan Mahmood2, Nabil Ahmed3, Lillian Lou4, Francisco Averhoff5, Ameer Abutaleb6, Shyamasundaran Kottilil6.

Method:
A total of 17 slums with an estimated total population of 50,000 in Islamabad were included in this project. The project includes free hepatitis C testing and treatment and utilizes trained community health workers (CHWs). The CHWs visit every household and provide hepatitis C testing and treatment. The project includes an adherence model for treatment initiation for adults in marginalized communities (i.e., slums) in Islamabad.

Results:
A total of 17 slums with an estimated total population of 50,000 in Islamabad were included in this project. The project includes free hepatitis C testing and treatment and utilizes trained community health workers (CHWs). The CHWs visit every household and provide hepatitis C testing and treatment. The project includes an adherence model for treatment initiation for adults in marginalized communities (i.e., slums) in Islamabad.

Background and aims: The safety and efficacy profile of Covid-19 vaccines in patients with MAFLD (metabolic associated fatty liver disease) remains unclear. MAFLD is a disease that affects millions of people worldwide and is associated with increased risk of HCC.

Method: In this prospective cohort, 50 participants with MAFLD and SARS-CoV-2 vaccination were recruited. Blood samples were collected before (day 0) and after (days 28, 57, and 180). Baseline vibration-controlled transient elastography and liver function tests were performed.

Results: No significant difference in proportion of patients with neutralizing antibody was observed between the two groups. In multivariable analysis, age and waist circumference were negatively associated with seropositivity of neutralizing antibody on day 57 while RBC and lymphocyte count were independent positive predictors on day 180 (Table).

Table: Factors associated with seropositive of neutralizing antibody on days 57 and 180, respectively.

<table>
<thead>
<tr>
<th>Characteristics</th>
<th>Univariable analysis</th>
<th>Multivariable analysis*</th>
<th>Univariable analysis</th>
<th>Multivariable analysis**</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age</td>
<td>OR 95% CI p</td>
<td>OR 95% CI p</td>
<td>OR 95% CI p</td>
<td>OR 95% CI p</td>
</tr>
<tr>
<td>Male (vs female)</td>
<td>1.054</td>
<td>0.997</td>
<td>1.054</td>
<td>0.997</td>
</tr>
<tr>
<td>Waist (cm)</td>
<td>0.940</td>
<td>0.564</td>
<td>2.045</td>
<td>0.564</td>
</tr>
<tr>
<td>BMI</td>
<td>1.286</td>
<td>0.589</td>
<td>1.028</td>
<td>0.760</td>
</tr>
<tr>
<td>CAP</td>
<td>0.989</td>
<td>0.589</td>
<td>1.006</td>
<td>0.474</td>
</tr>
<tr>
<td>LSM</td>
<td>1.082</td>
<td>0.634</td>
<td>1.299</td>
<td>0.103</td>
</tr>
<tr>
<td>BMI</td>
<td>1.087</td>
<td>0.701</td>
<td>0.981</td>
<td>0.703</td>
</tr>
<tr>
<td>ALT</td>
<td>1.010</td>
<td>0.577</td>
<td>1.024</td>
<td>0.275</td>
</tr>
<tr>
<td>ALP</td>
<td>1.009</td>
<td>0.952</td>
<td>1.051</td>
<td>0.002</td>
</tr>
<tr>
<td>OR</td>
<td>1.096</td>
<td>0.737</td>
<td>1.010</td>
<td>0.275</td>
</tr>
<tr>
<td>CRP</td>
<td>1.145</td>
<td>0.818</td>
<td>1.151</td>
<td>0.868</td>
</tr>
<tr>
<td>Fasting glucose</td>
<td>1.065</td>
<td>0.795</td>
<td>0.867</td>
<td>0.895</td>
</tr>
<tr>
<td>HOMA-IR</td>
<td>0.903</td>
<td>0.746</td>
<td>1.107</td>
<td>0.321</td>
</tr>
<tr>
<td>WBC</td>
<td>0.921</td>
<td>0.671</td>
<td>1.324</td>
<td>0.295</td>
</tr>
<tr>
<td>RBC</td>
<td>0.733</td>
<td>0.480</td>
<td>3.461</td>
<td>1.146</td>
</tr>
<tr>
<td>Lymphocyte</td>
<td>0.931</td>
<td>0.861</td>
<td>2.758</td>
<td>1.471</td>
</tr>
<tr>
<td>Hemoglobin</td>
<td>0.996</td>
<td>0.751</td>
<td>1.021</td>
<td>0.028</td>
</tr>
</tbody>
</table>

*Adjusted for age, sex, waist, CAP, LSM, WBC, ALP, and HOMA-IR.
**Adjusted for age, sex, CAP, LSM, WBC, RBC, lymphocyte, hemoglobin.

Conclusion: CoronaVac vaccination in MAFLD patients was safe and well tolerated. MAFLD patients showed a similar immune response to health controls.

Background and aims: Pakistan has a large burden of hepatitis C virus (HCV) infection, and access to care and treatment is limited. In order to increase access for underserved populations, a same-day testing and treatment initiation model program for adults in marginalized communities (i.e., slums) in Islamabad was launched on March 02, 2019. We describe the results of the program.

Method: A total of 17 slums with an estimated total population of 50,000 in Islamabad were included in this project. The project includes free hepatitis C testing and treatment and utilizes trained community health workers (CHWs). The CHWs visit every household and provide hepatitis C testing and treatment. The project includes an adherence model for treatment initiation for adults in marginalized communities (i.e., slums) in Islamabad.
Patients are seen every 4 weeks at the clinic and given refills on their medications and queried about adverse reactions, until the end of treatment. RNA testing is conducted at 12 weeks following completion of treatment to determine viral clearance (cure). The CHWs ensure referral and follow-up of HC infected persons.

**Results:** As of November 15, 2021, a total of 24,216 participants have been screened from seventeen slums, 514 (2.12%) tested positive for anti-HCV and were referred to receive testing for HCVRNA. Of those, 440 (85.6%) got tested for HCV RNA and 323 (73.4%) had detected RNA. Three hundred and eighteen individuals (98.5%) had initiated treatment, of which 284 (89.3%) had completed treatment. To date, 257 (90.5%) patients are eligible to test for Sustained Virologic Response (SVR), out of which 250 (97.3%) were tested; 241 (96.4%) were HCV RNA negative, four (1.6%) were loss to follow-up and five patients were (2%) HCV RNA positive. Those five patients were given Sofosbuvir and Velpatasvir and are on treatment.

**Conclusion:** Same day hepatitis C testing and treatment initiation is feasible among underserved communities in urban slums in Pakistan. CHWs can be effective in reaching “hard-to-reach” populations with limited access to health services and achieving high rates of linkage to care and adherence with treatment for hepatitis C.

**THU247**

**Bacterial and hepatitis C testing practices and seroconversions among dialysis facilities in Georgia**

Maia Butsashvili1, George Kanchelashvili1, Ana Aslanikashvili2, Tinatin Kuchuloria3, Shaun Shadaker4, Irina Tskhomelidze3, Maia Tsereteli2, George Kamkamidze1, Priti Patel1, Paige Armstrong2, 1Health Research Union, Tbilisi, Georgia; 2National Center for Disease Control and Prevention, Tbilisi, Georgia; 3Division of Viral Hepatitis, National Center for HIV, Viral Hepatitis, STD and TB Prevention, CDC, Atlanta, United States.

**Method:** All 27 dialysis centers in the country were invited to participate. Facility questionnaires were completed by the infection control representatives at each center from April to June, 2021. Respondents were asked about HBV and HCV screening practices, and the number of seroconversions among facility patients in the preceding year. Data entry, management and analyses were conducted using the statistical package SPSS v.22.0.

**Results:** A total of 22 (81.5%) dialysis centers participated in the survey. HBV screening is routinely performed upon admission at 21 facilities (95.5%). Susceptible patients are routinely vaccinated with the hepatitis B vaccine at about half (13; 59.1%) of facilities. Anti-HCV screening is performed at 15 institutions (68.2%) upon admission to the center, and anti-HCV screening is performed once every 6 months in 12 (54.5%) clinics for patients who were previously anti-HCV negative.

Ten (45.5%) of the dialysis facilities included in the study reported HBV and HCV seroconversions in the prior year. A total of 31 HBV seroconversions from 8 facilities and 39 HCV seroconversions from 7 facilities occurred. The largest number in a single facility was 25 total seroconversions of HBV or HCV infection.

**Conclusion:** The high seroconversion rate of HBV and HCV infections at dialysis units suggests opportunities for improved infection prevention practices and need for increased hepatitis B vaccination efforts. Surveillance could help identify cases and clusters early and contribute to preventing infection in this high-risk population.

**THU248**

**Innovative linkage model to re-engage loss-to-follow-up individuals in the national hepatitis C elimination program of Georgia**

Amiran Gamkrelidze1, Alexander Turdziladze1, Maia Tsereteli1, Vladimir Getia1, Ana Aslanikashvili1, Sophia Surguladze2, Irina Tskhomelidze3, Shaun Shadaker4, Paige Armstrong2, 1National Center for Disease Control and Public Health Georgia, Tbilisi, Georgia; 2The Task Force for Global Health, Tbilisi, Georgia; 3Division of Viral Hepatitis, National Center for HIV, Viral Hepatitis, STD and TB Prevention, CDC, Atlanta, United States.

**Background and aims:** The National Hepatitis C Elimination Program has made notable progress in Georgia. However, in the setting of COVID-19 related limitations, the number of individuals registering in the treatment program has declined over time, from an average of 996 per month in 2019 to 339 per month in 2021. As of September 30, 2021, 75% (n = 2,081, 548) of the adult population of Georgia has been screened for hepatitis C virus (HCV), but among antibody positive adults, 20, 913 (15%) had not completed a viremia test.

In 2019, the National Center for Disease Control and Public Health Georgia piloted a project to link to care those individuals who screened positive for anti-HCV but had not completed a viremia test. After success of the initial pilot, the model will be scaled up across Georgia.

**Method:** All anti-HCV positive adults (aged ≥18 years) who did not have record of viremia testing in the national HCV electronic database 3 months from the date of a positive result, and who were not registered in the HIV/AIDS program or with a correctional facility, were eligible for follow-up.

Using the phone number listed in the database, individuals were contacted by phone or home visit by patient navigators (trained epidemiologists and primary healthcare physicians) and referred to HCV care and treatment. If the first attempt was unsuccessful, one repeat attempt was made to contact the individual. Incentives were
provided to regional health personnel for each patient that was successfully linked to care, defined as presenting for viremia testing.

Results: As of October 1, 2020, 18, 030 persons were not linked to care; patient navigators attempted to reach 8, 907 (49%) with phone numbers in the database; 6, 718 (75%) were reached. The remaining 2, 189 could not be reached, had moved, or emigrated. Of those contacted, 1, 546 (23%) presented for viremia testing, and 811 (52%) were positive for HCV RNA or core antigen. Overall, 419 (52%) persons with chronic HCV infection were enrolled in the HCV treatment program as a result of this effort.

Conclusion: Program-wide implementation of the piloted model showed that this can be scaled up and is effective for re-engaging people in care. The main challenge in Georgia remains linkage-to-care, which is essential to meet elimination goals. Innovative approaches are necessary to reinforce linkage to care. This is especially important during the COVID-19 pandemic when there is an increased need for programs that can re-engage people in HCV care.

THU249
Combined COVID-19 vaccination and HIV and hepatitis C virus testing in high-risk populations at a mobile testing unit in Madrid, Spain
Jorge Valencia1, Pablo Ryan1, Guillermo Cuevas3, Julieta Domingorena2, Álvaro Vicario2, Marcela Villota-Rivas3, Jeffrey Lazarus4,4.1 Hospital Universitario Infanta Leonor, Department of Internal Medicine, Madrid, Spain; 2SMASD, Harm reduction Unit, Madrid, Spain; 3Barcelona Institute for Global Health (ISGlobal), Hospital Clinic, University of Barcelona, Barcelona, Spain; 4University of Barcelona, Faculty of Medicine, Barcelona, Spain
Email: Jeffrey.Lazarus@isglobal.org

Background and aims: The COVID-19 pandemic has hindered efforts to address HIV and hepatitis c virus (HCV) by reducing testing, particularly in marginalised groups, who have some of the highest rates of HIV and HCV and lowest rates of COVID-19 vaccination. This study aimed to explore the acceptability of combining HIV and HCV testing with COVID-19 vaccination in a mobile testing unit (MTU) in Madrid, Spain.

Method: From 9/28/2021 to 10/26/2021, 101 individuals from high-risk populations (e.g., homeless people, those with substance use and/or mental disorders, sex workers, refugees, undocumented migrants) were invited to get the COVID-19 vaccine at the MTU. If HCV antibody (Ab) positive, they were offered HCV-RNA point-of-care testing to confirm active infection. HIV and HCV-RNA-positive patients were offered linkage to care.

Results: All 101 participants accepted the combined intervention of which 69.3% were male, 30.7% of Spanish origin, most reported a precarious living situation or being homeless (59.4%) and being unemployed (70.3%), and 28.7% a history of incarceration. The mean age was 35.6 (SD: 11.9). Of the total, 11.9% reported a previous COVID-19 diagnosis, none had been vaccinated for COVID-19 and all subsequently received the Janssen vaccine without any adverse events. The process was also efficient, since it maximised the use of time that participants would have spent waiting for HIV and/or HCV test results or post-vaccine administration. This intervention can serve as an example of a novel model of care to increase HCV and HCV screening and linkage to care as well as COVID-19 vaccination in high-risk populations.

THU250
A model to eradicate HCV in undocumended migrants and low-income refugees in Italy
Marianantonietta Pisaturo1, Margherita Macera2, Loredana Alessio2, Stefania de Pascalis2, Lorenzo Onorato1, Maria Stanzione3, Gianfranca Stornaiuolo3, Vincenzo Messina1, Nicola Coppola1. 1university of Campania L.vanvitelli, mental health and preventive medicine, Naples, Italy; 2Vanitelli hospital, Naples, Italy; 3Caserta Hospital, Caserta, Italy
Email: marianantonietta.pisaturo@unicampania.it

Background and aims: To validate an innovative eradication model for HCV infection in undocumented migrants and low-income refugees living Southern Italy.

Method: a prospective, multicenter, collaborative study was started in June 2018 with The study was stopped in February 2020 due to the outbreak of SARS-CoV-2 infection in Italy and was resumed in February 2021. At the six 1st level centers participating to the study volunteer associations that deal with the first needs of disadvantaged people performed the enrolment and the screening for anti-HCV, HBSAg and anti-HIV; epidemiological data were collected in an electronic database. Anti-HCV-positive subjects were sent to two 3rd level centers for the clinical, virological and therapeutic evaluation. For the HCV-RNA-positive subjects HCV genotyping and a clinical, biochemical and ultrasound staging was performed. The HCV RNA-positive subjects have been treated with sofosbuvir-velpatasvir for 12 weeks and followed for 12 months from the end of therapy.

Results: Of the 3, 991 migrants observed in the study period, 3, 897 (97.6%) accepted to be screened. They were young (median age 26 years), predominantly male (85.9%) and came from North Africa (3.8%), from Sub-Saharan Africa (68.4%), from Eastern Europe (8.1%), from Indo-Pakistan (17%) and from other countries (2.7%). Of the 3, 897 enrolled subjects, 185 (4.7%) resulted anti-HCV positive. The Figure shows the HCV-cure cascade. All the 185 anti-HCV-positive subjects were linked to care at 3rdID and tested for HCV RNA and 53 (28.6%) resulted HCV-RNA positive. Of these, 46 (86.8%) started DAA regimen with sofosbuvir plus velpatasvir (15 with GT 1b, 10 with 1a, 16 with 3, 3 with 4 and 2 with 2). Forty-two completed the follow-up and 4 was still pending. Of these 42 subjects, 41 (97.6%) showed a
SVR12 and SVR 24, and one dropped-out in follow-up after the stop of DAA treatment. No subject had adverse event.

**Conclusion:** This model seems to be effective to eradicate HCV infection among a difficult-to-manage population, such as undocumented migrants and low-income refugees

**THU251 Enhancing the cascade of hepatitis C care in community-recruited high-risk people who inject drugs during the COVID-19 pandemic: the Alexandros program**

Vana Sypsa1, Sotiris Roussos2, Efrossini Tsirigiani3,4, Despina Trafal1, Dimitra Tisia2, Athena Gavalaki1, Zafiris Papanikolaou1, Ioanna Papagiouvanni3,5, Athena Tampaki5, Dimitrios Paraskevis2, George Kalaitzis5, Ioannis Goulis7, Angelos Hatzakis1,5,6, 1Medical School of National and Kapodistrian University of Athens, Department of Hygiene, Epidemiology and Medical Statistics, Athens, Greece; 2Medical School of National and Kapodistrian University of Athens, Department of Hygiene, Epidemiology and Medical Statistics, Athens, Greece; 3Fourth Department of Internal Medicine, Hippokratio Hospital, Aristotle University of Thessaloniki; 4Greek Organisation Against Drugs; 5Hellenic Scientific Society for the Study of AIDS and Sexually Transmitted Diseases and Emerging Diseases, Athens, Greece; 6Fourth Department of Internal Medicine, Hippokratio Hospital, Aristotle University of Thessaloniki, Thessaloniki, Greece; 7Hellenic Liver Patients Association “Prometheus”; 8Fourth Department of Internal Medicine, Hippokratio Hospital, Aristotle University of Thessaloniki, Thessaloniki, Greece

Email: vsipsa@med.uoa.gr

**Background and aims:** Despite the availability of effective treatment for chronic hepatitis C, treatment initiation rates remain low among People Who Inject Drugs (PWID) worldwide, especially among those not linked to opioid substitution treatment programs (OST). A community-based program was implemented in Thessaloniki (the second largest city in Greece) during September 2019-August 2021 with the aim to screen for HCV/HIV and improve access to care among high-risk PWID. We aim to provide data on the cascade of HCV care in this population.

**Method:** ALEXANDROS was a “seek-test-treat” community-based program where PWID were recruited using peer-driven chain referral with monetary incentives (Respondent-Driven Sampling). The program was implemented in five consecutive rounds during September 2019-August 2021 and PWID could participate in multiple rounds but only once in each round. Participation included interviewing, counselling, rapid HCV/HIV test and blood sample collection for testing of anti-HCV (+) participants (HCV genotype/biochemical evaluation). PWID eligible for DAAAs with available social security number were entered to the national HCV treatment registry and visited the program site for their prescriptions and assessment of sustained virological response. The personnel of the program, including a peer-navigator, assisted patients through all stages.

**Results:** In total, 1,101 unique PWID were recruited. The majority of participants were current PWID (54.0% with injection in the past 30 days), 15.0% were homeless and 79.7% were not linked to OST. Anti-HCV prevalence was 62.9% and 6.9% were HCV/HIV coinfected. Only 9.7% of anti-HCV (+) PWID reported previous treatment with DAAAs. Chronic HCV prevalence in anti-HCV (+) PWID was 67.6%. Among PWID which chronic HCV monoinfection, it was possible to identify the social security number for 97.4% of them, 96.9% were entered to the national HCV treatment registry to apply for free treatment with DAAs, 61.8% were linked to HCV care and 53.6% initiated treatment by September 2021.

**Conclusion:** Despite the disruptions due to the COVID-19 pandemic, ALEXANDROS was successful in reaching rapidly a population of PWID most in need (current injectors, homeless, low OST coverage) and in offering HCV testing, linkage to care as well as in encouraging HCV treatment initiation.

**THU252 SVR4 and SVR12 monitoring by using dried blood spot test: is it the best alternative for people who use drugs?**

Andrea Herranz1, María Victoria Fernández-Baca2, María Dolores Maca Romero3, María Paz Díaz2, Maria Carmen Gallegos Alvarez2, Ricardo M Arcay3, Francisco Salva3, Adoración Hurtado4, María Buti3,4, Ángels Vilella1, Jeffrey Lazarus1,4, 1Barcelona Institute for Global Health (ISGlobal), Hospital Clinic, University of Barcelona, Barcelona, Spain; 2Hospital Universitari Son Llàtzer, Microbiology Service, Palma, Spain; 3Hospital Universitari Son Espases, Microbiology Service, Palma, Spain; 4Hospital Can Misses, Microbiology Service, Eivissa, Spain; 5Universitari Vall d’Hebron, Liver Unit, Barcelona, Spain; 6Instituto Carlos III, CIBER Hepatic and Digestive Diseases (CIBERehd), Madrid, Spain; 7Hospital Universitari Son Llàtzer, Department of Gastroenterology, Palma, Spain; 8University of Barcelona, Faculty of Medicine, Barcelona, Spain

Email: Jeffrey.Lazarus@isglobal.org

**Background and aims:** People who use drugs (PWUD) are one of the key at-risk population groups for hepatitis C virus (HCV) infection and typically have difficulties in being linked to care and are often lost to follow-up. The Hepatitis C Free Balears project carries out micro-elimination strategies to facilitate the screening, treatment and follow-up of this population.

**Method:** This project has been implemented in 13 of 17 addiction service centres in the Balearic Islands and consists of four phases: 1) recruitment and HCV screening onsite via a point-of-care anti-HCV antibody test (Oraquick®) and a dried blood spot (DBS) test or blood sample collection for testing of anti-HCV (+) participants (HCV genotype/biochemical evaluation), PWID eligible for DAAs with available social security number were entered to the national HCV treatment registry and visited the program site for their prescriptions and assessment of sustained virological response. The personnel of the program, including a peer-navigator, assisted patients through all stages.

**Results:** Of 395 recruited patients, 150 (38%) were anti-HCV+, 1 (0.3%) was HBV-Ag+, 25 (6%) were anti-HIV+ and 60 (15%) had an active HCV infection. Of these 60, 43 (73%) initiated treatment, 17 (28%) are pending and 21 (35%) have already finished it. SVR4 and SVR12 monitoring were performed in 15 (75%) and 5 (25%) of those patients who completed treatment, respectively. Three (14%) SVR4 and three (14%) SVR12 tests were not performed, as the patients did
not show up at the settled appointments, and 3 (14%) SVR4 tests and 13 (62%) SVR12 tests are pending. The 93% (n = 14) SVR4 monitoring tests and the 100% (n = 5) SVR12 monitoring tests showed undetectable HCV-RNA. At the moment, only four patients performed both SVR4 and SVR12 tests, and all of them had concordant results.

**Conclusion:** DBS testing has been proven to be an alternative for HCV screening in PWUD by the Hepatitis C Free Balears team, since it is performed onsite and facilitates screening of drug users who otherwise would have not either reached or received care. It is also useful as a follow-up control method, since it simplifies circuits and reduces difficulties faced by PWUD. Although the SVR4 and SVR12 control tests results were concordant, more data are needed to know if the SVR4 control performed with DBS test is an alternative to lost to follow-up of this vulnerable population.

**THU253**

**Collateral benefit of Georgia national hepatitis C elimination program-improving blood transfusion safety in the country of Georgia**

Maia Alkhazashvili1, Evan Bloch2, Shaun Shadaker3, Tinatin Kuchuloria4, Tamar Samadashvili1, Vladimer Getia1, Alexander Turzdiladze1, Jan Drobeniuc1, Paige A Armstrong3, Amiran Gamkrelidze1, 1National Center for Disease Control and Public Health of Georgia, Tbilisi, Georgia; 2Johns Hopkins School of Medicine, Baltimore, United States; 3Centers for Disease Control and Prevention, Atlanta, United States; 4The Task Force for Global Health, Tbilisi, Georgia

**Background and aims:** In 2015, a national seroprevalence survey identified blood transfusion as a risk factor for transmission of hepatitis C virus (HCV) and hepatitis B virus (HBV) in Georgia. Based on recommendations from the HCV elimination program’s Technical Advisory Group, the EU-funded Technical Assistance and Information Exchange (TAIEX) with the support of the Global Fund, centralized nucleic acid testing (NAT) was implemented at the Richard Lugar Center for Public Health Research at the National Center for Disease Control and Public Health, Tbilisi, Georgia.

**Method:** One year of blood donor screening data (January-December, 2020) was analysed from the Unified Electronic Donor Database. Two samples were collected from all donors, one for primary serological testing by blood centers, and a second for NAT using the Procleix®Ultrio Elite Assay (multiplex for HCV, HBV, and HIV). In the event of a discordant result between NAT and serology (NAT positive, serology negative), additional discriminatory testing was performed. A subset of the discordant samples was retested using ARCHITECT i2000SR immunoassay for HBV surface antigen, HBV core antibody, HCV antibody, and HIV 1/2 Ab/Ag.

**Results:** A total of 54, 116 donations representing 39, 164 unique donors were evaluated. Overall, 671 donors (1.7%) tested positive for at least one infectious marker by serology or NAT. Sixty donations were serology/NAT discordant (serology-/NAT+). Discordance was more likely among females vs. males (adjusted odds ratio [aOR] 2.06; 95% confidence interval [95%CI]: 1.05–4.05), paid (aOR 10.15; 95%CI: 2.80–36.86) or voluntary (aOR 4.30; 95%CI: 1.27–14.56) vs. replacement donors, and repeat vs. first time (aOR 13.98; 95%CI: 4.06–48.12) donors. After repeat serologic testing was performed to confirm blood center reported results, a total of 12 donations (6 HBV+ donations, 5 HCV+ donations and 1 HIV+) were deemed NAT yield and would not have been detected with serology. Out of the total 54, 116 donations, the final NAT yield rate was 1 in 9, 019 for HBV, 1 in 10, 823 for HCV, and 1 in 54, 116 for HIV.

**Conclusion:** This project offers a regional model for NAT implementation, demonstrating the feasibility and clinical utility in a nationwide blood screening program. NAT is resource intensive and expensive to implement system-wide, and may not be feasible in all settings. Balancing cost and yield is important, and countries with high prevalence may benefit more from NAT testing implementation.

**THU254**

**Outcomes of a community led comprehensive HCV and HBV care provision model, including same-day “test and treat” to facilitate micro-elimination of HCV among people who inject drugs in Manipur, India**

Khumukcham Lokeshwar Singh1, Thangjam Dhabali2, Rajkumari Rosse3, Rajkumar Nalminikanta4, Samuraiatpam Rajesh Sharma1, Sanjay Sarin5, Giten Khwairakpam6, Sonjelle Shilton5, 1Jawaharlal Nehru Institute of Medical Sciences, Manipur, India; 2Babina Diagnostics, Manipur, India; 3Department of Medical Microbiology and Immunology, Manipur University, Manipur, India; 4Babina Diagnostics, Manipur, India; 5FIND, the global alliance for diagnostics, Geneva, Switzerland; 6TREAT Asia/amfAR, Thailand

**Background and aims:** The prevalence of hepatitis C virus (HCV) infection among people who inject drugs (PWID) in the state capital of Manipur, India, is 65%; however, access to and uptake of HCV care is poor, largely due to lengthy pre-treatment processes. We piloted a community-led, comprehensive, simplified hepatitis care model that includes same-day HCV testing and treatment initiation (“test and treat”) at drug rehabilitation centres in Manipur, to expand access to care for chronic hepatitis.

**Method:** Participants were screened using HCV antibody (Ab) and hepatitis B virus (HBV) surface antigen (HBSAg) rapid diagnostic tests. Positive HCV Ab samples were tested using a point of care platform for HCV RNA (Mol Ibio TrueNat). HCV RNA-positive participants eligible for treatment under national guidelines were initiated on sofosbuvir and daclastasvir on the same day and are followed until tests of cure (SVR). Participants who were HBSAg negative received HBV vaccine per the WHO rapid regimen. Positive HBSAg samples were sent to a referral lab for HBV DNA tests; and will be referred for treatment per national guidelines.

**Results:** Between 12–22 November 2021, 133 individuals were approached, of whom 103 (77%) were eligible and all consented to participate. To date, 98 (95%) participants have been screened; all were male and identified as PWID and had a median age of 27 (IQR 22–32) years. A total of 39 (40%) were HCV Ab positive; all were tested for HCV RNA, of whom 24 (61.5%) were HCV RNA positive. Of those with viremia, 23 (96%) were initiated on treatment on the same day,
with 1 awaiting HBV DNA results to be initiated on treatment. The median time from screening to HCV treatment initiation was 8 hours and 12 minutes (range 6:03–9:58). First SVR tests for sustained virologic response are due in April 2022. A total of 6 (6.1%) were HBsAg-positive. Of the 92 participants with negative HBsAg tests, 89 (97%) had not previously been vaccinated and all have completed at least 1 dose of the HBV vaccine.

Conclusion: Preliminary results show that community-led comprehensive hepatitis care which incorporates same day “test and treat” for HCV is feasible and effective in this context. HBV screening identified a large proportion who had not been vaccinated. Additional follow-up and implementation research would inform how this model could be replicable in other settings to increase equity in access to HCV and HBV screening, treatment, and prevention.

THU255
A novel hepatitis C intervention in Denmark to test and treat people who inject drugs

Jeffrey Lazarus1,2, Anne Øvrehus3, Jonas Demant4, Louise Krohn-Hehli5, Jannet van der Veen6, Nina Weis5,6, 1Barcelona Institute for Global Health (ISGlobal), Hospital Clinic, University of Barcelona, Barcelona, Spain; 2University of Barcelona, Faculty of Medicine, Barcelona, Spain; 3Odense University Hospital, Odense, Denmark; 4Users Academy, Copenhagen, Denmark; 5Copenhagen University Hospital, Department of Infectious Diseases, Hvidovre, Denmark; 6University of Copenhagen, Department of Clinical Medicine, Faculty of Health and Medical Sciences, Copenhagen, Denmark

Email: Jeffrey.Lazarus@isglobal.org

Background and aims: Providing testing and treatment for hepatitis C (HCV) for people who inject drugs (PWID) is critical in eliminating HCV, but reaching this population with traditional healthcare services can be challenging. Combining point-of-care (PoC) testing with peer support and counselling is a model of care (MoC) that can be effective for PWID. This study aims to investigate if a peer-led mobile van equipped with rapid PoC tests for HCV antibodies (Ab) and RNA could simplify testing and link PWID to care and treatment.

Method: In Copenhagen, Denmark, a peer-led mobile service providing counselling, Ab testing (In-Tec™) and linkage to standard care was equipped with a PoC HCV-RNA finger-prick test (Xpert HCV Viral Load Finger-Stick Point-of-Care Assay, Cepheid). Eligible HCV-RNA+ individuals were offered assisted referral to a fast-track hospital clinic for evaluation and treatment, with peer support available if needed.

Results: From 1 May 2019 to 25 October 2021, 1013 people were tested for HCV-RNA and 10.2% (n = 103) were positive. Nine additional individuals with HCV infection contacted the service to be linked to care. Of the 112 individuals with chronic HCV infection, 72.3% (n = 81) were evaluated for treatment at the hospital clinic, of whom 86.4% (n = 70) initiated direct-acting antiviral therapy and 37% (n = 3) are waiting to initiate treatment. Major reasons for not being evaluated for treatment included being undocumented (38.7%; n = 12) and being lost to follow-up (32.3%; n = 10). Among those who initiated treatment, 20% (n = 14) were connected to drug addiction treatment services. The peer-led service assisted all treated with communication with the hospital nurse, collection of treatment medicine and accommodation to follow-up visits.

Conclusion: We found that a peer-led mobile PoC service is an MoC that can engage PWID in HCV testing and link them to treatment, even during the COVID-19 pandemic. We identified being an undocumented migrant as a major cause for not accessing care. This poses a challenge for HCV elimination in Denmark due to the risk of onward transmission. Next steps include engaging with health authorities to provide care for these migrants.

THU256
Peer-led hepatitis C services reach poorly served populations at scale: a model for tackling health inequalities

Leila Reid1, Rachel Halford1,2, Stuart Smith1, Sean Cox1. 1The Hepatitis C Trust, London, United Kingdom; 2World Hepatitis Alliance, Geneva, Switzerland

Email: leila.reid@hepctrust.org.uk

Background and aims: England’s approach to HCV elimination includes significant involvement-including leadership-from people with lived experience of hepatitis C. This is unique worldwide, and is proving very effective, in particular in engaging, diagnosing and treating groups typically excluded from health services. This large-scale, national programme bears out emerging evidence on peer-based models for tackling health inequalities.

Method: England’s elimination programme tasked drug companies to not only treat but find people with HCV. This responds to a key challenge in the UK and many other countries: most people with HCV are hard to engage and undiagnosed.

Led by The Hepatitis C Trust, a national charity led by people with lived experience, England’s HCV peers work together nationally as well as forming part of local NHS HCV delivery networks to engage marginalised populations. Launched in 2019, the model has three core components:

Peer Support: at its core, HCT provide patient support from another person (a peer) with lived experience of HCV, drug use and/or prison. The Peer provides a bespoke approach, support from testing to diagnosis to treatment and with other conditions.

Partnership: collaboration is paramount to improving systems. Working closely with services and clinicians, HCT’s peer workers shorten pathways, ensure accessible clinics, improve patient understanding, and move services ever closer to those who need them most.

Patient-centred innovation: developed from patient feedback, HCT places the needs of people with HCV at the centre, regularly seeking feedback, adapting and innovating to reach new populations.

Results: Since 2019 HCT’s peer teams have:

engaged almost 75, 000 people at risk of HCV; 33, 324 through outreach and 39, 333 in prisons.

Trained 15, 401 health, care and prison staff

tested 18, 467 people in the community, and 17, 691 in prison. 15% of community tests find markers for current/past HCV (patient data is being collated).

Received 6, 517 referrals for support

62% have started treatment, and 94% for whom an SVR has been obtained (n = 1018) are cured

Feedback is consistently positive; patients highlight one to one relationships, shared experience and trust as pivotal to engagement.

Conclusion: HCT’s highly assertive outreach, partnership-based model has seen peers embedded in NHS and prison systems. Links across the peers-who work as part of regional teams and as a national body-generates innovation, rapid sharing of good practice and excellent reach.

People experiencing marginalisation and often very complex needs engage with the peer model, often their first experience of sustained service engagement.

This is an effective, transferable and likely cost-effective approach (a study is planned), which stimulates both system-level and individual-level change, both positively impacting health inequalities.
Background and aims: People who inject drugs (PWID) have the highest burden of hepatitis C virus (HCV) globally, but are often undertreated due to stigma and lack of access to services. Implementing efficient treatment algorithms for PWID is required to reach this population. The INTRO-HCV randomised control trial conducted in Norway over 2017–2019 found that integrating HCV treatment, using direct-acting antivirals (DAAs), into community settings improved treatment outcomes, but did not compare the longer-term health economic benefits. This study analyses the cost-effectiveness of integrated treatment compared to the standard referral pathway of care.

Method: A health state transition Markov model of HCV disease progression and treatment was developed based on the INTRO-HCV trial. Treatment cost and outcome data were analysed from the trial. Parameters related to disease progression came from published literature. The incremental cost-effectiveness ratio (ICER) was calculated in terms of cost per quality-adjusted life year (QALY) gained from the health provider’s perspective over a lifetime horizon and compared against a conventional (NOK 500,000) willingness-to-pay (WTP) threshold for Norway. Probabilistic and univariate sensitivity analyses were undertaken.

Results: Preliminary results suggest that compared to the standard treatment pathway, integrated treatment resulted in an ICER of NOK 305,000 per QALY gained, with an 80.7% probability of being cost-effective against the conventional WTP threshold. Sensitivity analyses suggest that the cost of DAA medications strongly affected the ICER, with a 30% lower DAA price resulting in integrated treatment having an ICER of NOK 176,000 per QALY gained and a 42.4% probability of being cost-saving.

Conclusion: Integrating HCV treatment for PWID in community settings is likely to be highly cost-effective and may become cost-saving even with moderate reductions in DAA price.

THU258
Characterization of HCV recent infections and re-infections among high-risk population from Georgia using global hepatitis outbreak and surveillance technology
Adam Kotorashvili 1, Amiran Gamkrelidze 1, Nato Kotaria 1, Maia Tsereteli 1, Ana Papkaia 1, Ketevan Galdavadze 1, Maia Alkhazashvili 1, Paata Imdadze 1, Tatin Kuchuloria 2, Lilia Ganova-Raeva 1, Sumathi Ramachandran 3, Saleem Kamili 3, Shaheen Sarah Thomas 3, Chhagan Bihari 3, Shiv Kumar Sarin 3, 1Institute of Medical Sciences, University of Bergen, Norway; 2Haukeland University Hospital, Norway; 3University of Bristol, Population Health Sciences, Bristol Medical School, UK

Background and aims: Global Hepatitis Outbreak and Surveillance Technology (GHOST), is a novel technology that identifies transmission links between specimens, creating a graphic display. GHOST was developed by the Centers for Disease Control and Prevention, and the National Center for Disease Control and Public Health of Georgia. GHOST uses next-generation deep sequencing of Hyper Variable Region 1 (HVR1) of HCV. Genotypes of the HCV strains were determined by HVR1 sequence data analysis. Two HR sites in the cities of Tbilisi and Zugdidi were selected. Samples were collected from HR beneficiaries with documented reinfection or seroconversion. All participants provided written informed consent for participation and completed a questionnaire on the relevant epidemiological information.

Overall, 58 people with a history of injecting drugs were invited to participate, including 33 (57%) in Tbilisi and 25 (43%) in Zugdidi; 52% agreed to participate (n = 30/58).

Results: Among the 30 enrolled participants, 17 (57%) had HCV reinfection and 13 (43%) seroconverted during the observation. In the 6 months prior to the study, 27 participants (90%) reported injecting drugs and 3 (10%) reported needle sharing. Among reinfected participants (n = 17), one (6%) received a blood transfusion, 13 (76.4%) had an invasive medical procedure, and 4 (23.5%) were incarcerated. Among participants with new infection, 5 (38.4%) received blood transfusion, 8 (62%) had an invasive medical procedure more than 1 year ago, and 5 (38%) were incarcerated prior to seroconversion.

Conclusion: This is the first molecular epidemiological report among the high risk PWID population of Georgia using GHOST. The detected transmission clusters and mixed genotype infections indicate a very high rate of exposure in studied communities. GHOST can be utilized for surveillance for early intervention on networks as well as successfully applied to other infectious diseases including HBV, HAV, and HIV.
as physical activity and alcohol consumption of the participants. In addition, anthropometric measurements, transient elastography and blood samples were collected for biochemical tests such as ALT, AST, total bilirubin, cholesterol, triglycerides and fasting blood sugar in participants who volunteered for screening. Liver stiffness measurement (LSM) of ≥8 kPa was used to define significant liver fibrosis. Univariable and multivariable analysis was done to determine the factors associated with liver fibrosis.

Results: A total of 2863 participants were screened with mean age of 43 ± 13.6 years, with 56% being males. Mean fasting blood sugar was 114.5 ± 49.78 mg/dl whereas median triglyceride was found to be 130.2 mg/dl (IQR: 95.4–181.2). The prevalence of significant liver fibrosis in the general population was 7.6% (95%CI: 6.65%–8.64%). The following factors were found to have a statistically significant (p < 0.001) association with significant liver fibrosis after adjusting for other factors: age (aOR: 1.73; 95%CI: 1.01–2.04), male gender (aOR: 1.73; 95%CI: 1.22–2.43), diabetes (aOR: 3.15; 95%CI: 2.23–4.44), morbid obesity (aOR: 7.53; 95%CI: 2.28–24.8) as seen in Table 1.

Conclusion: There is high prevalence of fibrosis in the general population screened for the present study. There is a need for large scale public health interventions with high-risk approach to detect and treat liver fibrosis and prevent its complications.

THU261
Prognostic value of liver function test for COVID-19 hospitalized patients with respiratory disease
Carlos Alventosa Mateu1, Elena Guillen Botaya1, Cecilia Albert-Antequera1, Irene Perez Alvarez2, Alejandro Fernandez Soro3, Eva Sanchez Ramos2, Salvador Benlloch1, Juan Jose Urquijo Ponce1, Francesc Puchades Gimeno1, Francisco Sanz Herrero4, Miguel Garcia Deltoro5, Mercedes Latorre Sánchez1, Inmaculada Castelló Miralles1, Cecilia Albert-Antequera2, Irene Perez Alvarez1, Digestive Diseases, Valencia, Spain; 4Consorcio Hospital General Universitario Valencia, Internal Medicine, Valencia, Spain; 5Consorcio Hospital General Universitario Valencia, Infectious Diseases, Valencia, Spain; 6Consorcio Hospital General Universitario Valencia, Microbiology, Valencia, Spain

Background and aims: Abnormal liver function tests (ALFT) have been associated with worse evolution in COVID-19 hospitalized patients with respiratory disease, but it is unclear if it is an independent prognostic factor. Our aim is to determine whether ALFT have a direct impact on the prognosis of these patients.

Method: A single-center, retrospective study of COVID-19 hospitalized patients with respiratory disease from February 15th, 2020, to February 28th, 2021. Patients with already known liver diseases were excluded. ALFT were defined as elevated total bilirubin (TBIL), aspartate transferase (AST), alanine transferase (ALT), alkaline phosphatase (ALP) and/or gamma-glutamyltransference (GGT) above the upper limit of normality (ULN) in our laboratory. COVID-19 respiratory disease was classified as mild (no pneumonia), moderate (pneumonia) and severe (pneumonia with respiratory failure). Worsening of respiratory disease was defined as mild/moderate to severe respiratory disease progression or death. An association of ALFT with moderate/severe disease, worsening of respiratory disease, hospital stay, need for intensive care unit (ICU) admission and mortality was assessed. Statistical analysis was based on T-test and logistic regression. They included an adjusted multivariable model for age, sex, Charlson Comorbidities Index (CCI) and liver steatosis and fibrosis prior to hospital admission (defined by Hepatic Steatosis Index and FIB-4 scores respectively). Significance was set at p < 0.05.

Results: The data of 2075 patients (51.5% males), average age 66.5 (SD 17.8) years, were analyzed. Despite excluding patients with already known liver diseases, the overall prevalence of liver steatosis was 57.8% and that of fibrosis was 18.4%. 1225 patients (51.9%) presented ALFT at hospital admission and 1572 (75.8%) during hospital stay. ALFT were significantly associated with moderate/severe disease, likelihood of worsening of respiratory disease, longer hospital stay (8 vs 11.9 days, p = 0.001) and higher rate of ICU admission, but not with higher mortality. Higher FIB-4 was also significantly associated with worsening of respiratory disease (OR = 1.98, p < 0.001). Age and CCI were associated with higher mortality. Female sex was a protective factor against unfavorable events. Among ALFT, TBIL was the most associated with worsening of respiratory disease (OR = 2.4, p < 0.001) and ALT with ICU admission (OR = 1.42, p < 0.001) and mortality (OR = 1.03, p = 0.04). The exclusion of patients with elevated ALT/AST prior to admission did not change the results.

Conclusion: According to our study, ALFT can be considered as an independent risk factor for worse evolution in COVID-19 hospitalized patients with respiratory disease. Liver fibrosis had only influence in worsening of respiratory disease.

Figure: Association of ALFT with the different clinical events.
Background and aims: Viral vector COVID-19 vaccines have been administered more commonly worldwide but their effectiveness in participants with cirrhosis is unknown. We explored the effectiveness of vaccination with the Janssen Ad.26.COV2.S compared to the mRNA Pfizer BNT162b2 or Moderna 1273-mRNA vaccine in participants with cirrhosis.

Method: This was a test-negative case control study among participants with cirrhosis. This study design is widely used in evaluations of vaccine effectiveness and has the advantage of minimizing biases associated with access to vaccination or health care. Cases were those who were SARS CoV2 PCR positive, controls were those who tested negative during the study period between March 15, 2021 and October 3, 2021. Participants who did not undergo SARS CoV2 PCR testing, who had COVID-19 before the study period, or received a liver transplant, were excluded. COVID-19 was classified based on individual chart review using the National Institute of Health (NIH) COVID-19 severity scale as asymptomatic, mild, moderate, severe or critical illness.

Results: A total of 955 cases and 955 matched controls were included in the study population. The two groups were well matched to all baseline characteristics. The Ad.26.COV2.S vaccine had an effectiveness of 64% against COVID-19 (adjusted Odds Ratio [aOR] 0.36, 95% CI 0.20–0.62, p = 0.005). Effectiveness was lowest with asymptomatic illness (aOR 0.42, 0.18–0.73, p = 0.03), and higher against mild (aOR 0.36, 0.15–0.63, p = 0.006), moderate (aOR 0.33, 0.14–0.49, p = 0.002) and severe/critical (aOR 0.24, 0.08–0.83, p = 0.04) COVID-19. In the same period, mRNA vaccines had a 73% effectiveness against overall COVID-19 (aOR 0.27, 0.19–0.37, p < 0.0001), progressively higher from asymptomatic (aOR 0.38, 0.23–0.59, p = 0.0004) to mild (aOR 0.29, 0.18–0.42, p < 0.0001), moderate (aOR 0.27, 0.18–0.36, p < 0.0001), and severe or critical illness (aOR 0.17, 0.06–0.32, p < 0.0001). There were no statistically significant differences between the viral vector and mRNA vaccines.

Conclusion: In participants with cirrhosis, the Ad.26.COV2.S demonstrated a 64% effectiveness against COVID-19, and a 74% effectiveness against severe or critical COVID-19, similar to that associated with mRNA vaccines.
lower anti-S after first dose. The spike-specific T cell response was evaluated in 14 cirrhotics, showing a heterogeneous magnitude of response, but on average the quantity and kinetics of decline of the spike-specific cellular responses diverged in cirrhotics compared to controls, with lower concentrations of both IFN-γ and IL-2, at all time-points. During follow-up, 4/133 (3%) COVID-19 naïve cirrhotics tested positive for anti-N: all asymptomatic, no hospitalization required. Neither unexpected nor severe adverse events emerged in our patients.

**Conclusion:** In COVID-19 naïve patients with cirrhosis undergoing SARS-CoV-2 mRNA vaccine, humoral and cellular responses appeared suboptimal compared to healthy controls, but the rates of post-vaccination infection remained low. The response after the third dose will be also presented.

**THU264**

The protective role of dairy protein on sarcopenic obesity in middle-aged and older women: a community-based, 12-year, prospective cohort study

Jun-Hyuk Lee1, Joo Hyun Oh2, Sang Bong Ahn2, Huiyul Park3, Joo Hyun Sohn4, Bo-Kyeong Kang2, Mi Mi Kim2, Chul-min Lee5, Dae Won Jun6, Eileen Yoon6, Hye Young Lee2, Hyunwoo Oh2. 1Nowon Eulji Medical Center, Eulji University School of Medicine, Department of Family medicine, Seoul, Korea, Rep. of South; 2Nowon Eulji Medical Center, Eulji University School of Medicine, Department of Medicine, Seoul, Korea, Rep. of South; 3Uijeongbu Eulji Medical Center, Eulji University School of Medicine, Department of Medicine, Seoul, Korea, Rep. of South; 4Hanyang University Guri Hospital, Hanyang University College of Medicine, Department of Medicine, Gyeonggi-do, Korea, Rep. of South; 5Hanyang University College of Medicine, Department of Medicine, Seoul, Korea, Rep. of South; 6Uijeongbu Eulji Medical Center, Department of Medicine, Gyeonggi-do, Korea, Rep. of South; 7Hanyang University College of Medicine, Department of Medicine, Seoul, Korea, Rep. of South; 8Uijeongbu Eulji Medical Center, Department of Medicine, Gyeonggi-do, Korea, Rep. of South.

**Email:** dr486@eulji.ac.kr

**Background and aims:** Changes in body composition during aging include decreased muscle mass and increased fat mass, especially in women. Individuals with sarcopenic obesity (SO) could be at higher risk of morbidities and mortality than those with either sarcopenia or obesity alone. Dairy products, which contain whey protein and all essential amino acids, could have a beneficial role in preserving muscle mass and reducing obesity. We aimed to analyze the effect of dairy protein on the development of SO in women using a large-scale, community-based prospective cohort.

**Method:** Our analysis included 4251 women from the Korean Genome and Epidemiology Study. Participants were categorized into three groups by the tertile of dairy protein intake, which was assessed using a semi-quantitative 103-food item food frequency questionnaire. Appendicular skeletal muscle mass was estimated using the anthropometric equation. Obesity was defined as a body mass index of 25 kg/m² or greater. Multiple Cox hazard regression analysis was conducted to examine associations between dairy protein intake and incident SO.

**Results:** During follow-up (mean, 9.6 years), 280 women newly developed SO. Using Cox proportional regression models, the hazard ratios (95% confidence interval) for incident SO of the middle and highest tertiles were 0.93 (0.70–1.24) and 0.72 (0.52–0.98) compared with lowest tertile after adjusting for confounding variables.

**Conclusion:** These findings indicate high dairy protein intake is inversely related to SO development in Korean women. Dairy protein intake could be an effective strategy to prevent incident SO.

**Keywords:** dairy protein; sarcopenia; obesity; sarcopenic obesity; women

**THU265**

Detection of microplastics in cirrhotic liver tissue

Thomas Horvatits1, Matthias Tamminga2, Beibei Liu1, Marcial Sebode3, Klaus Püschel3, Ansgar Lohse1, Samuel Huber3, Elke Fischer1. 1University Medical Center Hamburg-Eppendorf, I. Department of Medicine, Gastroenterology and Hepatology, Hamburg, Germany; 2University of Hamburg, Center for Earth System Research and Sustainability (CEN), Hamburg, Germany; 3University Medical Centre Hamburg-Eppendorf, Institute of Legal Medicine, Hamburg, Germany

**Email:** t.horvatits@uke.de

**Background and aims:** The contamination of ecosystem compartments by microplastics (MPs) is an ubiquitous problem. Tissue accumulation of MPs has been observed in mice, and recently MPs have been observed in human stool and placenta. However, whether MPs accumulate in human tissues, and the resulting consequences are still unclear. Aim of this study was to examine various human tissue samples for the presence of MPs, and to determine whether MPs may deposit in the liver, kidney or spleen.

**Method:** This proof-of-concept case series was conducted in Hamburg, northern Germany, Europe. Tissue samples from 6 patients with liver cirrhosis and portal hypertension and from 7 individuals without underlying liver disease were assessed. A reliable method for detection of MP particles in human tissue was developed. A total of 17 samples (11 human liver, 3 kidney and 3 spleen samples) were analysed according to the final protocol. Chemical digestion of the tissue samples, staining with Nile red, subsequent fluorescent microscopy and Raman spectroscopy were performed. Procedural blanks were processed and analysed during each series of analyses. Shape, size and types of MP polymers were assessed in all tissue samples.

**Results:** Considering the limit of detection, all samples (liver, spleen, kidney) from patients without liver disease tested negative for MPs (n = n.s.), whereas MPs in liver samples from patients with cirrhosis tested positive and MP concentrations (5 to 12 particles per g tissue) were significantly higher than those from blank samples (n = 6, p = 0.009, α = 0.05). Six different microplastic polymers (polystyrene (PS), polyvinyl chloride (PVC), polyethylene terephthalate (PET), polymethyl methacrylate (PMMA), polyoxymethylene (POM), and polypropylene (PP)) ranging from 4 to 30 µm in size have been detected, see figure 1.

**Figure 1:** Detection of microplastics in liver tissue using Raman spectroscopy.

**Table 1:** Characteristics of patients with liver cirrhosis.

- **S224 Journal of Hepatology 2022 vol. 77(51) | S119–S388**
Conclusion: This is the first study, assessing MPs in different types of human tissues. MPs were found only in liver tissues from patients with cirrhosis. Hepatic deposition may be the consequence of impaired intestinal barrier function due to portal hypertension and portal enteropathy. Future studies on the possible effects on human health are urgently needed.

Examples of MP particles found in human tissue samples displayed as fluorescence images (left column) and true colour microscope images (mid column) as well as related Raman-spectra. White scale bar indicates 10 µm, library reference spectra are displayed in red, particle spectra are given in green. S/N: signal to noise ratio

THU266
Patient Navigators: an innovative approach to improve hepatitis C case finding leveraging existing human immunodeficiency virus service delivery models to reach last mile patients in Nasarawa State, Nigeria
Chukwuemeka Agwuocha1,2, Olayinka Adisa1, Onyeka Nwobi1, Muhammad-Mujtaba Akanmu1, Caroline Boeke3, Magdalena Witschi3, Amy Azania3, Jibrin Kama1, Folu Lufadeju1, Owens Wiw1. 1Clinton health access initiative, Abuja, Nigeria; 2Clinton health access initiative, Abuja, Nigeria; 3Clinton Health Access Initiative, Abuja, Nigeria; 4Clinton health access initiative, United States
Email: cagwuocha@clintonhealthaccess.org

Background and aims: The natural history of Hepatitis C Virus (HCV) demonstrates an asymptomatic disease that often leads to liver degeneration in approximately three decades. In HIV/HCV coinfection, liver degeneration is accelerated with decompensated cirrhosis occurring in less than two decades resulting in higher mortality rates. The asymptomatic nature of HCV, increased rate of disease progression in HIV, low awareness, and poor care seeking behaviour emphasizes the need to improve HCV case finding in People Living with HIV (PLHIV).

In Nigeria, the Nasarawa State Government has committed to HCV elimination, with an initial focus on PLHIV, necessitating integration of services to screen ART patients for HCV. However, due to the COVID pandemic and the resultant scale-up of Differentiated Service Delivery (DSD) models within the HIV program, screening yield from facility-based case finding reduced significantly. To ensure last mile linkage to HCV screening, the Patient Navigator pilot was conducted from March-October 2021. This analysis aims to assess screening coverage before and during this pilot period.

Method: One healthcare worker across three secondary facilities i.e., General Hospitals Keana, Awe, and Uke, labelled patient navigator (PN) was charged with the responsibility of identifying unscreened PLHIV using facility screening records and enrolment data. These PNs were HIV program defaulter trackers, consequently integrating this service within the HIV program. The PN employed strategic patient tracking approaches like phone calls, community engagements and peer group meetings. Using laboratory screening registers, screening progress was compared pre-intervention (July 2020 to February 2021) versus during the intervention (March to October 2021).

Results: A total of 125, 560, and 923 were active on ART care as of January 2020 in General Hospitals Keana, Awe, and Uke respectively. Across sites, the first 4 months of the pre-intervention phase saw high screening numbers as all available patients presenting to facilities were screened. Subsequently, a decline in screening numbers across all facilities. However, the intervention phase demonstrated extended coverage, reaching the last mile patients leading to an increase in case finding by 18% in GH Keana, and 23% in GH Awe and GH Uke respectively.

Conclusion: The use of patient navigators demonstrates the feasibility and cost-effectiveness of increasing case-finding through HCV/HIV program integration.

THU267
The Community Pop-Up Clinic (CPC): a unique strategy to achieve HCV elimination in the inner city
Brian Conway1,2, Shawn Sharma1, Leo Yamamoto1, Rossitta Yung1, David Truong1. 1Vancouver Infectious Diseases Centre, Vancouver, Canada; 2Simon Fraser University, Burnaby, Canada
Email: bconway5538@gmail.com

Background and aims: A number of strategies have been proposed to help identify HCV-infected inner-city residents, engage them in care, provide them with Hepatitis C Virus (HCV) therapy, and achieve and measure cure. While many programs have successfully identified large numbers of subjects eligible for treatment, the rate of successful completion and cure is highly variable. The most relevant outcome measure for such programs may be the number of HCV cures achieved over time, and programmatic changes should be implemented and evaluated according to this metric. We have evaluated our Community Pop-Up (CPC) program in terms of this outcome measure, as a function of the resources required for its implementation.

Method: On a weekly basis, a team consisting of a physician, nurse and three support staff interact with up to 30 individuals over 4 hours in the inner city of Vancouver, at a community centre or single room occupancy dwelling to provide point-of-care HCV testing or ascertaining of previously identified HCV infection status. Treatment for HCV infection is offered in the context of a low-barrier treatment program, with medications delivered daily/weekly, at the place of residence, local pharmacy or at our community clinic. Strategies are in place to limit loss to follow-up and maximize engagement in care throughout treatment and thereafter, to ascertain if cure has been achieved.

Results: From 07/20–09/21 (15 months), we conducted 55 community pop-up clinics and screened a total of 774 individuals for their HCV status. Of 280 HCV-infected individuals by antibody test, 99 (35.4%) had documented HCV viral load result. Key demographic characteristics include: median age 43 (28–86) years, 77.5% male, F0/F1 (22, 55%), opioid antagonist therapy 26 (65%), HIV co-infected 2 (5%), fentanyl/cocaine/amphetamine use (24/12/18, 60%/30%/45%). Of 40 individuals on treatment, none have been lost to follow-up, 26 have demonstrated cure, with outcome results pending in the other 14 subjects. Strategies are in place to engage the remaining 49 viremic individuals in HCV treatment.
POSTER PRESENTATIONS

TU268

Age, gender and region-specific HBsAg and anti-HCV seroprevalence in Ghana: a nationwide hospital based cross-sectional study

Yvonne Nartey1, 2. 1Cape Coast Teaching Hospital, Internal Medicine, Cape Coast, Ghana; 2Karolinska Institute, Medical Epidemiology and Biostatistics, Stockholm, Sweden

Email: yvonne.nartey@ki.se

Background and aims: Hepatitis B (HBV) and Hepatitis C (HCV) viral infection continue to pose a significant global health burden and are responsible for high morbidity and mortality worldwide due to sequelae of end stage liver disease. Previous estimates in Ghana report a seroprevalence of anti-HCV of 3.3% and HBsAg of roughly 9%. These estimates fall short of describing age and gender-specific rates and have relied on small sample sizes in few centers. Particularly for HCV, there is a paucity of data from several regions in Ghana. Numerous challenges, including lack of focused and definitive testing and treatment strategies and policies limit the impact of current elimination efforts. Providing a robust programmatic foundation requires a scale-up of hepatitis testing nationwide, and this in turn requires up-to-date epidemiologic data to understand the burden of disease in all parts of the country and across all age groups. This study aimed to perform an epidemiological assessment of HBV and HCV infection in Ghana to determine age, gender, and region specific seroprevalence. Additionally, it aimed to convene a coalition of local stakeholders for policy development in Ghana.

Method: A nationwide cross-sectional study using de-identified data was collated from January 1st to October 30th 2021. Data from health information management systems for 2017–2021 was reviewed for 20 centers including teaching, regional, and district hospitals in 11 regions in Ghana. Sixty thousand labour ward, 54, 000 blood bank, and 48, 000 laboratory-based records were reviewed and analyzed for age and gender-specific HBV and HCV prevalence. Regional differences in seroprevalence were also determined.

Results: A stakeholder meeting was held in Accra, Ghana bringing together key players from the public and private sector involved in viral hepatitis elimination for policy planning. Crude prevalence among pregnant women was 6.36% (95% CI 5.70–7.02) for HBsAg; among blood donors was 5.09% (95% CI 4.91–5.28) for HBsAg and 3.22% (95% CI 3.08–3.38) for anti-HCV. From laboratory-based registers, overall seroprevalence was 8.90% (95% CI 8.65–9.16%) for HBsAg and 3.39% (95% CI 3.17–3.63) for anti-HCV. Analysis of age and gender-specific HBV and HCV prevalence. Regional differences in seroprevalence were also determined.

Conclusion: In the context of an established, multidisciplinary clinic serving the inner city, a 4 hour/week initiative staffed with 2 health care providers and 3 support staff led to successful HCV treatment of 40 individuals, with none lost to follow-up once treatment has been initiated and the possibility of 40–50 additional treatment starts in the short term. This represents a very cost effective and productive initiative to address HCV infection in similar populations.

TU269

The elimination of hepatitis C in the cherokee Nation: the impact of harm reduction

Jorge Mera1, Whitney Essex1, Molly Feder2, Homie Razavi3, Devin Razavi-Shearer1, 2. 1Cherokee Nation Outpatient Health Center, Tahlequah, United States; 2Cardea Services, Seattle, United States; 3Center for Disease Analysis Foundation, Lafayette, United States

Email: drazavishearer@cdfound.org

Background and aims: In the United States, American Indians/Alaskan Natives have the highest rates of HCV incidence, liver cancer and mortality compared to all other racial/ethnic groups. The Cherokee Nation (CN) a sovereign tribal nation, began a hepatitis C (HCV) elimination program in 2015 with a 6-fold increase in treatment in 2016. The primary aim of this study is to estimate what would need to be done to meet the World Health Organization’s (WHO) 2030 targets by 2025. In addition to examining increase in treatment, the implementation and lack of syringe service programs (SSP) were considered in the analysis.

Method: CN specific input data populated a dynamic Markov model. Three scenarios were considered. The Base scenario examined the impact of maintaining the current treatment and diagnosis levels into the future. The 2025 w/o SSP scenario examined how much treatment would need to be increased to attempt to meet the 2030 targets in 2025 without access to SSP. The 2025 w/SSP scenario examined the accompanying treatment uptake necessary to meet the 2030 goals in 2025 with a robust SSP program.

Results: In the Base scenario, it was estimated that the 90% diagnosis and 80% treatment targets would be met prior to 2025. By 2030, there is estimated to be an 84% reduction in mortality and a 50% reduction in incidence when compared to 2015 (Figure 1). 2025 w/o SSP required a large increase in treatment, from 162 to 400 annually. This scenario resulted in an 89% reduction in mortality by 2025 but only a 50% reduction in incidence by 2025. The 2025 w/SSP scenario required a modest increase in treatment to 255 individuals annually. This resulted in a 65% reduction in mortality and an 86% reduction in incidence by 2025 thus meeting all targets.

Conclusion: Ghana remains a region of high endemicity for HBV and moderate-high endemicity for HCV. Northern Ghana consistently demonstrates a higher disease burden than the rest of the country. Focused and targeted policies are essential to reach elimination targets.
Background and aims: The effectiveness of COVID-19 vaccines with rising prevalence of SARS-CoV-2 delta variant

Binu John1,2, Raphaella Ferreira1, Dustin Bastaich3, Akash Doshi4, Tamar H Taddei5, David Kaplan6, Seth Spector1,4, Bassam Dahman3, Sylvia Brakenhoff1, Robert De Man1, Robert De Knegt1, Patrick Bindels5, Evelien de Schepper2, Erasmus MC, University Medical Center, Gastroenterology and Hepatology, Rotterdam, Netherlands; 2Erasmus MC, University Medical Center, General Practice, Rotterdam, Netherlands; 3University of Miami, Coral Gables, United States; 4University of Pennsylvania, Philadelphia, United States; 5University of Virginia, Graduate School, Richmond, United States; 6University of Miami, Miami, United States.

Conclusion: The current HCV elimination program would meet almost all of the WHO targets prior to 2030. However, in the absence of SSP that provide access to all of those that need it, it is estimated that the incidence would not drop substantially enough by 2030. With the CN approving SSP an opportunity has opened for the CN to meet all targets by 2025. In the first year of the elimination program 222 individuals were treated thus increasing treatment to 255 for three years would be within the capacity of the program. To achieve this goal the CN should have a swift broad rollout of SSP. This combined with a slight increase in treatment will lead to early elimination and a positive impact on the population health of the CN.

THU270
Effectiveness of mRNA vaccines in patients with cirrhosis with rising prevalence of SARS-CoV-2 delta variant

Binu John1,2, Raphaella Ferreira1, Dustin Bastaich3, Akash Doshi4, Tamar H Taddei5, David Kaplan6, Seth Spector1,4, Bassam Dahman3

Background and aims: The effectiveness of COVID-19 vaccines with the increasing prevalence of SARS-CoV-2 B.1.617.2 delta variant among patients with cirrhosis is unknown. The aim of the study was to investigate the effectiveness of COVID-19 vaccination at varying community prevalence of the B.1.617.2 variant among patients with cirrhosis.

Method: This study used a test-negative case control design, where adults with cirrhosis who had a diagnosis of COVID-19 as documented by a positive SARS-CoV-2 Polymerase Chain Reaction (PCR) were considered as cases, and those with a negative SARS-CoV-2 PCR were considered controls. This study design is widely used in evaluations of vaccine effectiveness and has the advantage of minimizing biases associated with access to vaccination or health care. Participants who did not undergo SARS-CoV-2 PCR testing, who had COVID-19 before the study period, received a vaccine other than an mRNA vaccine, or received a liver transplant, were excluded. Patients were considered fully vaccinated 14 days after receipt of either the Pfizer BNT162b2 or the Moderna 1273-mRNA vaccine. COVID-19 was classified based on individual chart review using the National Institute of Health (NIH) COVID-19 severity scale as asymptomatic, mild, moderate, severe or critical illness. The weekly proportion of the delta variant in the United States was obtained using data from the Center for Disease Control COVID-19 genomic surveillance data.

Propensity score matching was used to match test positive cases and test negative controls. The propensity score of having COVID-19 was derived from a logistic regression that adjusted for the participant’s baseline variables.

Results: The study sample included 1,720 participants, including 860 cases and 860 controls. The effectiveness of mRNA vaccines against COVID-19 was inversely related to the community prevalence of the B.1.617.2 variant. For every 10% increase in the community prevalence of delta, the likelihood of COVID-19 after full vaccination increased by 5% (aOR 1.05, 1.02–1.07, p = 0.0001). At community delta prevalence of 10%, mRNA vaccines were 70% effective (aOR 0.30, 0.21–0.43, p < 0.0001). Vaccine effectiveness dropped to 62% (aOR 0.38, 0.30–0.48, p < 0.0001) when the community prevalence of the delta variant increased to 50%, to 52% (aOR 0.50, 0.38–0.67, p < 0.0001) at a community delta prevalence of 90% and to 50% (aOR 0.38–0.67, p < 0.0001) with a community delta prevalence of 99%.

Conclusion: Vaccine effectiveness is inversely associated with community prevalence of the delta variant, with effectiveness dropping from 30% at delta prevalence of 10%, down to 50% with a community delta prevalence of 99%. Further studies are needed to understand if booster doses are able to overcome the drop in vaccine effectiveness with increasing prevalence of delta variant, among patients with cirrhosis.

THU271
Epidemiology and management of hepatitis B and C in primary care in the Netherlands-data from the Rijnmond primary care database

Sylvia Brakenhoff1, Robert De Man1, Robert De Kneegt1, Patrick Bindels5, Evelien de Schepper2, Erasmus MC, University Medical Center, Gastroenterology and Hepatology, Rotterdam, Netherlands; 2Erasmus MC, University Medical Center, General Practice, Rotterdam, Netherlands

Background and aims: The Dutch guideline for general practitioners (GPs) advises bimannual surveillance of hepatitis B (HBV) patients and referral of every hepatitis C (HCV) patient. We aimed to study the prevalence, incidence and the management of hepatitis B and C in primary care.

Method: This is a retrospective cohort study using the Rijnmond Primary Care database (RPCD), including healthcare data of medical records of GPs of approximately 200,000 patients in the area of Rotterdam, the Netherlands. Patient records were selected based on laboratory results, International Classification of Primary Care (ICPC) codes and free text words.

Results: In total, 977 patients were included; 717 HBV, 252 HCV, and 8 HBV/HCV co-infected patients. Between 2013 and 2019, the prevalence of HBV and HCV declined from 5.21 to 2.99/1,000 person years (PYs; -43%) and 1.50 to 0.70/1,000 PYs (-53%) respectively. We observed that the majority of the patients had been referred to a medical specialist at least once (71% HBV and 85% HCV patients). However, among the 406 chronic hepatitis B patients, we observed that 36.2% of the patients did not receive adequate surveillance by their GP (>2 ALT checks within 3 years) or by a medical specialist. In addition, among the 153 chronic hepatitis C patients, 113 (73.9%)
POSTER PRESENTATIONS

THU273
Association of novel lifestyle- and whole foods base inflammation scores with metabolic dysfunction-associated fatty liver disease: a population-based study among Iranian adults

Elshaneh Taheri1, Roberd M Bostick2, Behzad Hatami1, Mohammadamin Pourhoseingholi1, Hamid Asadzadeh Aghdaei1, Alireza Moslem3, Alireza Mosusavijaraji4, Mohmadreza Zali1. 1Shahid beheshti university of medical sciences, Research institute for gastroenterology and liver disease center, Tehran, Iran; 2Emory University, Epidemiology, Atlanta, United States; 3Sabzevar university of medical sciences, Cellular and molecular research center, Sabzevar, Iran; 4Shahid beheshti university of medical sciences, Department of community medicine, Tehran, Iran

Background and aims: Chronic inflammation, associated with lifestyle and dietary patterns, may contribute to metabolic dysfunction-associated fatty liver disease (MAFLD) risk. Recently, a novel dietary inflammatory score based on weighted inflammatory scores of 19 components (whole foods) from food frequency questionnaire (FFQ) and lifestyle inflammatory score based on weighted inflammatory scores of 4 components of lifestyle (physical activity, adiposity, alcohol, and smoking) were proposed. The main aim of this study was to evaluate the associations of these novel inflammatory scores with MAFLD risk. The secondary aim of our study was to compare novel dietary- and lifestyle inflammatory scores-MAFLD associations with previous dietary inflammatory scores.

Method: We investigated associations of 19-component dietary and 4-component lifestyle inflammatory separately and jointly with MAFLD risk among Iranian adults aged 35-70 years of age at baseline phase of PERSIAN cohort study in Sabzevar city. MAFLD was defined as having a fatty liver index (FLI) ≥60, plus one of the following: being overweight or obese (body mass index [BMI] ≥25 kg/m2), a Type II diabetes mellitus (T2DM) diagnosis, or having any evidence of metabolic dysregulation. We also calculated previous well-known dieter-related inflammatory markers such as dietary inflammatory index (DII) and empirical dietary inflammatory pattern (EDIP) using information from 115-item FFQ. Higher score were considered more inflammatory status. We assessed inflammatory scores-MAFLD associations using multivariable unconditional logistic regression.

Results: Of 4241 participants of Persian Sabzevar Cohort study, 968 patients with MAFLD and 964 age- and gender adjusted controls were recruited in this nested case-control study. Among participants in the highest relative to the lowest dietary- and lifestyle inflammatory scores tertiles, the adjusted odds ratios (OR) and their 95% confidence intervals (CI) were 1.84 (1.61–2.07; p-trend <0.001)) and 1.96 (1.69–2.21; p-trend <0.001), respectively. Among those in the highest relative to the lowest joint dietary- and lifestyle inflammatory score tertiles, the adjusted OR (95% CI) was 2.56 (95% CI: 2.19–2.93; p-interaction <0.001). The third tertile ORs (95% CI) for the DII- and EDIP-MAFLD associations were 1.63 (1.05–5.62) and 1.71 (1.17–4.62), respectively.

Conclusion: More pro-inflammatory diets and lifestyles, separately and particularly jointly, are associated with higher risk of having MAFLD among adults. The associations of novel dietary- and lifestyle inflammatory with MAFLD were stronger than DII- or EDIP- MAFLD associations.

THU272
Point of care testing for hepatitis C in the priority settings of mental health, prisons and drug and alcohol facilities

Catherine Ferguson1, Lucy Ralton1, Erin McCartney1, Joshua Dawe2, Rachel Lambert2, Adam Adolphi2, Catherine Newington3, Ben Land1. 1South Australian health and education, Adelaide, Australia; 2Adelaide Medical Imaging, Adelaide, Australia; 3Flinders University, Medicine and Public Health, Adelaide, Australia

Background and aims: A key barrier to hepatitis C (HCV) diagnosis and treatment is the multi-stage process of conventional testing that requires multiple visits to pathology services and healthcare providers to obtain a HCV antibody (Ab) test, HCV RNA test, diagnosis, and linkage into care to commence treatment. Point of care testing for hepatitis C in the priority settings of mental health, prisons and drug and alcohol facilities (PROMPt) aims to overcome critical roadblocks to HCV testing in the community by providing HCV point-of-care testing (POCT) and direct referral into treatment. Over a 12 month period PROMPt aims to evaluate the effect of POCT on HCV testing rates, linkage to care and explore the acceptability of HCV POCT in facilities and services for individuals at high risk of HCV infection. Primary end points: 1. Number/proportion of participants who receive rapid POCT HCV Ab plus POCT RNA. HCV Ab/RNA positivity at each site. 2. Number/proportion of HCV RNA positive participants who are linked to care. Secondary end points: 1. Acceptability of HCV POCT to participants in each setting.

Method: Participants are offered POC HCV diagnostic testing using SD Bioline fingerstick Ab assay and those returning a positive HCV Ab result are offered a Cepheid finger stick HCV RNA Xpert assay. Project staff, including peer support workers, provide HCV education, pre- and post-test counselling, and linkage to care at the time of diagnosis.

Results: Interim analysis at 6 months reports 707 participants recruited across all 3 priority settings. 125/707 (18%) positive HCV Ab participants were reflexed to HCV RNA testing, resulting in 35 positive RNA participants 35/125 (28%). To date 27/35 (77%) RNA positive participants have commenced treatment. The complete 12 months of recruitment and final analysis of end points will be presented.

Conclusion: PROMPt has demonstrated high rates of HCV POCT testing and acceptability in 3 high priority settings. The hepatitis C infection rates have been lower than anticipated and the combined HCV Ab and RNA POCT approach to testing has allowed for efficient and economical testing scale up in each site.
Background and aims: Elimination of Hepatitis B Virus (HBV) and Hepatitis C Virus (HCV) requires continuous diagnosis and treatment. Ongoing pandemic COVID-19 has been affecting on health care system including on preventive care and testing of HBV and HCV. This study aimed to assess the impact of COVID-19 on hepatitis prevention and treatment in Japan. This international joint research conducted by three research groups of Ministry of Health, Labour and Welfare of Japan with the Task Force for Global Health and in cooperation with Japan Society of Hepatology (JSH).

Method: We conducted this cross-sectional study by a questionnaire survey in Japanese and English language on online Microsoft forms platform from 24 August to 03 October 2021. The electronic version of the questionnaire was disseminated by e-mail to all the members of JSH. The questionnaire was designed to address the impact of COVID-19 on hepatitis prevention and management, and perceived benefits of COVID-19 response; and demonstrated of hepatitis C virus screening.

Results: The questionnaire was sent to Japanese and English language on online Microsoft forms platform from 24 August to 03 October 2021. The electronic version of the questionnaire was disseminated by e-mail to all the members of JSH. The questionnaire was designed to address the impact of COVID-19 on hepatitis prevention and management, and perceived benefits of COVID-19 response; and demonstrated of hepatitis C virus screening.

Conclusion: In Japan, a greater decrease was noticed on HBV and HCV confirmatory testing, screening than treatment initiation. However, anxiety and fear of patients, lack of staff and facilities are major challenges to overcome such situation. Perceived benefits of COVID-19 on hepatitis were strengthened health care system, demonstration of hepatitis infrastructure and improved training in infectious disease testing and management.

Background and Aims: In Spain, HIV, HBV, and HCV prevalence are lower in females. A 2017 study reported that HBV and HCV prevalence among women in reproductive and sexual health clinics in the Valencian Community were 0.8% and 0.4%, respectively. However, the prevalence of HCV among women has increased significantly in recent years, particularly among injection drug users (IDUs). In our study, we aimed to evaluate the prevalence of HBV and HCV among women attending reproductive and sexual health clinics in Valencia, Spain.
THU277

mRNA COVID-19 vaccine effectiveness in liver transplant patients
Muhammad Khan1, Kamran Mushtaq1, Deema AlSoub1, Hussam Almasri1, Bisher Sawaf1, Saad AlKaabi1, Yasser Kamel1.
1Hamad Medical Corporation, Doha, Qatar

Background and aims: There is poor antibody response in up to 61% of the liver transplant patients after mRNA COVID-19 vaccination, and almost 20% of liver transplant recipients have undetectable antibody levels. However, antibodies are surrogate markers of disease protection and absence of seroconversion does not mean complete susceptibility to the disease. We hypothesized that COVID-19 vaccines are effective in liver transplant patients despite low seroconversion rates.

Method: We designed a test-negative case-control study to assess the vaccine effectiveness (VE) of COVID-19 vaccination in liver transplant recipients followed at our center in Hamad Medical Corporation. All liver transplant patients who were tested for SARS-CoV-2 infection between 1st of February till 30th of July in Qatar were included in the study. Case patients were identified as patients who had positive SARS-CoV-2 test on nasopharyngeal and throat swab while control patients were identified as patients who were tested negative during the same period. Information regarding demographic and clinical characteristics, transplant history, current immunosuppressive treatment was obtained from the medical records. Also, we recorded the type of COVID-19 vaccination, number of vaccine doses (one or two), COVID-19 complications, hospitalizations, and ICU admissions. VE was estimated by a test-negative case-control design in which symptomatic liver transplant patients who were tested negative for COVID-19 were recorded as controls, while patients who tested positive were considered cases. VE was defined as "1- OR (odds ratio)."

Results: A total of 136 liver transplant patients were included in the study. 13 (9.6%) patients were diagnosed with COVID-19 during the study period, out of which 7 (5.2%) needed hospitalization and 5 (3.7%) were admitted to the ICU. None of the patients died. The baseline characteristics, transplant history, comorbid conditions, and current immunosuppressive treatment for the participants is summarized in the table. Among the vaccinated patients, 86 (63.5%) had received Pfizer vaccine, and 92 (69.3%) of the patients had received both the doses, three weeks apart.

VE of mRNA based vaccines against any COVID-19 infection, hospitalization and ICU admission is shown. In liver transplant patients VE was 84.1% (38.2%-96.2%, p = 0.002) for any documented infection. VE was 88.5% (26.4%–98.9%, p = 0.003), and 92.8% (22.8%-99.8%, p = 0.003) for COVID-19 related hospitalizations and ICU admissions respectively.

Conclusion: In liver transplant patients, two doses of mRNA based SARS-CoV-2 vaccines is effective against any documented infection. The protection is higher against hospitalization and ICU admissions. Combined analysis of cellular and humoral response is needed to identify vaccine responders.

THU278

Evaluation of global progress towards HBV and HCV elimination
Sarah Blach1, Devin Razavi-Shearer1, Ellen Mooneyhan1, Chris Estes1, Kathryn Razavi-Shearer1, Ivane Gamkrelidze1, Homie Razavi1.
1Center for Disease Analysis Foundation, Lafayette, United States

Background and aims: The Polaris Observatory maintains mathematical models for hepatitis B (HBV) and hepatitis C (HCV) viruses which are updated annually and used to monitor progress towards elimination. The outcomes of this work, including country/territory progress reports are publicly available online. The objective of this
analysis was to evaluate progress towards elimination (by elimination target) among the countries with approved or estimated models, and to report on policy assessment surveys returned by country experts. **Method:** The year of elimination (by target) was extracted from 110 HCV and 167 HBV models available on the Polaris Observatory website (data from 2020). Results were summarized across countries by disease area and time period of elimination (target achieved before 2030, target achieved between 2031 and 2050, target achieved after 2050). Additionally, average country-level results from a qualitative policy assessment survey (administered in 2020 by the CDA Foundation, with responses from 47 countries) were used to score national viral hepatitis elimination policies. **Results:** Based on 2020 data, no countries were on track to achieve all HBV elimination targets by 2030; however, 85 countries were expected to achieve the target for prevalence among 5-year-olds, 40 countries were on track to achieve absolute mortality targets, and 7 were on track to achieve the diagnosis target. Based on 41 survey responses, 11 countries (26%) received the highest score of 10 for political will (“Government is fully committed to the elimination in any population who tests positive for the virus”). Nine countries were on track to achieve all relative HCV elimination targets by 2030, with 27 expected to achieve the diagnosis target and 18 expected to achieve the treatment target. When absolute targets were considered, 58 countries would achieve the mortality target and 44 would achieve the incidence target. Relative mortality and incidence targets would only be met by 18 and 10 countries, respectively. Based on 47 survey responses, 17 countries (36%) received a score of 10 for political will. Political will was found to be the strongest predictor of country achieving viral hepatitis elimination. Unfortunately, across the board, countries reported a lower political will score for HBV elimination as compared to HCV. **Conclusion:** Nuanced country reports on viral hepatitis elimination progress and policies are vital feedback mechanisms for policy makers. Although most countries were not on track to achieve all HBV or HCV targets, substantial progress has been made by countries with regards to individual targets. Substantial work is needed to increase political will for HBV and HCV elimination.

**THU279**

**The impact of vaccination on the global and regional pediatric prevalence of hepatitis B from 1985 to 2022**

Devin Razavi-Shearer, Ivane Gamkrelidze, Sarah Blach, Chris Estes, Ellen Mooneyhan, Kathryn Razavi-Shearer, Homie Razavi. Center for Disease Analysis Foundation, Lafayette, United States

**Background and aims:** The first vaccine to prevent the hepatitis B virus (HBV) was available in 1981. The rollout and coverage of the vaccine varied by country, but three dose coverage became widespread in 2001 when Gavi, the vaccine alliance, began to support these programs. This study aims to examine the impact of prophylaxis measures on the pediatric, under 18 years of age, prevalence of HBV between 1985 and 2022. **Method:** The Polaris Observatory maintains 166 country specific PRoGReSs Models. These models consider the impact of prophylaxis measures (timely birth dose, three dose, hepatitis B immunoglobulin, and anti-viral treatment of pregnant women) and treatment on the incidence and disease burden of HBV. These models were utilized to estimate the historical and current prevalence among the pediatric population at the country and regional level. For countries in which models were not available, a regional prevalence was applied to the population of said missing country. **Results:** Modeled countries represented 99.6% and 99.7% of all estimated pediatric cases in 1985 and 2022 respectively. Globally it was estimated that in 1985 the pediatric HBV prevalence was 5.23%, representing 101.9 million infections, this dropped to 1.0%, 23.8 million infections, by 2022 (Figure 1). This represents an 81% reduction in prevalence. High income and upper middle-income countries saw the largest drop, 96%, whereas lower middle- and low-income countries only saw a reduction of 74–75%. Discrepancies in regional reductions were also observed of 95% in Europe, 91% in the Americas, 88% in Asia, 77% in Oceania and 72% in Africa. **Conclusion:** Countries and regions that historically provided timely birth-dose as well as additional mother to child transmission prophylaxis measures have greatly reduced the burden of HBV in their pediatric population. While all regions have reduced the pediatric prevalence, the reductions have been highly inequitable with lower-middle- and low-income countries continuing to bear the brunt of the disease. Without additional assistance to provide timely birth dose and other prevention measures these inequities will continue well into the future.

**Figure 1: The Global HBV Pediatric Prevalence, 1985–2022.**
Background and aims: The estimated prevalence of hepatitis C virus (HCV) infection in India is 0.32%, which comprises a considerable proportion of the global HCV burden. The incarcerated population is disproportionately affected by HCV and significant scale-up of access to testing and treatment is needed in order to achieve the 2030 global targets for the elimination of HCV. The objective of this intervention was to provide early diagnosis and management of HCV and evaluate the feasibility and efficacy of a decentralised HCV micro-elimination care model in 19 prisons across states of Punjab, Haryana and Union Territory of Chandigarh in the northern part of India.

Method: Anti-HCV antibody rapid diagnostic test (RDT) was performed for the inmates at time of admission or via screening camps. Inmates with positive HCV RDT results received reflex blood draw for HCV RNA testing and pre-treatment investigations. Liver staging was determined by APRI and FIB-4 scores (non-cirrhotic APRI <2 and FIB-4 <3.5 and cirrhotic as APRI >2 and FIB-4 >3.5). Non-cirrhotic patients were initiated on treatment by the prison medical officer trained by the health department of the respective states. The cirrhotic cases were referred to specialist care at the model treatment centers set up by the states. Test of cure (SVR12) was assessed with an HCV RNA test done 12 weeks after completion of treatment.

Results: A total of 30, 670 inmates, which represent 100% of the prison population in the 19 prisons at the time the intervention started, were screened from November 2019 to January 2022. Of the 13.11% (n = 4022) HCV antibody-positive, 90.42% (n = 3637) received a confirmatory viral load test, of which, 75.19% (n = 2735) were HCV RNA-positive. 74.04% (n = 2052) of those testing HCV RNA positive were initiated on treatment, and 56.87% (n = 1167) had completed treatment as of January 2022. Of those who completed treatment, 48.67% (n = 568) were assessed for SVR cure assessment, with SVR achieved in 89.26% (n = 507) inmates. The median days and IQR for the turnaround time from RDT screening to viral load result completion was 6 days, IQR 4–12 days (n = 2553); between viral load results and treatment initiation was 6 days, IQR 0–15 days (n = 1622) and total median time between RDT screening and treatment initiation was 16 days with an IQR of 10–30 day (n = 1597).

Conclusion: This simple decentralised HCV testing and treatment model in prison settings has shown to be feasible, effective, and replicable in the Indian context. As this care model is fully transitioned to government partners, additional efforts are being made to re-engage individuals released from incarceration that had not completed all steps in the HCV care cascade.

Background and aims: In the last decade, innovative treatments and health policies for Hepatitis C Virus (HCV) are leading to the reduction of the burden of HCV-related diseases. Direct-Acting Antiviral (DAA) therapy has shown a high rate of viral eradication, and there is evidence that HCV cure reduces HCV complications and is cost-saving in most western countries in the long term. The aim of this analysis is to evaluate the trend of hospitalizations in patients with HCV chronic infection and HCV-related liver complications in Italy and to discuss the impact of the introduction of DAAs in 2015.

Method: The analysis was based on records of hospital discharge (SDO) at national level from 2012 to 2019. SDO collect information related to all discharges from public and private hospitals in Italy. Data was extracted based on primary and secondary diagnosis for HCV, cirrhosis and hepatocellular carcinoma (HCC). We calculated the annual incident hospitalizations with diagnosis of HCV and HCV-related complications. Analyses were stratified by age cohort (40–59, 60–79 and 80+ years) and divided into two distinct periods: (1) 2012–2015, in which DAAs were not available or had just been approved, and (2) 2016–2019, in which DAAs were available initially with prioritized access and later with universal access. The trend of alcoholic liver complications was also evaluated with the same methodology as comparison.

Results: Annual incident hospitalizations for cirrhosis reduced from 73 new cases per 100,000 inhabitants in 2012 to 44 in 2019 (-39%). Each year, patients with age ≥80 years represent around 20% of new hospitalizations. For alcoholic liver related complications, a reduction of only 9% was observed, and patients with age ≥80 years only represent around 5% of new hospitalizations. From 2012 to 2019, incident cases of HCC also reduced from 52 to 45 per 100,000 inhabitants (-14%) and incident cases of HCV reduced from 113 to 49 per 100,000 inhabitants (-57%). For cirrhosis, HCC, and HCV the reduction is becoming more evident in recent years. Hospitalizations for chronic HCV infection, cirrhosis complications and HCC. This reduction is becoming more evident in recent years. Alcohol related liver complications are decreasing at a slower rate and affect younger patients on average. Overall, these data confirm
the clinical benefit of viral eradication by DAA and the long-term economic benefit of reduced expenses for severe liver complications.

**THU282**

**Hepatitis B birth dose coverage remains dramatically low in The Gambia and has been disrupted by the COVID-19 pandemic**

Gibril Ndow1, Esu Ezeani1, Cecile de Bezenac2,3, Julien Randon-Furling4, Umberto D’Alessandro1, Yusuke Shimakawa3, Maud Lemoine6, 1MRC Unit The Gambia at LSHTM, Fajara, Gambia; 2Turing Institution, LONDON, United Kingdom; 3The Alan Turing Institute, LONDON, United Kingdom; 4Sorbonne University, Paris, France; 5Pasteur Institution, Paris, France; 6Imperial College London, Hepatology, LONDON, United Kingdom.

Email: m.lemoine@imperial.ac.uk

**Background and aims:** Africa has the lowest coverage of hepatitis B birth dose (HepB-BD) vaccination (11%) worldwide and lags far behind the 90% coverage target recommended by the WHO for viral hepatitis elimination by 2030. We aimed to assess i. the coverage and limiting factors of HepB-BD vaccination and ii. the impact of the COVID-19 pandemic on HepB-BD coverage in The Gambia, in the first African country to introduce in 1990 hepatitis B vaccination at birth.

**Method:** we analysed data form the Health and Demographic Surveillance system (HDSS) in four areas in The Gambia. HepB-BD coverage was calculated at birth (0–1 day), day 7 and day 28 in children born between 2015 and 2021. We also performed multiple comparisons tests and a logistic regression to identify factors associated with lack of timely delivery.

**Results:** between 1 January 2015 and 31 July 2021, 77,913 births were recorded; of them 77,515 live births with complete information were analysed. 3, 494/77,515 babies (4.5%) received a timely HepB-BD (D0–1). The median age at first dose was 20 days (IQR: 12–31 days). HepB-BD was administrated at D7 and D28, in 7, 308/77, 515 (9.4%) and 38, 239/77, 515 (49.3%) babies, respectively. Whilst timely HepB-BD coverage steadily increased over time (Figure 1), a major disruption was observed between March and August 2020, corresponding to the first wave of COVID-19 outbreak in The Gambia. Between March and August 2020, the HepB-BD coverage dropped from 9% (July 2019 to Feb 2020) to 5%.

**Conclusion:** more than 30 years after adoption of the HepB-BD vaccination, only minor progress has been made in HepB-BD coverage in The Gambia, putting at risk the HBV elimination goals.

**THU283**

**Hepatitis B prevalence and the impact of vaccination in Georgia: results from a nationwide serosurvey**

Nino Khetsuriani1, Amiran Gamkrelidze2, Shaun Shadaker3, Maia Tseteli4, Maia Alkhasahvili5, Nazibrola Chitadze6, Irina Tskhomedelie4, Lia Gvinjila7, Francisco Averhoff8, Gavir Cloherty4, Qian An1, Giorgi Chakhunashvili1, Jan Drobeniec3, Paata Imnadze2, Khatuna Zakhashvili2, Paige A Armstrong9, 1Centers for Disease Control and Prevention, Global Health, Tbilisi, Georgia; 2Centers for Disease Control and Prevention, Division of Viral Hepatitis, Atlanta, United States; 3National Center for Disease Control and Public Health, Tbilisi, Georgia; 4Task Force for Global Health, Tbilisi, Georgia; 5Centers for Disease Control and Prevention, Eastern Europe and Central Asia Regional Office, Tbilisi, Georgia; 6Abbott Diagnostics, Abbott Park, United States. Email: nck7@cdc.gov

**Background and aims:** Georgia introduced routine infant hepatitis B (HepB) vaccination in 2001 with >90% coverage over the last decade. In 2015, a nationwide serosurvey demonstrated an anti-hepatitis B core antibody (anti-HBc) prevalence of 25.9% and hepatitis B surface antigen (HBsAg) prevalence of 2.9% among adults ≥18 years. No prevalence data were available for children. In 2021, we assessed hepatitis B virus (HBV) infection prevalence among children and updated estimates for adults in a combined COVID-19, hepatitis C and HBsAg serosurvey of persons aged ≥5 years.

**Method:** We used a stratified, multi-stage cluster design. We collected data on demographics, medical and exposure history; we tested blood samples for anti-HBc and, if positive, for HBsAg. Nationally representative weighted proportions and 95% confidence intervals (CI) for anti-HBc and HBsAg were calculated. Participants aged 5–20 years had been eligible for routine HepB vaccination as infants.

**Results:** Among children aged 5–17 years, 0.7% were anti-HBc+ and 0.03% were HBsAg+ (Table). Among adults ≥18 years, 21.7% were anti-HBc+ and 2.7% were HBsAg+. Anti-HBc prevalence increased with age from 1.3% among 18–23-year-olds to 28.6% among ≥60 years. HBsAg prevalence was lowest (0.2%) among 18–23-year-olds and highest (8.6%) among 35–39-year-olds. Males had higher HBsAg prevalence than females (3.6% versus 2.0%; p = 0.003). Anti-HBc prevalence was highest in Samegrelo-Zemo Svaneti, Adjara, and Imereti regions. Higher education and income were associated with lower anti-HBc, and unemployment—with higher HBsAg prevalence.

**Table. National anti-HBc and HBsAg prevalence by age and sex, Georgia, 2021**

<table>
<thead>
<tr>
<th>Age, years/sex</th>
<th>No. tested</th>
<th>Anti-HBc+, weighted % (95% CI)</th>
<th>HBsAg+, weighted % (95% CI)</th>
</tr>
</thead>
<tbody>
<tr>
<td>All ages ≥5</td>
<td>8, 710</td>
<td>17.1 (16.3-17.9)</td>
<td>2.2 (1.8-2.6)</td>
</tr>
<tr>
<td>Children 5-17</td>
<td>1, 473</td>
<td>4.7 (3.1-6.1)</td>
<td>0.03 (0-0.2)</td>
</tr>
<tr>
<td>Adults ≥18</td>
<td>7, 297</td>
<td>21.7 (20.4-23.2)</td>
<td>2.7 (2.2-3.4)</td>
</tr>
<tr>
<td>18-23</td>
<td>322</td>
<td>1.3 (0.6-2.1)</td>
<td>0.0 (0-0.1)</td>
</tr>
<tr>
<td>24-29</td>
<td>430</td>
<td>3.8 (2.7-5.1)</td>
<td>0.9 (0.4-2.4)</td>
</tr>
<tr>
<td>30-34</td>
<td>565</td>
<td>11.7 (8.2-16.5)</td>
<td>2.9 (1.7-7.0)</td>
</tr>
<tr>
<td>35-39</td>
<td>864</td>
<td>27.9 (23.4-32.6)</td>
<td>8.6 (5.7-12.1)</td>
</tr>
<tr>
<td>40-49</td>
<td>1, 283</td>
<td>27.4 (23.9-31.3)</td>
<td>3.0 (2.0-4.5)</td>
</tr>
<tr>
<td>50-59</td>
<td>1, 517</td>
<td>28.2 (25.0-31.7)</td>
<td>3.0 (1.6-5.1)</td>
</tr>
<tr>
<td>≥60</td>
<td>2, 476</td>
<td>28.6 (26.1-31.2)</td>
<td>1.7 (1.2-2.2)</td>
</tr>
</tbody>
</table>

**Sex (adults)**

<table>
<thead>
<tr>
<th></th>
<th>Male</th>
<th>Female</th>
</tr>
</thead>
<tbody>
<tr>
<td>HBsAg+</td>
<td>2, 409</td>
<td>23.1 (20.9-25.9)</td>
</tr>
<tr>
<td>HBsAg+</td>
<td>4, 628</td>
<td>20.5 (19.1-22.1)</td>
</tr>
</tbody>
</table>

Figure: Monthly proportion of timely HepB-BD from 1st Jan. 2015 to 31st July 2021. Circled in red is the disruption observed in the immediate wake of the first CoViD 19 outbreak (the black vertical line shows the date of the 1st case, 17 March 2020). Magenta dashed vertical lines are change points detected using general fluctuations tests (Bai-Perron). Blue horizontal segments show the mean timely BD rate for each period between change points.

Factors associated with lack of timely HepB-BD were: births on Friday or Saturday (OR: 3.2 (95% CI: 2.0 to 3.5), p value <10\(^{-5}\)) high maternal age (OR: 1.5 (1.4 to 1.6), p <10\(^{-12}\)) for mothers older than 20 with respect to (wrt) mothers younger than 20, and OR: 1.8 (1.6 to 2.1), p <10\(^{-15}\) for older than 25 wrt younger than 25), delivery outside the hospitals (OR: 4.6 (3.7 to 5.8), p <10\(^{-15}\)) especially home delivery (OR: 2.1 (95% CI: 1.9 to 2.3), p <10\(^{-15}\)), born to a primiparous mother (OR: 1.8 (1.6 to 2.2), p <10\(^{-12}\)) and delivery during the first COVID-19 outbreak (17 March 2020–1st August 2020) (OR:1.7 (1.4 to 1.9, p <10\(^{-11}\)) among all babies born after June 2019).

**Conclusion:** more than 30 years after adoption of the HepB-BD vaccination, only minor progress has been made in HepB-BD coverage in The Gambia, putting at risk the HBV elimination goals.
Progress towards HCV elimination in the country of Georgia: insights from modelling and national survey

Joséphine Walker1, Irina Tskholmelidze2, Shaun Shadaker3, Maia Tserteli1,2, Senad Handanagic3, Paige A Armstrong1, Amiran Gamkrelidze4, Peter Vickerman1. 1University of Bristol, Population Health Sciences, Bristol, United Kingdom; 2Task Force for Global Health, Tbilisi, Georgia; 3Centers for Disease Control and Prevention, Division of Viral Hepatitis, Atlanta, United States; 4National Center for Disease Control and Public Health, Tbilisi, Georgia

Email: jogwalker@gmail.com

Background and aims: A national serosurvey in 2015 found the country of Georgia had high hepatitis C virus (HCV) prevalence, with 5.4% of adults (~150,000 people) chronically infected. In April 2015, Georgia launched a national program to eliminate HCV infection (reduce prevalence by 90%). We developed an HCV transmission model to capture current and historical dynamics of HCV infection in Georgia, and project long-term impact of the elimination program. A follow-up serosurvey in 2021 provided data which was used to validate the model and update impact projections.

Method: The original model was calibrated to the 2015 serosurvey and surveys among people who inject drugs (PWID), accounting for age, sex, PWID status, and liver disease state. We compare model projected prevalence overall and by age group, sex, and among ever infected drugs to 2021 serosurvey prevalence, and filter the original 532 parameter sets to match the serosurvey results. We used logistic regression to assess which input parameters or model characteristics affect fit. We used program data on 77,168 persons treated May 2015-February 2022 to estimate current incidence of HCV infection, cases and deaths averted. We project the impact of reductions in treatment rates that occurred during in the COVID-19 epidemic.

Results: The original modelled adult hepatitis C prevalence for 2021 (2.7%, 1.9–3.5%) was higher than the observed serosurvey prevalence (1.8%, 1.3–2.4%); across all groups uncertainty bounds overlap. Only 14% of 532 model runs fits within the 95% confidence interval of all hepatitis C prevalence estimates; 32% fit overall, 28% fit in females, 43% fit in males, 85% fit in ever-injected drugs. Runs that fit the 2021 serosurvey data tend to have lower total population and lower general population hepatitis C incidence, suggesting the model underestimated the initial burden of infection. After filtering, modelled hepatitis C adult prevalence is slightly higher than the observed prevalence (2.1%, 1.6–2.4%). Hepatitis C incidence in March 2022 is estimated to be 0.05 (95% credible interval (CrI) 0.03–0.11) per 100 person-years in general population, and 1.14 (0.08–6.4) per 100 person-years in PWID, a 60% decrease since 2015. As of March 2022, 9, 186 (5, 396–16, 720) infections and 842 (489–1324) deaths have been averted, with benefit accumulating to 26, 154 (15, 850–47, 627) infections and 3, 971 (2, 516–5, 336) deaths averted if tracked to 2030. Treatment numbers went from 996/month in 2019 to 406/month March 2020–March 2022 during the COVID-19 pandemic, resulting in 14, 127 fewer treatments, 471 (242–817) fewer infections averted by March 2022. At 406 treatments/month, elimination can be reached in 2031.

Conclusion: The impact of HepB vaccination in Georgia is demonstrated by a low HBsAg prevalence among children that is below the 0.5% European regional hepatitis B control target and meets the ≤0.1% seroprevalence target for elimination of mother-to-child transmission of HBV. Chronic HBV infection remains a problem among adults born before routine infant HepB vaccination. Focusing efforts on screening, treatment, and preventive interventions among adults, along with sustaining high immunization coverage among children, can help Georgia achieve elimination of hepatitis B as public health threat by 2030.
significant burden on healthcare resources. Alcohol is a modifiable risk factor and interventions such as €1.00 MUP may have an immediate impact on reducing admissions for acute alcohol conditions. Larger sample sizes and longitudinal data are awaited.

**THU286**

Is hepatic steatosis individually a risk factor for colorectal adenoma?

Yuvraj Singh1, Maya Gogtay1, Anuroop Yekula1, Kartikeya Tripathi2, George Abraham1,2,4, Saint Vincent Hospital, Internal Medicine, Worcester, United States; 2University of Massachusetts Medical School, Baystate campus, Department of Gastroenterology, Springfield, United States; 4Mass Chan Medical School, Internal Medicine, Worcester, United States; 3American College of Physicians, Philadelphia, United States

Email: yuvraj.singh@stvincenthospital.com

**Background and aims:** Most colorectal cancers (CRC) originate from adenomatous lesions. Data suggests that obesity, insulin resistance, and metabolic syndrome are risk factors for CRC. Non-alcoholic fatty liver disease (NAFLD) is one of the manifestations of metabolic syndrome. Many studies have correlated metabolic syndrome with a risk of CRC but there is a paucity of evidence on NAFLD and its association with CRC. We aim to study the association between moderate to severe hepatic steatosis detected on vibration-controlled transient elastography (VCTE) and colorectal adenomas.

**Method:** This retrospective cohort study was approved by the institutional review board (IRB). We included adult patients who underwent VCTE and colonoscopy. Other causes of liver diseases, such as autoimmune hepatitis, alcohol use disorder, viral hepatitis, and primary biliary cirrhosis were excluded. Steatosis was categorized as S0-S1 (mild) and S2-S3 (moderate/severe) based on the controlled attenuation parameter (CAP) grade of VCTE. Colonoscopy findings were stratified on the biopsy results i.e., hyperplastic, adenoma, CRC, inflammatory or normal mucosa. Continuous variables were assessed using the Mann Whitney U test and categorical variables using chi-square with p <0.05 considered statistically significant. A multinomial logistic regression analysis (MLRA) was done between colorectal adenoma and significant covariates.

**Results:** Out of the 415 patients analyzed, 206 patients met inclusion criteria. 124 had moderate/severe steatosis and 82 had no/mild steatosis. Descriptive analysis showed that BMI (p = 0.001), aspirin (p = 0.01), smoking (p = 0.004), and adenoma (p = 0.02) were significantly different between both groups. In the MLRA model; aspirin had a hazard ratio (HR) of 3.5 [2.39–10.45] (p = 0.03) and obesity OR = 2.9 [1.07–6.78] (p = 0.02) in association with colorectal adenoma.

**Conclusion:** Our study indicated that moderate/severe hepatic steatosis is associated with an increased risk of colorectal adenoma detection on colonoscopy. Several patients were excluded due to the non-availability of colonoscopy reports, many of whom were less than 45 years of age. Current guidelines do not recommend earlier screening for CRC after detection of hepatic steatosis for patients. We recommend prospective studies to understand this positive association better. Further studies would be needed to determine if the increase in adenoma detection lowers the risk for the detection of CRC.

**THU287**

No effect of HBSAg positivity on antibody response after COVID-19 vaccine

Ganbolor Jargalsaihan1,2, Enkhtuul Batbold1,2, Delgersaikhan Zulkhnu1,2, Oyungerel Lkhagva-Ochir1,2, UurtSaikhi Baatsuren1,2, Myagmarjarg BudeeBazar3,4, KhatanZul Ganbold1,2, Sumiya Byambabaatar1,2, Byambasuren Ochirsum1,2, Munkhzaya Munkhbaatar1,2, Purevjargal Bat-Ulziib, Bishguurmaa Rechindorj1,2, Ariunbolor Byambasaikhan1,2, Naranbaatar Dashdorj1,2, Katy Shaw-Saliba3, Irini Sereti3, Sally Huangberger4, Renee Kidzon4, Naranjargal Dashdorj1,2, Onom Foundation, Ulaanbaatar, Mongolia; 3The Liver Center, Ulaanbaatar, Mongolia; 4National Institute of Health, Bethesda, Maryland, United States

Email: dashdorj@onomfoundation.org

**Background and aims:** Immune responses to vaccines may vary based on nutritional status, underlying comorbidities and/or concomitant infections. Despite the high burden of chronic HBV infection worldwide it is not known if this affects the immune response following COVID-19 vaccination. We aimed to evaluate antibody levels in people with chronic Hepatitis B virus (HBV) infection, compared to control group among those receiving either their third or fourth COVID-19 vaccination.

**Method:** Samples from a subset of participants in the InVITE study (ClinicalTrials.gov Identifier: NCT05096091) were assessed for SARS-CoV-2 IgG level (MINIVIDAS 3.0, BIOMEREUX, France) and HBSAg (HISC-5000, Sysmex, Japan). Chronic HBV infection was defined as HBSAg>0.03mIU/ml. T-tests were used to compare mean IgG levels and a regression analysis was performed to control for age, sex, history of COVID-19, number of vaccines received, obesity, and time since previous vaccine.

**Results:** Participants who received BBIBP CoV (n = 377), ChAdOx1 nCoV-19 (n = 196), BNT162b2 (23), Sputnik V (n = 17) vaccines as their initial two-dose COVID-19 vaccine regimen. Of the 613 participants included in this analysis, 104 with chronic HBV and 504 controls. Overall characteristics included: 6.5% older than 60 years, 62% female, 20% with history of COVID-19, 17% receiving a fourth dose of vaccine, 20% obese, and 48% had greater than 6 months since previous vaccine; these were well balanced between groups. The IgG levels between groups were not significantly different (p = 0.265), with mean (std) of control 32.3 (13.6) BAU/ml, chronic HBV, 34.0 BAU/ml (14.4). Only history of COVID-19 was significantly associated with increased antibody levels in the regression model (p = 3.0 × 10⁻³).

**Conclusion:** This study showed no difference in SARS-CoV-2 IgG levels between control and HBsAg positive groups. SARS-CoV-2 IgG level was higher in participants with previous COVID-19 infection than those without COVID-19 infection.

**THU288**

Prevalence of hepatitis B and C virus in the Uzbekistan Hepatitis Elimination Program (UHEP) patients

Erkin Musabaev1, Chris Estes2, Shakhllo Sadirova3, Shokhista Bakieva1, Krestina Brigida1, Kathryn Razavi-Shearer2, Bakhodir Yusupaliev4, Homie Razavi2, Research Institute of Virology, Tashkent, Uzbekistan; 2Center for Disease Analysis Foundation, Lafayette, United States; 3Center for Disease Analysis Foundation, Tashkent, Uzbekistan; 4Ministry of Health, Tashkent, Uzbekistan

Email: homie.razavi@centerforda.com

**Background and aims:** Chronic infection with hepatitis B and C viruses (HBV and HCV) is a major contributor to liver disease and liver-related mortality in Uzbekistan. There is a need to better
quantify the number of undiagnosed cases, the characteristics of infected patients, and the risk factors associated with disease. 

**Method:** In the capital city of Tashkent, 13 clinics were established to diagnosed and treat chronic HBV and HCV infection among the general adult population. Patients underwent testing for HBV and HCV infection, along with follow-up biochemical measures and questionnaire items. Nurses were trained to use rapid HCV and HBV tests to screen large numbers of people and an electronic medical system was put in place to record the test and questionnaire results. The prevalence of previously undiagnosed HBV and HCV was estimated and adjusted to the Uzbekistan population. Regression analyses quantified risk of infection based on demographic factors. 

**Results:** HBV and HCV screening was conducted on 62,000 people over a 12-month period that included a 6-month shutdown due to the COVID-19 pandemic. Before the shutdown, 30,000 people were screened while another 32,000 were screened in conjunction with COVID-19 testing. Complete dataset was available for 53,841 HBV patients and 54,396 HCV patients. Age-adjusted adult prevalence of previously undiagnosed chronic HBV and HCV infection were estimated at 3.23% (3.00–3.37%) and 3.02% (2.80–3.16%), respectively. Prevalence was significantly higher in males for both HBV and HCV, while increasing age was significantly associated with higher HCV prevalence. The most commonly reported risk factors among HCV+ patients were dental procedures and medical injections, and 2.5% of HCV+ patients had APRI score >2.5. Among HBV+ patients 1.2% had eGFR <30 while for HCV+ patients the portion was 3.3%.

**Conclusion:** This program represents the first of its kind in terms of scope (HBV and HCV testing) and size providing a detailed estimate of viral hepatitis infection. A large population of patients chronically infected with HBV and HCV remains undiagnosed in Uzbekistan. There should be further efforts to screen, diagnose and treat these patients in the general population to achieve the WHO 2030 elimination targets.

---

**Figure:** (abstract: THU288): aPR = Adjusted prevalence ratio.
THU289
Evaluation of the clinical and economic value of sofosbuvir/velpatasvir (SOF/VEL) in patients with chronic hepatitis C in Spain during the last 5 years
Rafael Esteban1, Raquel Domínguez-Hernández2, Helena Cantoreo1, Miguel Ángel Casado2. 1Hospital Universitari Vall d’Hebron, Barcelona, Spain; 2Pharmacoeconomics and Outcomes Research Iberia (PORIB), Pozuelo de Alarcón, Spain; 3Gilead Sciences, Madrid, Spain.
Email: rdominguez@porib.com

Background and aims: The introduction of direct-acting antivirals in the therapeutic arsenal for the treatment of hepatitis C virus (HCV) infection represented a paradigm shift. Sofosbuvir/velpatasvir (SOF/VEL) has added value to HCV treatments, achieving high response rates that lead to a cure in most HCV chronic patients. The aim of this analysis was to evaluate the long-term impact on health and economic outcomes of patients with chronic hepatitis C treated with SOF/VEL during the first 5 years after its approval in Spain (2017–2022).

Method: A previously developed lifetime Markov model was adapted to estimate HCV morbidity and mortality comparing two treatment alternatives: SOF/VEL versus previous therapies (peginterferon and ribavirin in double/triple therapy with telaprevir or boceprevir). The target population (30, 488 patients) entered the model during the first 5 years (22% 1st year, 26% 2nd, 22% 3rd, 13% 4th, 17% 5th) and were distributed among the fibrosis stages in treated or untreated. In SOF/VEL, all patients (100%) were treated regardless of fibrosis stages (F0–F4) with an average weighted sustained viral rate (SVR) of 98.9% from real-world data. In previous therapies, only 49% of ≥F2 stages HCV patients were treated, with 61% SVR. All parameters required for the analysis were obtained from real-world data and the literature. Only direct healthcare costs associated with disease management were included. A discount rate (3%) was applied to costs and healthcare outcomes. The results were measured as the number of cases of decompensated cirrhosis (DC), hepatocellular carcinoma (HCC), and liver transplant as well as their costs associated, in addition to liver-related deaths, comparing both alternatives. An alternative analysis was performed with a reduction in the SVR rate of SOF/VEL to 95%.

Results: In the analysis of SVR rate (98.9%), the lifetime results showed that SOF/VEL decreased liver-related mortality by 85% (4, 017 cases avoided) as well as avoided cases of liver complications: 4, 367 DC (-92%), 2, 536 HCC (-80%) and 474 LT (-87%), having the greatest impact on DC. In economic terms, the costs associated with SOF/VEL in the management of liver complications generated a total saving of 197 million euros. In the alternative analysis, a variation in the SVR rate (95%) decreased the impact on the reduction of avoided liver-related events between 75 and 86%.

Conclusion: SOF/VEL significantly decreases HCV morbidity and mortality adding value to the management of patients with chronic hepatitis C reducing the clinical and economic burden of the disease and contributing to the goal of disease elimination in Spain.

THU290
The value of increased HCV testing and treatment strategies in Spain to achieve elimination goals
José Luis Calleja Panero1, Jaime Espin2, Ankita Kaushik3, Manuel Hernández Guerra3, Rob Bissey4, Adam Igloi-Nagy5, Alon Yehoshua3. 1Universidad Autónoma de Madrid, Hospital Universitario Puerta de Hierro, Madrid, Spain; 2Escuela Andaluza de Salud Pública, Granada, Spain; 3Gilead Sciences, Inc., Foster City, United States; 4Hospital Universitario de Canarias, Tenerife, Spain; 5Maple Health Group, LLC, New York City, United States.
Email: alon.yehoshua@gilead.com

Background and aims: In 2015, Spain launched a national eradication strategy for Hepatitis C virus (HCV) through prevention, screening, diagnosis, and link-to-care, resulting in the highest HCV treatment rate of any European country and substantial reductions in HCV prevalence. To achieve the goal of HCV elimination, it is necessary to scale up the diagnosis, treatment, and management of HCV infection in the general population, migrants and people who inject drugs (PWID). Our aim was to assess the prevalence, incidence, and cost effectiveness of scaling up compared to status quo scenarios.

Method: A compartmental dynamic transmission model was developed in visual basic for applications (VBA). The model comprises two modules: the first represents the cascade of HCV care and the second represents the progression of liver disease. Direct and indirect costs, as well as utilities to estimate quality of life were considered as model inputs. Outcomes included the prevalence and incidence of HCV infection as well as the incremental cost per quality-adjusted life year (QALY) and per life year (LY). Outcomes for a hypothetical elimination strategy were compared to those expected with the status quo staying in place. Costs and effects were discounted at 3.0%; the model time horizon is until the year 2030 in the base case and extended to 2040 in scenario analysis.

Results: The base case analysis found that scaling up testing and treatment reduced both the prevalence and incidence of HCV over time resulting in incremental costs per QALY and LY of €13, 291 and €12, 285 respectively, compared to the status quo. Excluding indirect costs from the analysis brought the incremental costs per QALY and LY to €13, 761 and €12, 720, respectively. Main drivers of the cost-effectiveness results included cost of diagnosis, cost of treatment, proportion of people who are unaware, percentage of population of people who inject drugs, and various calibration parameters related to HCV infection prevalence. Scenario analyses found that reducing the screening intervals decreased the prevalence of HCV infection over time; extending screening to include migrants upon arrival in Spain also decreased the prevalence over time with the same or better cost effectiveness metrics.

Conclusion: This analysis demonstrated that scaling up testing and treatment with direct acting antivirals (DAAs) is an efficient strategy for reducing the incidence and prevalence of HCV infection among
key populations of interest in Spain. Given the global burden of HCV infection, and its associated liver-related morbidity and mortality, increasing access to testing and treatment among key populations of interest may be a successful strategy to achieve HCV elimination goals in Spain.

**THU291**

**National hepatitis elimination profiles: progress towards HBV and HCV elimination in five European countries**

Lindsey Hiebert1, Isabelle Nassar1, Vanessa Nunez2, Loreta Kondili2, Sema Mandal3, Graham Foster4, Francisco Javier Garcia-Samaniego Rey5,6, Philip Bruggmann7,8, Paolo Bonanni3, Camila Picchio9,10, Rui Marinho11, Jeffrey Lazarus10, John Ward1. 1Task Force for Global Health, Coalition for Global Hepatitis Elimination, Decatur, United States; 2Istituto Superiore di Sanità, Italy; 3UK Health Security Agency, United Kingdom; 4Queen Mary University of London, United Kingdom; 5Allianza para la Eliminación de las Hepatitis Víricas en España, Spain; 6Hospital Universitario La Paz, Spain; 7Swiss Hepatitis, Switzerland; 8Arud Centre for Addiction Medicine, Switzerland; 9University of Florence, Italy; 10University of Barcelona, Institute of Global Health (ISGlobal); 11University of Lisbon (FMUL)

Email: lriebert@taskforce.org

**Background and aims:** To achieve WHO goals for hepatitis elimination, Member States (MS) are in various stages of national planning and policy development. To track country-level progress and identify feasible next steps, CGHE is developing National Hepatitis Elimination Profiles (NHEPs). The status of hepatitis elimination in European countries is described.

**Method:** Together with local partners, profiles were prepared for England (EG), Italy (IT), Portugal (PT), Spain (ES) and Switzerland (CH). For comparison, key indicators include policies for prevention, testing, and treatment. Country-specific data were collected from peer-reviewed reports, ministries of health (MoH), ECDC, WHO and other credible sources, Partners in MoH, clinical practice, and civil society organizations (CSO) validated data.

**Results:** All MS have an HCV action plan; ES, IT, and CH have HBV action plans. EG, ES, and CH have set HBV and HCV elimination goals, while PT has goals for HCV. For CH and ES, the hepatitis AP and goals were prepared by clinical associations and CSO. All MS have >95% coverage of infant 3-dose HepB vaccination. All MS have policies for routine HBV screening of pregnant women; IT recommends maternal HCV screening. All countries recommend HepB birth dose vaccination (Hep-BD-V) for newborns of HBsAg+ mothers. PT recommends universal HepB-BD- V ≤24 hours of birth; PT has >50% coverage, the WHO 2020 target. The 4 countries with data distribute 27–139 needle-syringes per person who injects drugs (PWID) per year, 14%-70% of the WHO 2020 target. At least two MS have safe injection programs for persons who are incarcerated. All countries have risk-based HBV and HCV screening; IT recommends HCV testing for persons born 1969–1989. All have removed most restrictions to HCV treatment. However, some MS require HCV genotyping (CH, IT, PT) and specialty care (ES, IT, PT) (Figure). Data suggest 3 countries have reduced HCV mortality rates approaching or exceeding the 2030 WHO target (≤2/100,000). As feasible next steps, local partners prioritize community awareness of hepatitis, expanded adult testing, and micro-elimination programs for key populations (PWID, INC).

**Conclusion:** NHEPs reveal advances and challenges to hepatitis prevention and care and lessons learned for overcoming barriers. With NHEPs, local coalitions (CSO, MoH, clinical) can advocate for policies expanding HBV and HCV services, accelerating progress toward hepatitis elimination.

**THU292**

**Economic investment and strategies to eliminate hepatitis C in Mexico**

Ellen Mooneyhan1, Alethse De la Torre Rosas2, Daniel Bernal Serrano2, David Kershenobich2, Maria Jesus Sanchez2, Leandro Soares Sereno2, Ivane Gamkrelidze1, Sarah Blach1, Homie Razavi1. 1Center for Disease Analysis Foundation, Lafayette, United States; 2National Center for the Prevention and Control of HIV (CENSIDA), Mexico City, Mexico; 3The National Institute of Health Sciences and Nutrition Salvador Zubirán (INCMNSZ), Tlalpan, Mexico; 4Pan American Health Organization, Mexico City, Mexico; 5Pan American Health Organization, Washington DC, United States

Email: emooneyhan@cdafound.org

**Background and aims:** In July 2020, the Mexican Government initiated the National Program for Elimination of Hepatitis C (HCV) under a procurement strategy that secured universal, free access to HCV screening, diagnosis, and treatment for 2020–22. This analysis quantifies the clinical and economic burden of HCV under a continuation (or an end) to this agreement.

**Method:** A modeling and Delphi approach was used to evaluate the current and future disease burden (from 2020 to 30) and economic impact (from 2020 to 35) of the historical paradigm (Historical Base), compared to HCV elimination (Elimination). The elimination cost analysis was stratified assuming the agreement continues (Elimination-Agreement to 2035) or terminates (Elimination-Agreement to 2022). We also analyzed the price of HCV treatment needed to achieve net-zero cost (defined as the difference in cumulative direct costs between the scenario and the Historical Base), starting at a base price of 77,838 MXN per person per treatment. Elimination is defined by the World Health Organization as a 90% reduction in new infections, 80% diagnosis coverage, 80% treatment coverage, and 65% reduction in mortality, by 2030.

**Results:** A viremic prevalence of 0.55% (0.38–0.60) was estimated in Mexico on January 1, 2021, corresponding to 745,000 (677,000–812,000) viremic infections. In the Historical Base, cases of advanced liver disease and liver-related deaths are projected to rise 75%–80% and annual direct costs are projected to remain at 2.4–2.5 billion MXN, with cumulative direct costs reaching 39.7 billion MXN. Elimination could save 23,500 lives and divert 6.5 billion MXN in healthcare costs. Under Elimination-Agreement to 2035, annual direct costs are projected to peak at 2.6 billion MXN, with cumulative direct costs...
of 31.2 billion MXN. Under the Elimination Agreement to 2022, annual direct costs would peak at 8.1 billion MXN, estimating 74.2 billion MXN in cumulative direct costs. The price of HCV treatment must decrease to 11,000 MXN per patient to achieve net-zero cost by 2035.

Figure: Direct Medical Costs, 2020–2035 annual direct medical costs, b) cumulative direct medical cost

Conclusion: To achieve HCV elimination at net-zero cost or below, the Mexican Government could either extend the procurement agreement through 2035 or reduce the cost of HCV treatment from 77,838 MXN to 11,000 MXN per person per treatment, starting in 2023. Otherwise, the Mexican Government must increase national budget allocation to the elimination program in order to achieve elimination by 2030.

THU293 Assessing the cost-effectiveness of integrated screening of viral hepatitis C, HIV, and tuberculosis
Ketevan Goginashvili1, Ekaterine Adamia1. 1Ministry of Internally Displaced Persons from the Occupied Territories, Labour, Health and Social Affairs of Georgia, Policy Department, Tbilisi, Georgia
Email: kogoginashvili@moh.gov.ge

Background and aims: Georgia has made significant progress in reducing the burden of communicable diseases, which is due to effective measures taken to manage these diseases. The aim of the study was to evaluate the cost-effectiveness of integrated screening for the early detection of hepatitis C, HIV/AIDS, and tuberculosis, introduced at the level of primary health care since 2018.

Method: A pre and post-intervention study focused on comparing of two different methods of hepatitis screening using the cost-effectiveness evaluation. For the purpose of the study: the costs, screening coverage, and prevalence rates were compared for two different screening methods 1) integrated screening for hepatitis C, tuberculosis, and HIV/AIDS; 2) Separate screening of all three diseases in Samegrelo region.

Method: In Samegrelo region, primary health physicians conducted an average of 0.68 integrated screenings per adult person for hepatitis C, tuberculosis, and HIV/AIDS in 2019–2020, the mean screening cost was 9.4 GEL per person and the hepatitis C prevalence rate was 6.5% (p <0.05). While in 2017–2018, Separate screening of all three diseases per adult person in the same region was 0.35, expenditure on hepatitis screening was GEL 17.4 and the prevalence rate was 6.9% (p <0.05). The Cost-effectiveness coefficient was 13.8 and 49.7 for integrated screening and for hepatitis screening respectively (p = 0.01).

Results: In Samegrelo region, primary health physicians conducted an average of 0.68 integrated screenings per adult person for hepatitis C, tuberculosis, and HIV/AIDS in 2019–2020, the mean screening cost was 9.4 GEL per person and the hepatitis C prevalence rate was 6.5% (p <0.05). While in 2017–2018, Separate screening of all three diseases per adult person in the same region was 0.35, expenditure on hepatitis screening was GEL 17.4 and the prevalence rate was 6.9% (p <0.05). The Cost-effectiveness coefficient was 13.8 and 49.7 for integrated screening and for hepatitis screening respectively (p = 0.01).

Table: Clinical and economic outcomes for integrated screening of three diseases and hepatitis C screening

<table>
<thead>
<tr>
<th>Screening per person</th>
<th>Integrated screening of three diseases</th>
<th>Hepatitis C screening</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Screening mean cost per adult person GEL</td>
<td>9.4</td>
<td>17.4</td>
<td>&lt;0.05</td>
</tr>
<tr>
<td>Hepatitis C prevalence rate</td>
<td>6.5%</td>
<td>6.9%</td>
<td>&lt;0.05</td>
</tr>
<tr>
<td>Cost-effectiveness coefficient</td>
<td>13.8</td>
<td>49.7</td>
<td>0.01</td>
</tr>
</tbody>
</table>

Conclusion: This study provides evidence that adherence to the integrated screening of Hepatitis C, HIV/AIDS, and tuberculosis is more cost-effective and increases the rate of screening coverage compared to single hepatitis C screening alone.

THU294 Eliminating chronic hepatitis B in the northern territory of Australia through a holistic care package delivered in partnership with the community
Jane Davies1, Joshua Saul Davis1, Kelly Hosking2, Paula Binks3, Catherine Gargan4, Belinda Greenwood-Smith2, Sarah Bukulatji3, Terese Ngurrwuthun3, Amanda Dhagapan1, Phillip Wilson2, Teresa De Santis2, Karen Fuller4, Melita McKinnon1, Mikaela Mobbs4, Emily Vintour-Cesar4, 1Menzies School of Health Research; 2Northern Territory Government, Department of Health, Darwin City, Australia; 3Miwatj Health Aboriginal Corporation; 4Katherine West Health Board Aboriginal Corporation
Email: jane.davies@menzies.edu.au

Background and aims: Hep B PAST is a partnership project developed to eliminate chronic hepatitis B (CHB) from the Aboriginal population of the Northern Territory (NT) in Australia. Preliminary results from the project demonstrate significant improvements in the cascade of care for those living with CHB. The project aims to: Improve hepatitis B related health literacy Improve the cascade of care for people living with CHB

Method: Aim 1: Using a participatory action approach (PAR) the “Hep B Story” educational app was designed, translated (forward and back translation) launched in pilot language Yolu, and evaluated, with the process then repeated for the seven next most widely spoken NT Aboriginal languages.

Aim 2: Reviewing existing pathology and vaccination data from electronic health record systems, individuals in consenting health services were allocated to one of six hepatitis B zero-status codes (Hep B: Fully vaccinated, Hep B: Immune by Exposure, Hep B: Infected On Treatment, Hep B: Infected NOT On Treatment, Hep B: Non-Immune, No data) triggering an appropriate follow-up response for all clients. To support primary care to manage recalls and follow-ups as appropriate, we delivered hepatitis B education to remote doctors, nurses, and Aboriginal Health Workers (AHWs). Using a PAR, a hepatitis B management education course for AHWs was developed, delivered, and evaluated.

Results: The Hep B Story App is now available in English and eight Aboriginal languages spoken in the NT and roll out and evaluation is underway. All client files in participating health services have been reviewed, with approximately 30, 000 Aboriginal clients allocated a hepatitis B serocode and appropriate care pathway. Hepatitis B education has been delivered to over 150 general practitioners and nurses in the NT, and to approximately 100 AHWs. The cascade of care for those living with hepatitis B in the NT has significantly improved, now exceeding National Hepatitis B Strategy Targets, with 90% allocated a serocode (national target = 80%), 61% engaged in care (national target = 50%), and 21% receiving antiviral treatment (national target = 20%)

Conclusion: This project is demonstrating the effectiveness of a partnership approach with communities, with AHWs at the centre of the care model, and creating a community led, culturally acceptable, in-language health promotion tool in improving client outcomes for CHB. The preliminary findings from the project demonstrate
improvements in clinical care whilst preserving Aboriginal languages
and empowering community through increased health literacy.

THU295
Hepatitis C prevalence and elimination in Pakistan: a bottom-up approach accounting for provincial variation
Ellen Mooneyhan1, Huma Qureshi2, Hassan Mahmood2, Samra Mazhar2, Mohammad Tariq3, Nabeel Ahmed Maqbool3, Ambreen Khan3, Masood Anwar3, Sarah Blach4, Homie Razavi4, Sabeen Shah5, Saeed Sadqi Hamid6, Tanweer Hussain1, Saira Khowaja7, Uzma Khan7, Syeda Zahida Sarwar3, Khalid Mahmood8,9, Gul Sabeen Azam Ghorezai10, Farooq Azam11, Ayub Rose12, Mohammad Khalil Akhter13, Aamir Ghafoor Khan13, Mujahid Aslam14, Ahmad Nawaz15,16. 1Center for Disease Analysis Foundation, United States; 2Ministry of National Health Services, Regulations and Coordination, Islamabad, Pakistan; 3Chemonics International, Pakistan; 4Center for Disease Analysis Foundation, Lafayette, United States; 5Indus Hospital and Health Network, Karachi, Pakistan; 6Aga Khan University and Hospitals, Karachi, Pakistan; 7IRD Pakistan, IRD Global, Karachi, Pakistan; 8Pakistan; 9Punjab Hepatitis Control Programme, Lahore, Pakistan; 10Punjab Hepatitis Control Program, Primary and Secondary Healthcare, Lahore, Pakistan; 11Balochistan Hepatitis Control Programme, Quetta, Pakistan; 12Chemonics International/USAID, Quetta, Pakistan; 13Chemonics International/USAID, Peshawar, Pakistan; 14Health Department Khyber Pakhtunkhwa, Peshawar, Pakistan; 15Lady Reading Hospital, Peshawar, Pakistan

Method: Using a Delphi method, epidemiologic HCV data for the four provinces of Pakistan (accounting for 97% of the country’s population) were reviewed with 21 provincial and national subject-matter experts over 10 virtual meetings. Province-level estimates were then aggregated and inputted into a mathematical model to estimate the national HCV disease burden in the absence of intervention (Base), and if the World Health Organization (WHO) elimination targets of a 90% reduction in new infections, 80% diagnosis coverage, 80% treatment coverage, and 65% reduction in mortality, are achieved by 2030 (WHO Elimination).

Results: An estimated 9, 746, 000 (7, 573, 000–10, 006, 000) Pakistanis are living with viraemic HCV as of January 1, 2021, corresponding to a viraemic prevalence of 4.3% (3.3–4.4). Under the Base, it is estimated that 21% (2, 010, 000) of the infected Pakistani population has been diagnosed with HCV and only 2% (215, 000) of those infected received treatment in 2021. WHO Elimination would require an annual average of 18.8 million people screened, 1.1 million treated, and 46, 700 new infections prevented between 2021–2030. WHO Elimination would reduce total infections by 7, 040, 000, save 152, 000 lives and prevent 104, 000 incidence cases of hepatocellular carcinoma between 2015 and 2030.

Conclusion: Recent blood surveys, programmatic data, and expert panel input from the four provinces of Pakistan uncovered a higher number of HCV infections and lower number of patients treated than has been estimated using national extrapolations, which demonstrates the benefits of a bottom-up approach. Screening and treatment must increase 20-fold and 5-fold, respectively, from current levels, to curb the HCV epidemic in Pakistan and achieve elimination by 2030.

THU296
Association between immunosuppressants and poor antibody responses to inactivated SARS-CoV-2 vaccines in patients with autoimmune liver diseases
Hu Li1, Yuting Wang1, Ling Ao1, Mingxia Ke1, Zhi-wei Chen1, Min Chen1, Ming-Li Peng1, Ning Ling1, Peng Hu1, Dachuan Cai1, Dazhi Zhang1, Hong Ren1. 1Key Laboratory of Molecular Biology for Infectious Diseases (Ministry of Education), Institute for Viral Hepatitis, Department of Infectious Diseases, the Second Affiliated Hospital of Chongqing Medical University

Email: renhong0531@vip.sina.com

Background and aims: To evaluate the safety, antibody responses and explore the impact of immunosuppressants on inactivated SARS-CoV-2 vaccines in patients with autoimmune liver diseases (AILD).

Method: In this prospective study, 76 adult patients with AILD and 136 healthy subjects were enrolled at least 21 days since the second dose of vaccines (BBIBP-CoronaVac or CoronaVac). All adverse events (AEs) after the COVID-19 vaccination were recorded and graded. The anti-RBD-IgG and neutralizing antibodies (NAbs) were determined. In addition, SARS-CoV-2 specific B cells were also analyzed.

Results: All AEs were mild and self-limiting, and the incidence was similar between AILD patients and controls within 7 days and 30 days after COVID-19 vaccination. The anti-RBD-IgG and NAbs were detectable in 74 (97.4%, 100% in healthy controls, p = 0.13) and 48 (63.2%, 84.6% in healthy controls, p <0.001) patients. The titers of anti-RBD-IgG (p = 0.02) and NAbs (p <0.001) were both significantly lower in AILD patients than healthy controls. In multiple regression analysis, immunosuppressive therapy was an independent risk factor for the low-level anti-RBD-IgG responses (AOR: 4.7; 95% CI, 1.5–15.2; p = 0.01) and reduced probability of NAbs seropositivity (AOR, 3.0; 95% CI, 1.0–8.9; p = 0.04) in AILD patients. However, regardless of with or without immunosuppressants, the RBD-specific MBCs responses were comparable between patients with AILD and healthy controls.

Conclusion: The COVID-19 inactivated vaccine is safe and achieves efficient antibody responses in patients with AILD. In addition, immunosuppressants are significantly associated with poor antibody responses to the SARS-CoV-2 vaccine.

THU297
“Like what? You think I have that?!” Impact of stigma on pharmacy-based identification and treatment of hepatitis C in Victoria, British Columbia
Marion Selfridge1,2, Tamara Barnett1, Kellie Guarasci1, Karen Lundgren1, Anne Drost1, Chris Fraser1,3. 1Cool Aid Community Health Centre, Victoria, Canada; 2University of Victoria, Canadian Institute of Substance Use Research, Victoria, Canada; 3University of British Columbia, Department of Family Medicine, Vancouver, Canada

Email: msselfridge@coolaid.org

Background and aims: Canada is currently on target to reach the 2030 WHO goal of HCV elimination. Continued high rates of treatment initiation are required to meet this goal. Novel models have proven successful to engage populations who use drugs (PWUD) in HCV therapy with a simplified, task-shifted cascade of care: Tayside, Scotland pharmacy-based HCV screening and treatment has demonstrated excellent outcomes and progress towards local HCV elimination. The EPIC Study seeks to determine whether pharmacy-based treatment successes can be replicated at community pharmacies in Victoria BC.

Method: Four community pharmacies known to work with PWUD and provide opioid agonist therapy (OAT) were provided training sessions to equip staff with a standardized tool kit of resources. In fall 2020, pharmacy staff were trained to provide verbal informed consent and perform point of care HCV OraQuick antibody screening. Pharmacies were supported by a study nurse to link to HCV RNA testing when antibody positive patients were identified, with initiation of HCV treatment offered to those found to be RNA positive.
The study nurse worked with pharmacy staff to strategize adherence and support as needed by study subjects. Qualitative interviews have been conducted with five pharmacy staff to explore their experiences with testing and monitoring HCV treatment and the feasibility of involving pharmacists in the HCV care cascade.

**Results:** To date pharmacy staff completed 171 HCV OraQuick tests finding 53 tested positive for HCV antibodies: 23 people were HCV RNA negative, (20 previously treated and 2 self-cleared), 8 unk/LTF. Of the 22 RNA positive participants, 1 is pending treatment start, 21 people have started treatment, with 8 achieving SVR. While great success has been achieved in treating identified people, less than half of projected OraQuick tests have been completed. Although the onset of the Covid 19 pandemic was a fundamental barrier incorporating HCV testing at pharmacies, stigma related to HCV and illicit drug use continues to impact this process. Pharmacists described feeling hesitant about approaching participants, especially after receiving negative responses from clients about HCV testing. Some worried their relationship would change with clients as asking about HCV implied risky drug use.

**Conclusion:** This innovative and novel approach to HCV therapy in PWUD attempted to use a pharmacy-based approach to find people with limited connection to primary health care to test and treat HCV. Increased training of pharmacy staff related to stigma around drug use and HCV is required both before and ongoing for successful integration of pharmacy-led HCV testing and treatment in Canada.

---

**THU298**

**Improved clinical and economic outcomes in an intensive care unit with a focus on hepatology through interprofessional cooperation between physicians, staff nurses, and pharmacists**

Schmid Stephan¹, Schlosser Sophie¹, Karsten Güelow¹, Vlad Pavel¹, Alexander Mehrl¹, Martina Mueller-Schilling¹, Alexander Kratzer²

¹University Hospital Regensburg, Department of Internal Medicine I, Gastroenterology, Hepatology, Endocrinology, Rheumatology, and Infectious Diseases, Regensburg, Germany; ²University Hospital Regensburg, Hospital Pharmacy, Regensburg, Germany

Email: stephan.schmid@ukr.de

**Background and aims:** Since 2015, the medical intensive care unit (ICU) with a focus on hepatology of the Department of Internal Medicine 1 at the University Hospital Regensburg, Germany, has a particular emphasis on interprofessional collaboration with staff nurses and hospital pharmacists. The hospital pharmacists have access to the hospital information system and the electronic charting program. Consultations take place on a daily basis. Furthermore, weekly joint rounds within the antibiotic stewardship program are performed. Furthermore, there is a joint training and teaching of medical, nursing and pharmacy students within the intensive care training ward Regensburg (TM A-STAR project). The study aims to investigate to what extent the newly introduced structural changes affect clinical and economic outcomes.

**Method:** We examined clinical performance data and consumption figures for antibiotics and other drugs over a 10-year period from
2011 to 2021. Data from the hospital pharmacy, hospital administration, electronic charting, and hospital information systems were included in the analyses. An electronic platform was developed to improve documentation. The years 2020 and 2021 were considered separately due to the COVID-19 pandemic and the care of numerous COVID-19 patients in the ICU.

Results: It could be shown that the pharmacist’s recommendations regarding drug administration were mainly related to indication (43.6%), dosage (27.6%), interactions (9.4%), and side effects (4.1%). Antibiotic consumption was reduced by 12.2% from 2015 to 2019. Encouragingly, this included a 23.4% reduction in carbapenem use. Antibiotic spending was reduced by 24.9% overall.

An analysis of the intensive care G-DRGs showed that the case-mix points increased significantly by 31.6% during the period under review. Similarly, patient severity of illness as measured by the SAPS II score increased by 21.4%. The proportion of mechanically ventilated patients exceeded 50%.

In another analysis, antibiotic spending per case-mix point was calculated. While spending was EUR 60.22 per case-mix point in 2015, this could be reduced by 42.9% to EUR 34.37 per case-mix point by 2019.

Conclusion: Through close interprofessional collaboration between physicians, staff nurses, and pharmacists, the consumption of antibiotics and other drugs (e.g., albumin) was significantly reduced, thus improving patient care. There was also a positive economic effect—with a simultaneous increase in case-mix points, expenditure on antibiotics was significantly reduced.

Responsible use of resources and high-performance medicine are not contradictory. In our view, a close interprofessional collaboration between physicians, staff nurses, and pharmacists will be of outstanding importance in the future, particularly in intensive care medicine.

THU299
Need to implement the screening strategy to advance HCV elimination in Italy: a cost-consequences analysis
Andrea Marcellusi1, Kristi Tata2, Francesco Mennini1, Massimo Andreoni1, Loreta Kondili3, Tor Vergata University, CEIS, Rome, Italy; 2University Hospital Center of Tirana, Tirana, Albania; 3Tor Vergata University, Rome, Italy; 4Istituto Superiore di Sanità, Center for Global Health, Rome, Italy
Email: loreta.kondili@iss.it

Background and aims: In Italy, the HCV disease burden is the highest of western Europe. A graduated screening strategy that covers the birth cohort population from 1948–1988 is cost-effective to achieve HCV elimination in Italy. A dedicated fund for HCV screening could permit free of charge testing of the population from 1969–to 1989, but if the screening is not implemented to other birth cohorts the HCV elimination targets could not be achieved. Based on the HCV infection burden, by a cohort of age and fibrosis stage previously estimated, we evaluated the cost-consequences of a delay of HCV diagnosis in the next 5 years in Italy.

Method: We used a previously designed and validated probabilistic model to estimate the clinical, and economic outcomes of different screening coverage uptakes, considering the HCV disease costs by the fibrosis stage as reported by the PITER cohort real-life data. The model starts with a decision probabilistic tree that simulates 5 years of HCV testing in the general population cohort born between the years 1948–1967 (15, 485, 565 individuals to be tested) with different coverage rates lower in the lack of active screening and higher in case of screening implementation. The first part of the model identified and categorized HCV chronic patients by the fibrosis stage. A Markov model was considered for 10 years horizon time. The simulations consider two alternative coverage rates and timing during the five years simulated scenarios: 1) Incremental approach (coverage rates equal to 10%, 20%, 25%, 30% respectively at years 1, 2, 3, and 4) and 2) Fast approach (50% of the target population each year at years 1, 2, 3 and 4).

Results: The overall estimated number of HCV active infections to be diagnosed in the target population was 106, 200. The incremental approach scenario estimated 62% of the target population diagnosed vs 94% diagnosed in the fast approach scenario. An increase in overall costs was observed in the fast approach scenario up to year 5, but at year 6 the cost starts to decrease due to a higher number of diagnosed patients versus the incremental approach in which the disease costs continue to increase. (Figure 1). At ten years’ time-horizon, the model estimated a cumulative not mutually exclusive reduction of 5, 406 persons living in the HCC health state, 4, 614 in decompensated cirrhosis and 11, 081 liver-related deaths. A cost reduction of €74 million was estimated if a fast approach was adopted versus the incremental one.

Conclusion: A delay in HCV diagnosis in the general population from 1968–to 1948, yet not addressed for the HCV free of charge screening, will have important clinical and economic consequences in Italy.

THU300
Evaluation of access to treatment for hepatitis C: a large retrospective cohort from a tertiary care hospital in Turkey
Merve Eren Durmuş1,2, Gökhan Koker3, Yeşim Çekin5, Serkan Ocal5, Ayhan Çekin5, ‘Antalya Education and Research Hospital, Gastroenterology, Antalya, Turkey; 3Antalya Education and Research Hospital, Gastroenterology, Turkey; 4Antalya Education and Research Hospital, Internal Medicine, Antalya, Turkey; 5Antalya Education and Research Hospital, Medical Microbiology, Turkey; 2Antalya Education and Research Hospital, Gastroenterology, Turkey
Email: drmerveerun@gmail.com

Background and aims: Hepatitis C virus (HCV) infection is a major public health issue. According to 2015 data, approximately 71 million people have chronic HCV viremia in the world. It is one of the leading causes of liver-related morbidity and mortality globally. The seroprevalence of anti-HCV in our country has been detected 0.5–1%. Due to its silent progress many patients may be unaware of the situation. In our study, we aimed to determine the rate of the anti-HCV positive patients who were able to access to treatment.

Method: Subjects who had anti-HCV positivity between 2014–2019 have been reviewed retrospectively. The data of the patients were recorded and patients referred for further evaluation and accessed to treatment were identified.

Results: The clinics that requested anti-HCV tests were divided in to two groups. Group 1 included gastroenterology, infectious diseases and internal medicine along with its other subspecialties; and the rest of the clinics are defined as Group 2. There were 3924 anti-HCV positive patients in 5-years period. 2350 of them were tested for HCV viremia (%59.9), HCV-RNA were positive in 1447 of them (%29.2), corresponding to 48.8 of the patients who have been tested. Among the patients with HCV-RNA positivity, 948 of them were tested for
HCV genotype (%24.1). Of these patients, 251 were genotype 1A, 438 were genotype 1B, 26 were genotype 2, 193 were genotype 3, 39 were genotype 4 and one patient was genotype 5. Only 589 of them could access treatment (%15). Numbers of patients in each step of the treatment cascade are presented in Figure 1. Although the departments in Group 2 detected more anti-HCV positivity, the number of the ones that could access treatment were lower.

**Conclusion:** World Health Organization has been set international targets for the elimination of HCV infection by 2030, which is a public health threat. According to our study, there are significant deficiencies in several stages of the treatment cascade, which is consistent with world data. The rate HCV- RNA testing was low among all clinics. However, Group 2 has lower referral rates according to Group 1 indicating a lower level of awareness. Knowledge of all physicians should be improved to prevent losses and delays in the diagnosis and treatment of HCV infection independent of their departments.
Hepatitis E Virus Capsid Antigen (HEV-Ag): a practical diagnostic biomarker in the HEV outbreak scenario

Simón Lyttton¹, Rakibul Hassan Bulbul², Mamunur Rashid².
¹SeraDiagLogistics; ²Bangladesh Institute Of Tropical And Infectious Diseases Hospital, Chittagong, Bangladesh
Email: simon.lyttton@t-online.de

**Background and aims:** The increased global incidence of hepatitis E virus (HEV) infections, warrants accurate and affordable diagnostics across different geographical regions. The soluble and highly conserved HEV open reading frame 2 (ORF2) capsid antigen (HEV-Ag) is detectable in self-limited acute enteric hepatitis by HEV-Ag ELISA which is a promising serological assay in settings where HEV RNA testing is not feasible. Our aim was to assess the HEV-Ag biomarker in an HEV outbreak in a low income country.

**Method:** A prospective single center longitudinal study during HEV outbreaks in the Chittagong, Bangladesh region between October 2018 and October 2019 was conducted based on recruitment of acute jaundice cases with clinical signs and symptoms of suspect HEV infections. Acute HEV infection was defined as a positive test result for anti-HEV IgM antibodies.

**Results:** Forty four of the 51 enrolled enteric hepatitis cases (86%) were confirmed HEV by anti-HEV IgM ELISA at day 0 hospital entry. The anti-HEV-IgM and IgG were positive in all patients and did not reveal significant differences; neither between the time points day 0 and follow-up hospitalization on day 2-6 or day 7–10 nor between RNA-positive (n = 36) versus RNA-negative (n = 8) HEV groups. The HEV-Ag positivity was higher in viral RNA-positive (29/36, 81%) than the viral RNA-negative (1/8, 12%) group, r = 0.77, p < 0.0001. All non-HEV cases; n = 7 tested negative anti-HEV IgM and HEV-Ag and 5 of 7 (71%) tested anti-HAV IgM positive.

**Conclusion:** The HEV-Ag ELISA is a reliable and practical diagnostic tool in this acute HEV outbreak.

**Bulevirtide is broadly active against all HDV genotypes expressing envelopes from HBV genotypes A–H and a large panel of clinical isolates**

Savrina Manhas¹, Bin Han¹, Simin Xu¹, Lindsey May¹, Dong Han¹, Tahmineh Yazdi¹, Silvia Chang¹, Thomas Aeschbacher¹, Rishi Aryal¹, Ross Martin¹, Yang Liu¹, Roberto Mateo¹, Vithika Suri¹, Dmitry Manuilov², John F. Flaherty¹, Julius Hollnberger²,³, Stephan Urban⁴, Tomas Cihlar⁴, Evgenia S Svarovskaia⁴, Hongmei Mo¹. 
¹Gilead Sciences, Inc., Foster City, United States; ²University Hospital Heidelberg, Department of Molecular Virology, Heidelberg, Germany; ³German Center for Infection Research (DZIF), Heidelberg; ⁴University Hospital Heidelberg, Heidelberg, Germany
Email: savrina.manhas1@gilead.com

**Background and aims:** Bulevirtide (BLV) is a 47-amino acid lipopeptide derived from the HBV large envelope protein (LHBsAg). BLV binds to the HDV/HBV host entry receptor sodium taurocholate cotransporting polypeptide and acts as a potent HDV entry inhibitor. BLV has been approved for treatment of HDV in the European Union and is under late stage clinical evaluation in the United States. Based on sequence divergence, there are eight HDV genotypes (HDV-1 to HDV-8) and eight HBV genotypes (GTA to GTH). To determine the activity of BLV against diverse HDV/HBV variants sequences, the antiviral activity of BLV against HDV-1 to HDV-8 enveloped with HBV GTA-H and against 137 clinical isolates from study participants with HDV infection was assessed.

**Method:** HDV viruses were produced by co-transfection of Huh7 cells with HDV genome and HBV envelope plasmids. Subsequently, virus containing supernatant was collected, titered and used to infect primary human hepatocytes (PHHs). For the HDV phenotyping assay, PHHs were pre-treated with BLV and then infected with clinical plasma or a lab strain of HDV. After five days, immunofluorescence staining was performed to determine cells that were positive for HDV antigen (HDAg). The concentration of BLV decreasing the HDV HDAg positive cells by 50% was expressed as a mean EC50 value from at least two independent experiments.

**Results:** For HDV lab strains, the median EC50 of BLV against HDV-1 to HDV-8 pseudotyped with HBV GTA-D envelopes ranged from 0.35 nM to 0.64 nM. Similarly, for HDV-1 to HDV-8 lab strains pseudotyped with HBV GTE-H envelopes, the median EC50 of BLV ranged from 0.21 nM to 0.61 nM. Across HDV-1 to HDV-8 lab strains enveloped with HBV GTA-H envelopes, the median EC50 of BLV ranged from 0.26 nM to 0.64 nM. Additionally, the median EC50 of BLV against HDV-1 with envelopes carrying common polymorphisms in the LHBsAg PreS1 region that corresponds to the BLV sequence region for HBV GTA, GTB, GTC and GTD were 0.57, 0.59, 0.43 and 0.33 nM, respectively. The activity of BLV was also evaluated against 165 clinical isolates with a total of 137 out of 165 clinical isolates having sufficient infectivity to be tested for BLV activity. Most clinical isolates tested (n = 122) belonged to HBV genotype D/HDV genotype 1 (D/1) and had a median EC50 value of 0.33 nM. Similarly, the median EC50 values for clinical isolates of A/1 (n = 9), E/5 (n = 5) and A/6 (n = 1) were 0.54, 0.36, and 0.70 nM, respectively (Figure).

**Conclusion:** BLV demonstrated potent broad spectrum antiviral activity against HDV-1 to HDV-8 enveloped with HBV GTA to GTH and against a larger panel of HDV clinical isolates showing similar EC50 values across different HBV/HDV genotypes irrespective of the presence of polymorphisms. These results support that BLV has broad genotype coverage potential for the treatment of patients with chronic HDV infection.
THU303
A persistent HBV infection features spontaneous cccDNA loss and new rounds of infection
Bai-Hua Zhang1, Yuanping Zhou1, Stephen Horrigan3, Fabien Zoulim1, David Baltimore3, Yong-Yuan Zhang1.
1Hospital Beaujon AP-HP, Hepatology, Clichy, France; 2United States; 3Laboratoire d'Amniologie et Histo-comparatit, Paris, France; 4California Institute of
Technology, Biology, Pasadena, United States
Email: yongyuanzhang50@gmail.com

Background and aims: Clinical evidence shows frequent replacement of serum wild type viral population with mutants in chronic HBV infection, which indicates cccDNA turnover and new rounds of infection. We hypothesized that HBV infection is maintained by new rounds of infection. This hypothesis can be tested in HBV infected uPA/SCID chimeric mice by blocking new rounds of infection using anti-HBs antibody. Since anti-HBs Ab mainly functions extracellularly, its administration in HBV infected chimeric mice is expected to have a therapeutic impact on HBV infection level only if it is sustained with new rounds of infection.

Method: An optimized AAV vector that carries human anti-HBs Ab genes was used to express sustained high level of anti-HBs antibody. HBV infected uPA/SCID chimeric mice were treated with AAV vector expressing malaria antibody or anti-HBs antibody day 49 post infection. Serum HBV DNA and HBsAg level were monitored until day 183 and liver HBV DNA was determined through 20 random samplings of each autopsied liver.

Results: Two key findings were observed: I. Dynamic cccDNA status and spontaneous cccDNA loss: average cccDNA level ≤ 1 copy/cell was detected in 260 (46%) of 566 cccDNA samplings of 18 HBV infected human livers from chimeric mice, suggesting cccDNA was already lost spontaneously in a fraction of infected cells. II. Anti-HBs treatment profoundly impacts HBV infection level: i) Viremia was significantly lowered by up to >100-fold; ii) Intrahepatic rcDNA level was significantly lowered by 4, 000 to 10, 000 copies/cell; iii) The number of cccDNA samplings with cccDNA level ≤ 1 copy/cell was significantly expanded (50.2%, 244/486) in anti-HBs treated animals compared to malaria antibody or anti-HBs antibody day 49 post infection. Serum HBV DNA and HBsAg level were monitored until day 183 and liver HBV DNA was determined through 20 random samplings of each autopsied liver.

Conclusion: cccDNA level is dynamic with spontaneous cccDNA loss, which mediates spontaneous HBV clearance and but can be replenished by new rounds of infection in infected human livers of chimeric mice. New rounds of infection prolong HBV persistent infection. Therapeutic blocking of new rounds of infection profoundly impacts both rcDNA and cccDNA level including a nearly complete cccDNA elimination in one animal with HBV functional cure. Our study identifies an opportunity to durably terminate persistent HBV infection through blocking new rounds of infection.

THU304
Functional and mitochondrial dynamics alterations in patients with chronic hepatitis B and advanced fibrosis
Dimitri Loureiro1, 2, Issam Tout1, 2, Cheikh Mohamed Bed1, 2, Morgan Kea1, 2, Ahmad Sleiman1, 2, Boyer Nathalie1, 2, Stephanie Narguet1, 2, Nathalie Pons-Kerjean2, 2, Corinne Castelnau1, 2, Nathalie Giuly1, 2, Vassili Soumelis3, Jamel El Benna3, Patrick Soussan3, Richard Moreau3, Valérie Paradis1, 2, Abdel Mansouri1, 2, Tarik Asselah1, 2.
1Hospital Beaujon AP-HP, Hepatology, Clichy, France; 2Center Recherche Sur l’Inflammation, U1149, Paris, France; 3Hospital Beaujon AP-HP, Pharmacy, Clichy, France; 4Hospital Saint-Louis, Laboratoire d’Immunoologie et Histo-comparatit, Paris, France; 5Paris Diderot University, U1135, Paris, France
Email: dimitri.loureiro@inserm.fr

Background and aims: Patients with chronic hepatitis B (CHB) have an increased risk of advanced fibrosis and hepatocellular carcinoma (HCC). In experimental models, hepatitis B virus (HBV) infection causes oxidative stress and alters hepatic mitochondria. The aim of the study is to investigate the role of mitochondrial stress in the progression of fibrosis in CHB.

Method: 132 treatment-naïve CHB mono-infected patients with available liver biopsies specimen were included in this study. Patient demographics and laboratory parameters were recorded at the time of the biopsy. Liver mitochondrial DNA (mtDNA) damage was screened by long PCR and sequencing and levels by Slot blot. The expression of the main genes of cytochrome c oxidase subunits, mitophagy, mitochondrial peptides and chaperonins, TNFα and IL6, inducible NO synthase and MnSOD were investigated by RT-qPCR and Western-blotting. Patients with CHB and advanced fibrosis (F3-F4 Metavir score; n = 43) were compared to patients with no-mild-moderate fibrosis (F0-F2; n = 89). In vitro, HBV and HBx were transiently expressed in HepG2 cells and the superoxide anion formation, peroxynitrite, nitration of mitochondrial chain complexes, INOS, MnSOD protein levels and mtDNA depletion were assessed.

Results: Whereas 100% of patients with F3-F4 exhibited multiple mtDNA deletions, 50% of those with F0-F2 (x2= 6.8;p < .001) carried a single mtDNA deletion. Significant decreases were observed in patients with F3-F4 compared to those with F0-F2 for the mRNAs of MT-CO1 (0.55 ± 0.36 and 1.20 ± 0.75, p < .001), HSP90 (0.70 ± 0.28 and 1.06 ± 0.57, p < .001), HSPA9 (0.83 ± 0.36 and 1.10 ± 0.44, p < .05), Lon Peptidase 1, LONP1 (0.83 ± 0.22 and 1.06 ± 0.33, p < .05), PRK1 (0.45 ± 0.26 and 1.12 ± 0.57, p < .0001), PINK1 (0.59 ± 0.17 and 1.06 ± 0.26, p < .0001), Liver TNFα (1.72 ± 0.2 and 0.99 ± 0.2; p < .05), IL6 (7.82 ± 0.90 and 1.14 ± 0.26; p < .05). Protein levels significantly decreased in F3-F4 for MT-CO1 (2.55 ± 0.88 and 3.44 ± 0.80, p < .01), LONP1 (0.67 ± 0.31 and 1.07 ± 0.51, p < .05), HSP90 (0.67 ± 0.31 and 1.20 ± 0.77, p < .05) MT-ATP8 (0.14 ± 0.03 and 0.30 ± 0.06, p < .05). INOS and MnSOD proteins are significantly increased in patients with F3-F4 with MnSOD activity decreased in these patients (p < .05).

In HepG2 cells, HBV or HBx expression increase mitochondrial superoxide formation at 24 and 48 h (p < .05), increase iNOS protein levels, but only HBV increase MnSOD protein expression by 2-fold (p < .05). Then, an increase of peroxynitrite as well as mtDNA depletion (p < .01) and nitration of the mitochondrial respiratory chain complexes were observed.
Here, we setup an innovative method based on reverse virus replication. We hypothesized that Lonafarnib treatment may have side effects on antigen (L-HDAg), blocking virus assembly. Given the importance of molecules currently tested in clinical trials, the farnesyl transferase against hepatitis D virus (HDV) are absent. Among the antiviral chronic viral hepatitis and to date, efficient therapeutic approaches

**Background and aims:**

Email: e.verrier@unistra.fr

Strasbourg, France

Hospitalo-Universitaire, Pôle Hépato-digestif, Nouvel Hôpital Civil, Hepatiques UMR_S1110, Strasbourg, France;2CIRI-Centre International Strasbourg, Inserm, Institut de Recherche sur les Maladies Virales et

**Hepatitis histology**

<table>
<thead>
<tr>
<th>Metavir</th>
<th>Activity A0</th>
<th>A1</th>
<th>A2</th>
<th>A3</th>
<th>A4</th>
<th>A5</th>
<th>A6</th>
</tr>
</thead>
<tbody>
<tr>
<td>F0</td>
<td>26</td>
<td>6</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>F1</td>
<td>32</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>F2</td>
<td>12</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>F3-F4</td>
<td>15</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>F5</td>
<td>5</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>F6</td>
<td>4</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**Results:** We demonstrated that FTI treatment of HBV-HDV co-infected cells leads to an accumulation of intracellular HDV RNAs and a marked increase in the levels of edited HDV RNAs not only within the infected cells but also in the viral particles that are secreted. Interestingly, these viral particles were less infectious, probably due to an enrichment in edited genomes that are packaged, leading to unproductive infection given the absence of S-HDAg synthesis after viral entry.

**Conclusion:** Taken together, we setup an innovative quantification method allowing the investigation of HDV RNAs editing during HDV infection in a simple, fast, clinically-relevant assay and demonstrated for the first time the dual antiviral activity of FTI on HDV infection.

**THU306**

**Characterization of circulating hepatitis B Virus RNAs in vitro and chronic hepatitis B patients**

Doobyun Kim1, Delphine Bousquet1,2, Marie-Laure Plissonnier1, Hyoseon TaK7, Xavier Grand1, Chloé Goldsmith5, Françoise Berly1, Bordes Isabelle1, Alexia Paturel1,2, Aaron Hamilton4, Marinhia Heil4, Massimo Levrero1,2,5, Barbara Testoni1, Fabien Zoulim1,2,6, 1Cancer Research Center of Lyon, Chronic Viral Hepatitis: virus/host interactions, pathogenesis and novel antiviral strategies, Lyon, France; 2Université de Lyon, Lyon, France; 3University of Canberra, Bruce, Australia; 4Roche Diagnostics, Pleasanton, United States; 5Sapienza University of Rome, Roma, Italy; 6La Croix-Rousse Hospital, Lyon, France

Email: fabien.zoulim@inserm.fr

**Background and aims:** Circulating HBV RNA (CirB-RNA) is a promising non-invasive biomarker for cccDNA transcriptional activity. However, the molecular characteristics and circulating particles containing cirB-RNA in vitro and in vivo remain to be fully defined.

**Method:** Supernatants from cultured hepatocytes infected by HBV and treated or not with lamivudine, and sera from 9 untreated [4 HBeAg (+) and 5 HBeAg (-)] and 1 HBeAg (+) ETV-treated chronic hepatitis B (CHB) patients were subjected to iodixanol/Sucrose ultracentrifugation for buoyant density. Each density fraction was analyzed for HBV DNA/RNA by specific qPCR and droplet digital (dd) PCR. Viral and extracellular vesicles (EVs)-associated proteins were detected by ELISA and Western Blotting. 5′ CirB-RNA sequencing by ONT MiniION was used to identify CirB-RNA species. Longitudinal serum samples before and at two time points after NUC therapy initiation were obtained from two additional patients [HBeAg (+) TDF-treated CHB and HBeAg (-) ETV-treated CHB].

**Results:** After ultracentrifugation, CirB-RNA was mainly detected in core-associated virion-like particles, in 2 log10 less amount than HBV DNA. However, CirB-RNA was the predominant species in lighter density fractions (1.17–1.18 g/ml) deprived of viral proteins, both in cell supernatant and in serum. The enrichment for EVs in these fractions was confirmed by detection of CD9 and CD81 by Western Blotting, immunoprecipitation assay, Nanoparticle tracking analysis and Transmission Electron Microscopy. Distribution of CirB-RNA did not differ significantly according to HBeAg status, while in a patient with low HBsAg level, CirB-RNA was mainly detected in the EVs-enriched fractions. Lastly, CirB-RNA profiling by 5′ RACE and ONT MiniION sequencing identified different proportions of pgRNA-derived transcripts according to HBeAg status and HBsAg level.

**Conclusion:** Our results indicate that EVs-enriched compartment also contributes to the circulation of HBV-RNAs. Moreover, different HBV-RNA transcripts in addition to pgRNA can be detected in vivo. Altogether, these data could significantly contribute to the characterization of cirB-RNAs as new viral biomarker.
Background and aims: Circulating HBV RNA (CirB-RNA) reflects the transcriptional activity of the intrahepatic cccDNA, thus representing a promising non-invasive serum biomarker for the reduction or inactivation of cccDNA pool. Although several studies have suggested that cellular releasing pathways may determine the fate of these RNAs, the specific regulators of the shuttle machinery involved remain largely unknown.

Method: Expression of candidate shuttle proteins were analyzed by Western Blotting and RT-qPCR in cell lysate and supernatant from HBV-infected HepG2-NTCP cells and Primary human hepatocytes (PHHs). Shuttle protein interaction with CirB-RNAs was investigated by RNP-IP (Ribonucleoprotein-Immunoprecipitation) and Biotin pull down assay. Adapted iodixanol/Sucrose density ultracentrifugation allowed to isolate exosome-enriched fractions from sera of 5 untreated [2 HBeAg (+) and 3 HBeAg (-)], 2 HBeAg (-) chronic infection and 2 NUC-treated chronic hepatitis B (CHB) patients.

Results: Among the RNA-binding proteins analyzed, heterogeneous nuclear ribonucleoprotein A1 (hnRNPA1) expression was increased in both cell lysates and supernatants of HepG2-NTCP cells and PHHs upon HBV infection. hnRNPA1 was also detected in the serum of CHB patients and, after density ultracentrifugation of serum samples, hnRNPA1 was mostly detected in the exosome-enriched fractions. Loss-of-function studies in HepG2-NTCP cells indicated that hnRNPA1 downregulation was associated to reduced expression of exosome-enriched fractions from sera of 5 untreated [2 HBeAg (+) and 3 HBeAg (-)], 2 HBeAg (-) chronic infection and 2 NUC-treated chronic hepatitis B (CHB) patients.

Conclusion: Altogether, our data suggest that hnRNPA1 directly binds to HBV RNAs and can function as a novel shuttling mechanism for the export of HBV RNAs in vivo.
Genotypes A and B had 4 to 6 amino acid changes, respectively, and genotype D had 8. Despite their sequence differences, HDV genotype 1 viruses containing HBV genotype A-H preS1 representative sequences and the most prevalent HBV genotype A-D polymorphisms were fully susceptible to BLV with EC_{50} values that ranged from 0.28 nM to 0.85 nM.

**Conclusion:** BLV demonstrated potent activity against HDV harboring the polymorphisms in the PreS1 region corresponding to the BLV sequence across HBV genotypes A-D, indicating the broad-spectrum antiviral activity of BLV for the treatment of patients infected with HDV viruses.

**THU310 RIPK1 plays a survival role in the liver of mice with active HDV replication**

Gracian Campos1, Sheila Maestro2, Carla Usai1, Mirja Hommel1, Cristina Olague Micheltorena1, Africa Vales Arangueren1, Rafael Aldabe1, Gloria González-Aseguiuola1,1 CIMA Universidad de Navarra, Gene therapy and regulation of gene expression, Pamplona, Spain; 2Viralgene; 3Blizard Institute

**Email:** ggasegui@unav.es

**Background and aims:** Hepatitis delta virus (HDV) infection represents the most severe form of viral hepatitis; however, the molecular mechanisms involved in the severity of the disease remain unknown. The absence of mouse models in which HDV-induced liver damage occurs has prevented the study of this important aspect of antiviral activity of BLV for the treatment of patients infected with HDV viruses.

**Method:** The present study is to elucidate the mechanisms involved in HDV-mediated liver damage.

**Results:** Surprisingly, the absence of TNF-α induced apoptosis as the main cell death mechanism in RIPK1-edited mice. Interestingly, depletion of macrophages had no effect on the exacerbation of liver disease associated with the RIPK1 knockdown in hepatocytes. Interestingly, depletion of macrophages had a significant detrimental effect, indicating that these cells play a protective role.

**Conclusion:** Our investigations demonstrate the protective role of RIPK1 in HDV-induced liver pathology and strongly suggest that the RIPK1-caspase-8 axis influences the pathogenesis of HDV infection. More experiments are needed for a better understating of the mechanism involved.

**Background and aims:** EASL guidelines suggest that treatment with nucleos (t)ide analogue therapy (NA) can be stopped in HBeAg negative patients after three years of viral suppression. Recently, the combination of HBsAg and HBV-RNA level at the time of NA cessation has been linked to a better prediction of off-treatment response compared to HBsAg alone in mixed cohorts of HBeAg negative and positive patients. In this study we investigated the association of relapse after NA cessation with baseline serum HBV-RNA level in a large cohort of HBeAg negative patients.

**Method:** Serum level of HBV-RNA, HBsAg and HBcAg were determined in 154 HBeAg negative patients, participating in a prospective, multicenter therapeutic vaccination trial (ABX-203, NCT02249988) or in an observational register trial (Terminator 2), before stop of NA therapy. Importantly, vaccination showed no impact on relapse. HBV DNA ≥ 2,000 IU/ml 24 weeks after NA cessation was defined as virological relapse, while clinical relapse comprised attendant ALT levels ≥ 2 ULN. The lower limit for the quantification of HBV-RNA was 10 copies/ml. For the comparison of continuous and categorical variables the Mann-Whitney U and the Fisher’s exact test were used. Kaplan-Meyer analysis with the log-rank test was used for the calculation of cumulative relapse rates.

**Results:** The majority of patients were male (n = 115/154; 75%) with a median age of 53 years. Two thirds of patients were treated with entecavir (n = 94/154; 61%), while the rest received tenofovir. Median HBV-RNA, HBsAg and HBcAg BL level was 0 copies/ml, 950 IU/ml and 1585 kU/ml, respectively. No significant correlation was found between HBV-RNA and HBsAg (r = −0.253, p = 0.055) or HBV-RNA and HBcAg (r = 0.044, p = 0.73), respectively. Virological relapse occurred in 53% of patients (N = 82/154), including 8 patients (10%) developing an ALT flare. BLHBV-RNA level did not differ significantly between virological relapsers and off-treatment responders (p = 0.86) or between virological relapsers and clinical relapsers (p = 0.36), respectively. Further, no significant difference occurred in proportions of detectable HBV-RNA BL level between off-treatment responders (N = 10/72; 14%) and relapsers (N = 13/82; 16%) (p = 0.68). Relapse prediction could not be improved by combining predefined HBsAg cut-offs (100 IU/ml, p = 0.0016) or HBcAg cut-offs (3 log U/ml, p = 0.07) with a HBV-RNA cut-off of ≤ 10 copies/ml (p = 0.003) (figure).

**Figure:** A) Cumulative relapse rates after NA cessation according to end of treatment (EoT) grouped by serum RNA baseline levels and proportion of patients with virological relapse grouped by B) BL HBsAg level ± HBV-RNA level or C) BL HBcAg level ± HBV-RNA level.
Conclusion: In a cohort of exclusively HBeAg negative patients no improvement in relapse prediction was achieved by considering HBV-RNA BL levels.

THU312
A versatile small animal immunocompromised model for chronic hepatitis E
Siddharth Sridhar1, Shusheng Wu2, Jianwen Situ2. 1The University of Hong Kong, Microbiology; 2The University of Hong Kong, Microbiology Email: sid8998@hku.hk

Background and aims: Hepatitis E virus (HEV) is an important cause of chronic hepatitis in immunocompromised persons. We aimed to develop a small animal model of chronic hepatitis E using immunocompromised rats infected with Orthohepevirus species C (HEV-C; rat hepatitis E virus), which is an emerging cause of human hepatitis.

Method: Female 6–8 week old Sprague-Dawley rats were divided into 3 groups (6 rats per group): immunocompetent (group 1), low-dose immunosuppressed (group 2) and high-dose immunosuppressed (group 3). Rats in groups 2 and 3 were immunosuppressed using a combination of tacrolimus (5 mg/kg vs 7.5 mg/kg respectively), mycophenolate mofetil (25 mg/kg vs 30 mg/kg respectively), and prednisolone (10 mg/kg vs 4 mg/kg respectively). Drugs were administered 10 days prior to infection and continued thereafter. Filtered stool supernatants containing 2.5 × 10^5 copies/ml of HEV-C were administered to rats intravenously. Stool supernatants were either from infected humans (3 rats per group) or rats (3 rats per group). Stool and serum viral loads in infected rats were monitored. Antibody responses and liver histology were assessed. Ethics approval was obtained.

Results: HEV-C infections in group 1 rats were fleeting with transient viremia (figure). Group 2 and 3 rats developed higher viral loads in both stool and serum (figure). No differences in viral loads between infected humans (3 rats per group) or rats (3 rats per group). Group 3 rats showed significantly higher viral loads compared to group 1 and 2 rats (p < 0.05). The viral load in stool and serum of group 3 rats was significantly higher than that of group 1 and 2 rats (p < 0.05). The viral load in stool and serum of group 3 rats was significantly higher than that of group 1 and 2 rats (p < 0.05).

Conclusion: We designed a versatile gradable immunocompromised rat model of chronic hepatitis E infection using immunosuppressants commonly taken by transplant recipients. This model will enable convenient investigation of pathogenicity and antivirals for HEV infections. This work establishes capacity to perform chronic HEV research without using large animal models or genetically modified rats. Further evaluation of this model for studying antivirals is required.
Background and aims: Hepatocellular Carcinoma (HCC) is the first cause of death among chronic hepatitis B (CHB) patients. PAGE-B and FIB-4 may predict the occurrence of HCC among all CHB patients. We aimed to compare the predictive capacity of PAGE-B and FIB-4 for the occurrence of HCC in CHB patients at 1, 3 and 5 years of follow-up in the ANRS CO22 HEPATHER cohort.

Method: CHB patients included in the ANRS CO22 HEPATHER cohort between August 6, 2012 and December 31, 2015 were eligible. Exclusion criteria were chronic HCV, HDV co-infection, liver-transplantation, or history of HCC. Primary outcome was the time between inclusion and occurrence of HCC. Predictive performances were compared by the AUROC at year 1, 3 and 5. Two cutoffs were determined for each score, maximizing respectively sensitivity then specificity, to establish three different risk groups.

Results: Among 5,214 patients, with a median follow-up of 5.6 years (IQR: 4.3–6.9), 69 experienced HCC. Median scores values were of 10 (IQR: 6–14) for PAGE-B and 1.0 (IQR: 0.7–1.5) for FIB-4. Corrected AUROCs of PAGE-B and FIB-4 at year 1, 3 and 5 were 0.91 (0.8–0.97), 0.85 (0.81–0.97) and 0.81 (0.76–0.86) and 0.85 (0.70–0.97), 0.83 (0.77–0.89) and 0.80 (0.75–0.86), respectively. No significant difference between the AUROCs of the two scores was estimated at any time. Best cut-offs to identify patients at lower and higher risk of HCC were 10 and 18 for PAGE-B score, and 1.0 and 2.2 for FIB-4, respectively. Cumulative probability of HCC according to these new risk groups are depicted on the figure above.

Conclusion: PAGE-B and FIB-4 scores showed good and equivalent predictive performances for HCC in chronic hepatitis B patients in a French nationwide cohort, and could be used in clinical practice.

Background and aims: The Hepatitis E virus (HEV) is the most common cause of acute viral hepatitis worldwide and mainly transmitted via the fecal-oral route or consumption of contaminated food products. Due to the lack of efficient cell culture systems for the propagation of HEV, limited data regarding HEV sensitivity to chemical disinfectants are available. Consequently, preventive and evidence-based hygienic guidelines on HEV disinfection are lacking. In this study we evaluated different principal components of hand disinfectants as well as commercial hand disinfectants for their virucidal activity against HEV using a recently described high titer cell culture HEV model.

Method: We used a robust HEV genotype 3 cell culture model which allows quantification of viral infection of quasi-enveloped and naked HEV particles. For HEV genotype 1 infections the primary isolate Sar55 in a faecal suspension was applied. Standardized quantitative suspension tests using end point dilution and large-volume-plating were performed for the determination of virucidal activity of alcohols (1-propanol, 2- propanol, ethanol), WHO disinfectant formulations and five different commercial hand disinfectants against HEV. Iodixanol gradients were conducted to elucidate the influence of ethanol on quasi-enveloped viral particles.

Results: Naked and quasi-enveloped HEV was resistant to alcohols as well as alcohol-based formulations recommended by WHO. Of the tested commercial hand disinfectants only one product displayed a virucidal activity against HEV. This activity could be linked to phosphoric acid as essential ingredient. Finally, we observed that ethanol and possibly non-active alcohol-based disinfectants disrupted the quasi-envelope structure of HEV particles, while leaving the highly transmissible and infectious naked virions intact.

Conclusion: Different alcohols and alcohol-based hand disinfectants were insufficient to eliminate HEV infectivity with the exception of one commercially ethanol-based product which including phosphoric acid. These findings have strong implications for the efficient prevention measures to reduce viral transmission in clinical practice.

Figure: Incidence curves of HCC among low-risk groups (blue curves), intermediate risk groups (red curves) and high risk groups (orange curves) for PAGE-B and FIB-4, according to the new thresholds founded in the study.

Conclusion: PAGE-B and FIB-4 scores showed good and equivalent predictive performances for HCC in chronic hepatitis B patients in a French nationwide cohort, and could be used in clinical practice.
Background and aims: This study evaluated the diagnostic accuracy of the Elecsys® HCV Duo immunoassay on the cobas 801 analyser (Roche Diagnostics International Ltd) for the detection of hepatitis C virus (HCV) infection vs commercially available comparators.

Method: This international, multicentre study was conducted at seven sites (August 2020–March 2021). Blood donor samples and clinical laboratory samples (from routine diagnostic testing, pregnant women and patients on haemodialysis) were used for specificity analyses, while confirmed HCV-positive samples and seroconversion panels were used for sensitivity analyses. All samples were pseudonymised or fully anonymised residual serum or ethylenediamine-tetraacetic acid–plasma. The Elecsys HCV Duo immunoassay was compared with two registered antigen-antibody (Ag-Ab) combination assays: the Monolisa HCV Ag-Ab ULTRAV2 and Murex HCV Ag/Ab Combination. The Elecsys HCV Duo immunoassay provides parallel, but separate, read-out of HCV Ag and Ab results (while other combination assays show a combined result only). We compared the HCV Ab (anti-HCV) module with the Elecsys Anti-HCV II and Alinity s Anti-HCV assays; no neutralisation method was available to test the HCV Ag module singularly.

Results: In all blood donor samples (n = 20634), the specificity of the Elecsys HCV Duo immunoassay was 99.94% (95% confidence interval [CI], 99.89–99.97). In all clinical laboratory samples (n = 2531), the specificity of both the Elecsys HCV Duo immunoassay and the Elecsys HCV Duo anti-HCV module was 99.92% (95% CI, 99.71–99.99), vs 99.84% (95% CI, 99.59–99.96) for the Monolisa HCV Ag-Ab ULTRAV2 and 99.76% (95% CI, 99.48–99.91) for the Elecsys Anti-HCV II assay, respectively. The sensitivity of the Elecsys HCV Duo immunoassay in confirmed HCV-positive samples (n = 257) was 99.6% vs 96.1% for the Monolisa HCV Ag-Ab ULTRA V2 assay. The Murex HCV Ag/Ab Combination assay could not detect 19% of the seroconversion panels and the Elecsys Anti-HCV II assay could not detect 20%. The former found HCV infections 2 days later (58 panels; 11 undetected) and the latter 18 days later (40 panels; 8 undetected) vs the Elecsys HCV Duo immunoassay.

Conclusion: The Elecsys HCV Duo immunoassay had comparable specificity and better sensitivity vs the comparator assays, including anti-HCV tests. The Elecsys HCV Duo immunoassay may be an alternative diagnostic tool in countries where nucleic acid testing is not possible.
genotype D with only 2 splice variants identified (Sp1* and Sp13*). The frequency of variants was generally highest in Phase II (123/165 75% of patients), a phase typically associated with enhanced immune activation, followed by Phase I (69/99 70% of patients). In Phase II there was significantly higher number of patients with splice variants across all genotypes A to D compared to the number of patients without splice variants (p = 0.0004). Splice variants were associated with reduced hepatitis B e antigen (HBeAg) levels and statistically reduced likelihood of achieving HBsAg loss (functional cure) in Phase II patients for Sp1 and Sp13 (p = 0.0014 and 0.0156, respectively, Figure 1 A and B).

**Method:**
Ten male mice (5 PXB SCID-M with hepatocyte donor: JFC uPA-SCID mouse model, using an agent-based modelling (ABM) approach) were inoculated intravenously with 1 × 10⁶ copies/ml SCID-Mlivers without humanized livers, SCID-M). We developed an ABM that accounts for two types of agents: hepatocytes and virus in the blood, attempting to recapitulate the stochastic process of HCV infection of hepatocytes in SCID-M mice. The ABM simulates a series of infection stages including initial infection of uninfected cells, infected cells in a non-productive viral eclipse phase, and infected cells in a productive infection phase releasing HCV virion, which then proceed to infect additional hepatocytes. Several model parameters (e.g., virion production cycle) were calculated based on the in vivo experimental design. Model parameter fitting was done using a Genetic Algorithm (GA) with the EMEWS framework on the Midway2 high-performance computing cluster at the University of Chicago.

**Results:**
While in SCID-M HCV was rapidly cleared (Fig. 1a, dashed lines), a productive infection was established in SCID-MhL (Fig. 1a, solid lines). After an initial viral decline, the virus resurged, followed by a transient decline (in 4 mice) that eventually stabilized at high steady state levels (Fig. 1). To account for a transient decline, a decrease in viral production was assumed reminiscent of our previous observation of such transient HCV decline seen in chimpanzees (Gastroenterology; 128 (4):1056–66). The ABM quantitatively reproduces the multi-phase HCV kinetic patterns observed (Fig. 1b and c). The ABM predicts that: (1) the viral eclipse phase lasts between 1 and 20 h; (2) Once the infected cell passes the eclipse phase, the viral production rate is not constant, but rather increases over time. Initially all mice started with a long production cycle of 1 virion per 9–15 h but gradually reaching 1 virion per hour after 12 hr; (3) Within 5 days, the virion production reaches a steady state production rate of 1–3 virions per hour in each infected cell; and (4) a viral production drop of 83%–98% starting between 2–5 days p.i. in 4 mice.

**Conclusion:**
Conclusion: HBsAg splice variants detected in patient serum are not merely a by-product of HBV replication, differing markedly by HBV genotype and phase of CHB natural history. Their frequency was generally highest in Phase II, the “immune clearance” phase of CHB natural history, suggesting an immune escape phenotype. The contribution of splice variants to the likelihood of achieving functional cure on therapy requires further investigation.

**THU319 Understanding acute HCV infection kinetics in humanized mice via an agent-based modeling approach**
Zhengzhen Shi1, Yuji Ishida2,3, Nicholson Collier4,5, Michio Imamura3,6, Chise Tateno2,6, Jonathan Ozik4,5, Jordan Feld7, Harel Dahari1, Kazuaki Chayama3,8,9.

**Background and aims:** uPA-SCID chimeric mice with humanized livers (SCID-MhL) are a useful tool for studying HCV infection in the absence of an adaptive immune response. Here we sought to analyse the role of sodium taurocholate co-transporting polypeptide (NTCP) in extra hepatic cells may make these cells susceptible to HBV infection of uninfected cells, infected cells in a non-productive viral eclipse phase, and infected cells in a productive infection phase releasing HCV virion, which then proceed to infect additional hepatocytes. Several model parameters (e.g., virion production cycle) were calculated based on the in vivo experimental design. Model parameter fitting was done using a Genetic Algorithm (GA) with the EMEWS framework on the Midway2 high-performance computing cluster at the University of Chicago.

**Results:** While in SCID-M HCV was rapidly cleared (Fig. 1a, dashed lines), a productive infection was established in SCID-MhL (Fig. 1a, solid lines). After an initial viral decline, the virus resurged, followed by a transient decline (in 4 mice) that eventually stabilized at high steady state levels (Fig. 1). To account for a transient decline, a decrease in viral production was assumed reminiscent of our previous observation of such transient HCV decline seen in chimpanzees (Gastroenterology; 128 (4):1056–66). The ABM quantitatively reproduces the multi-phase HCV kinetic patterns observed (Fig. 1b and c). The ABM predicts that: (1) the viral eclipse phase lasts between 1 and 20 h; (2) Once the infected cell passes the eclipse phase, the viral production rate is not constant, but rather increases over time. Initially all mice started with a long production cycle of 1 virion per 9–15 h but gradually reaching 1 virion per hour after 12 hr; (3) Within 5 days, the virion production reaches a steady state production rate of 1–3 virions per hour in each infected cell; and (4) a viral production drop of 83%–98% starting between 2–5 days p.i. in 4 mice.

**Conclusion:** The ABM provides novel insights into the HCV life cycle in vivo. The model suggests a partial block of virion production possibly due to an early stage of innate immune response.

**THU320 Presence of sodium taurocholate co-transporting polypeptide and hepatitis B replication markers on placenta: another home for the virus?**
Garima Garg1, Meenu Mn1, Kajal Patel1,2, Shashank Purwar1, Saman Mkhupadhayay1, Nitu Mishra1, Sumit Rawat1, Shashwati Nema2, Debasis Biswas1, Anirudh Kumar Singh1, Ashish Kumar Vyas1, Ashok Kumar, India; 2All India Institute of Medical Sciences Bhopal, Microbiology, India; 3All India Institute of Medical Sciences Bhopal, Pathology, India; 4Gandhi Medical College Bhopal, India; 5Bundelkhand Medical College Sagar, India

**Background and aims:** The role of sodium taurocholate co-transporting polypeptide (NTCP), in facilitating the binding of the virus on surface of hepatocytes is well documented. Expression of NTCP in extra hepatic cells may make these cells susceptible to HBV infection.
infection and support cellular proliferation akin to hepatocytes. Placental replication of HBV is not well explored/studied. In this study we have assessed the expression of NTCP and HBV replication markers (HBeAg, HBcAg, and HBV DNA) in placental cells, to investigate if these cells act as host/reservoir for HBV.

**Method:** Twenty HBsAg+ve pregnant women along with 10 healthy controls were enrolled after obtaining informed consent. The HBV DNA in placenta was detected by qPCR using primers for X and core ORF. Expression of NTCP in placenta was analyzed by qRT-PCR and was further investigated by immunohistochemistry (IHC) along with HBV replication biomarkers, HBsAg, HBeAg, and HBcAg.

**Results:** HBV infected females showed increased expression of NTCP in trophoblasts of placenta compared to control group (3.62 ± 0.96 Vs 2.06 ± 1.3) and it was correlated with the maternal HBV DNA load. Membranous and/or Cytoplasmic immunostaining of NTCP, and cytoplasmic staining of HBeAg and HBcAg in trophoblasts along with presence of HBV DNA indicated that trophoblasts are not only susceptible to HBV infection but may also be a probable site for viral replication.

**Conclusion:** This is the pioneer study, which demonstrates expression of NTCP on placenta which may facilitate the entry of HBV. Furthermore, the study establishes the presence of HBeAg in trophoblasts indicating these cells may act as replication host/reservoir. Correlation of NTCP expression with maternal viral load and presence of HBeAg in placenta indicates its probable role in vertical transmission of HBV. Our preliminary finding suggest that NTCP blocking strategy may be used for therapeutic intervention of vertical transmission.

**Disclosure-Conflict of interest:** There are no conflict of interest among the authors.

**THU321**

Exploring dynamic changes in HBCrAg and HBV RNA in e-Antigen negative HBV/HIV patients on antiretroviral therapy: still evidence of integrated activity after 5 years of treatment

Ruth Byrne1, Mark Anderson2, Gavin Cloherty2, Kate Childs3, Ivana Carey1, Mark Nelson1, Kosh Agarwal3. 1Chelsea and Westminster Hospital, London, United Kingdom; 2Abbott Diagnostics, Department of Infectious Diseases, Chicago, United States; 3Kings College Hospital, Institute of Liver Studies, London, United Kingdom

Email: ruthbyrne@nhs.net

**Background and aims:** Hepatitis B core-related antigen (HBCrAg) and pre-genomic (pg) HBV RNA are surrogates of covalently closed circular (ccc) DNA and have emerged as new HBV biomarkers. There is growing evidence for their role in predicting treatment durability and successful cessation of nucleos(t)ide analogue therapy in chronic HBV. Limited data exist on their utility predicting outcomes in HBV/HIV co-infection. We aimed to evaluate the value of longitudinal measurement of HBCrAg and HBV RNA in two cohorts of HBV/HIV co-infected patients.

**Method:** Two cohorts of e-antigen negative HBV/HIV co-infected patients were retrospectively studied. Patients were classified into 2 groups: those who started tenofovir (TDF) based antiretroviral therapy (ART) at baseline (Cohort A, n = 30) and those already established on TDF based ART with suppressed HBV DNA for 5 years at baseline (Cohort B, n = 37). HBCrAg and HBV RNA were tested at baseline, year 3 and year 5. HBCrAg was measured by automated CLEIA-method (Lumipulse G 1200 HBcAg, Fujirebio). HBV RNA was measured by real-time PCR research assay Abbott Diagnostic with LLQ 1.65 log10 U/ml.

**Results:** Cohort A: at baseline 11 patients (37%) had undetectable HBCrAg and 10 (33%) had HBV RNA below the limit of detection. After 3 years of ART all patients had completely suppressed HBV DNA, 40% still had detectable HBCrAg and 43% had HBV RNA below the limit of detection. After 5 years of therapy there were still 10 patients (33%) with detectable HBCrAg (median 4.4 log10 U/ml; range 3.3–4.1) and 10 patients (33%) with detectable HBV RNA (median 1.96 log10 U/ml; range 1.78–3.6). Cohort B: at baseline all patients had been on TDF based ART for 5 years and had undetectable HBV DNA, 17 patients (46%) had undetectable HBCrAg and 20 (54%) had HBV RNA below the limit of detection. After 3 years 45% still had detectable HBCrAg and 32% had detectable HBV RNA. After 5 years, there were still 15 patients (41%) with detectable HBCrAg (median 3.7 log10 U/ml; range 3.0–5.4) and 11 (30%) with detectable HBV RNA (median 2.19 log10 U/ml; range 1.78–3.6). The impact of HBV genotype, pre therapy HIV viral load and nadir CD4 count on HBV markers in both cohorts was analysed and no significant effect found.

**Conclusion:** HBCrAg and HBV RNA are sensitive biomarkers for continued transcription of cccDNA in HBeAg negative HBV/HIV co-infected patients despite long term suppression of HBV DNA by TDF based ART. TDF withdrawal studies are needed in HBV/HIV cohorts but as ART moves into a new era of TDF-sparing two drug regimens, these biomarkers may have clinical utility identifying those who can stop TDF safely with minimal risk of HBV reactivation.

**THU322**

Next-generation sequencing of Swiss HEV isolates allows for reconstitution of functional clones

Jérôme Gouttenoire1, Roland Sahl2, Daniela Müllhaupt1,Montserrat Fraga Christian1, Darius Moradpour1. 1Lausanne University Hospital (CHUV) and University of Lausanne, Division of Gastroenterology and Hepatology, Lausanne, Switzerland; 2Lausanne University Hospital (CHUV) and University of Lausanne, Institute of Microbiology, Lausanne, Switzerland

Email: jermoe.gouttenoire@chuv.ch

**Background and aims:** Hepatitis E acquired in Switzerland is caused primarily by a specific hepatitis E virus (HEV) subtype which has been provisionally designated as 3 s and recently assigned as a distinct group to 3 h (3 s/p/h). Here, we analyzed HEV from patients with severe outcomes of hepatitis E by a newly developed next-generation sequencing (NGS) protocol and assembled subgenomic replicons as well as full-length clones.

**Method:** Illumina RNA sequencing coupled with HEV-specific sequence enrichment was carried out on plasma samples from 24 patients with hepatitis E acquired in Switzerland and severe outcomes (severe acute hepatitis, acute-on-chronic liver failure and neurologic complications). Viral genomes reconstituted by DNA synthesis and molecular cloning were functionally characterized in cell culture.

**Results:** The entire HEV genomes from plasma of 24 patients could be sequenced successfully, confirming the predominance of subtype 3 s.
Results: The combination of Vonafexor and peg-IFNα led to an improved anti-HBV effect on all parameters analyzed in both dHepaRG and PHH cells, including intracellular decrease in HBV RNAs, viremia and HBsAg secretion. The effect was more pronounced on HBsAg secretion where a synergy between Vonafexor and peg-IFNα was observed (see figure below). At therapeutically relevant concentrations of the combination Vonafexor and peg-IFNα, no toxicity was observed using 4 different assays (Cell titer Glo, Neutral red, Sulforhodamine stainings, and LDH release), thus ruling out potential toxicity as an alternative explanation for improved anti-HBV effects. Interestingly, similar improved anti-HBV activities were also observed with other FXR agonists, thus demonstrating the class effect of those observations.

Conclusion: The novel FXR agonist HEC96719 has strong inhibitory effect against HBV replication in PHH cells and AA/HBV mice, thus represent a promising agent for HBV cure.

THU324
Combined effect of Vonafexor and Interferon-alpha on HBV replication in primary human hepatocytes
Romain Barnault1, Raphael Darteil2, Pietro Scalforo2, Jacky Vonderscher2, David Durantel1, 1INSERM U1111-CIRI, HepVir team, Lyon, France; 2ENYO pharma SA, Bioserra 1, Lyon, France
Email: david.durantel@inserm.fr

Background and aims: Despite its adverse safety and tolerance profile, as well as a limited effect in inducing a HBsAg-loss, pegylated interferon-alpha (peg-IFNα) continues to be used as first line therapy for chronic hepatitis B (CHB) patients. It is hypothesized that an immune-stimulator will be a necessary component of future combination therapies for curing CHB, therefore, it is essential to either use alternative compounds to peg-IFNα, or to introduce a second compound which may increase its efficacy and lead to lowering its dosing, which may reduce associated side effects. Several FXR agonists were shown to have some anti-HBV properties in vitro. Moreover, the combination of peg-IFNα2a with Vonafexor, a synthetic non-steroidal, non bile-acid and highly selective FXR agonist, has been shown in an on-going open-label phase II trial (NCT04365933) to significantly reduce HBsAg levels in HBe-negative patients after only 16 weeks of treatment (Poster 2844, EASL 2021). The aim of this work was to further evaluate the underlying mechanism of action by determining whether an increased anti-HBV effect of this combination could be recapitulated in cell culture models.

Method: We used experimentally HBV-infected differentiated HepaRG cells and primary human hepatocytes (PHH), as well as standard molecular and cellular virologic methods to study the combination of Vonafexor and peg-IFNα, and compare the combination to respective monotherapies. The cytotoxicity of the combination was also evaluated to exclude its contribution to the improved antiviral effects.

Results: The combination of Vonafexor and peg-IFNα led to an improved anti-HBV effect on all parameters analyzed in both dHepaRG and PHH cells, including intracellular decrease in HBV RNAs, viremia and HBsAg secretion. The effect was more pronounced on HBsAg secretion where a synergy between Vonafexor and peg-IFNα was observed (see figure below). At therapeutically relevant concentrations of the combination Vonafexor and peg-IFNα, no toxicity was observed using 4 different assays (Cell titer Glo, Neutral red, Sulforhodamine stainings, and LDH release), thus ruling out potential toxicity as an alternative explanation for improved anti-HBV effects. Interestingly, similar improved anti-HBV activities were also observed with other FXR agonists, thus demonstrating the class effect of those observations.

Conclusion: The novel FXR agonist HEC96719 has strong inhibitory effect against HBV replication in PHH cells and AA/HBV mice, thus represent a promising agent for HBV cure.
**Conclusion:** We were able to recapitulate, in cell culture models, the improved anti-HBV effect of combining Vonafexor and peg-IFNα. We also observed that the effect is achieved without inducing toxicity. This study provides support for the existence of a mechanism of action underlying the antiviral activity in combining Vonafexor and peg-IFNα, details of which should be explored further to eventually assist in identifying efficacy predictive factors in clinical trials.

**THU325**  
**Hepatitis Delta virus quasispecies conservation and variability in ribozyme region**

Beatriz Pacín Ruiz1,2,3, Maria Francesca Cortese1,2,3, Sara Sopena Santistevé1, Josep Gregori1, Selene García-García1,2,3, David Tabernero1,2,3, Rosario Casillas1,2,3, Marta Vila1,2,3, Ariadna Rando-Segura2, Adriana Palom3, Mar Rivero Barciela4, Franciso Rodríguez-Frias1,2,3, Maria Buti4.  
*Vall D’Hebron Research Institute, Barcelona, Spain, Liver Unit, Barcelona, Spain; 2 InstitutoDe Salud Carlos III, Madrid, Spain, Centro De Investigación Biomédica En Red, Enfermedades Hepáticas y Digestivas (CIBERehd), Madrid, Spain; 3 Vall D’Hebron University Hospital, Biochemistry and Microbiology/Liver Pathology Unit, Barcelona, Spain; 4 Vall D’Hebron University Hospital, Liver Unit, Internal Medicine Department, Barcelona, Spain*

**Email:** beatriz.pacin@vhir.org

**Background and aims:** Around the 5% of hepatitis B virus (HBV) infected patients are co-infected with Hepatitis D virus (HDV). HDV genome is characterized by an 85 nucleotides-length domain with autocatalytic activity called ribozyme, which covers a key role in HDV replication. Of note, HDV presents a high rate of evolution and circulates as a mixture of variants forming a quasispecies (QS). Here, we analyzed by Next Generation sequencing (NGS) the ribozyme QS in longitudinal samples to study its conservation and identify possible mutations that could potentially affect HDV replication.

**Method:** Thirty-two patients with chronic hepatitis delta (CHD) were selected and two serum samples were collected per patient with a mean follow-up of 2.25 years. Viral genotype was determined by analyzing HDV delta antigen sequence. The HDV RNA region between nt 663 and 899, corresponding to ribozyme, was analyzed by NGS (MiSeq Illumina, San Diego, USA). Conservation was studied by calculating QS information content. Nucleotide substitutions were identified by aligning sample QS with its genotype consensus sequence.

**Results:** All patients were infected by genotype 1 HDV. A median of 5040 reads/sample was obtained. The ribozyme was overall highly conserved. A hyper-conserved region was identified between nt 715–769, whereas the more variable portion was between nt 739–769, although more the 90% of nt showed a maximum of conservation. When looking QS evolution between the two follow-up samples, limited distance was observed. Eleven mutations were observed. Of them, 3 mutations (T23C, T64del, and T69C) presented a high frequency (respectively 5.51, 98.60, and 8.20%) in viral QS and were selected in the two patients’ sample.

**Conclusion:** As expected and considering its role in viral replication, the ribozyme QS was highly conserved without changes between the two samples. The mutations observed interested domains involved in ribozyme excision activity (L3) and structural stabilization (P4), and they could potentially interfere with viral replication. Thanks to its high rate of conservation, the ribozyme could be a valuable target of gene therapy. Further in vitro studies are required to evaluate the effects of the mutations in HDV expression. Funding: Instituto de Salud Carlos III (grant P11/02233), co-financed by the European Regional Development Fund (ERDF).

**THU326**  
**Exosomal cargo as a key player of the immune response after direct-acting antiviral treatment in chronic hepatitis C patients**

Eirini Karamichali1, Pelagia Foka1, Vaia Valiakou1, Petros Eliadias2, Domniki Loukaki-Gkountara1, Konstantina Andressaki1, Georgia Papadopoulou1, Urania Georgopoulou1, Ioannis-Georgios Koskinas2, 1Hellenic Pasteur Institute, Molecular Virology, Athens, Greece; 2Hellenic Pasteur Institute, Laboratory of Molecular Biology and Immunobiotechnology, Athens, Greece; 3 Medical School of Athens, Greece, 2nd Department of Internal Medicine, Hippokration General Hospital, Athens, Greece

**Email:** koskinasj@yahoo.gr

**Background and aims:** HCV infection causes severe liver disease. Direct-acting antivirals (DAAs) eradicate HCV but host immunity fails to fully recover. Exosomes are extracellular vesicles secreted by all cell types. They are masters of intercellular communication in health and disease. It has been demonstrated that HCV infection can be transmitted by exosomes between hepatocyte-like cells establishing a productive infection. Viruses exploit exosomes to establish persistent infection and escape the immune response. Exosomal cargo promotes disease progression possibly by “dampening down” host immune responses.

We aimed to elucidate the role of exosomes in the immune response of chronic HCV patients at various stages of liver fibrosis, before and after DAAs treatment.

**Method:** Whole blood from 40 chronic HCV patients with characterized fibrosis was collected before and after DAAs administration and used for isolation of exosomes and peripheral blood mononuclear cells. The existence of specific T-cell subpopulations was assessed by FACS. Exosomal cargo was analyzed for immunosuppressive factors by immunoblotting, FACS and ELISA.

**Results:** The (%)ratio of cytotoxic (CTL) over total T-lymphocytes (CD3/CD8) remained unaffected by DAAs treatment and fibrosis stage. Conversely, the Tregs (CD4/CD25/FOXPD3) subpopulation post-DAAs treatment was statistically decreased in mild fibrosis (stages F0-F1-F2), but remained stable in advanced fibrosis and cirrhosis.

Figure: (abstract: THU325): Logo representation of the nucleotide sequence corresponding to the ribozyme region in the genomic sense (nt 688-771). At the bottom are indicated the different regions of the ribozyme and to which of them each nucleotide group corresponds.
(stages F3–F4). Importantly, the active form of the immunosuppressive cytokine TGF-β was detected in the eosomal cargo and matching serum, albeit varying between fibrosis stages. We observed that the TGF-β levels of both sera and exosomes before DAAs treatment were statically increased in advanced fibrosis (F3). Treatment with DAAs statistically reduced serum TGF-β levels by 50% in the advanced stages of fibrosis and cirrhosis, whereas it did not alter TGF-β levels in exosomes in the different stages of fibrosis. Finally, we confirmed the presence of the immunosuppressive PD-L1 molecule in exosomes isolated from the same samples both before and after treatment.

Conclusion: HCV-manipulated exosomes may confer continuing immune suppression in the otherwise cured HCV patients bearing advanced liver disease. Despite DAAs-mediated HCV eradication, the presence of immunosuppressive factors in the eosomal cargo supports the notion of a remaining “viral fingerprint” that could promote liver disease in susceptible individuals.

THU327
Therapeutic suppression of HBV transcripts promotes reappearance of the SMCS/6 complex and cccDNA silencing in vivo without affecting posttranslational modifications of cccDNA-bound histones
Lena Allweiss1, 2, Moritz Calaminus1, Katja Giersch3, Tassilo Volz1, Andrea Pirou3, Marc Luettehgamann3, 4, Maura Dandri1, 2. 1University Medical Center Hamburg-Eppendorf, I. Department of Internal Medicine, Hamburg, Germany; 2German Center for Infection Research (DZIF), Hamburg-Lubeck-Borstell-Riens, Germany; 3University Medical Center Hamburg-Eppendorf, Department of Medical Microbiology, Virology and Hygiene, Germany; 4Leibniz Institute for Experimental Virology, Department of Viral Immunology, Hamburg, Germany
Email: L.allweiss@uke.de

Background and aims: There is a strong need to explore interventions able to suppress the hepatitis B virus (HBV) reservoir, the cccDNA, since its silencing may promote a functional cure of chronic hepatitis B (CHB). We previously showed that treatments with siRNA targeting all HBV transcripts or pegylated interferon α (peg-IFNα) strongly reduce all HBV markers, including HBx, thus enabling reappearance of the host restriction factor “structural maintenance of chromosome 5/6” (SMCS/6) complex and cccDNA suppression in vivo (Allweiss/Giersch, Gut 2021). The aim of this study was to investigate the epigenetic landscape of cccDNA-bound histones in HBV-infected humanized mice after siRNA or peg-IFNα treatment.

Method: HBV-infected human liver chimeric mice received siRNA or peg-IFNα for 4 or 6 weeks, respectively, or were left untreated. RNA in situ hybridisation demonstrated suppression of HBV transcripts in human hepatocytes. Active and repressive posttranslational modifications (PTMs) of cccDNA-bound histones and SMCS/6 occupancy were analysed by chromatin immunoprecipitation-qPCR (ChIP-qPCR) and compared with PTMs on host genes.

Results: In untreated mice with high HBV replicative activity, canonical transcriptionally active PTMs (H3K27ac, H3K4me3) were highly enriched on the cccDNA minichromosome while the repressive mark H3K27me3 was undetectable. This pattern was consistent with active transcription and similar to the active host gene promoter GAPDH. Remarkably, neither siRNA nor peg-IFNα provoked significant PTM changes on the cccDNA despite strong reduction of HBV transcription. Consistent with previous results, only NSE4 occupancy, a subunit of the SMCS/6 complex, became detectable on the cccDNA after siRNA and peg-IFNα treatment.

Conclusion: Despite shutting down cccDNA transcription in a great proportion of human hepatocytes, siRNA or peg-IFNα treatment did not alter the pattern of the analysed cccDNA-bound histone PTMs. In line with the function of SMCS/6 as a DNA micro-compaction machine (Serrano, Molecular Cell 2020), the data suggest that SMCS/6 could mediate silencing through physical cccDNA compaction rather than through epigenetic changes.

THU328
Updated national prevalence estimates of chronic hepatitis B virus infection in countries within the European (EU) and European Economic Area (EEA): a systematic review
Sandra Bivege1, 2, Adam Trickey3, Zak Thornton1, Becky Scanlan1, Anna McNaughton1, Aaron G. Lim1, Lina Nerlander2, Hannah Fraser1, Josephine Walker1, Matthew Hickman1, 2, Peter Vickerman1, 2, Helen Johnson3, Erika Duffell1, Ellen Brooks-Pollock1, Hannah Christensen1, 3, University of Bristol, Population Health Science, Bristol Medical School, Bristol, United Kingdom; 2University of Bristol, NIHR HPRU in Behavioural Science and Evaluation, Bristol, United Kingdom; 3European Centre for Disease Control, Stockholm, Sweden
Email: hannah.christensen@bristol.ac.uk

Background and aims: Hepatitis B virus (HBV) is a leading public health problem globally. In Europe, the burden of HBV disproportionately affects at-risk groups, including men who have sex with men (MSM), migrants and prisoners. There are no recent population-level estimates of HBV prevalence in Europe.

Method: We undertook a systematic review to update estimates of chronic HBV (CHB) prevalence for the EU/EEA and UK in key sentinel and at-risk population groups. Databases were searched for original research articles in English published between 1/1/2018 to 24/2/2021. Titles and abstracts were screened to identify articles containing relevant information on CHB prevalence in Europe as measured by HBsAg status, with full text screening undertaken to confirm inclusion. Sentinel groups included first-time blood donors (FTB), general population (GP) and pregnant women; at-risk groups included MSM, migrants and prisoners. The updated estimates were incorporated into an existing HBV prevalence database (spanning 2005–2017) developed by the European Centre for Disease Control using the same inclusion/exclusion criteria. External grey literature data were obtained from country experts.

Results: A total of 5678 articles were title and abstract screened, of which 307 were full-text screened. A total of 41 published studies were included in the review, consisting of studies in GP (n = 12), migrants (n = 17), pregnant women (n = 5), MSM (n = 3) and prisoners (n = 4). Additional estimates from grey literature were also included (n = 109), comprising of GP (n = 11), migrants (n = 7), pregnant women (n = 16), MSM (n = 6), prisoners (n = 8) and FTB (n = 61). Weighted CHB prevalence estimates from the existing and updated database indicated a low HBV prevalence (≤2%) among sentinel populations in all regions with exceptions in Romania, Bulgaria, Italy and Greece (reported prevalences 3.4–7.6%). Prevalence among prisoners varied considerably across all regions (range 2.1–25.2%) and 56% countries lacked data. Studies among migrants recorded some of the highest HBV prevalences, and estimates in this sub-population were typically higher in Southern European regions (range 5.0–12.2%). Reported HBV prevalence among MSM was low (≤2%), except in Belgium and Estonia (range 2.3–3.4%). Studies on MSM and migrants were absent in Eastern Europe.

Figure: Updated HBsAg prevalence estimates in high-risk groups in the EU/EEA and UK. Maps show the weighted average prevalence in each country.

Conclusion: This review builds on previous estimates in the EU/EEA and UK, providing an additional 150 prevalence estimates across the region (updated total; n = 582). HBV prevalence was higher in Southern and south-Eastern Europe compared to other regions. Furthermore, CHB prevalence remains high among high-risk groups,
indicating that further interventions targeting these groups are required to reduce the burden of HBV in Europe.

THU329
Relevance of HEV detection in ejaculate of chronically infected patients
Mathias Schemmerer1, Marc Luetghehtmann2, Hans Bock3, Jörn Schattenberg4, Samuel Huber5, Susanne Polywka2, M Mader6, Ansgar Lohe3, Daniel Todt6,7, Eike Steinmann6, Jürgen Wenzel1, Thomas Horvatits3, Sven Pischke5, 1University Medical Center Regensburg, Institute of Clinical Microbiology and Hygiene, National Consultant Laboratory for HW and HEV, Regensburg, Germany; 2University Hospital Hamburg-Eppendorf, Microbiology, Germany; 3University Hospital Düsseldorf, Gastroenterology, Germany; 4University Medical Center Mainz, Gastroenterology, Germany; 5University Medical Center Hamburg-Eppendorf, Department of Medicine, Germany; 6Ruhr-University Bochum, Department of Molecular and Medical Virology, Germany; 7European Virus Bioinformatics Center (EVBC). Jena, Germany
Email: mathias.schemmerer@ukr.de

Background and aims: Recently, HEV particles have been detected in the ejaculate of 2 out of 3 chronically infected patients. HEV RNA in the ejaculate can be significantly higher than in serum or plasma. However, it was unclear whether these viral particles in the ejaculate are infectious, and how often HEV generally occurs in the ejaculate of chronically infected individuals.

Method: After a previous cell culture model failed to demonstrate the infectivity of HEV particles from the ejaculate of two chronically infected patients (Horvatits et al. Journal of Hepatology 2021), we now used an alternative cell culture model based on overconfluent PLC/PRF/5 cells (Schemmerer et al. Viruses 2019) to study these particles for infectivity. Furthermore, we monitored HEV viral load in blood, urine, stool and ejaculate in 9 chronically infected patients.

Results: For the first time, HEV particles from ejaculate were shown to be infectious in overconfluent PLC/PRF/5 cells (figure). HEV replicated to high viral loads of 10^9 HEV RNA copies per ml. Moreover, HEV was detected in the ejaculate of 7 out of 9 chronically infected patients (age 36–67 years, median 56 years). In 5 of the patients the viral loads were significantly higher (more than 2 log) compared to their serum, while in 2 patients, viral loads were lower than in their serum (more than 1 log).

Conclusion: In the context of chronic HEV infection, HEV particles can be detected in the ejaculate of 78% (7/9) of infected men, usually with significantly higher viral loads than in serum. In this regard, it should be noted that the gap between high viral load in ejaculate compared to viral load in blood may even be much higher than previously suspected. After the infectivity of HEV particles from ejaculate could not be demonstrated so far, it could now be shown that they are infectious in PLC/PRF/5 cells. While there is probably no danger from this ejaculate for immunocompetent sexual partners, safer sex practice should be followed if the sexual partners are immunocompromised.

THU330
HDV-mediated inhibition of HBV in superinfection mouse model: the role of type I Interferon
Beatriz Pacín Ruiz1,2,3, Gracián Camps4, Maria Francesca Cortese1,2,3, Josep Gregori1,2,4, David Tabernero1,3, Selene García-García1,2,3, África Vales Aranguren4, Cristina Olague Micheltorena5, Adriana Rando-Segura1, Josep Quer4, Rafael Esteban1,3, Mar Riveiro Barciela1,2, Maria Buti5, Glória González-Aseguinolaza4, Francisco Rodríguez-Prias1,2,3, 1Vall D’hebron University Hospital, Biochemistry and Microbiology/Liver Pathology Unit, Barcelona, Spain; 2Vall D’Hebron Research Institute, Liver Unit, Barcelona, Spain; 3Instituto De Salud Carlos III, Centro De Investigación Biomédica En Red, Enfermedades Hepáticas Digestivas (CIBERehd), Madrid, Spain; 4University of Navarra, Center for Applied Medical Research (CIMA), Pamplona, Spain; 5Vall D’Hebron University Hospital, Liver Unit, Department of Internal Medicine, Barcelona, Spain
Email: beatriz.pacin@vhir.org

Background and aims: While Hepatitis B virus (HBV) replication does not significantly activate the innate immune response, it has been observed that in the presence of Hepatitis Delta virus (HDV) there is an increased type I interferon (INF) response. The aim of this study is to analyze the potential role of the INF response on the HBV inhibition upon HDV super-infection in a novel HBV-expressing transgenic (HBVtg) mouse model knock out for the INF alpha-receptor (IFNαR KO).

Method: Wild type (WT) and IFNαR KO HBVtg mice were intravenously administered with 5 × 10^10 viral genomes of adeno-associated vector (AAV) expressing luciferase (LUC) or HDV. While Hepatitis B viremia was weekly monitored during the experiment, liver HbcAg expression and HBV-DNA levels were analyzed at 21 days after AAV injection. At this timepoint, the complexity of the HBV quasispecies (QS) at the 5′ end of the X gene expression and HBV-DNA levels were analyzed at 21 days after AAV injection. At this timepoint, the complexity of the HBV quasispecies (QS) at the 5′ end of the X gene (nt 1255–1611) and 3′ end of the X gene (nt 1596–1912) was analyzed by next-generation sequencing (NGS) (MiSeq Illumina, San Diego, USA). Nucleotide substitutions were identified by aligning sample QS with its genotype master sequence and QS complexity was calculated using Rare Haplotype Load (RHL) index (threshold 1%).

Results: Both liver HbcAg expression and viremia was higher in HBVtg × IFNαR KO than in WT HBVtg mice under steady state conditions. AAV-HDV infection induced the decrease of hepatic HbcAg expression and HBV-DNA levels in HBVtg mice. This effect disappeared in HBVtg × IFNαR KO mice. Likewise, viremia was reduced from day 7, reaching the lowest levels at day 21 after vector administration in HBVtg mice, while HBV serum levels in HBVtg × IFNαR KO animals remained constant until the end of the experiment. Similar ALT serum levels presented by HBVtg and HBVtg × IFNαR KO mice excluded differential liver damage as the reason for the HBV repression observed in HBVtg animals. An overall higher number of changes was observed in 5′ HBX region than in 3′ HBX region (42.72 vs. 15.61). In 5′ HBX the RHL index was higher in presence of HDV. This index was even more pronounced in wt HBVtg than IFNαR KO.

Conclusion: The limited inhibition of HBV expression in presence of HDV in IFNαR KO mice suggested that IFN type I is essential for HDV-mediated HBV inhibition. The higher QS variability in presence of HDV might contribute to the inhibition of HBV replication. This variability is more pronounced in wt mice, thus suggesting a possible role of IFN-dependent activation of mutagenic enzymes. Further studies are required to better characterize the molecular mechanisms involved in HBV inhibition and viability, and to identify novel therapeutic strategies for HDV-infected patients. Funding: Instituto
**THU331**

Assessment of Myrcludex or heparin antiviral activity on HBV infection using a 3-dimensional primary human hepatocyte culture system

Juliette Besombes¹, Charlotte Pronier¹, Jeremy Bomo¹, Philippe Grippon¹, Vincent Thibault¹. ¹CHU Rennes-Pontchaillou Hospital, Virology, Rennes, France

Email: vincent.thibault@chu-rennes.fr

**Background and aims:** Despite effective vaccination, Hepatitis B Virus (HBV) infection remains responsible for significant morbidity and mortality worldwide. Robust in vitro models mimicking the complex liver architecture are still lacking and culture of differentiated primary human hepatocytes (PHH) remains fastidious. Three dimensional (3D) culture models of PHH have been developed offering a microenvironment closer to in vivo conditions. Here, we describe the characterization of a 3D cell culture model based on the formation of PHH spheroids supporting HBV infection. We focus on the effect of Heparin and Myrcludex B (MyrB) on HBV infection.

**Method:** PHH (freshly collected or cryopreserved) were first incubated overnight in ultra-low-attachment plates to make them aggregate in spheroids before being embedded in a collagen matrix. HBV infection was performed 2 days after seeding using a 50-fold concentrated culture supernatant of HepG.2.2.15 cells or HBV purified from chronically infected patients’ plasmas using different multiplication of infection (MOI). Susceptibility to infection was monitored by the secretion of HBe antigen (HBeAg) in the supernatant. HBV infection under different concentrations of Heparin (4 and 133 μg/ml) or MyrB (50 to 800 nM) was evaluated.

**Results:** After defining the optimal MOI of 400 HBV genome equivalents (GE)/cell, long-term HBV infections for at least 38 days were obtained with this model. The dose-response study showed that HBV infections at a low MOI of 10 GE/cell, similar to the one used in vivo in animal models, were possible even though HBeAg secretion was weak. We confirmed that high concentration of heparin (133 μg/ml) blocked HBV infection with an average inhibition of HBeAg secretion (p < 0.05) at 14 days post infection (dpi). Conversely, heparin at therapeutic concentration (4 μg/ml) in the culture medium promoted infection with a 130% increase in HBeAg secretion (p < 0.05). In this model, 50 nM MyrB efficiently blocked HBV infection with an average inhibition of HBeAg secretion of 63%, at 7 dpi. An increase of MyrB concentration from 50 to 800 nM did not improve the inhibition of infection. The level of HBeAg secretion was comparable when MyrB (100nM) was present only at the time of infection or maintained throughout the culture duration with an inhibition of HBeAg secretion of 84% at 14 dpi, whatever the condition. Adjunction of MyrB in the culture medium at 4 and 8 dpi resulted in a decrease in HBeAg secretion of 61% and 25%, respectively, at 14 dpi (p < 0.05 compared to without MyrB).

**Conclusion:** This 3D PHH culture system supports long-term HBV infection. Activity of MyrB even when added at distance from infection suggests late or secondary infections. Heparin activity on HBV infection depended on its concentration in the medium, yet the mechanism underlying this effect remains partially unexplained. Optimization and characterization of this model are warranted.

**THU332**

Concordance of the Xpert hepatitis B viral load test and conventional quantitative PCR in detecting and quantifying viremia using stored plasma and dried blood spot samples in West Africa

Gibril Ndow¹, Amie Ceesay¹, Yusuke Shimakawa², Alpha Omar Jallow¹, Haddy Nyang¹, Baboucarr Bittaye¹, Francis Mendy¹, Ousman Secka¹, Umberto D’Alessandro¹, Mark Thurfs², Isabelle Chemin³, Maud Lemoine³. ¹MRC Unit The Gambia at LSHTM, Disease Control and Elimination, Fajara, Gambia; ²Institut Pasteur, Unité d’épidémiologie des maladies émergentes, Paris, France; ³Imperial College London, Metabolism, Digestion and Reproduction, London, United Kingdom; ⁴INSERM U1052, Center de Recherche en Cancérologie, CNRS UMR5286, Lyon, France

Email: gibril.ndow@lshtm.ac.uk

**Background and aims:** The new Xpert hepatitis B virus (HBV) viral load test (Cepheid, USA) provides an opportunity to scale up and decentralise hepatitis B diagnosis, treatment and monitoring in resource-limited settings where HBV is endemic and molecular diagnostics to quantify HBV DNA are scarce. We assessed the concordance between the new Xpert HBV viral load test and the conventional quantitative PCR (Abbott, USA) in quantifying HBV viremia using stored plasma and dried blood spot (DBS) samples.

**Method:** Paired plasma and DBS (Whatman 903 Protein Saver cards) samples were collected from adults with chronic HBV infection followed up in the PROLIFICA (Prevention of Liver Fibrosis and Cancer in Africa) programme in The Gambia. Samples were stored in −80°C for at least 12 months before analysis.

For each plasma sample, HBV DNA was quantified using both realtime qPCR (Abbott, detection limit 26 IU/ml in plasma) and Xpert (detection limit 3.2 IU/ml in plasma). For DBS, HBV DNA was quantified using Xpert.

Concordance of the Xpert HBV test and the conventional qPCR in detecting and quantifying HBV viremia in plasma was assessed by kappa statistics, and the agreement between the two assays was assessed using the Bland-Altman plot. The concordance of HBV viremia between paired plasma and DBS samples was also assessed by kappa statistics.

**Results:** We analysed 266 stored plasma samples from patients at various hepatitis B disease stages. Of these, HBV viral load results were discordant between the Xpert and the conventional qPCR: 130 (48.9%) and 63 (23.7%) were detectable and undetectable by both assays, respectively. The results were discordant in 71 (26.7%) samples that were detectable by Xpert but not qPCR, and 2 (0.8%) samples that were detectable by qPCR but not Xpert. In 110 samples with quantified viral load results from both assays, the mean difference between the two assays was 0.316 log IU/ml (95% limits of agreement – 1.189, 1.820) with only 6/110 results (5.45%) being outside the limits of agreement (figure 1), indicating good agreement.

From 91 paired plasma and DBS samples analysed by Xpert assay, the mean bias between plasma and DBS was statistically significant at 1.831 log IU/ml (95% limits of agreement: 0.660–3.001). Bias was smaller at lower viral loads. The kappa statistic was 0.10 indicating very poor agreement between results. After excluding samples with error or invalid result by either sample type (n = 40), kappa statistic was 0.34 indicating a poor agreement.
THU333

A high-throughput viral integration sequencing method reveals that mitochondrial DNA is frequently targeted by HBV integration

Domenico Giosa1, Daniele Lombardo1, Cristina Musolino2, Valeria Chines1, Giuseppina Raffa1, Deborah D’aliberti1, Francesca Casuscelli di Tocco1, Carlo Salta1, Riccardo Aiese Cigliano1, Orazio Romeo1, Angela Aliibrandi1, Giuseppe Navarra1, Giovanni Raimondo1, Teresa Pollicino2, University Hospital of Messina, Clinical and Experimental Medicine, Messina, Italy; 2University Hospital of Messina, Human Pathology, Messina, Italy; 3University of Milano Bicoca, DIPARTIMENTO DI MEDICINA E CHIRURGIA (SCHOOL OF MEDICINE AND SURGERY), Milan, Italy; 4Sequenom Biotech SL, Barcelona; 5University of Messina, Dipartimento di Scienze chimiche, biologiche, farmaceutiche e ambientali, Messina, Italy; 6University of Messina, Dipartimento di Economia, Messina, Italy

Email: tpollicino@unime.it

Background and aims: Although research on HBV DNA integration has made relevant progress, important aspects remain unclear. Development of new integration detection methods may help in improving knowledge in the field and in better understanding HBV-related tumorigenesis. Our aim was to conduct a high-throughput integration detection on tumor (T) and non-tumor tissues (NT) from HBsAg-positive patients using a highly sensitive method for assaying HBV integration.

Method: We studied T from 7 patients with hepatitis B-related HCC and paired NT from 6 of the 7 cases. HBV integration sites were recovered by semi-nested ligation-mediated PCR from host DNA (fragmented by sonication and ligated to asymmetric DNA linkers) and the use of forward or reverse HBV-specific primers. Targeted sequences were further enriched by nested-PCR with forward or reverse MiSeq HBV primers and forward or reverse MiSeq plinkers. PCR products were subjected to paired-end sequencing, and reads were aligned to a hybrid genome including human genome (GRCh38,p10) and HBV genome (NC_003977).

Results: A total of 3, 339 unique HBV integration sites were detected in the 7 patients: 2, 913 integrations in T and 426 in NT. The average number of integration sites in T and NT was 416 and 71, respectively. All patients had HBV integrations, with an average of 256.8 integrations per individual patients. The detected integration sites were randomly distributed across the whole genome and no hotspot was detected. Compared to individual chromosomes, a significant enrichment of virus integration sites was observed in mitochondrial DNA (mtDNA) both in T (p <0.0001) and NT (p <0.0001), after normalization of the number of integrations to chromosome length. We found a total of 20 unique HBV integrations in mtDNA from the tissue samples obtained from 4/7 patients (17 breakpoints in T from 4/4 patients and 3 breakpoints in NT from 2/4 patients). HBV integration in mtDNA was associated with HBV DNA (p = 0.01) and pgRNA amounts (p = 0.02). In mtDNA, the integration breakpoints were preferentially located in mitochondrial genes in T (17/17 vs 0/3; P < 0.0001) and in the D-loop region in NT (2/17 vs 3/3; P = 0.001). RNR2, ATP6, ND4, and ND5 mitochondrial genes were identified as recurrent sites of integration in T. Moreover, in T of individual patients, HBV integrations were detected in CYTB, COX1, ND1, and ND2 genes. Furthermore, we found that HBV RNAs are imported into mitochondria.

Conclusion: The new HBV integration sequencing method importantly increased the detection efficiency of HBV integration breakpoints. We detected a significant number of integration DNA from both T and NT. HBV integrations in mtDNA preferentially involved OXPHOS mitochondrial genes in T, suggesting that there is selection for mitochondria harboring HBV integration in these genes or for cells containing these mitochondria during hepatocarcinogenesis.

THU334

Enhanced T cell responses in patients and mouse model of hepatitis B and comorbid non-alcoholic fatty liver disease

Nishi Patel1, Dan Boghici2, Micol Rava3, Matteo Iannaccone4, Konstantin Koro5, Craig Jenne2, Carla Osiowy2, Carla Coffin2, 1University of Calgary, Cumming School of Medicine, Calgary, Canada; 2University of Calgary, Cumming School of Medicine, Calgary, Canada; 3San Raffaele Hospital, Division of Immunology, Transplantation and Infectious Diseases, Milano, Italy; 4Alberta Precision Laboratories, Calgary, Canada; 5Public Health Agency of Canada, National Microbiology Laboratory, Winnipeg, Canada

Email: nishi.patel@ucalgary.ca

Background and aims: Individuals living with hepatitis B and comorbid non-alcoholic fatty liver disease (NAFLD) are at an increased risk for hepatocellular carcinoma. Large cohort studies show a positive association between hepatic steatosis and reduced hepatitis B virus (HBV) replication. The objective of this study is to determine the viral and immune factors and mechanisms that contribute towards lower HBV replication in patients and mouse model of hepatitis B and NAFLD.

Method: 55 patients with hepatitis B and NAFLD were recruited from 3 Canadian liver clinics. Plasma, sera, and peripheral blood mononuclear cells (PBMCs) were isolated from blood. A parallel mouse model study of HBV and NAFLD was performed using 1.3.32DH transgenic mice that included healthy, NAFLD, and HBV control groups (N = 10/group). The mice were followed for 8 weeks and then sacrificed to obtain plasma, sera, PBMCs, and liver tissue (for histopathological scoring and viral antigen staining). HBV biomarkers were quantified using in-house and/or standard clinic assays in both patient and mice samples. Next-generation sequencing of HBV surface and core genes was performed using the Illumina MiSeq platform. A panel of 13 pro-and-anti-inflammatory cytokines was measured using multiplex Luminex assay. PBMCs phenotypic profile and ex vivo HBV-specific T cell responses were characterized through flow cytometry and IFN-gamma ELISPOT, respectively.

Results: In 55 patients with hepatitis B and NAFLD (35% female; mean age of 45 ± 10.6 years), 52 (95%) were HBeAg negative. The mean HBV DNA, qHBsAg, and HBV pgRNA levels were 3.2 ± 1.8 log10 IU/ml, 2.9 ± 1.2 log10 pg/ml, and 2.1 ± 1.3 log10 copies/ml, respectively. Hepatitis B patients with NAFLD clinical factors (i.e., dyslipidemia, hypertension, and metabolic syndrome) had lower levels of qHBsAg (p <0.001). Similarly, mice with HBV and NAFLD had lower levels of HBV DNA (p = 0.022) and nucleic acid related antigen (p = 0.044) at 8 weeks. Greater frequency of immune escape mutations in HBV surface gene
PHNOM PENH, CAMBODIA; 3Institut de Recherche en Science de la Santé (IRSS), Unité de Recherche Clinique de Nanoro (URCN), Nanoro, Burkina Faso; 4National Hospital Organization Nagasaki Medical Center, Clinical Research Center, Nagasaki, Japan

Methods: Hospital based cross-sectional study was performed in a total of 1565 pregnant women who visited three hospitals in Siem Reap for their antenatal care from Feb-Sep 2020. The sero-markers such as HBsAg, HBsAb, HBeAb, HBeAg and HBeAb were detected from their blood samples using chemiluminescent enzyme linked. Viral titer was measured by real-time PCR. Full HBV genomes were amplified by direct sequencing. The study has been approved by ethical committees of Hiroshima University and Cambodia.

Results: The age of pregnant women participated in this study ranged from 15 to 47 years old with the mean age of 28.3 ± 5.6 years old. The prevalence of HBsAg, HBeAg, and HBcAb were 4.28%, 38.53%, 23.13%, respectively. Among the HBsAg positives, the prevalence of HBeAg and HBeAb were 41.79% and 55.22%, respectively. The overall mean viral titer was 2.22 × 10^6 copies/ml, where 5.30 × 10^6 copy/ml for HBeAg+ and 5.58 × 10^3 copy/ml for HBeAb+. Thirty-seven samples were able to perform full-genome sequencing. HBV genotype C1 was predominant (70.27%), followed by B4 (16.22%) and B2 (13.51%). All HBV genotype B were found to be recombinant B/C. By full genome analysis on 37 HBV isolates, mutation at a determinant region of surface protein was 24.32%. Additionally, the combination mutation was found in 2.70% and double mutation in 29.73% and V149I mutation at core region in 2.70%, all of which were highly associated to hepatocellular carcinoma occurrence.

Conclusions: The findings from our study demonstrated the intermediate level of HBV infection endemicity, genotype distribution and mutation pattern among pregnant women in Siem Reap. These findings contribute to the establishment of HBV screening program and the management of HBsAg positive for pregnant women in Cambodia.

THU336
Genotype distribution and mutations associated with hepatocellular carcinoma risk among hepatitis B carriers in Goto Islands, Japan

Serge Ouoba1,2, Ko Ko1, Shintaro Nagashima1, Bunthen E1,3, Kazumi Yamasaki1, Kazuki Takahashi1, Junko Tanaka1, Hiroshima University, Department of Epidemiology, Infectious Disease Control and Prevention, Graduate School of Biomedical and Health Sciences, Hiroshima, Japan; 2Ministry of Health, Payment Certification Agency, Phnom Penh, Cambodia; 3Institut de Recherche en Science de la Santé (IRSS), Unité de Recherche Clinique de Nanoro (URCN), Nanoro, Burkina Faso; 4Ministry of Health, National Maternal and Child Health Center, Phnom Penh, Cambodia; 5Ministry of Health, National Immunization Program (NIP), Phnom Penh, Cambodia; 6World Health Organization Country Office, Expanded Program on Immunization, Phnom Penh, Cambodia

Background and aims: Hepatitis B virus (HBV) genotype and specific mutations are associated with the risk of hepatocellular carcinoma (HCC). Using stored serum of a cohort of HBsAg-positive patients in

Figure 1: Cytokine levels based on NAFLD clinical factors in hepatitis B patients (Mann-Whitney U test). *p <0.05. **p <0.01.

Conclusion: Heightened T cell responses observed in patients and mouse model of hepatitis B and NAFLD contribute towards suppression of HBV replication.

THU335
Hepatitis B Virus sero-prevalence and genotype distribution among pregnant women in Siem Reap, Cambodia

Bunthen E1,2, Ko Ko1, Shintaro Nagashima1, Serge Ouoba1,3, Kanon Abe1, Aya Sugiyama1, Kazuki Takahashi1, Rattana Kim4, Veerit Ohk1, Md. Shafiqul Hossain5, Junko Tanaka1, Hiroshima University, Department of Epidemiology, Infectious Disease Control and Prevention, Graduate School of Biomedical and Health Sciences, Hiroshima, Japan; 2Ministry of Health, Payment Certification Agency, Phnom Penh, Cambodia; 3Institut de Recherche en Science de la Santé (IRSS), Unité de Recherche Clinique de Nanoro (URCN), Nanoro, Burkina Faso; 4Ministry of Health, National Maternal and Child Health Center, Phnom Penh, Cambodia; 5Ministry of Health, National Immunization Program (NIP), Phnom Penh, Cambodia

Background and aims: The latest report hepatitis B virus (HBV) infection prevalence in Cambodia was 4.4% among mothers and 0.56% among their 5–7 years old. High infection prevalence in women of childbearing age showed potential of vertical transmission, threatening WHO target of eliminating hepatitis virus infection by 2030. This study aimed to estimate HBsAg prevalence among pregnant women, and then to examine their genomic structure and the mutation pattern.

Method: Hospital based cross-sectional study was performed in a total of 1565 pregnant women who visited three hospitals in Siem Reap for their antenatal care from Feb-Sep 2020. The sero-markers such as HBsAg, HBsAb, HBeAb, HBeAg and HBeAb were detected from their blood samples using chemiluminescent enzyme linked. Viral titer was measured by real-time PCR. Full HBV genomes were amplified by direct sequencing. The study has been approved by ethical committees of Hiroshima University and Cambodia.

Results: The age of pregnant women participated in this study ranged from 15 to 47 years old with the mean age of 28.3 ± 5.6 years old. The prevalence of HBsAg, HBeAg, and HBcAb were 4.28%, 38.53%, 23.13%, respectively. Among the HBsAg positives, the prevalence of HBeAg and HBeAb were 41.79% and 55.22%, respectively. The overall mean viral titer was 2.22 × 10^6 copies/ml, where 5.30 × 10^6 copy/ml for HBeAg+ and 5.58 × 10^3 copy/ml for HBeAb+. Thirty-seven samples were able to perform full-genome sequencing. HBV genotype C1 was predominant (70.27%), followed by B4 (16.22%) and B2 (13.51%). All HBV genotype B were found to be recombinant B/C. By full genome analysis on 37 HBV isolates, mutation at a determinant region of surface protein was 24.32%. Additionally, the combination mutation was found in 2.70% and double mutation in 29.73% and V149I mutation at core region in 2.70%, all of which were highly associated to hepatocellular carcinoma occurrence.

Conclusion: The findings from our study demonstrated the intermediate level of HBV infection endemicity, genotype distribution and mutation pattern among pregnant women in Siem Reap. These findings contribute to the establishment of HBV screening program and the management of HBsAg positive for pregnant women in Cambodia.
Goto Islands, we studied the genotype distribution and the mutations related to the progression of liver disease.

**Method:** A total of 910 samples from a cohort of Hepatitis B surface Antigen-positive patients between 1980 and 2017 underwent genomic analyses. Partial and full HBV genomes were amplified by direct sequencing using an in-house developed primer set to identify HBV genotype and mutations related to HCC risk. Phylogenetic tree was performed by the neighbor-joining method.

**Results:** Men represented 57.4% of the cohort and the mean age at the start of the cohort was 45.5 ± 17.3 years. The median follow-up duration was 14.6 years. At entry, 61% were asymptomatic carriers but a 172% increment of hepatocellular carcinoma was found at the end of follow-up. The mean viral load was $2.0 \times 10^4$ copies/ml, and the prevalence of HBeAg and HBeAb were 26.5% and 71.2%, respectively. The predominant circulating genotype was genotype C2 (96.2%), followed by genotype B (3.4%) and A (0.6%). Three main clusters of cases were found having 95.61%-99% homology and were closely related to HBV isolates from China and Japan. A total of 92 isolates underwent full genome analysis and mutations related to HCC occurrence were observed. Double mutation (A1762T/G1764A) was found in 73.5%, combination mutation (C1653 T and A1762T/G1764A or T1753C and A1762T/G1764A) in 29.4%, and V149I mutation in the core region in 26.9% of the isolates.

**Conclusion:** Genotype C, which is known to be associated with HCC risk, is the predominant circulating genotype in Goto islands, suggesting a large influence from East Asia. Mutations related to hepatocellular carcinoma occurrence were also found. In addition to the improvement of countermeasures against HBV infection in Goto Islands, genomic surveillance of HBV is essential to reduce the burden of the infection.

Figure: (abstract: THU336)
THU337
Comprehensive analysis of the different phases of chronic hepatitis B virus infection
Michael Basic1,2, Qingyan Wu2, Anja Schollmeier2, Christoph Sarrazin1,2, Stefan Zeuzem1, Eberhard Hildt2,4, Kai-Henrik Peiffer1,2.
1University Hospital Frankfurt, Frankfurt am Main, Germany; 2Paul Ehrlich Institute, Langen (Hessen), Germany; 3St. Joseph’s Hospital in Wiesbaden, Wiesbaden, Germany; 4German Center for Infection Research, Braunschweig

Background and aims: Chronic Hepatitis B virus (HBV) infection was classified into four active phases by the EASL: 1. HBeAg-positive chronic infection, 2. HBeAg-negative chronic hepatitis, 3. HBeAg-negative chronic infection and 4. HBeAg-negative chronic hepatitis. Recently, it was observed that released HBsAg amounts, ratios of L-, M- and S-proteins and morphology of subviral particles varied by viral genotype (Gt). Further, HBsAg composition was described to be distinct during the different phases of infection. Here, we characterized different phases of chronic HBV infection regarding HBsAg, core and particle assembly in vivo and in vitro.

Method: Sera of patients infected with GtA or GtD of different disease phases according to the EASL classification were analyzed by Western blot (WB) and density gradient centrifugation. For in vitro studies, HBV genomes of GtA, GtB, and GtD of patients with HBeAg-negative chronic infection and presence of precore mutation G1896A were cloned into pUC-18 and expressed in Hepatoma cells. Corresponding HBeAg-positive wildtype genomes were used for comparison. Expression and localization of HBsAg and core protein, replication, particle morphology and infectivity as well as subcellular localization were analyzed.

Results: In the sera of patients, the ratio of HBsAg proteins differed among genotypes but not among the different disease phases. Density of HBsAg-particles varied among genotypes but not between the stage of infection. In vitro, the HBeAg-negative genomes showed a reduction in HBsAg expression in comparison to the corresponding HBeAg-positive genomes. By WB analyses, intracellular accumulation of LHBs and core protein was found. Further, perinuclear accumulation of LHBs and core protein was observed in HBeAg-negative genomes by immunofluorescence analyses (see fig.). Reintroduction of precore G1896A mutation did not restore HBsAg expression and did not affect intracellular distribution of HBsAg. Furthermore, immunofluorescence microscopy analyses and subcellular fractionation showed a strong intranuclear localization of assembled core protein.

Conclusion: In contrast to other studies, consistent ratios of HBsAg and similar particle densities were observed among the four different phases of active HBV infection. In comparison to HBeAg-positive genomes, HBeAg-negative genomes are characterized by an enhanced intranuclear localization of assembled core protein and a perinuclear accumulation of HBsAg in vitro. This is further reflected by an impaired release of HBsAg. Interestingly, neither HBeAg nor presence of precore G1896A mutation seem to be causative for the observed characteristics in HBsAg and core virology in genomes derived from patients with HBeAg-negative chronic infection. Further analyses of the underlying mechanisms might also affect novel antiviral strategies.

THU338
Human stem cell-derived hepatic and intestinal culture systems to study HEV transmission along the gut-liver axis
Viet Loan Dao Thi1,2, Michael Dill1,4, Sarah Prallet1, Ann-Kathrin Mehner1, Sabrina Schweiggert1,2, Center for Integrative Infectious Disease Research (CIID) University Hospital Heidelberg, Department of Infectious Diseases, Virology, Heidelberg, Germany; 1German Centre for Infection Research (DZIF), Heidelberg, Germany; 2University Hospital Heidelberg, Division of Gastroenterology, Heidelberg, Germany; 2German Cancer Research Center (DKFZ), Experimental Hepatology, Inflammation and Cancer (F240) Deutsches Krebsforschungszentrum, Heidelberg, Germany

Email: vietloan.daothi@med.uni-heidelberg.de

Background and aims: The intestine and the liver are anatomically and functionally linked, often referred to as the gut-liver axis. They cooperate in nutrient uptake and metabolism, as well as provide immunity to pathogens, due to their organization as barrier tissues. Enterically transmitted hepatitis E virus (HEV), the most common cause of acute hepatitis in the world, is dependent on this axis: Once in the gastrointestinal tract, HEV passes the intestinal epithelium to gain access to the blood stream from where it reaches the liver and infects hepatocytes. Conventional cell culture systems fail to recapitulate the intricacy of this axis. Human induced pluripotent and adult tissue stem cell derived organoid culture systems that reflect in vivo-like organ complexity, allow for better and authentic recapitulation of these human epithelial tissues, including polarization and cellular differentiation.

Method: The human induced pluripotent stem cell line iPSC.C3A was differentiated to hepatocyte-like cells (HLCs), which were embedded into Matrigel domes to initiate the formation of hepatic organoids. iPSC.C3A cells were also differentiated to small intestinal organoids using a commercially available kit. In addition, we differentiated human LGR5-positive bipotent cholangiocyte organoids to mature hepatic organoids.

Results: Following organoid formation of iPSC-derived HLCs and further differentiation of both, HLCs-derived and cholangiocyte organoids into mature hepatic organoids, we observed a strong increase in albumin expression, by qRT-PCR analysis and, partially, by IF staining. Both intestinal and hepatic organoid culture systems supported authentic HEV infection using the HEV GT3 Kernow-C1 p6 strain, as evidenced by an increase in HEV viral genomes and the upregulation of interferon-stimulated genes. Interestingly, even immature, bipotent cholangiocyte organoid progenitors were readily permissive for HEV infection.

Conclusion: We have established novel hepatic and intestinal culture systems supporting authentic HEV infection. We will use these systems to study tissue-specific determinants of HEV infection, including the analysis of an HEV-induced innate immune response. In the future, we will combine both systems to study HEV transmission along the gut-liver axis.

Keywords: Hepatitis E virus, induced pluripotent stem cells, hepatic organoids, intestinal organoids, cholangiocyte organoids, gut-liver axis.
THU339
A novel class of glycanspecific human monoclonal antibodies neutralizing the hepatitis E virus
Katja Dinkelborg1,2, George Ssebyatika3, Elina Muriel Guzmán4, Prossie Lindah Nankya3, Luisa J Ströh1, Lucas Hueffner1, Volker Kinast5,6, Toni Luise Meister6, Heiner Wedemeyer2,7, Eike Steinmann6,7, Thomas Pietschmann1,7, Thomas Krey3,4,7,8,9, Patrick Behrendt1,2,7, FWINCORE, Centre for Experimental and Clinical Infection Research, a Joint Venture between the Medical School Hannover (MHH) and the Helmholtz Centre for Infection Research (HZI), Experimental Virology; 2Hannover Medical School, Department of Gastroentrology, Hepatology and Endocrinology; 3Institute of Experimental Virology; 4Hannover Medical School, Department of Biochemistry, University of Lübeck, Center of Structural and Cell Biology in Medicine, Germany; 5Hannover Medical School, Department of Medical Microbiology and Virology; 6Carl von Ossietzky University Oldenburg, Department of Medical Microbiology and Virology; 7Ruhr University Bochum, Department of Molecular and Medical Virology; 8German Center for Infectious Disease Research (DZIF); 9Hannover Medical School, Excellence Cluster 2155 RESIST; 10Centre for Structural Systems Biology (CSSB)

Background and aims: Acute viral hepatitis is most commonly caused by infection with the hepatitis E virus (HEV). It can lead to chronic infection in immunocompromised hosts, as well as severe hepatitis with the risk of liver failure in certain cases. Four main human pathogenic genotypes (gt 1–4) have been described. They differ in their worldwide distribution and route of infection. HEV infected cells secrete glycosylated isoforms of the viral capsid protein (open reading frame 2, pORF2) that are hypothesized to help the virus evade the humoral immune response of infected individuals. However, a gt1 protein-based vaccine has been developed in China and large cohort studies showed that the generated antibody titre correlated with protection from infection. Here, we aimed to generate human monoclonal antibodies neutralising HEV.

Method: Memory B cells of two acutely infected individuals were selected by recognizing the protruding domain (pdomain) of pORF2. Heavy and light chain of the B cell receptor were sequenced and single chain variable fragments (scFv) or monoclonal antibodies (mAb) were expressed in Expi293F cells. To analyse binding, Enzyme-linked Immunosorbet Assays (ELISA) and Biacore experiments were performed. Neutralisation assays were performed using three different HEV strains (gt3: Kernow C1 p6 G1634R and HEV-83–2–27; gt1: Sar55). Additionally, selected scFvs in complex with HEV gt3 pdomain were crystallised and structures were analysed.

Results: In vitro neutralization assays led to the identification of 16 hit candidates. ELISA confirmed the identification of at least four mAbs specifically recognizing the non-glycosylated, infectious form of pORF2. Further experiments confirmed neutralisation of genotype 1 and 3 viral strains by selected mAbs. Titration of identified mAbs determined the half-maximal inhibitory concentration of the best neutralizers at ≤0.01 µg/ml. ELISA using patient sera over the course of acute or chronic infection with HEV confirmed the specificity of a subgroup of identified mAbs to infectious viral particles. Additionally, the specific mAbs but not the non-specific mAbs were unaffected in their ability to neutralize HEV by glycosylated pORF2 isoforms. Structure analysis confirmed that specific mAbs directly bind the glycosylation site, which is highly conserved between different HEV genotypes.

Conclusion: Here, we identified a novel subgroup of human mAbs neutralising different genotypes of HEV. They specifically bind to infectious viral particles and neutralisation is not disrupted by the presence of secreted isoforms of pORF2. These antibodies may serve as a novel therapeutic option for severe and chronic HEV infection, for which effective and specific treatment is currently lacking in the clinic. Furthermore, we offer new insights for the development of cross-genotype effective vaccines against HEV in the future.

THU340
Increased lymphocyte trafficking and myeloid activation in patients with chronic hepatitis delta
Ester García-Pras1, Thais Leonel1, Sergio Rodriguez-Tajes1, Mireia García-López1, Sabela Lens2, Zoe Mariño1, Alba Díaz2, William Fundora2, Xavier Forns1, Sofia Pérez-del-Pulgar1, Liver Unit, Hospital Clinic, University of Barcelona, IDIBAPS, CIBERehd, Barcelona, Spain; 2(2)Pathology Department, Biomedical Diagnostic Center, Hospital Clinic, CIBEREHD, Barcelona, Spain; 3(3) Hepatobioiliapancrican and Liver Transplant Department, Hospital Clinic, Barcelona, Spain
Email: egpras@clinic.cat

Background and aims: Hepatitis Delta virus (HDV) is a satellite virus of hepatitis B virus (HBV), as it requires the HBV envelope proteins (HBsAg) to form viral particles. Compared to HBV monoinfection, chronic hepatitis delta (CHD) represents the most aggressive form of viral hepatitis leading to a faster progression towards cirrhosis, liver decompensation and hepatocellular carcinoma. Immune-mediated liver damage upon HDV infection is an important factor of HDV pathogenesis. The aim of the study was to analyze intrahepatic gene expression in CHD patients compared to HBV-infected patients and healthy controls.

Method: Formalin fixed paraffin embedded (FFPE) liver biopsies from 21 anti-HDV positive patients were included in the study. Patients were classified as HDV+ and HDV- based on whether or not they had detectable HDV-RNA in serum. Untreated HBV monoinfected patients and healthy donors were used as control groups. Gene expression analysis of immune-regulatory pathways was performed by using the nCounter® Host Response Panel of Nanostring. Differential expression between groups was considered if log2 fold-change>1 and p<0.05, FDR adjusted by Benjamin-Yekutieli.

Results: The median age of the patients was 51 years; 62% were male, 62% had liver cirrhosis and 43% were on nucleos (t)ide analog (NA) treatment. Gene expression analysis revealed 223 genes significantly upregulated in HDV+ patients compared to healthy donors and 198 compared to HDV- patients. Chemokines were the molecules with the highest differential expression between groups, being CXCL9, CXCL10, CXCL11 (and its cognate receptor CXCR3) the most relevant. Consequently, genes involved in trafficking and activation pathways of myeloid cells (CCR2, CCR5, CCL18) and lymphocytes (CD2, CD5, CD69, CD40L, CD20, CD79A) were significantly upregulated in HDV+ compared to healthy donors and HDV- patients. Consistent with increased immunopathogenesis associated with HDV infection, apoptotic (BCL-2, TNF), cytotoxic (CZMH, CZMA and PRF-1) and inflammasome (NLRP1, PYCARD y AIM2) pathways were enriched in CHD patients. Immune activation and liver damage pathways were also increased in untreated HBV patients, but significantly less pronounced compared to HDV+ patients. Remarkably, some innate (IFI1, IFIT2 and IFIT3) and adaptive (CD2, CC5 and IL17RE) response molecules persisted upregulated after HDV clearance.

Conclusion: HDV infection induces innate and adaptive responses that contribute to aggravating the progression of liver disease. A strong recruitment and activation of myeloid cells and lymphocytes elicits inflammation and cell death processes in CHD. The resolution of HDV infection might not be able to completely reverse altered signaling pathways, due to molecule sequelae or the persistence of HBV.
Background and aims: Circulating HBsAg can be derived from both intrahepatic cccDNA and integrated HBV DNA. Functional cure may be dependent on the origins of the HBsAg. We sought to correlate cccDNA and integrated DNA from liver tissues of HBeAg (+) and (-) CHB participants with serum virological parameters and intrahepatic HBcAg and HBsAg immunostaining patterns.

Method: Liver tissues from untreated CHB participants of the North American Hepatitis B Research Network (HBRN) were evaluated. For cccDNA analysis, DNA prep was heat denatured and digested by plasmid-safe ATP-dependent DNase (PSAD) to remove rcdNA and integrated DNA prior to qPCR quantification. Mitochondrial DNA COX3 gene qPCR was used for cccDNA normalization. For integrated DNA detection, 100 ng of total DNA was subjected to HBV-enriched next generation sequencing (NGS) assay. Enriched DNA library was sequenced by Illumina Miniseq. The resulting HBV-host junction sequences were identified by ChimericSeq. Integrated DNA quantity was estimated based on percent of HBV-host junction reads per HBV reads and HBV sequence distribution. Serum HBV RNA was measured by Abbott research assay, HBcrAg by Fujirebio Europe, and qHBsAg by Roche Diagnostics’ Elecsys platform.

Results: The cohort [24 HBeAg (+), 32 HBeAg (-)] was predominantly Asian (75%) with mean age of 44 years. The intrahepatic cccDNA, serum HBV DNA, RNA, HBcrAg and qHBsAg were higher among the HBeAg (+) participants (Table). HBeAg (-) vs. (+) participants had larger proportion of integrated HBV DNA in liver (Figure). There were significant Pearson’s correlations between cccDNA and serum RNA [r = .53, p < .001] and HBcrAg [r = .41, p = .002]. The correlations between serum DNA and RNA were strong among both HBeAg (+) and (-) CHB (Table). Correlations between serum qHBsAg levels with serum DNA or RNA were moderate for HBeAg (+) but very weak for HBeAg (-) participants (Table). The majority [88%] of HBeAg (+) samples had positive intrahepatic HBsAg stain compared to 13% of HBeAg (-) samples. In contrast, 96% of HBeAg (+) and 88% of HBeAg (-) livers had positive HBsAg stain. Granular cytoplasmic HBsAg staining was noted in 57% and 64% of HBeAg (+) and (-) livers respectively. Membranous HBsAg stain pattern was noted in only 14% of HBeAg (-) compared to 78% of HBeAg (+) samples. There was a significant inverse relationship between HBV RNA and integrated HBV DNA that may explain the low level of membranous HBsAg stain in HBeAg (-) livers.

Conclusion: Serum RNA and HBcrAg reflect the intrahepatic cccDNA concentrations. Participants with HBeAg (-) CHB had high levels of integrated HBV DNA in the liver. The HBsAg derived from the integrated DNA likely contributed to the discordant serum DNA and RNA correlations to qHBsAg and the HBsAg immunostaining patterns in HBeAg (-) participants. These findings are important for the design and monitoring of therapies aiming for HBV functional cure.
Method: Liver tissue from C57Bl/6 and HBV-transgenic mouse strains (tg[Alb1HBV][44Bri [Alb/HBs], tg1.4HBV-s-mut and tg1.4HBV-s-rec [F1 generation Alb/HBs×tg1.4HBV-s-mut]) was analysed using transmission electron microscopy (TEM). HBV replication was characterized on RNA and protein level. All-in-one liver cell preparation enabled extraction of primary murine hepatocytes, liver sinusoidal endothelial cells and Kupffer cells and remaining non-parenchymal cells (rNPC). Responsiveness to poly(I:C) treatment (Tlr3) and transfection (Rig-I) was determined using quantitative RT-PCR and multiplex-based cytokine assay.

Results: TEM visualised viral particles (tg1.4HBV-s-rec), nuclear spot formations (tg1.4HBV-s-mut and tg1.4HBV-s-rec) and malformation of the endoplasmic reticulum (Alb/HBs). Viral replication did not differ comparing tg1.4HBV-s-rec and tg1.4HBV-s-mut, except HBsAg levels. A distinct cell type-dependent and mouse strain-dependent gene expression pattern for interferon (Ifnb, Ifi15), cytokine (Tnf, Il1b, Il10) and chemokine (Ccl2, Ccl5) was observed by quantitative RT-PCR and validated using a multiplex-based cytokine assay. Emphasizing that tg1.4HBV-s-rec-derived liver cells responded to poly(I:C) with significantly suppressed expression levels, compared to the other mouse strains. Contrary, rNPC of tg1.4HBV-s-rec mice showed the highest induction for Il10, Tnf, Il1b and Ccl5 in response to poly(I:C). In all HBV-transgenic mice, the induction of Ccl2 was significant lower in PMH but increased in rNPC.

Conclusion: Production of HBV particles and release of HBsAg in tg1.4HBV-s-rec mice led to suppressed hepatic Tlr3 and Rig-I signaling. However, rNPC seemed be more potent in producing poly(I:C)-induced inflammatory cytokines.

THU343 Profiling at single hepatocyte level indicates variance in viral replication associated with HBeAg status in chronic hepatitis B patients

Alfonso Blázquez-Moreno1, Nadia Neto1, Hinrich Göhlmann1, Cheng-Yuan Peng2,3,3, Jeroen Aerssens1, Janssen Research and Development, Beerse, Belgium; CMIUH (China Medical University Hospital), Taichung, Taiwan, China; China Medical University, School of Medicine, Taiwan

Email: mtueffe1@its.jnj.com

Background and aims: Chronic infection with hepatitis B virus (CHB) is characterized by heterogeneity of viral replication across hepatocytes. Here we report on an approach that assesses multiple viral parameters at one single hepatocyte level: status of hepatitis B virus (HBV) surface antigen (HBsAg) and core antigen (HbcAg), presence of covalently closed circular DNA (cccDNA) and quantification of HBV RNA. We applied this method to liver biopsy samples collected from 7 treatment-naive male patients covering for HBV e-antigen (HBeAg) positive (n = 4) and negative (n = 3) CHB phases.

Method: Cryosections from the liver core biopsies were fluorescently stained for 4′, 6-diamidino-2-phenylindole (DAPI), cytokeratin 18 (CK18), HBsAg and adjacent HbcAg. For each patient, up to 96 (range 60–96, average 85) individual hepatocytes (DAPI and CK18 positive) were randomly collected using a RareCyte Finder II, separately deposited into tubes and subjected to simultaneous DNA and RNA extraction using DNA/RNA Zymo columns. HBV RNA and cccDNA, together with mitochondrial RNA and DNA as positive controls, were measured using the Bio-Rad digital droplet polymerase chain reaction system.

Results: HBeAg (+) vs HBeAg (-) patients showed contrasted expression of viral markers, with higher percentages of individual hepatocytes positive for HBsAg (median: 88% vs 16%), HbcAg (median: 82% vs 1%), HBV RNA (94% vs 21%) and cccDNA (37% vs 17%). The percentage of infected hepatocytes (positive hepatocytes for either cccDNA, RNA or HBsAg) was higher in HBeAg (+) vs HBeAg (-) patients (median: 99% vs 53%). Quantitative assessment of HBV RNA demonstrated that expression levels within individual hepatocytes was higher in HBeAg (+) vs HBeAg (-) patients (median: 84 vs 0 HBV RNA counts/cell). Within HBeAg (+) subjects, cccDNA-positive hepatocytes showed higher transcriptomic activity (median: 87 vs 72 RNA counts/cell) than cccDNA-negative hepatocytes, compared to HBeAg (-) subjects (median: 0 vs 0 RNA counts/cell). Interestingly, CHB patients with lower (<300 IU/ml) peripheral HBsAg levels had also the lowest proportion of HBsAg (+) hepatocytes (<32%), whereas patients with peripheral HBsAg levels >1000 IU/ml showed large variation in percentage of HBsAg (+) (range 31–100%). Peripheral levels of HBV DNA or alanine aminotransferase were not associated with any of the hepatocyte-derived readouts.

Conclusion: We demonstrated that CHB patients at different stages of disease show diverse profiles of viral markers measured at single hepatocyte level.

THU344 Human stem cell-derived hepatocytes as a model for hepatitis D virus infection

Huanting Chu1,2, Bingqian Qu1, Angga Prawira1, Lars Maurrer1, Rebecca Fu1, Florian Lempp1, Charlotte Decker1, Zhenfeng Zhang1, Dirk Grimm1,2,3, Viet Loan Dao Th1,2, Stephan Urban1,3, University Hospital Heidelberg, Department of Infectious Diseases; German Centre for Infection Research (DZIF), Partner Site Heidelberg

Email: chihuanting@gmail.com

Background and aims: An estimated 12–15 million people worldwide are suffering from chronic hepatitis D virus (HDV) infection without a curative therapeutic regimen so far. Primary human hepatocytes represent the most physiological model for HDV research, but their application is restricted. Hepatoma cells can also support the entire HDV life cycle via gene editing techniques, but they only partially resemble hepatocytes due to their aberrant nature. Recently, human pluripotent stem-cell derived hepatocyte-like cells (HLCs) have been proposed as an attractive cell culture system for hepatitis B, C, and E viruses. Here, we show that HLCs support the entire HDV life cycle and propose this model as a new platform for the study of HDV biology and the evaluation of antiviral treatments.

Method: We optimized a stem cell-based differentiation protocol which yields HDV-permissive HLCs (Fig A). Mature HLCs were inoculated with HDV in the presence of 4% Polyethylene Glycol 8000 (PEG8000) and 1.5% dimethyl sulfoxide (DMSO), with samples being harvested for immunofluorescence and quantitative RT-PCR analysis. Adeno-associated viruses (AAVs) encoding hepatitis B virus S antigen (HBsAg) were transduced to HDV infected HLCs for viral assembly and secretion. The supernatant was taken to subsequently infect HuH7 cells to determine infectivity of secreted HDV particles.
Hepatitis B viral load variation between the first and third trimesters of pregnancy

Stuart Gallacher1, Alan Yeung2,3, Megan Glancy2,3, Ewan Forrest4, Stephen Barclay1, 1NHS Greater Glasgow and Clyde, Department of Infectious Diseases, Brownlee Centre, Glasgow, United Kingdom; 2Glasgow Caledonian University, School of Health and Life Sciences, Glasgow, United Kingdom; 3Public Health Scotland, Glasgow, United Kingdom; 4NHS Greater Glasgow and Clyde, Department of Gastroenterology, Glasgow Royal Infirmary, Glasgnow, United Kingdom Email: stuart.gallacher3@nhs.scot

Background and aims: Hepatitis B virus (HBV) infection may be transmitted vertically, with maternal HBV viral load (VL) >5.3 log10 IU/ml may prevent unnecessary treatment.

Results: HBV infection of HLCs was assessed by measuring HDV RNA by quantitative RT-PCR and immunofluorescence staining of delta antigen (HDAg) (Fig B and C). HDV infection could be completely blocked by Myrcludex B, suggesting NTCP-dependent entry in HLCs. In agreement, staining with Atto565-NHS-ester-coupled Myrcludex B (Fig D) is consistent with the HDV-induced HLCs assembled and released infectious HDV progeny particles, showing that HLCs can recapitulate the entire HDV life cycle (Fig E and F). We further found that HLCs could be infected with HDV genotypes 1 from Ethiopia, 2 and 4 from Japan, and 3 from Peru. Finally, HDV infection of HLCs could be inhibited by IFN-α and IFN-λ, treatment (Fig G). Further testing of other antivirals is currently being performed.

Conclusion: HLCs provide an attractive, genetically tractable, and physiologically relevant platform for studying pan-genotype HDV life cycle and evaluating antiviral treatments.

THU345
Hepatitis B viral load variation between the first and third trimesters of pregnancy

Leywun Li1, Peter Revill2, Ran Yan1, Calvin Chan1, Hua Tian1, Julie Ma1, Luisa M Stamm1, Man-Fung Yuen3, Alexander Thompson4, Kathryn M Kitinos1, Assembly Biosciences, South San Francisco, United States; 2Victorian Infectious Diseases Reference Laboratory, Melbourne, Australia; 3The University of Hong Kong, Department of Medicine, Hong Kong, China; 4St Vincent’s Health Australia, Fitzroy, VIC, Australia Email: lewynl@assemblybio.com

Background and aims: Vebicorv (VBR) is a first-generation core inhibitor being developed for the treatment of chronic hepatitis B virus infection (CHBV). In Study 202 (NCT03577171), treatment-naïve HBeAg positive CHBV patients were randomized to VBR+entecavir (ETV) or placebo+ETV for 24 weeks. Eligible patients then received open label VBR+ETV in Study 211 (NCT03780543) for ≥52 weeks. In Study 211, 19 patients discontinued (Dced) VBR and remained on ETV at end of study. Following VBR DC, a mean HBV DNA increase of 1.0 log10 IU/ml was observed, with 11/19 patients having a maximal increase of >1 log10 IU/ml. Here we further characterize the patients who Dced VBR and remained on ETV and describe the results of next
generation sequencing (NGS) analyses to characterize viral quasispecies during treatment.

**Method:** Viral nucleic acids were purified from Study 202 baseline (BL), Week (Wk) 4, and rebound (if possible) patient plasma and whole genome NGS (Illumina MiSeq) was conducted. 18/19 patients had NGS data available: 11 with ≥1 log_{10} IU/ml HBV DNA maximal increase and 7 with <1 log_{10} IU/ml HBV DNA maximal increase after VBR DC. To determine sequence diversity, Shannon entropy was calculated from demultiplexed FASTQ read files using an in-house pipeline with genotype-specific reference sequences. The pipeline includes data quality control, read trimming and alignment, variant calling, and annotation in a workflow orchestrated by Nextflow. The pipeline calculated from demultiplexed FASTQ read files using an in-house pipeline with genotype-specific reference sequences. The pipeline includes data quality control, read trimming and alignment, variant calling, and annotation in a workflow orchestrated by Nextflow.

**Results:** Patients with <1 log_{10} IU/ml HBV DNA increase had significantly lower HBeAg and HBcAg (p < 0.05) and trended lower for HBV DNA and pregenomic RNA with most having ALT >ULN at BL compared to patients with ≥1 log_{10} IU/ml HBV DNA increase. At BL, similar diversity levels were observed across the viral genome in both groups. At Wk 4, diversity remained stable for patients with <1 log_{10} IU/ml HBV DNA increases, while diversity increased at Wk 4 for patients with ≥1 log_{10} IU/ml HBV DNA increases (p < 0.01) (Figure). For patients with ≥1 log_{10} IU/ml HBV DNA increase, diversity returned towards BL levels at rebound following VBR DC.

**Conclusion:** Greater sequence diversity was observed during initial HBV DNA decline during HBV treatment among patients with lower rebound when VBR was DCed and ETV continued. The early differences in sequence diversity may reflect differences in HBV specific immune responses (also reflected in ALT levels) and viral load set points between these 2 groups, although the mechanism needs to be further defined.

**Background and aims:** The country of Georgia launched its national Hepatitis C Virus (HCV) Elimination Program in 2015, and a serosurvey the same year showed prevalence of HCV antibody (anti-HCV) and HCV RNA among adults aged ≥18 years was 7.7%, and 5.4%, respectively. Since then, over 76,000 people with chronic HCV have been treated, with a cure rate of 98.9%. To monitor progress, a second serosurvey was conducted in 2021 to estimate the prevalence of hepatitis C, hepatitis B, and anti-SARS-CoV-2. This analysis reports hepatitis C results of the serosurvey and progress towards elimination.

**Method:** The serosurvey used a stratified, multi-stage cluster design with systematic sampling. Adults and children ≥5 years consenting (or assenting with parental consent) to the interview and blood draw were eligible to participate. All blood samples were tested for anti-HCV and if positive, HCV RNA. Nationally representative weighted proportions and 95% confidence intervals (CI) were calculated and compared with 2015 age-adjusted estimates for adults.

**Results:** A total of 7,237 adults and 1,473 children participated in the survey. For adults, the median age was 46 years (interquartile range: 32–60), and 53.3% (95% CI: 51.3–55.2) were female. The prevalence of anti-HCV was 6.8% (95% CI: 5.9–7.7), which was not significantly different from 2015 (7.7% [95% CI: 6.6–8.8]; p = 0.20). The HCV RNA prevalence was 1.8% (95% CI: 1.3–2.4), compared to 5.4% [95% CI: 4.5–6.3] in 2015 (p < 0.001). This represents a 67% reduction in persons with chronic HCV infection, despite the program having treated 51% of the estimated 150,000 infected. HCV RNA prevalence decreased among all age groups, most notably among those aged 40–59 years (9.3% in 2015 to 2.2% in 2021; p < 0.001). Substantial decreases were also observed among both males (9.0% to 3.1%; p < 0.001) and females (2.2% to 0.6%; p < 0.001). HCV RNA prevalence also decreased from 51.1% to 17.8% among persons who ever injected drugs, and 13.1% to 3.8% among those who received a blood transfusion (both p < 0.001). No children tested positive for anti-HCV or HCV RNA.

**Conclusion:** These results demonstrate the substantial progress made since Georgia launched its HCV Elimination Program in 2015. The 67% reduction in chronic HCV infections during 2015–2021 also supports treatment as a means for prevention, as the reduction is larger than would be expected based on those treated alone. These findings can inform strategies to meet HCV elimination targets.
Background and aims: Previous analysis showed that central nervous system drugs were the most prescribed in patients with hepatitis C. This sub-analysis describes the use, drug-drug interactions (DDIs), and clinical impact of antipsychotic use in real-world patients treated with Pangenotypic Direct Action Antivirals (DAAP).

Method: Retrospective observational study, using the BIG-PAC database (Atrys Health), in HCV patients treated from 2017 to 2020 with DAAs. Potential DDIs between concomitant medication and the DAAs, Sofosbuvir/Velpatasvir [SOF/VEL] and Glecaprevir/Pibrentasvir [GLE/PIB], were evaluated using the University of Liverpool Hepatitis Interactions database. The risk of DDIs, the report of related adverse effects (AEs), and the clinical actions linked to the management of DDIs with antipsychotics (dose reduction; change of antipsychotic or pDAAs) compared to SOF/VEL, [73% vs 43% of patients (p < 0.001)] were analyzed. Regarding antipsychotics, there was a higher number of active ingredients with potential DDIs for GLE/PIB vs SOF/VEL (6 vs 2, respectively), linked to a higher percentage of patients at risk of DDIs (51% vs 23%, p < 0.001, respectively). Two AE were reported with GLE/PIB for quetiapine and paliperidone, and none with SOF/VEL. The AE reported with quetiapine and GLE/PIB (extrapyramidal symptoms) occurred at a dose of <300 mg/day.

Results: 187 patients prescribed antipsychotics were included, 150 treated with SOF/VEL [median age: 53 years; men: 59%; F3/4: 44%] and 37 with GLE/PIB [median age 48 years; men: 60%; F3/4: 46%]. The mean pill number was 5.0 and 5.9 tablets/patient, respectively. Accounting for all comedication, GLE/PIB was associated with a higher risk of single and multiple DDIs (>2 comedations with DDIs with pDAAs) compared to SOF/VEL, [73% vs 43% of patients (p < 0.001)] and [24% vs 15% (p = 0.002)], respectively.

Regarding antipsychotics, there was a higher number of active ingredients with potential DDIs for GLE/PIB vs SOF/VEL (6 vs 2, respectively), linked to a higher percentage of patients at risk of DDIs (51% vs 23%, p < 0.001, respectively). Two AE were reported with GLE/PIB for quetiapine and paliperidone, and none with SOF/VEL. The AE reported with quetiapine and GLE/PIB (extrapyramidal symptoms) occurred at a dose of <300 mg/day.

Conclusion: This analysis confirms that the greater use of SOF/VEL in patients with antipsychotic treatment may be due to its favorable DDI profile, which implies a lower number of adverse effects and required clinical actions.
Viral hepatitis A/E: Clinical aspects

THU353
Detection of highly variable RNA-containing viral particles on CNT-based electrochemical impedimetric DNA-nanosensors
Andrei Babenka1, Victor Hyharovitch1, Halina Grushevskaya2, Igor Lipnevich3, Nina Krylova4, Elena Lebedeva5, Uladzimir Davydau6, Svetlana Marchuk1, Dmitry Borisovets7, Sergei Zhavoronok1, 2Belarusian State Medical University, Minsk, Belarus; 3Belarusian State University, Minsk, Belarus; 4Vitebsk State Medical University, Viciebsk, Belarus; 5Institute of Experimental Veterinary Medicine named after S.N. Vyshelessky, Minsk, Belarus
Email: labmdbt@gmail.com

Background and aims: Due to the high variability of RNA-containing viruses genome, neither PCR nor ELISA methods give a 100% guarantee. For example, in the case of infection with the hepatitis E virus (HEV), the likelihood of a false negative diagnosis is considered very high. One of the possible ways to overcome this problem in general and for the diagnosis of HEV in particular, may be the use of alternative, non-PCR technologies. CNT-based electrochemical impedimetric DNA-nanosensors make it possible to recognize HEV RNA/cDNA using short probes (less than 20 bp), which sharply increases the likelihood of capturing variable genomes. This ensures high specificity of recognition. We offer a novel highly-performed and selective impedimetric DNA sensor with redox-active nanoporous transducer based on bundles of carbon nanotubes (CNTs) for diagnosing of HEV RNA in clinical samples.

Method: A target double-stranded (ds) cDNA was synthesized by reverse transcription of the total RNA isolated by standard commercial spin-column based kits from the whole blood, serum, feces and urine of patients with confirmed acute HEV diagnosis. A non faradaic impedimetric DNA-sensor is fabricated by depositing the two most conserved region of the HEV genome and, according to preliminary estimates, is able to recognize about 99% of all sequences.

Conclusion: In untreated chronic hepatitis D, HDV-RNA and HBsAg levels show positive correlation mostly in younger people. Normal ALT levels are associated with significantly increased HBsAg levels. Monitoring of HDV-RNA and HBsAg serum levels in patients with chronic hepatitis D provides insight in the design of new therapeutic strategies.
of the HEV genome presented in the GeneBank database (more than 500) and sequenced in Belarus (more than 100). DNA-nanosensors are interdigital electrode structures with the sensitive coating. The electron-dense layers of the probe oligonucleotide and CNTs were fabricated by Langmuir-Blodgett technique. The impedance DNA-nanosensors are utilized as measured capacitance C entering a resistor (R) -capacitor (C) -oscillator. Impedance measurements are performed using the non faradaic impedance spectroscopy at quasi-resonance frequencies of the RC-oscillator.

Results: The capacitive characteristics of the DNA sensors in the frequency range from 100 kHz to 1 MHz after hybridization with targeted DNA at various concentrations have been investigated. It was found that the addition of molten target DNA at low concentrations leads to a significant decrease in capacity over the entire frequency range. Interacting the probe ss-DNA and target ss-cDNA molecules form homoduplexes on the sensor surface that leads to increasing the electron density of the nucleotide CNT-cover, providing capacity reduction due to an emerging screening surface effect.

Conclusion: The novel highly-performed and high-sensitive electrochemical method reliably detects the presence or absence of HEV in a sample in dose-dependent manner and does not demand expensive consumable materials.

THU352
Hepatitis B Delta: assessment of knowledge and practices of French non academic hepatogastroenterologists
Jean-François David Cadranel1, Honore Zougmore1, Bertrand Hanslik1, Jean-René Ngele1, Xavier Gausse1, Denis Ouzan4, Thierry Thévenot6, Philippe Halton5, Dominique Roulot1, Veronique Loustaud-Ratti2, Tristan Lemagoarou1, GHPSO DE CREIL, liver and diseases department, CREIL, France; 2Hospital Center Régional D’Orléans Hospital La Source, liver and diseases department, Orléans, France; 3Arnault Institute Tzanck, liver and diseases department, Saint-Laurent-du-Var, France; 4Centre hospitalier régional universitaire de Besançon, liver and diseases department, Besançon, France; 5liver and INFECTIOUS diseases department, MARSEILLE, France; 6liver and DIGESTIVE diseases department, bobigny, France; 7liver and ANDF DIGESTIVE diseases department, limoges, France; 8GHPSO DE CREIL, DIM, Creil, France
Email: jcadranel5@gmail.com

Background and aims: Hepatitis B virus (HBV) and Hepatitis delta virus (HDV) are a global public health problem. HDV infection is a complication of HBV infection and can cause more severe liver disease, including cirrhosis and hepatocellular carcinoma. This study was conducted in France (Ile-de-France) to evaluate the knowledge and practices concerning the diagnosis and treatment of HBV and HDV among HGEs practicing in non-academic settings.

Method: A Google form questionnaire was sent to senior or junior non-academic from May to September. The following data were evaluated: demographic data, predominant specialty, status, modality of diagnosis and treatment of BD hepatitis among HGs practicing in non-academic settings.

Results: 129 HGs (H 58, 1%) of age : 44, 8 (13, 4) answered this survey. The search for delta infection in all HBs antigen positive pts was performed by 89.1% of HGs and by 10%: juniors 77.8%, seniors 84.4%, p = 0.009; in any pts carrying HBs antigen with anti HBe: juniors 67%, seniors 92%, p = 0.002, in any pts infected with HIV (juniors 83.8%, seniors 95.4%, p = 0.064. Concerning fibrosis assessment, among the non-invasive markers of fibrosis: the fibrotest was never used by 47% of the respondents, the fibrometer was never used by 55% of the respondents. APRI and FIB 4 were not used; the delta fibrosis score adapted to hepatitis Delta was used by 13% of the HGE. Fibrosis assessment was mainly done by Fibroscan® in 77% of cases and liver biopsy in 81% of cases. Treatment was proposed for patients >F2 in 49% of cases, whatever the transaminase level, and for all patients by 35% of the Gs. The HGE proposed treatment with pegylated interferon in 48.4% of cases, Buleviride in 43% of cases, and a combination of the two in 42% of cases. Half of the HGs referred their patients to an academic colleague. Among the criteria for treatment efficacy, a decrease or normalization of transaminases was retained by 84% of the HGs; 60% of the HGs defined VR by a cancellation or a 2-log decrease of viral replication; and a PVR by a disappearance of RNA after 12 (45.4%) or 24 months (16%) with normal transaminase activity. Discussion: The number of respondents to this survey is low despite the number of reminders, reflecting the rarity of the disease or its lack of awareness in non-academic settings, HGs often refer their patients to another colleague, the search for BD infection is not systematically performed, elastometry and liver biopsy are most often used to assess fibrosis.

Conclusion: The results of this survey show a certain degree of ignorance of BD hepatitis by non-academic HGs; the modalities of diagnosis and the need for systematic screening of BD infection in any HBsAg patient should be recalled by the learned societies.
**THU354**  
Microarray analysis of virus-specific IgM and IgG antibodies significantly improves the serological diagnosis of hepatitis E virus infection  
David Springer¹, Christian Borsodi², Stephan Aberte³,  
Lukas Weseslindtner¹.  
¹Medical University of Vienna, Center for Virology, Vienna, Austria  
Email: lukas.weseslindtner@meduniwien.ac.at

**Background and aims:** Due to the limited availability of PCR, the rapid decrease of viral RNA in the blood, and the possibility of unspecific reactivity in serological assays, the laboratory diagnosis of hepatitis E virus (HEV) infection remains challenging. Therefore, we evaluated a commercial microarray for HEV-specific IgM and IgG antibodies featuring nine target antigens (HEV Virachip<sup>®</sup>, Viramed).  

**Method:** The evaluation panel comprised 408 serum samples first characterized by HEV-PCR (in-house) and Anti-HEV- IgM- and IgG-ELISAs (Wantai-HEV-IgG/IgM ELISA<sup>®</sup>, Wantai Biological Pharmacy Ent). Based on these results and additional IgG avidity testing, samples were staged as early viremic (serum PCR+, IgM+; IgG 2; n = 94), progressed non-viremic (serum PCR-, IgM+, IgG+; n = 80) and past HEV infection (PCR-, IgM-, IgG+; n = 117). Additional 117 samples negative for all HEV parameters served as controls.  

**Results:** Microarray results significantly concurred with the ELISAs in 94.8% of IgM positive and 97.7% of IgG positive samples, indicating a high concordance of the applied serological assays. However, IgM and IgG antibodies against specific antigens included in the microarray (e. g., IgM and IgG against O2–1C4 and O2-1N, respectively) were earlier detectable in 14.9% of still ELISA-IgM negative and 35.3% of ELISA-IgG negative samples. In addition, samples with negative PCR but positive IgM ELISA results (progressed HEV infection) were reliably identified as HEV infection by the microarray and constituted a specific infection stage based on the serological microarray profile. Finally, we calculated an algorithm to identify HEV infection (with PCR positivity as reference) with the highest accuracy using all serological parameters provided by the microarray (ROC-AUC 0.90, p <0.005).  

**Conclusion:** Microarray analysis of HEV-specific IgM and IgG antibodies displays high sensitivity to diagnose HEV infection, especially in the early phase of the infection, and identifies the progressed infection stage when PCR from serum already tests negative.

**Viral hepatitis B/D: Clinical aspects except therapy**

**THU355**  
Hepatitis delta virus reflex testing in patients with hepatitis B improves the HDV screening cascade: 10 years of real-world experience from Avicenne University Hospital, France  
Segolene Brichler1,2,3, Dominique Roulot1,2,3,4, Samira Dziri1,3,  
1Avicenne Hospital, AP-HP, Bobigny, France; 2Paris Nord University, Bobigny, France; 3INSERM U955, Creteil, France; 4Avicenne Hospital, AP-HP, Hepatology Unit, Bobigny, France  
Email: segolene.brichler@aphp.fr

**Background and aims:** Due to the limited availability of PCR, the rapid decrease of viral RNA in the blood, and the possibility of unspecific reactivity in serological assays, the laboratory diagnosis of hepatitis E virus (HEV) infection remains challenging. Therefore, we evaluated a commercial microarray for HEV-specific IgM and IgG antibodies featuring nine target antigens (HEV Virachip<sup>®</sup>, Viramed).  

**Method:** The evaluation panel comprised 408 serum samples first characterized by HEV-PCR (in-house) and Anti-HEV- IgM- and IgG-ELISAs (Wantai-HEV-IgG/IgM ELISA<sup>®</sup>, Wantai Biological Pharmacy Ent). Based on these results and additional IgG avidity testing, samples were staged as early viremic (serum PCR+, IgM+; IgG 2; n = 94), progressed non-viremic (serum PCR-, IgM+, IgG+; n = 80) and past HEV infection (PCR-, IgM-, IgG+; n = 117). Additional 117 samples negative for all HEV parameters served as controls.  

**Results:** Microarray results significantly concurred with the ELISAs in 94.8% of IgM positive and 97.7% of IgG positive samples, indicating a high concordance of the applied serological assays. However, IgM and IgG antibodies against specific antigens included in the microarray (e. g., IgM and IgG against O2–1C4 and O2-1N, respectively) were earlier detectable in 14.9% of still ELISA-IgM negative and 35.3% of ELISA-IgG negative samples. In addition, samples with negative PCR but positive IgM ELISA results (progressed HEV infection) were reliably identified as HEV infection by the microarray and constituted a specific infection stage based on the serological microarray profile. Finally, we calculated an algorithm to identify HEV infection (with PCR positivity as reference) with the highest accuracy using all serological parameters provided by the microarray (ROC-AUC 0.90, p <0.005).  

**Conclusion:** Microarray analysis of HEV-specific IgM and IgG antibodies displays high sensitivity to diagnose HEV infection, especially in the early phase of the infection, and identifies the progressed infection stage when PCR from serum already tests negative.

**THU356**  
T cell epitope mapping of hepatitis B virus in chronic infection  
Marie Viau<sup>1</sup>, Marianne Tuelfer<sup>2</sup>, Christina Heeke<sup>1</sup>, Kamilla Kjærgaard Munk<sup>1</sup>, Mohammad Kadivar<sup>1</sup>, Georg Lauër<sup>2</sup>, Jacques Bollekens<sup>3</sup>, Sine Reker Hadrup<sup>2</sup>,  
<sup>1</sup>Technical University of Denmark, Department of Health Technology, Kgs. Lyngby, Denmark;  
<sup>2</sup>Janssen Pharmaceuticals, Infectious Diseases and Vaccines, Beerse, Belgium;  
<sup>3</sup>Massachusetts General Hospital, Department of Medicine, Boston, United States  
Email: macviu@dtu.dk

**Background and aims:** Affecting more than 250 million patients worldwide, chronic hepatitis B virus (HBV) infection still poses a substantial global health threat, without available curative therapy. CD8 T cells are known to be crucial for the elimination of the virus, however, in chronically infected patients, the cellular immune response proves inefficient. Thus, uncovering the full repertoire of HBV epitopes and functionality of the HBV-specific CD8 T cells is highly relevant for understanding the immune response. Identification of HBV epitopes recognized by T cells has historically been limited to few HLA types and selected viral proteins. Here, we have performed a large-scale screening covering HBV genotypes A-H to identify T cell recognition restricted by 12 different HLA molecules, in patients with acute and chronic hepatitis. This data is substantially extending the present knowledge about the T cell recognition of HBV.

**Method:** A library of >1, 900 peptide-MHC combinations was used extending the present knowledge about the T cell recognition of HBV.

**Conclusion:** T cell epitope mapping of hepatitis B virus in chronic infection
selecting specific 8–11mers from HBV genotypes A-H, predicted to bind to 12 different HLA types.

**Results:** Performing the large-scale multimer screening we found a total of 212 unique peptide-MHC, which were recognized by CD8 T cells across all patient groups. Out of these, 189 peptide-MHC have not previously been described. Furthermore, 45% of the peptide-MHCs were recognized in multiple patients. T cell recognition was detected in both acute and chronic patients, with no significant difference observed between chronic and HBsAg loss patients. Interestingly, T cells recognizing the identified peptides display different level of functional responses upon peptide stimulation, which will be further investigated.

**THU357**

The Comparison of tenofovir alafenamide fumurate with tenofovir disoproxil fumarate in preventing hepatitis B transmission in mothers with high viral load: a retrospective cohort study

Yunxia Zhu1, Jinhua Wang2, Ming Wang2, Xin Zhou1, Shuangxia Zhang1, Shujie Zhang1, Bo Yang1, Pinge Yang1, Zhongjie Hu3.

1Beijing Youan Hospital, Capital Medical University, Obstetrics and Gynecology, Beijing, China; 2Beijing Obstetrics and Gynecology Hospital, Capital Medical University, Department of Gynecologic Oncology, Beijing, China; 3Beijing Youan Hospital, Capital Medical University, Hepatology, Beijing, China

Email: zyxnon7@163.com

**Background and aims:** Tenofovir disoproxil fumarate (TDF) is most commonly utilized in the prevention of maternal-to-child transmission of the hepatitis B virus. The previous studies show antiviral prophylaxis with tenofovir alafenamide fumurate (TAF) was also generally safe for both mothers and infants and reduced the mother-to-child transmission (MTCT) rate to 0%. However, few safety and effectiveness results have been published regarding the comparison of two drugs during pregnancy for the prevention of MTCT of HBV, especially for the early markers of bone metabolism like alkaline phosphatase (ALP) and Z value for bone mineral density (BMD) of infants.

**Method:** We performed a prospective cohort study involving women who had HBV DNA ≥2010^5 IU/ml and initiated TAF or TDF for preventing MTCT during gestational weeks 24–28 weeks. All enrolled patients had normal liver function and had not received antiviral therapy before pregnancy. We collected the name, ID, age, and drug duration of the maternal, monitoring HBV viral load and ALP at the same time besides infants’ HBV marks and their Z value for BMD. The primary outcomes were the decrease in virus load and the rates for MTCT, which was defined as the proportion of infants who had a serum HBV DNA level of more than 20 IU per milliliter (i.e., above the lower limit of detection) or who were positive for hepatitis B surface antigen (HBsAg). The secondary outcomes were the changes in serum ALP expression of the mother and the BMD of newborns.

**Results:** A total of 61 patients received TAF treatment and 73 patients received TDF.1 pairs of patients were matched by Propensity Score Match (PSM). The levels of HBV-DNA decline in TDF-treated mothers were compared to TAF treated mothers (3.70 ± 0.91 log10IU/ml vs 3.43 ± 1.30 log10IU/ml, P > 0.05) before delivery. The rates of MTCT in the TAF group were similar to the TDF group (with the transmission of 0.00% [0 of 39] vs 0.00% [0 of 29], p > 0.05) in the per-protocol analysis. As for BMD, no significant difference in the Z value of newborns was found between the two groups. However, the expression level of ALP was significantly higher in the TDF group than TAF group.

**Conclusion:** TDF and TAF use in MTCT for highly viremic mothers was equally effective and the study showed both two drugs have no statistically different effect on neonatal BMD. However, TAF has less influence on serum ALP in pregnant women than TDF.

**THU358**

Detection of notable hepatitis B virus serologic activity after hepatitis B surface antigen seroclearance

Danny Ka-Ho Wong1,2, Takako Inoue3, Lung Yi Loey Mak1,2, Yan Yue James Fung1,2, Ka-Shing Cheung1, Wai-Kay Seto1,2, Yasuhiro Tanaka4, Man-Fung Yuen1,2, The University of Hong Kong, Medicine, Hong Kong; 3The University of Hong Kong, State Key Laboratory of Liver Research, Hong Kong; 4Nagoya City University Hospital, Clinical Laboratory Medicine, Nagoya, Japan; 5Kumamoto University, Gastroenterology and Hepatology, Kumamoto, Japan

Email: dannykhwong@gmail.com

**Background and aims:** Undetectable serum hepatitis B surface antigen (HBsAg) measured by conventional assays (lower limit of detection ~0.05 IU/ml) is regarded as functional cure to chronic hepatitis B (CHB). It has been demonstrated that some HBV proteins are detectable in hepatocytes after HBsAg seroclearance (SC). We evaluated the use of two novel investigational assays to detect hepatitis B core-related antigen (HBcAg) and HBsAg in serial patient samples collected before and after SC.

**Method:** Serum samples were collected from 98 CHB patients (72 males and 26 females) with SC at the following 7 time-points: 5 years and 3 years before SC, at the time of SC, and 1 year, 3 years, 5 years and 10 years after SC. HBsAg and HBcAg were measured using the iTACT-(stands for Immunoassay for Total Antigen including Complex via pre-Treatment)-HBsAg and iTACT-HBcAg assays (Fujirebio, Tokyo, Japan) respectively. The lower limit of quantitation (LLOQ) of the iTACT-HBsAg and iTACT-HBcAg assays are 0.0005 IU/ml and 2.1 log U/ml respectively, which are 100 times and approximately 10 times more sensitive than the current HBsAg and HBcAg assays (LLOQ 3 log U/ml). Anti-HBs was measured by the Lumipulse Presto anti-HBs assay (LLOQ 10 mIU/ml).

**Results:** The median age of SC was 52 years (IQR: 45–57). A total of 572 samples (142 collected before SC and 430 collected after SC) were tested. HBsAg was detectable by iTACT-HBsAg in all the 142 samples collected before SC (median level: 10.9 IU/ml) and in 165/430 (38.4%) samples collected after SC (median level for those with detectable HBsAg: 0.0082 IU/ml). 61.6% of samples collected after SC had detectable anti-HBs. Of these anti-HBs positive samples, 70 (26.4%) had detectable HBsAg, HBcAg was detectable in 78.9% of samples collected after SC and 66.4% after SC. There was a positive correlation between HBsAg and HBcAg levels (r = 0.330, P <
Comparison of on-treatment ALT or FIB-4 as an on-treatment biomarker of hepatitis B treatment for liver cirrhosis patients

Conclusion: The iTACT-HBsAg assay could detect a low level of HBsAg in >20% patients even at 10 years after SC. A relatively stable expression of HBCrAg was also detected in >60% patients after SC. The findings suggested that the threshold of SC may be raised using an ultrasensitive HBCrAg assay and that expression of HBV proteins could still be detected after SC. The association between the expression levels of these proteins and disease progression deserves further studies.

THU359 Comparison of on-treatment ALT or FIB-4 as an on-treatment biomarker of hepatitis B treatment for liver cirrhosis patients

Conclusion: Among HBV-related liver cirrhosis patients who started antiviral therapy, complete virological response and improvement of FIB-4 index at one-year was independently associated with future HCC risk, while ALT normalization and serological biomarkers were not. This indicates HBV DNA and FIB-4 index can be better on-treatment clinical end points of antiviral therapy for cirrhotic patients.

THU360 Liver fibrosis burden determines risk of hepatocellular carcinoma among patients with hepatitis B surface antigen seroclearance

Background and aims: Hepatitis B surface antigen (HBsAg) seroclearance is regarded as functional cure in chronic hepatitis B infection (CHB). We investigated the risk of hepatocellular carcinoma (HCC) in CHB patients after achievement of HBsAg seroclearance.

Method: 337 Asian CHB patients (69.1% male) who developed spontaneous HBsAg seroclearance between April 1996 to October 2012 with retrievable blood samples before HBsAg seroclearance were recruited and prospectively followed up for a median duration of 12.7 (interquartile range [IQR] 9.5–16.2) years. Blood levels of Enhanced Liver Fibrosis (ELF) were determined. Variables of interest included gender, age of HBsAg seroclearance (ageSC), presence of diabetes mellitus (DM), ELF score, and antibody to HBsAg (anti-HBs). Independent risk factors of HCC were determined by univariate then multivariate Cox regression and Kaplan Meier survival analysis.

Results: The median ageSC was 51.6 (IQR 42.6–58.1) years old, and 24.6% patients had DM. ELF at a median interval of 3.4 (IQR 0.4–4.9) years before HBsAg seroclearance was 9.5 (IQR 9.0–10.1). 216/337 (64.1%) developed anti-HBs at a median time of 2.3 (IQR 0–4.0) years after HBsAg seroclearance with median level of 42 (IQR 18–138) ml/l. Nine cases of HCC were diagnosed at a median time of 6.8 (IQR 2.6–7.9) years after HBsAg seroclearance. At Cox regression analysis, ageSC (hazard ratio [HR] univariate: 1.118, multivariate: 1.096, both p < 0.001) and ELF (HR 1.17, p = 0.876) and gender (HR 1.695, p = 0.514) were not significant variables. The area under receiver-operating characteristic curve value for ELF was 0.856 (95% confidence interval [CI] 0.714–0.997, p < 0.001). By maximizing the Youden’s index, ELF <10.8 was associated with lower risk of HCC with 77.8% sensitivity and 90.2% specificity. Among patients with ageSC ≥50 (known to be associated with residual risk of HCC; n = 190), ELF <10.8 before HBsAg seroclearance was associated with >97% reduction in risk of HCC development [Figure 1].
Conclusion: ELF <10.8 was associated with markedly reduced risk of HCC development upon long-term follow-up among CHB patients with ageSC ≥50. Ongoing HCC surveillance is required for patients who achieved HBsAg seroclearance at an older age and had advanced liver fibrosis before HBsAg seroclearance. [Supported by SK Yee Medical Foundation [reference number: 2171213]]

THU361
Estimating the prevalence of hepatitis delta infection among foreign-born adults with chronic hepatitis B in the United States
Robert Wong1, Carol Bros gast, Steven Wong2, Jordan Feld3, Jeffrey Glenn4, Saeed Sadiq Hamid5, Kate Moraras6, John Ward7, Heiner Wedemeyer8, Chihan Yurdaydın9, Robert G. Gish10.
1Stanford University School of Medicine, Veterans Affairs Palo Alto Healthcare System, Palo Alto, United States; 2Immunology Program, University of California San Francisco Parnassus Campus, San Francisco, United States; 3Wong Consulting, LLC, United States; 4University Health Network, Toronto, Canada; 5Stanford University School of Medicine, Stanford, United States; 6Aga Khan University Hospital, Karachi, Pakistan; 7Hepatitis B Foundation, Doylestown, United States; 8UnitedHealthcare Services, United States; 9Hannover Medical School, Department of Gastroenterology, Hepatology and Endocrinology, Germany; 10Koç University School of Medicine, Department of Gastroenterology and Hepatology
Email: rwong123@stanford.edu

Background and aims: Suboptimal awareness and testing for hepatitis delta virus (HDV) infection among adults with chronic hepatitis B (CHB) contributes to the poor understanding of the true prevalence of HDV and appropriate policy development. Our recent study estimated 1.47 million (M) foreign-born (FB) persons with HBsAg were living in the United States (US) in 2018. FB persons with CHB contribute to the majority of the burden of HDV infection in the US, given the high burden of HDV in many world regions from which FB patients emigrate from. This study aims to provide an estimate of HDV prevalence among FB adults with CHB in the US.

Method: We updated analyses of CHB prevalence among FB adults in the US by performing systematic reviews and meta-analyses (surveys published from 1980 to 2019) that combined country-specific CHB prevalence rates with number of FB living in the US in 2019 by US Census Bureau. To estimate HDV prevalence among FB adults with CHB, we combined country-specific HDV prevalence rates (anti-HDV or HDV RNA positive) for persons with CHB from meta-analyses and applied these estimates to the number of FB with CHB in the US by country of birth to estimate the number of FB CHB patients with combined HDV infection.

Results: In 2019, the overall FB population in the US was 48.0M, among which the estimated prevalence of CHB was 3.10% (95% CI 2.98–3.23), resulting in 1.49M (95% CI 1.33–1.66) FB adults with CHB, which accounts for nearly 80% of all adults with CHB in the US. Among FB adults with CHB, overall estimated pooled prevalence of HDV infection was 9.22% (95% CI 9.00–9.44), resulting in 137,158 FB CHB adults with HDV (95% CI 129,366–145,949). World region-specific estimates of HDV infection among adults with CHB were 8.73% in Asia, 6.98% in the Americas, 22.52% in Oceania, 11.18% in Africa, and 14.08% in Europe. Representing 76,817 (Asia), 19,327 (Americas), 2,789 (Oceania), 25,442 (Africa), and 12,782 (Europe), FB CHB adults with HDV infection in the US.

Conclusion: This analysis provides an estimate of the number of FB adults with CHB living in the US who are also infected with HDV, which is expected to further grow with patterns of increased immigration into the US. The burden of HDV will be even greater when factoring in US-born CHB patients who have combined HDV infection acquired primarily through high-risk activities.

THU362
Terry Cheuk-Fung Yip1, Mandy Sze-Man Lai1, Vincent Wai-Sun Wong1, Yee-Kit Tse1, Yan Liang2, Vicki Wing-Ki Hui2, Henry LY Chan3,4, Grace Lai-Hung Wong1. 1The Chinese University of Hong Kong, Medical Data Analytics Centre (MDAC), Department of Medicine and Therapeutics, Institute of Digestive Disease, Faculty of Medicine, Hong Kong; 2The Chinese University of Hong Kong, Medical Data Analytics Centre (MDAC), Department of Medicine and Therapeutics, Faculty of Medicine, Hong Kong; 3Union Hospital, Department of Internal Medicine, Hong Kong; 4The Chinese University of Hong Kong, Medical Data Analytics Centre (MDAC), Faculty of Medicine, Hong Kong
Email: wonglaihung@cuhk.edu.hk

Background and aims: Patients with chronic hepatitis B (CHB) are aging with more comorbidities such as diabetes mellitus (DM). In contrast, the reimbursement of antiviral treatment has been less restrictive over time, leading to better coverage. We aimed to examine whether the resulting change in patients’ clinical characteristics over time affects the accuracy of risk scores for hepatocellular carcinoma (HCC).

Method: Adult CHB patients who received entecavir or tenofovir for at least 6 months between January 2005 and March 2020 were identified using a territory-wide electronic healthcare database in Hong Kong. DM was defined by any use of non-insulin antidiabetic agents, continuous use of insulin for ≥28 days, haemoglobin A1c ≥6.5%, fasting glucose ≥7 mmol/L, and/or diagnosis codes. Four HCC risk scores for treated CHB patients including PAGE-B and modified PAGE-B (mPAGE-B) scores; cirrhosis, age, male sex, and DM (CAMD) score; and Real-world Effectiveness from Asia Pacific Rim Liver Consortium for hepatitis B virus (REAL-B) score were studied. The accuracy of scores was assessed by area under the time-dependent receiver operating characteristic curves (AUCROCs) with death as a competing risk. Comparisons were done based on 1,000 bootstrap samples.

Results: Of 48,706 patients included, 2,792, 11,563, 15,471, and 18,880 patients started antiviral treatment in 2005–08, 2009–12, 2013–16, and 2017–20 respectively; their mean age at treatment initiation were 50, 52, 54, and 57 years respectively. DM prevalence rose from 16% in 2005–08 to 19% in 2009–12, 21% in 2013–16, and 24% in 2017–20, whereas the prevalence of cirrhosis dropped from 21% to 17%, 9%, and 5% respectively through the 4 periods. The median follow-up time was 5, 5, 5, and 2 years in 2005–08, 2009–12, 2013–16, and
2017–20 respectively; 7.4%, 6.8%, 5.2%, and 1.9% of patients developed HCC respectively. PAGE-B and modified PAGE-B scores performed well across the 4 periods with comparable AUROCs ranging from 0.75–0.77 for PAGE-B score (p = 0.726) and 0.76–0.80 for mPAGE-B score (p = 0.150). For the other two scores with DM as a predictor, CAMD score was less predictive in the most recent period (p = 0.025). REAL-B score tended to be less predictive in the most recent period (p = 0.085) (Figure).

Conclusion: Two PAGE-B scores performed well regardless of the change in clinical characteristics of CHB patients over time. HCC risk scores that have DM as a predictor may however be less predictive in recent years.

THU364
Risk prediction of hepatocellular carcinoma in chronic hepatitis B patients outside current treatment criteria
Gi-Ae Kim1, Seungbong Han2, Young-Suk Lim3, Gwang Hyeon Choi4, Jonggi Choi5, Dong Hyun Sinn5, Yong Han Paik6, Jeong-Hoon Lee6, Ju-Yeon Cho7. 1Kyung Hee University School of Medicine, Department of Internal Medicine, Korea, Rep. of South; 2Korea University, Department of Biostatistics; 3Asan Medical Center, Department of Gastroenterology, Liver Center; 4Seoul National University Bundang Hospital, Department of Internal Medicine, Seongnam-si, Korea, Rep. of South; 5Samsung Medical Center, Department of Medicine, Korea, Rep. of South; 6Seoul National University College of Medicine, Department of Internal Medicine and Liver Research Institute, Korea, Rep. of South; 7Chosun University, Department of Internal Medicine, Korea, Rep. of South
Email: limys@amc.seoul.kr

Background and aims: A considerable number of chronic hepatitis B (CHB) patients outside the current treatment criteria develop hepatocellular carcinoma (HCC), suggesting many patients at high risk are left untreated and risk prediction for this population is called for. Thus, we aimed to investigate the risk of HCC in CHB patients who are not indicated for antiviral treatment including a broader range of HBV DNA levels and develop a risk prediction model for them.

Method: This multi-center study recruited 9,058 treatment-naïve, non-cirrhotic CHB patients with ALT <2 × upper limit of normal: 6, 549 for training cohort from Asan Medical Center and 2, 109 for validation cohort from two tertiary hospitals in Korea. A risk prediction model for HCC was developed using predictors based on multivariable cox models, and bootstrapping was performed for validation.

Results: In the training cohort, 363 patients (5.2%) developed HCC during 8.0 years of median follow-up. By multivariable cox regression analysis, HCC risk was the highest with HBV DNA levels of 6–7 log10 IU/ml (adjusted hazard ratio [aHR] 4.98; P < 0.001), and lowest with >8 log10 IU/ml (aHR 0.90; P = 0.71) and ≤4 log10 IU/ml (aHR 1.00; reference). HBV DNA levels, male sex, older age, and lower platelet counts were independent predictors of HCC but ALT levels did not predict HCC risk (p = 0.33). An ALT-independent 24-point risk prediction model (“ABC model 1”) was developed including the 4 independent predictors: sex, age, platelet counts, and HBV DNA levels combined with HBeAg status. HCC risk was calculated to range widely (0.19%–72.46%) at 10 years. The model showed good prediction performance with a concordance index (c-index) of 0.845. The area under receiver operating curves in the validation cohort was 0.79 (CI, 0.71–0.88) and 0.85 (CI, 0.72–0.99) at 5 and 10 years. A calibration plot showed a satisfactory calibration function. The model excluding HBeAg status (“ABC model 2”) showed a c-index of 0.843.

Conclusion: Incorporating the parabolic association between HBV DNA levels and HCC risk with the risk prediction models for untreated non-cirrhotic CHB patients is reliable for risk estimation. Our novel risk prediction model may help identify patients at high risk but left untreated and serve as a steppingstone to extend treatment indication.

Funding: Patient Centered Clinical Research Project (grant number: H0010062) and the National Research Program for Cancer Control through the National Cancer Center (grant number: HAC1C0110), funded by the Ministry of Health and Welfare, Republic of Korea.

Background and aims: Diabetes mellitus (DM) is common among patients with chronic hepatitis B infection (CHB) and has been associated with increased risk hepatocellular carcinoma (HCC) and liver decompensation. We investigated the factors associated with adverse clinical outcomes among CHB patients with DM.

Method: 624 Asian CHB patients (64.4% male, 65.1% antiviral-treated for median duration of 5.5 years) who had concomitant DM (median duration of 8.0 years) were prospectively recruited for transient elastography and followed-up (FU) for a median of 3.2 (interquartile range [IQR] 2.9–5.3) years. Adverse clinical outcome was defined as any liver decompensation event including ascites, variceal bleeding, hepatic encephalopathy (HE), HCC, liver transplantation (LT) or death. Variables of interest included age, cigarette smoking, antiviral therapy, liver stiffness (LS), controlled attenuation parameter (CAP), liver function, renal function, and glycemic control as reflected by individual mean glycated hemoglobin (HbA1c) during FU period. Good glycemic control was defined as mean HbA1c 6.5–7.0%. Advanced fibrosis and cirrhosis were defined by LS ≥9.0 and ≥12.0 kPa, respectively for normal alanine aminotransferase (ALT) or ≥12.0 and 13.5 kPa, respectively for raised ALT.

Email: loeymak@gmail.com

Advanced fibrosis and cirrhosis were defined by LS ≥9.0 and ≥12.0 kPa, respectively for normal alanine aminotransferase (ALT) or ≥12.0 and 13.5 kPa, respectively for raised ALT.

Suboptimal glycemic control is associated with adverse clinical outcomes in patients with chronic hepatitis B and diabetes mellitus
Lung Yi Loey Mak1,2, Rex Wan-Hin Hui1, Ka-Shing Cheung1, Danny Ka-Ho Wong1,2, Yan Yue James Fung1,2, Man-Fung Yuen1,2, Wai-Kay Seto1,2,3. 1The University of Hong Kong, Medicine, Hong Kong, Hong Kong; 2The University of Hong Kong, State Key Laboratory of Liver Research, Hong Kong, Hong Kong; 3The University of Hong Kong-Shenzhen Hospital, Shenzhen, China, Medicine, Shenzhen, China
Email: loeymak@gmail.com

Background and aims: Diabetes mellitus (DM) is common among patients with chronic hepatitis B infection (CHB) and has been associated with increased risk hepatocellular carcinoma (HCC) and liver decompensation. We investigated the factors associated with adverse clinical outcomes among CHB patients with DM.

Method: 624 Asian CHB patients (64.4% male, 65.1% antiviral-treated for median duration of 5.5 years) who had concomitant DM (median duration of 8.0 years) were prospectively recruited for transient elastography and followed-up (FU) for a median of 3.2 (interquartile range [IQR] 2.9–5.3) years. Adverse clinical outcome was defined as any liver decompensation event including ascites, variceal bleeding, hepatic encephalopathy (HE), HCC, liver transplantation (LT) or death. Variables of interest included age, cigarette smoking, antiviral therapy, liver stiffness (LS), controlled attenuation parameter (CAP), liver function, renal function, and glycemic control as reflected by individual mean glycated hemoglobin (HbA1c) during FU period. Good glycemic control was defined as mean HbA1c 6.5–7.0%. Advanced fibrosis and cirrhosis were defined by LS ≥9.0 and ≥12.0 kPa, respectively for normal alanine aminotransferase (ALT) or ≥12.0 and 13.5 kPa, respectively for raised ALT.

Email: loeymak@gmail.com

Diabetes mellitus (DM) is common among patients with chronic hepatitis B infection (CHB) and has been associated with increased risk hepatocellular carcinoma (HCC) and liver decompensation. We investigated the factors associated with adverse clinical outcomes among CHB patients with DM.

Method: 624 Asian CHB patients (64.4% male, 65.1% antiviral-treated for median duration of 5.5 years) who had concomitant DM (median duration of 8.0 years) were prospectively recruited for transient elastography and followed-up (FU) for a median of 3.2 (interquartile range [IQR] 2.9–5.3) years. Adverse clinical outcome was defined as any liver decompensation event including ascites, variceal bleeding, hepatic encephalopathy (HE), HCC, liver transplantation (LT) or death. Variables of interest included age, cigarette smoking, antiviral therapy, liver stiffness (LS), controlled attenuation parameter (CAP), liver function, renal function, and glycemic control as reflected by individual mean glycated hemoglobin (HbA1c) during FU period. Good glycemic control was defined as mean HbA1c 6.5–7.0%. Advanced fibrosis and cirrhosis were defined by LS ≥9.0 and ≥12.0 kPa, respectively for normal alanine aminotransferase (ALT) or ≥12.0 and 13.5 kPa, respectively for raised ALT.

Email: loeymak@gmail.com
Results: The median age was 62.1 (IQR 56.0–67.9) years old, and 25.2% were smokers or ex-smokers. 17.5% had cirrhosis at recruitment. Mean HbA1c was 6.9%, with 24.0% and 46.3% patients having levels of <6.5% and >7.0% (both are defined as suboptimal glycemic control, respectively). A total of 45 events (HCC, n = 29; ascites, n = 10; variceal bleeding, n = 7; HE, n = 7; death, n = 13; LT, n = 0) were observed during FU. Using multivariate Cox regression analysis, age (hazard ratio [HR] 1.038), smoking history (HR 2.814), LS (HR 1.037), suboptimal glycemic control (HR 3.362) [Figure 1] and albumin (HR 0.921; all p < 0.05) were independently associated with adverse clinical outcomes, while CAP (HR 0.995, univariate p = 0.082), antiviral therapy (HR 2.311, multivariate p = 0.088) and HBV DNA (HR 1.0002, univariate p = 0.065) were not significant variables. For the specific outcome of HCC, multivariate Cox regression showed that smoking history (HR 2.706), LS (HR 1.032) and mean HbA1c >7.0% (HR 2.252; all p < 0.05) were independent variables.

Conclusion: Suboptimal glycemic control (<6.5% or >7%) and history of cigarette smoking are associated with liver decompensation and HCC in CHB patients with DM.

THU365
Statin use and surface antigen loss in patients with chronic hepatitis B
Shahed Iqbal1, Ruidong Li2, Silpa Suthram3, Jeffrey Wallin1, James Trevaskis3, Anastasia Hyrina4, Simon Fletcher4, Meghan Holdorf5, 6Gilead Sciences, Inc., Biomarker Sciences, FOSTER CITY, United States; 5Gilead Sciences, Inc., Research Data Science, FOSTER CITY, United States; 4Gilead Sciences, Inc., Discovery Virology, FOSTER CITY, United States
Email: shahed.iqbal1@gilead.com

Background and aims: Statin use has been associated with reduced risk of liver outcomes (e.g., cirrhosis, liver cancer). One explanation is that the lipid composition of hepatitis B surface antigen (HBsAg) contains cellular cholesterol that is modified by statin use. We explored the association between statin use and sAg loss in patients with chronic hepatitis B (CHB).

Method: Adults (≥18 years) with CHB were identified from the IQVIA Ambulatory EMR database using International Classification of Disease (ICD) codes (ICD 9: 070.22–23, 070.32–33, ICD 10: B18.0, B18.1) or by HBsAg positive test. SAg loss was defined by having a negative HBsAg or positive hepatitis B surface antibody test. HIV disease, cancer, long-term steroid use, chronic liver disease, other hepatitis, or pregnancy were exclusion criteria. Statin use was measured using WHO recommended defined daily dose for statin. Due to limited data, virologic measures (e.g., HBV DNA) were not included in the model.

Results: Patients with CHB (N = 12, 314) diagnosed between 2001–2020 were included (mean age: 49.5 years, 47% men). The study comprised Caucasian (39%), Asian (27%), African American (10%) and other races (2%). Mean BMI was 26.1; 17% (n = 2054) of patients had any antiviral use and 4% (n = 505) had sAg loss (median time to sAg loss = 820 [121–4516] days). Current statin use (>28 days during follow-up) was recorded for 11.5% (n = 1421) of patients (2.4% used statin for 1–2 years and 2.2% for >2 years). Compared to no statin use, current statin use of >28–365 days (odds ratio[OR], 95% confidence interval [95% CI] = 1.9, 1.5–2.5), and 1–2 years (OR, 95% CI = 2.3, 1.4–3.4) were associated with sAg loss, but >2 years was not (OR, 95% CI = 1.2, 0.6–2.0). Current statin use was also associated with sAg loss (OR, 95% CI = 1.5, 1.2–2.0) after adjusting for age, sex, and race. In a stratified analysis, statin use was associated with sAg loss among patients who did not use antiviral (OR, 95% CI = 2.1, 1.6–2.7) but not among those who did (OR, 95% CI = 0.7, 0.2–1.5).

Table: Statin use and sAg loss in patients with chronic hepatitis B (N = 12, 314)

<table>
<thead>
<tr>
<th>Variable</th>
<th>Odds Ratio</th>
<th>95% Confidence interval</th>
<th>p-Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Statin use (yes vs. no)</td>
<td>1.5</td>
<td>(1.2, 2.0)</td>
<td>0.002</td>
</tr>
<tr>
<td>Age ≥45 to 65 vs. 18–44 yrs</td>
<td>1.6</td>
<td>(1.3, 2.1)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Age ≥65 vs. 18–44 yrs</td>
<td>1.5</td>
<td>(1.1, 2.1)</td>
<td>0.013</td>
</tr>
<tr>
<td>Male vs. Female</td>
<td>1.3</td>
<td>(1.0, 1.5)</td>
<td>0.027</td>
</tr>
<tr>
<td>African American vs. Caucasians</td>
<td>1.7</td>
<td>(1.3, 2.2)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Asian vs. Caucasians</td>
<td>1.1</td>
<td>(0.9, 1.4)</td>
<td>0.317</td>
</tr>
<tr>
<td>Other race vs. Caucasians</td>
<td>0.9</td>
<td>(0.4, 1.6)</td>
<td>0.683</td>
</tr>
</tbody>
</table>

Conclusion: In this large cohort of CHB patients, while statin use was associated with spontaneous sAg loss with dose response correlation up to two years of statin use, the interplay between age, virologic parameters, antiviral use, and statins need further research. These findings provide impetus for exploring the therapeutic role of statins in patients with CHB.

THU366
Patient engagement in hepatitis B clinical trials: ‘HBV cure’ is a motivation for participation in all ethnically diverse patients
Almuthana Mohamed1, Akudo Nwaogu1, Dusan Jovovic1, James Lok1, Maria Guerra Veloz1, Khin Aye Wint Han1, Jeya Anice Sundararaj1, Andrew Ayers1, Ivana Carey1, Kosh Agarwal1, King’s College Hospital, Institute of Liver Studies, London, United Kingdom
Email: almuthana700@gmail.com

Background and aims: Despite advances in treatment, chronic hepatitis B (CHB) remains a global health challenge. Clinical trials are key to the development of novel therapies for ‘HBV cure’. Patient enrolment can be challenging, especially in ethnic minorities, with reported participation rates of less than 20%. This study aimed to explore the experiences of patients enrolled in phase I or II CHB clinical trials at our hospital, and their motivation for participation.

Method: In this study, a constructivist research paradigm was implemented with the use of questionnaires as the primary modality of data collection. The questionnaire was carefully designed to contain a mixture of question styles, including open and Likert style questions. Baseline patient characteristics, including age and ethnicity, were also collected. The questionnaire was sent to all individuals enrolled in phase I or II CHB clinical trials at King’s College Hospital between 2019 and 2021. Open space answers underwent emergent coding and thematic analysis, whilst the results of the Likert scale questions were expressed as median (± IQR). Quantitative data analysis was performed using SPSS.

Results: Online questionnaires were sent to 83 CHB patients who had recently participated in clinical trials at our hospital and a total of 50 patients responded to our survey (60.3%). The ethnic distribution of
our cohort was representative of our local CHB population spread and the global burden of CHB. As shown in figure 1, the majority of our cohort resided within the Greater London region (80.7%). Most responders to the survey had undergone higher levels of education (86%). However, those from Sub-Saharan Africa were less likely to respond compared to other ethnicities (p = 0.0048). Thematic analysis of the qualitative data found that the concept of finite therapy and curative options are key drivers that encourage patients to participate in clinical trials. Whilst most responders to the survey (78%) would participate in future clinical trials, a significant proportion (n = 12, 24%) expressed difficulty in attending the extra clinic appointments.

Table 1: Patient characteristics of all subjects included in analysis

<table>
<thead>
<tr>
<th>Characteristics</th>
<th>Total Cohort</th>
<th>Responders</th>
<th>Non-responders</th>
<th>P-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age (Years)</td>
<td>83</td>
<td>50</td>
<td>33</td>
<td></td>
</tr>
<tr>
<td>18-40</td>
<td>26</td>
<td>17</td>
<td>9</td>
<td></td>
</tr>
<tr>
<td>41-60</td>
<td>41</td>
<td>23</td>
<td>18</td>
<td></td>
</tr>
<tr>
<td>61-65</td>
<td>16</td>
<td>10</td>
<td>6</td>
<td>0.004</td>
</tr>
<tr>
<td>Gender</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Male</td>
<td>58</td>
<td>36</td>
<td>22</td>
<td></td>
</tr>
<tr>
<td>Female</td>
<td>25</td>
<td>14</td>
<td>11</td>
<td>0.004</td>
</tr>
<tr>
<td>Ethnicity</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Caucasian</td>
<td>18</td>
<td>13</td>
<td>5</td>
<td></td>
</tr>
<tr>
<td>Sub-Saharan African</td>
<td>33</td>
<td>26</td>
<td>7</td>
<td></td>
</tr>
<tr>
<td>Asian</td>
<td>13</td>
<td>12</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>South Asian</td>
<td>7</td>
<td>1</td>
<td>6</td>
<td></td>
</tr>
<tr>
<td>Other/Mixed</td>
<td>12</td>
<td>6</td>
<td>4</td>
<td>0.0048</td>
</tr>
<tr>
<td>Level of Education</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Primary School</td>
<td>-</td>
<td>1</td>
<td>-</td>
<td></td>
</tr>
<tr>
<td>Secondary school</td>
<td>-</td>
<td>7</td>
<td>-</td>
<td></td>
</tr>
<tr>
<td>College Degree</td>
<td>-</td>
<td>10</td>
<td>-</td>
<td></td>
</tr>
<tr>
<td>Undergraduate Degree</td>
<td>-</td>
<td>19</td>
<td>-</td>
<td></td>
</tr>
<tr>
<td>Postgraduate Degree</td>
<td>-</td>
<td>14</td>
<td>-</td>
<td></td>
</tr>
<tr>
<td>Geographic Distribution</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Within Greater London</td>
<td>67</td>
<td>37</td>
<td>30</td>
<td></td>
</tr>
<tr>
<td>Outside of London</td>
<td>16</td>
<td>13</td>
<td>3</td>
<td>0.0559</td>
</tr>
</tbody>
</table>

Conclusion: 'HBV cure' is a motivation for patients’ participation in early phase clinical trials. Whilst most patients are happy to be re-involved in clinical trials, provisions must be taken to minimise the potential disruption of extra clinic appointments. Further work needs to be done in wider education for CHB patients to optimise participation in clinical trials.

THU367 Anti-HDV reflex testing increases the number of hepatitis D cases diagnosed in both academic and community centers

Adriana Palom1, Ariadna Rando-Segura2, Francisco Rodríguez-Frias2,3, Ana Barreira1,3, Jordi Llaneras1, Mar Riveiro Barciela1,2, Rafael Esteban1,3, Maria Buti1,3, Francisco Rodríguez-Frías2,3, Ana Barreira1,3, Jordi Llaneras1, Mar Riveiro Barciela1,2, Rafael Esteban1,3, Maria Buti1,3, 1Hospital Vall Hebron, Liver Unit, Barcelona; 2Hospital Vall Hebron, Department of Microbiology, Barcelona; 3Centro de investigación biomédica en red de enfermedades hepáticas y digestivas, Madrid

Email: mbuti@vhebron.net

Background and aims: Although EASL guidelines recommend anti-HDV testing in all HBsAg-positive individuals, HDV still remains underdiagnosed. In a study in Barcelona (Spain) in a catchment population of 400,000 inhabitants, only 9.4% of HBsAg-positive (HBsAg+) patients were tested for anti-HDV (Palom et al. AASLD 2021). We describe the initial results of a nontargeted HDV screening program using anti-HDV reflex testing of all HBsAg+ individuals and compare the results with those obtained before implementation of this strategy.

Method: We reviewed 2144 consecutive HBsAg+ samples sent to a central laboratory (January 2018–October 2021). Before reflex testing, we determined the rate of anti-HDV testing in 1553 HBsAg+ samples (January 2018–December 2020). Prospective anti-HDV reflex testing was done in all HBsAg+ serum samples (January to October 2021).

The overall prevalence of anti-HDV+ among those tested was similar before and after reflex implementation: 9.4% (11/117) and 8.6% (49/572), respectively. However, the absolute number of patients diagnosed with HDV increased from 3 cases in 2018, 2 cases in 2019 and 6 cases in 2020, to 49 cases in 10 months of 2021. Among 56 anti-HDV+ patients, HDV-RNA was detectable in 33 (66%) of 50 tested. HDV-RNA positive patients were more likely to be young, white, and HBeAg-negative, 69% had undetectable HBV-DNA and 58% elevated ALT.

Conclusion: In summary, anti-HDV reflex testing in all HBsAg+ individuals led to 5-fold increase in chronic hepatitis D diagnoses. Before reflex testing, a large percentage of HBsAg+ individuals were not tested for anti-HDV, particularly in primary care centers. The cost-effectiveness of anti-HDV reflex testing should be evaluated to inform testing guidelines.

THU368 HBVoice: a framework to enhance advocacy for patients and communities affected by hepatitis B virus infection

Phillippa Matthews1, Kathryn Jack2, Su Wang3, Jane Abbott4, Kathleen Bryce5, Benny Cheng6, Indrajit Ghosh7, Alistair Story8, Jacki Chen9, Chris Munoz10, John Bell11, Steven Riddell11, Amanda Goldring11, Chun Goddard12, Kate Moraras13, Chari Cohen13, Kenneth Brown11, Ahmed Elsharkawy14, Jeffrey Lazarus15, 1The Francis Crick Institute, London, United Kingdom; 2Nottingham University Hospitals NHS Trust Queen's Medical Centre Campus, United Kingdom; 3World Hepatitis Alliance, United Kingdom; 4Barts Health NHS Trust, United Kingdom; 5Royal Free London NHS Foundation Trust, United Kingdom; 6Waverley Care Milestone, United Kingdom; 7Mortimer Market Centre, United Kingdom; 8Find and Treat, University College Hospitals, London, United Kingdom; 9Rutgers Robert Wood Johnson Medical School, New Brunswick, United States; 10Yellow Warriors Hospitals, London, United Kingdom; 11British Liver Trust, United Kingdom; 12Sheffield Children’s NHS Foundation Trust, United Kingdom; 13Hepatitis B Foundation, Doylestown, United States; 14University Hospitals Birmingham, United Kingdom; 15Global Health-Trasplante Capilar en Turquía-1.960 c, Barcelona, Spain

Email: philippa.matthews@crick.ac.uk

Background and aims: Hepatitis B virus (HBV) is hidden from public view, with a long history of stigma and neglect, despite an estimated 300 million individuals being chronically infected worldwide. To make progress towards WHO elimination targets, it is essential to improve awareness of HBV among patients, the public, healthcare workers, funders, industry, academia and policy makers. As new HBV drugs enter clinical trials, the engagement of a diverse community is urgently required to deliver studies that engage and represent real-world populations. We present the rationale and groundwork for a
.new network, ‘HBVoice’, to increase HBV patient representation. Our aim is to develop this activity by promoting dialogue, connecting to a wider community and relevant stakeholders, and stimulating engagement between sectors.

**Method:** We have drawn on the published literature and data, and personal testimony in the public domain, alongside dialogue with patients. The British Liver Trust, Hepatitis B Foundation and the World Hepatitis Alliance. Context is also provided by the first externally led patient forum focused on HBV, convened by the Hepatitis B Foundation in partnership with the U.S. Food and Drug Administration (FDA) in 2020.

**Results:** We have established an expanding interdisciplinary group, representing healthcare workers, academia, non-governmental organisations, and people living with HBV. We are expanding to include hosting webinars, sharing lived experience of HBV infection, linking the HBV community to opportunities for involvement in clinical research, production of educational materials, political advocacy, and developing plans for industry funding to support a sustainable platform for patient engagement.

**Conclusion:** We highlight the urgent need for patient voice to be better addressed, supporting advances towards 2030 elimination goals.

**THU369**

**HBeAg-positive patients with HBsAg < 135IU/ml or HBcrAg < 3.6logU/ml have more chance to be HBsAg loss after nucleos (t)ide analogue cessation**

Yandi Xie1, Minghui Li2, Xiaojuan Ou3, Sujun Zheng2, Yinjie Gao3, Xiaoyuan Xu3, Yang Yang3, Anlin Ma4, Jia Li3, Lai Wei5, Yuemin Nan3, Huanwei Zheng1, Bo Feng1, 1Peking University People’s Hospital, Peking University Hepatology Institute, Beijing, China; 2Beijing Ditan Hospital, Capital Medical University, Department of Hepatology Division, Beijing, China; 3Beijing Friendship Hospital, Capital Medical University, Liver Research Center, Beijing, China; 4Beijing Youan Hospital, Capital Medical University, Complicated Liver Diseases and Artificial Liver Treatment and Training Center, Beijing, China; 5The Fifth Medical Center, General Hospital of PLA, Department of Infectious Diseases, Beijing, China; 6Peking University First Hospital, Department of Infectious Diseases, Beijing, China; 7The Second Hospital of Xingtai, Department of Infectious Diseases, Xingtai, China; 8China-Japan Friendship Hospital, Department of Infectious Diseases, Beijing, China; 9Tianjin Second People’s Hospital, Department of Liver Disease, Tianjin, China; 10Beijing Tsinhua Changgung Hospital, School of Clinical Medicine, Tsinghua University, Department of Hepatopancreatobiliary Disease, Beijing, China; 11The Third Hospital of Hebei Medical University, Department of Traditional and Western Medical Hepatology, Shijiazhuang, China; 12Shijiazhuang Fifth Hospital, Department of Liver Disease, Shijiazhuang, China Email: xxyfyb_1@sina.com

**Background and aims:** Cessation of nucleos (t)ide analogue (NAs) may increase hepatitis B virus (HBV) surface antigen (HBsAg) loss rate in chronic hepatitis B (CHB) patients. We aimed to identify predictor of HBsAg loss using serum quantitative HBsAg, HBV RNA and hepatitis B core-related antigen (HBcrAg) in CHB patients who stopped NAs treatment.

**Method:** Initially HBV e antigen (HBeAg)-positive CHB patients without cirrhosis who met the stopping criteria were included in 12 hospitals in China. Enrolled patients ceased NAs and were followed up with clinical and laboratory assessments every 3 months for 24 months after NAs cessation or until clinical relapse (CR).

**Results:** This is a multicenter prospective cohort study, in which 158 patients were included. Patients were divided into two groups according to the HBsAg status when NAs cessation. Group A included patients with HBsAg positive when NAs cessation (n = 139) and Group B included patients with HBsAg negative when NAs cessation (n = 19). In Group A, the 12-month and 24-month cumulative rates of HBsAg loss were 4.3% and 9.4%, respectively. End of treatment (EOT) HBsAg (hazard ratio (HR) = 0.152, p < 0.001), EOT HBcrAg (HR = 0.257, p = 0.001) were found to independently predict possibility of HBsAg loss. To predict HBsAg loss, the area under the receiver operating characteristic (AUROC) value of the EOT HBsAg and HBcrAg were...
0.952 (p < 0.001) and 0.765 (p < 0.001), respectively. Cumulative rates of HBsAg loss stratified by EOT HBsAg, HBV RNA or HBcAg levels, results showed that patients with EOT HBsAg ≤ 135 IU/ml (59.2% vs 1.3%, P < 0.001) or HBcAg ≤ 3.6 log10U/ml (17% vs 5.4%, P = 0.027) had higher 24-month cumulative HBsAg loss rate. In Group B, none of the patients had virological relapse (VR) or CR after NAs cessation. Only 1 (5.3%) patient had HBsAg reversion with HBV DNA detectable but less than 2000 IU/ml and without ALT elevation.

**Conclusion:** Some patients may get HBsAg loss after NAs cessation. An EOT HBsAg ≤ 135 IU/ml or HBcAg ≤ 3.6 log10U/ml identified a population with more chance to be HBsAg loss after NAs cessation. Patients with HBsAg negative when NAs cessation had a low risk of HBsAg reversion after NAs discontinuation.

**THU370**

**Serum markers of cccDNA transcriptional activity (HBcAg and pre-genomic HBV RNA) and large HBsAg (LHBs) protein are predicting response to pegylated interferon in HDV infection**

Ivana Carey1, Mark Anderson2, Christiana Moigboi1, Gavin Cloherty2, Geoffrey Dusheiko1, Kosh Agarwal1, 1King's College Hospital, Institute of Liver Studies, London, United Kingdom; 2Abbott Diagnostics, Department of Infectious Diseases, North Chicago, United States

**Background and aims:** Hepatitis delta virus (HDV) requires HBsAg envelope for propagation. The large, (LHBs), containing preS1+preS2 +S mediates HBV attachment to the NTCP receptor. A response to pegylated-interferon (Peg-IFN) treatment is achieved in less than 50% of patients, and unless HBsAg loss is achieved, patients are at risk of late relapse. We aimed to compare baseline and post treatment virological serum biomarkers (total HBsAg and LHBs levels, HBcAg and pgRNA concentrations, HDV genotypes and HDV RNA viral load) in HDV-positive responders versus non-responders (NR) to Peg-IFN.

**Method:** Serum samples of 33 HDV RNA-positive patients (median age 38 yrs, 21 (63%) males, 2 (6%) HBeAg+, 12 (36%) with compensated cirrhosis) were tested at the start and 3 years after late relapse. We aimed to compare baseline and post treatment virological serum biomarkers (total HBsAg and LHBs levels, HBcAg and pgRNA concentrations, HDV genotypes and HDV RNA viral load) in HDV-positive responders versus non-responders (NR) to Peg-IFN.

**Results:** Among 33 HDV RNA-positive patients (median age 38 yrs, 21 (63%) males, 2 (6%) HBeAg+, 12 (36%) with compensated cirrhosis) were tested at the start and 3 years after late relapse. We aimed to compare baseline and post treatment virological serum biomarkers (total HBsAg and LHBs levels, HBcAg and pgRNA concentrations, HDV genotypes and HDV RNA viral load) in HDV-positive responders versus non-responders (NR) to Peg-IFN.

**Conclusion:** Some patients may get HBsAg loss after NAs cessation. An EOT HBsAg ≤ 135 IU/ml or HBcAg ≤ 3.6 log10U/ml identified a population with more chance to be HBsAg loss after NAs cessation. Patients with HBsAg negative when NAs cessation had a low risk of HBsAg reversion after NAs discontinuation.

**Background and aims:** Hepatitis delta virus (HDV) requires HBsAg envelope for propagation. The large, (LHBs), containing preS1+preS2 +S mediates HBV attachment to the NTCP receptor. A response to pegylated-interferon (Peg-IFN) treatment is achieved in less than 50% of patients, and unless HBsAg loss is achieved, patients are at risk of late relapse. We aimed to compare baseline and post treatment virological serum biomarkers (total HBsAg and LHBs levels, HBcAg and pgRNA concentrations, HDV genotypes and HDV RNA viral load) in HDV-positive responders versus non-responders (NR) to Peg-IFN.

**Method:** Serum samples of 33 HDV RNA-positive patients (median age 38 yrs, 21 (63%) males, 2 (6%) HBeAg+, 12 (36%) with compensated cirrhosis) were tested at the start and 3 years after late relapse. We aimed to compare baseline and post treatment virological serum biomarkers (total HBsAg and LHBs levels, HBcAg and pgRNA concentrations, HDV genotypes and HDV RNA viral load) in HDV-positive responders versus non-responders (NR) to Peg-IFN.

**Results:** Among 33 HDV RNA-positive patients (median age 38 yrs, 21 (63%) males, 2 (6%) HBeAg+, 12 (36%) with compensated cirrhosis) were tested at the start and 3 years after late relapse. We aimed to compare baseline and post treatment virological serum biomarkers (total HBsAg and LHBs levels, HBcAg and pgRNA concentrations, HDV genotypes and HDV RNA viral load) in HDV-positive responders versus non-responders (NR) to Peg-IFN.

**Conclusion:** Some patients may get HBsAg loss after NAs cessation. An EOT HBsAg ≤ 135 IU/ml or HBcAg ≤ 3.6 log10U/ml identified a population with more chance to be HBsAg loss after NAs cessation. Patients with HBsAg negative when NAs cessation had a low risk of HBsAg reversion after NAs discontinuation.

---

**THU371**

**A decision-making model for prediction of a stable disease course in chronic hepatitis B patients**

Imlri Ofri1,2, Noam Peleg3, Moshe Leshno4, Amir Shlomai1,2, 1Rabin Medical Center, Belinson Hospital, Department of Medicine D, Petah Tikva, Israel; 2Tel Aviv University, The Sackler Faculty of Medicine, Tel Aviv, Israel; 3Rabin Medical Center, Belinson Hospital, The Institute of Gastroenterology, Petah Tikva, Israel; 4Tel Aviv University, The Coller Faculty of Management, Tel Aviv, Israel

**Background and aims:** Patients with chronic Hepatitis B (CHB) infection are regularly monitored for HBV DNA and liver enzyme levels in order to assess disease progression and the need for antiviral therapy. Identifying patients with a stable course of disease (i.e. long-lasting low HBV DNA and normal liver enzymes) can potentially prolong the intervals between visits, withhold unnecessary tests, resulting in reduced expenses. Accordingly, we aimed to find predictors for a stable disease course in patients with CHB.

**Method:** An inception cohort of 579 patients with CHB, who were followed in a tertiary referral center between January 2004 to December 2018, was retrospectively analyzed. Patients with low and steady viral load titer (<2000 IU/ml) and normal ALT levels (<40 IU/ml) in 6 consecutive clinic encounters were considered to have a stable course of CHB. A stepwise multivariate logistic regression analysis and a random forest decision tree model were used to identify predictors of a stable disease course.

**Results:** Following exclusion for various reasons, a total of 220 patients, with no active anti-viral treatment, were included in the final analysis. 64 had a stable disease course, whereas 156 had an unstable course. Patients with a stable disease were older and had lower baseline levels of AST, ALT and HBV DNA. In a multivariate analysis, age (OR 0.95, 95% CI 0.928–0.98), baseline ALT (OR 1.083, 95% CI 1.014–1.127) and Log HBV-DNA (OR 1.056 95% CI 1.032–1.08), were significantly associated with a stable disease. In a decision tree model, patients between 46–67 years old, with Log HBV-DNA below 5 IU/ML and ALT below 40.5 IU/ML had the best probability (0.91) for a stable disease course.

**Conclusion:** Integrating baseline viral DNA, ALT levels and patients’ age can predict the disease course in patients with CHB. Thus, stratification of CHB patients according to these simple parameters can determine the required intervals between scheduled clinic visits and may economize patients’ management.
Results: Among 6,719 adults with HDV who met inclusion criteria, 12 months continuous enrolment before and after ≥1 inpatient claim or ≥2 outpatient claims spaced 30 days apart for HDV infection based on ICD-9/10-CM diagnosis codes were identified from 01/01/2015 to 12/31/2019. Patients were required to have ≥12 months continuous enrolment before and after their first date of HDV infection diagnosis in the study period. All-cause healthcare-related resource utilization and costs were assessed in the 12 months pre- and post-HDV diagnosis period.

Conclusion: In a large national US healthcare claims database, representing ~80% of the US insured population, patients experienced significantly greater overall healthcare resource utilization and costs following diagnosis of HDV infection. These findings underscore a need for more effective strategies for the screening, diagnosis, and treatment of HDV, which may translate into cost savings for the healthcare system.

THU373
Validation of an internal hepatitis D virus DNA quantitative assay: developing assay suitable for global clinical application and clinical trials assessment
Natalie Bolton1, Dazhuang Shang1, Kosh Agarwal1, Ivana Carey1.
1King’s College Hospital, Institute of Liver Studies, London, United Kingdom
Email: natalie.bolton@nhs.net

Background and aims: Patients co-infected with both hepatitis B virus (HBV) and hepatitis D virus (HDV) have an increased risk of developing severe liver disease. HDV displays high genetic diversity, with previous studies identifying eight distinct genotypes. Robust, standardised assays for quantifying HDV viral load are needed to assess treatment impact, including standardisation of viral load reported units; two units currently used are copies/ml and international units (IU)/ml, with differing correction factors between these. This retrospective study aimed to assess the quality of an existing internal, pan-genotypic HDV RNA quantitative nucleic acid amplification test (NAAT), utilising the World Health Organisation (WHO) HDV international standard (WHO-HDV-IS), in a diverse South London population.

Method: Data was collected on 163 specimens taken from 89 HBV and HDV co-infected patients between January 2020 and October 2021, with HDV infection confirmed by a positive result on DIA.PRO Delta Ab (Total) assay. HDV viral load was quantified using an internal HDV RNA quantitative assay (Cobas® TaqMan® 48). Assay quality was assessed each run by inclusion of one negative internal control, two positive internal controls (low and high viral load dilutions of the same patient specimen), and the WHO-HDV-IS (genotype 1). Results for the WHO-HDV-IS were analysed using a previously described calculation to determine the correction factor for the assay. HDV genotyping was performed by direct sequencing and phylogenetic tree analysis using neighbor-joining distances analyses software.

Results: 84 (52%) of samples had a viral load below the limit of detection of the HDV RNA quantitative assay (6.40 × 10^2 copies/ml) whilst 5 (3%) did not have viral load analysed. Within the remaining 74 (45%) samples with quantifiable viral load the median HDV RNA level was 1.31 × 10^5 copies/ml. 40 (45%) and 34 (40%) of the patients were infected with genotype 1 and genotype 5 HDV, respectively. The internal low and high positive controls were found to be genotype 5. The correction factor calculation determined that the correction factor for the in-house HDV RNA quantitative assay was 1.06, meaning the limit of detection can be recalculated from 6.40 × 10^2 copies/ml to 6.76 × 10^1 IU/ml.

Conclusion: The correction factor of 1.06 shows that our internal HDV RNA quantitative NAAT calibrates extremely well in comparison with the WHO-HDV-IS. Despite the WHO standard derivation from genotype 1 HDV (the most prevalent genotype worldwide), our assay accurately quantitates HDV RNA in genotype 5 patients. More work is needed in the future to improve sensitivity and further standardize pan-genotypic HDV RNA quantification, in particular the introduction of a panel of standards across genotypes 1–8. Developing standardized assays suitable for HDV RNA quantitation in clinical trials of new therapeutic agents is an urgent need.
Early increase in HBeAg-positive CHB patients who achieved HBeAg loss after one year of peginterferon (± lamivudine) treatment. Serum HBV DNA, HBeAg and HBsAg were quantified at end of treatment (EOT) and at weeks 8 and 12 post-treatment; the peak value was used for analysis. An ALT flare was defined as ALT ≥5 ULN during the first 6 months after EOT.

Results: A total of 67 patients were included, the majority of whom were Caucasian (78%) and had HBV genotype A/D (52/27%). ALT flares occurred in 18%, after a median of 20 weeks (IQR 20–24). Patients who experienced flares had a median post-treatment HBeAg increase of 0.71 log, compared to a decline of 0.19 log in patients without a flare (p = 0.003). Among patients with an HBeAg increase of 0.5 log, 53% experienced a flare, versus 8% of the patients without an HBeAg increase (p < 0.001). In contrast, HBsAg kinetics were not associated with ALT flares (p = 0.313). As expected, patients with flares also experienced a more prominent HBV DNA rebound; we observed a median HBV DNA increase of 4.79 log vs 0.66 log in patients with and without flares (p = 0.005). Among patients with an HBV DNA increase of >3 log, 60% experienced a flare, versus 8% of the patients with <3 log HBV DNA increase. Patients with both HBeAg and HBV DNA increase experienced a flare in 86% versus 8% in patients without a concomitant increase (p < 0.001). Consistent results were observed in the subset of patients with HBV DNA <200 IU/ml at EOT (n = 36), 67% of the patients with an HBeAg increase >0.5 log experienced a flare, compared to 4% of patients without an HBeAg increase (p < 0.001).

Conclusion: Early increase in HBeAg levels after therapy withdrawal predicts subsequent ALT flares, and a combined increase of HBeAg and HBV DNA identifies patients at very high risk of flares. These findings suggest that HBeAg could be used to guide off-treatment follow-up. Our findings warrant further confirmation among patients treated with other finite treatment regimens.
Their liver, and an adequate quality of life can be achieved, resulting in favorable outcomes, assuming adherence to therapy and lack of other insults to disease or improved outcomes during follow-up. Interestingly, 4 of them developed it. The majority of individuals (95%) had stable liver transplant. Diabetes (50.5%), hypertension (49.8%), HIV infection (30.9%), substance abuse (28.7%), and smoking history (28.1%) were the top five comorbidities.

Conclusion: The prevalence of chronic hepatitis delta is currently very low (<5%) among positive HBsAg carriers in Portugal, with lower rates in recent years. We show that HDV infection has favorable outcomes, assuming adherence to therapy and lack of other insults to their liver, and an adequate quality of life can be achieved, resulting in longer overall survival. Therefore, HDV co-infection does not seem to have a significant clinical impact in Portuguese patients.

THU377 Impact of hepatitis B virus infection on liver-related death among people tested for HBV in British Columbia: results from a large longitudinal population-based cohort study
Makuza Jean Damascene1,2,3, Dahn Jeong2,3, Mawuena Binka2, Prince Adu2, Sofia Bartlett2, Amanda Yu2, Stanley Wong2, Georgine Cua1,2, Hector Velasquez1,2, Maria Alvarez2, Mel Krajden2, Mohammad Ehsanul Karim1, Naveed Janjua1,2, 1The University of British Columbia, School of Population and Public Health, Vancouver, Canada; 2BC Centre for Disease Control, BC HTC, Vancouver, Canada; 3Rwanda Biomedical Center (RBC), IHDPC, Kigali, Rwanda

Background and aims: A substantial number of people are living with hepatitis B virus (HBV) infection in Canada, which may result in higher morbidity and mortality among them. However, data on the contribution of HBV infection to liver-related mortality in Canada is limited. We assessed the impact of HBV infection on liver-related deaths in British Columbia (BC), Canada.

Method: We used data from the BC Hepatitis Testers Cohort (BC-HTC), a large population-based cohort that integrates data on HCV, HBV testing and diagnoses with data on primary care visits, hospitalizations, deaths and medication dispensations. Individuals who tested for HBV in the BC-HTC were followed from the first test date among HBV positive individuals and last test date among HBV negative individuals until the end of the study period (2020/06/30) or liver-related death. Liver-related mortality rates were computed for HBV positive and negative individuals. Multivariable Cox proportional hazards model was used to assess the impact while adjusting for confounders. Propensity scores (PS) pair matching analysis was conducted as a sensitivity analysis to assess the robustness of the main findings.

Results: Among 194,573 adults with HBV, 9,376 (4.8%) were coinfected with HDV. Among them, 38,847 HBV-positive individuals were matched to HBV-negative individuals until the end of the study period (2020/06/30) or liver-related death. Liver-related mortality rates were computed for HBV positive and negative individuals. Multivariable Cox proportional hazards model was used to assess the impact while adjusting for confounders. Propensity scores (PS) pair matching analysis was conducted as a sensitivity analysis to assess the robustness of the main findings.

Figure 1: The 30 PYS Cumulative incidence rate for people HBV tested positive vs. those HBV tested negative in BC from 1990–2015. (A) Cumulative incidence of liver-related mortality in individuals with and without HBV infection, over 30 PYS of follow-up. Solid lines: cumulative incidence of liver-related mortality; dashed lines: 95% confidence intervals. (B) Cumulative incidence of liver-related mortality in all individuals, over 30 years of follow-up. Solid lines: cumulative incidence of liver-related mortality; dashed lines: 95% confidence intervals. PYS, Person years; CI, confidence interval; HBV, hepatitis B virus.

Results: During the study duration, 40,704 people tested positive for HBV. Among them, 38,847 HBV-positive individuals were matched to HBV-negative individuals. The mean follow-up time for the study sample was 13.46 (standard deviation 6.53) years. A higher
proportion of those testing positive compared to negative were males (54% vs 43%), born in 1945–64 (46% vs 30%) and of East Asian ethnicity (63% vs 14%). The liver-related mortality rate was higher among people with HBV infection than those without [2.76 per 1,000 PYs (95%CI: 2.64, 2.89) vs. 0.66 per 1,000 PYs (95%CI: 0.65, 0.68), respectively]. In multivariable analysis, HBV infection was associated with increased liver-related mortality [adjusted hazard ratio (aHR): 3.35; 95%CI: 3.02, 3.71]. We found similar results in the PS-matched analysis (aHR: 3.36; 95%CI: 3.17, 3.57).

**Conclusion:** HBV infection is associated with a higher risk of liver-related mortality. Findings highlight an urgent need for HBV screening and diagnosis and continued monitoring for liver-related diseases to prevent mortality.

**THU379**
**Comparable risk of hepatocellular carcinoma between immune-tolerant and active phase in hepatitis B e antigen-positive patients**

Han Ah Lee1, Seung Up Kim2, Yeon Seok Seo3, Chai Hong Rim4. 1Inje University College of Medicine, Internal Medicine, Seoul, Korea, Rep. of South; 2Yonsei University College of Medicine, Internal Medicine, Seoul, Korea, Rep. of South; 3Korea University College of Medicine, Internal Medicine, Seoul, Korea, Rep. of South; 4Korea University College of Medicine, Radiation Oncology, Seoul, Korea, Rep. of South Email: crusion3@naver.com

**Background and aims:** Antiviral therapy is not indicated for patients with chronic hepatitis B (CHB) in the immune-tolerant (IT) phase. We compared the treatment outcomes between untreated IT-phase and treated immune-active (IA) phase in patients with CHB.

**Method:** We systematically searched four databases including Pubmed, Medline, Embase, and Cochrane database until August, 2021. The cumulative incidence of hepatocellular carcinoma (HCC) and mortality in IT and IA cohorts and that of CHB phase change in IT cohort was investigated. Studies regarding patients who have

![Figure](abstract: THU379)
clinically or pathologically diagnosed liver cirrhosis were excluded. Random effects model was used for pooled analyses. The study adhered PRISMA and referenced Cochrane handbook v6.2 for methodologic regards.

**Results:** A total of 13 studies involving 19 cohorts, including 11, 903 patients were included. Quantitative quality assessment was performed and five studies were regarded to have high and moderate quality; therefore none of 13 studies were dropped from formal analysis for quality issue. The overall median of median follow-up period was 62.4 months, (range: 51–103 months). The overall median value of median age was 40 (range: 29–53.5), and proportion of male was 59.6% (31.8–68.9). Possible publication bias was noted in pooled analyses of Egger's test p = 0.082 and 10-year HCC incidence (Egger's test p = 0.019).

The pooled HCC incidence rate at 5-years was 1.1% (95% confidence interval [CI]: 0.6–2.0%) in all cohorts. No statistical difference in HCC incidence rate at 5-years was observed between IT [1.1% (95% CI, 0.4–2.8%)] and IA cohorts [1.1% (95% CI, 0.5–2.3%) (p = 0.976). The pooled odds ratio of comparative series between IT and IA cohorts was 1.05 (95% CI, 0.32–3.45; p = 0.941). Pooled HCC incidence rate at 10-years was 3.5% (95% CI, 2.4–5.1%) in all cohorts. No statistical difference in HCC incidence rate at 10-years was observed between IT [2.7% (95% CI, 1.0–7.3%)] and IA cohorts [3.6% (95% CI, 2.4–5.5%) (p = 0.587). No statistical difference in pooled mortality rates at 5-years was observed between IT [1.9% (95% CI, 1.1–3.4%)] and IA cohorts [1.0% (95% CI, 0.3–2.9%) (p = 0.285). Finally, pooled incidence rate of CHB phase change in IT cohort was 36.1% at 5 years (95% CI, 29.5–43.2%).

**Conclusion:** The long-term risks of HCC and mortality were similar between the IT and IA phase. However, various definitions of CHB phase in different studies have to be considered.

**THU380**

**Evidence of extensive transcriptionally active HBV integrations involving genetic regions crucial for cell proliferation in the setting of HBeAg positive infection**

Romina Salpini1, Luca Carioti1, Arianna Battisti1,2, Lorenzo Piermatteo1, Alessandro Tavelli1, Eugenia Quiros-Roldan3, Antonella Cingolani2, Chiara Papalini5, Stefania Carrara6, Massimo Puoti3, Loredana Sarmati8, Antonella D’Arminio Monforte9,10, Francesca Ceccherini Silberstein1, Carlo Federico Perno1, Valentina Sivicher1, 1University of Rome “Tor Vergata”, Department of Experimental Medicine, Rome, Italy; 2Blizard Institute, Barts and The London SMD, QMUL, London, United Kingdom, Barts Liver Centre, United Kingdom

**Email:** rsalpini@yahoo.it

**Background and aims:** HBV integration into the human genome can mediate oncogenic activity. Limited information is available about initial HBV integration events, particularly in the early phases of infection. Here, we characterize chimeric HBV-human RNAs reflecting transcriptionally active HBV integrations in the setting of eAg positive phases of HBV infection.

**Method:** Liver tissues from 42 eAg+ chronically infected patients (27 with eAg+ hepatitis [eAg + CH] and 15 with eAg+ infection [eAg + CI]) were studied to perform total RNA-seq by NGS [Illumina, median (IQR) RNA reads per sample: 22 (18–27) millions]. An ad-hoc bioinformatic pipeline was applied to recognize chimeric HBV-human transcripts (present in >2 reads), resulting from HBV integration. Role of genes involved in HBV integration was assessed by GeneCards and Protein Atlas.

**Results:** Patients with eAg+CI were significantly younger than eAg+CH [27 (22–29) vs 29 (25–35) years, p < 0.0001]. Median (IQR) serum HBV DNA and HBsAg were 8.0 (5.7–8.6) logIU/ml and 4.4 (4.1–4.8) logIU/ml respectively, with no significant difference according to HBV infection status. Overall, >1 chimeric HBV-human RNA was revealed in almost all patients (98%, 41/42) for a total number of 1048 unique HBV-human transcripts, reflecting an abundance of transcriptionally active HBV integration events. The number of unique chimeric transcripts in each patient did not differ in eAg+CH and eAg+CI groups (median [IQR]): 13 (11–22) and 14 (10–39); P = 0.46, highlighting an early occurrence of HBV integration in young patients with no or limited fibrosis. 69.6% of integration events originated from HBsCore, indicating double stranded linear DNA as a major source of HBV integration. Moreover, 20.7% of chimeric transcripts involved HBsAg coding region, posing the basis to produce truncated/aberrant HBsAg forms. Notably, by gene ontology, 18% (189/1048) of HBV-human chimeric transcripts involved human exons and splicing signals, crucial for gene expression. Among them, 35.4% corresponds to genes playing a pivotal role in modulating cell survival/proliferation, including genes (BIRC6, SYF2, EVI5, BTG1) known to be dysregulated in HCC.

**Conclusion:** Transcriptionally active HBV integrations occur frequently in the eAg-positive phases of HBV infection, even in young patients with no or limited liver fibrosis. These events result in the production of chimeric HBV–human aberrant transcripts, that mostly involve genes regulating crucial intracellular pathways, that could confer a proliferative advantage to the hepatocytes. This is further evidence to support early treatment initiation in eAg positive chronic infection.

**THU381**

**In the setting of HIV-infection, HBV-reactivation is revealed by highly sensitive assays in a conspicuous fraction of anti-HBe-positive/HBsAg-negative patients switching to tenofovir-sparing therapy**

Romina Salpini1, Stefano D’Anna2, Mohammad Alkhatib1, Lorenzo Piermatteo1, Alessandro Tavelli1, Eugenia Quiros-Roldan3, Antonella Cingolani2, Chiara Papalini5, Stefania Carrara6, Massimo Puoti3, Loredana Sarmati8, Antonella d’Arminio Monforte9,10, Francesca CECCHERINI SILBERSTEIN1, Carlo Federico Perno1, Valentina Sivicher1, 1University of Rome “Tor Vergata”, Department of Experimental Medicine, Rome, Italy; 2Blizard Institute, Barts and The London SMD, QMUL, London, United Kingdom, Barts Liver Centre, United Kingdom

**Email:** rsalpini@yahoo.it

**Background and aims:** Tenofovir-sparing antiretroviral therapy (ART) is increasingly used in the setting of HIV-infection, raising the issue to properly identify those anti-HBe-positive/HBsAg-negative patients (pts) who can safely suspend this drug. Here, we aim at unravelling HBV replication kinetics after tenofovir withdrawal in HIV-infected anti-HBe-positive/HBsAg-negative pts. For each pt, a plasma sample is analyzed at T0 and during the first 12 months of TDF/TAF-sparing ART (T1). HBV-reactivation (HBV-R) during TDF/TAF-sparing ART is defined as HBV-DNA>1IU/ml in pts with negative HBV-DNA at T0 or a >2-fold increase in HBV-DNA from T0 to T1. HBV-DNA and -RNA are quantified by highly sensitive droplet digital PCR (HS-ddPCR, LLOD:1IU/ml) and anti-Hbc by Fujifilm (anti-Hbc>15COI indicating active HBV reservoir based on Salpini, 2020).

**Method:** This study includes 101 HIV-infected anti-HBe-positive/HBsAg-negative pts from ICoNA cohort, treated with TDF/TAF-containing ART for >12 months and switching to TDF/TAF-sparing ART: 73 with LAM and 28 with no active HBV drugs. At switching (T0) 98% of pts has undetectable HBV-RNA.

For each pt, a plasma sample is analyzed at T0 and during the first 12 months of TDF/TAF-sparing ART (T1). HBV-reactivation (HBV-R) during TDF/TAF-sparing ART is defined as HBVDNA=>1IU/ml in pts with negative HBV-DNA at T0 or a >2-fold increase in HBV-DNA from T0 to T1. HBV-DNA and -RNA are quantified by highly sensitive droplet digital PCR (HS-ddPCR, LLOD:1IU/ml) and anti-Hbc by Fujifilm (anti-Hbc>15COI indicating active HBV reservoir based on Salpini, 2020).

**Results:** At T0, despite TDF/TAF therapy, 34 (33.7%) pts have detectable HBV-DNA by HS-ddPCR (median[IQR]: 2–5IU/ml). Among the remaining 67 pts, 9% has detectable HBV-DNA by HS-ddPCR (median[IQR]: 6–7IU/ml) and anti-Hbc>15COI, indicating a transcriptionally active cccDNA.
THU382
Absence of hepatitis B virus (HBV) in at-risk infants receiving early antiretroviral therapy in a cohort of HIV-transmitting mothers in KwaZulu-Natal, South Africa

Jane Millar1, Gabriela Cromhout2, Noxolo Mchunu2, Philip Gould3, Philippa Matthews3, Anna McNaughton1, 2, 4, 5.
1 University of Oxford, Department of Paediatrics, Oxford, United Kingdom; 2 University of KwaZulu-Natal, HIV Pathogenesis Programme, South Africa; 3 University of Oxford, Nuffield Department of Medicine, Oxford, United Kingdom; 4 Department of Infectious Diseases and Microbiology, Oxford University Hospitals NHS Foundation Trust, Oxford, United Kingdom; 5 University of Bristol, Population Health Science, Bristol Medical School, Bristol, United Kingdom

Email: anna.mcnaughton@bristol.ac.uk

Background and aims: Both HIV and hepatitis B virus (HBV) prevalence are high in KwaZulu-Natal (KZN), South Africa (ZA). HIV coinfection can negatively impact HBV prognosis, and is associated with an increased likelihood of HBV mother-to-child transmission (MTCT) in the absence of appropriate treatment/prophylaxis. This study worked with an established cohort of HIV-transmitting mother-child pairs in KZN, in which HIV-positive infants were treated with antiretrovirals (ART) within 48hrs of life. We generated a detailed characterisation of HBV serological makers in the maternal cohort, and tested the infants at-risk of HBV MTCT.

Method: Maternal serum samples (n = 175) were screened for active HBV infection (HBsAg), exposure to HBV (anti-Hbc) and vaccination responses (anti-HBs- positive in the absence of other HBV markers). HBV vaccination has been part of the routine ZA infant immunization schedule since 1995, with the first dose given at age 6 weeks. HBV infections in HBsAg-positive mothers were further characterised with HBsAg and HBV DNA testing. Infants of HBV infected mothers were screened for HBsAg.

Results: Evidence of HBV exposure was present in 31.4% (55/175) mothers and HBV infection was present in 8.6% (15/175). Anti-HBc responses were absent in 53.3% (8/15) HBV-positive cases, suggesting it may be a poor biomarker in HIV-positive cohorts. A lone anti-HBs profile, indicating HBV vaccination, was present in 8.0% (14/175) mothers. HBV DNA was detectable in 46.7% (7/15) HBsAg-positive mothers, with 26.7% (4/15) also HBsAg-positive. Where HBV-DNA was detected, median viral load was 3.8log10 IU/ml (range 1.9-8.2log10 IU/ml). Among HBV-infected mothers, CD4+ counts were lower in those also testing HBV DNA positive (mean 264 vs 643; p = 0.003). Using a threshold of >5.3 log10 IU/ml, 20% (3/15) HBV-positive mothers were defined as high risk of MTCT. Screening of infants found no cases (0/15) of HBV MTCT.

Conclusion: Within this vulnerable cohort of HIV-transmitting mothers, we found evidence of a high HBV prevalence, and indications that 20% of the HBV-positive mothers are also high-risk for HBV MTCT. ART regimens prescribed to the infants early in life contained agents active against HBV (lamivudine), and this may have prevented MTCT in high-risk cases. Larger studies, incorporating long-term follow-up would be informative. Prevention of HBV MTCT at a population level requires consistent antenatal HBV screening and birth-dose immunisation of infants, together with specific antiviral prophylaxis.
**THU384**

**Analysis from national hospital discharge records database in Spain: increased baseline comorbidity burden including liver severity among HDV coinfection versus HBV monoinfection patients**

Maria Buti1, Ankita Kaushik2, Mertxell Ascaino3, Josep Darba4, Narindra Kachru5, 1Hospital Universitario Valle Hebron, Liver Unit, Barcelona, Spain; 2Gilead Sciences, HEOR-Global Value and Access, California, United States; 3BCN Health Economics and Outcomes Research St, Barcelona, Spain; 4University of Barcelona, Department of Economics, Barcelona, Spain

Email: mbuti@vhebron.net

**Background and aims:** Hepatitis D virus (HDV) is considered as the most severe form of chronic viral hepatitis, given its relatively rapid progression to cirrhosis and liver-related complications. This retrospective study compares baseline characteristics of adult patients with HDV coinfection versus (vs.) hepatitis B virus (HBV) mono-infection in a national hospital database in Spain.

**Method:** The study population included subjects ≥18 years having ≥1 ICD-9-10-CM diagnosis code for HDV or HBV in the Spanish National Health System’s Hospital Discharge Records Database (Conjunto Mínimo Básico de Datos) from 01/01/2000 to 12/31/2019 (study period). HDV and HBV cohorts were identified from 01/01/2001 to 12/31/2018 (identification period) with their first diagnosis defined as the diagnosis date, having ≥12 months of continuous enrollment before and after the diagnosis date. Baseline characteristics were assessed over the entire duration prior to diagnosis date. Descriptive statistics were summarized, and comparisons were made via chi-square tests.

**Results:** The study reported 12,317 patients diagnosed with HDV or HBV, of which 3,079 met the inclusion criteria: 1,592 HDV and 2,920 HBV patients. HDV patients [mean age 42.7 ± 14.4 | Charlson Comorbidity Index (CCI) score 0.92] were significantly younger than HBV patients [mean age 46.6 ± 15.9; p = 0.0034 | CCI score 0.77]. The male to female ratio (roughly 3:1) was similar across the two cohorts. Both the cohorts were largely covered by public insurance (93.7% HDV vs. 95.4% HBV; p = 0.3311) and roughly half were seen by gastroenterologists (44.7% HDV vs. 50.3% HBV; p = 0.1673) followed by other specialists (36.5% HDV vs. 29.8% HBV; p = 0.0763). HDV patients were significantly more likely to have compensated cirrhosis (49.7% vs. 29%; p < 0.0001), compensated cirrhosis (26.4% vs. 9.8%; p < 0.0001) and liver transplant (5% vs. 1.8%; p = 0.0109) than HBV patients, whereas hepatocellular carcinoma rates were at 5.7% and 3%, respectively. Further, HDV patients reported significantly higher rates of HCV (8.8% vs. 3.6%; p = 0.0043), HIV (13.8% vs. 3.3%; p < 0.0001) and substance abuse (18.9% vs. 7%; p < 0.0001) than HBV patients.

**Conclusion:** In a national hospital Spanish database, HDV coinfection patients had greater comorbidities and significantly higher liver disease severity than HBV monoinfected patients. These findings underscore the need for early screening and diagnosis, and eventual treatment of HDV to mitigate future disease progression.
systematic literature review and meta-analysis to examine whether HDV RNA positivity (HDV RNA+) vs. RNA negativity (HDV RNA–) is associated with increased risk of advanced liver disease events (ALDEs), including compensated cirrhosis (CC), decompensated cirrhosis (DCC), hepatocellular carcinoma (HCC), liver transplant (LT), and liver-related mortality (LRM).

Method: PubMed, Embase and Cochrane Central were searched in August 2021. Observational, case-control, and cross-sectional studies along with clinical trials reports addressing the clinical question of the review were included. Data extraction focused on data related to the relative rate of progression to advanced liver disease events for HDV RNA+/detectable versus HDV RNA–/undetectable patients and quality evaluation was based on the modified Risk of Bias in Non-randomised Studies-of Interventions (mROBINS-I) checklist. Data were pooled using the Hartung-Knapp-Sidik-Jonkman method for random-effects models for both risk (RR) and hazard ratios (HRs). We assessed the proportion of variability due to between-study heterogeneity with the I² statistic.

Results: Among a total of 2, 034 studies identified, 34 met analysis inclusion criteria. After meta-analysis, presence of HDV RNA+ was associated with a significantly increased risk of any ALDE (mean effect [95% CI]: RR: 1.85 [1.11, 3.09]; HR: 2.39 [1.56, 3.68]). When compared to HDV RNA– patients, HDV RNA+ was associated with a significantly higher risk of progressing to CC (RR 2.19 [1.60, 2.99]; HR 2.91 [1.94, 4.29]), LT (HR 7.07 [1.61, 31.00]), and LRM (RR 1.92 [1.02, 3.63]; HR 4.58 [2.72, 7.70]).

Conclusion: This comprehensive systematic review and meta-analysis demonstrates that HDV RNA+ patients have significantly greater risk of liver disease progression compared to HDV RNA– patients. These findings highlight the need for improved HDV screening in patients with chronic HBV, leading to early detection of HBV/HDV, linkage to care, and timely initiation of appropriate antiviral therapies to reduce the risk of liver-related morbidity and mortality.

THU387

The serum markers of cccDNA transcriptional activity have a role in predicting long-term outcomes in children with perinatally acquired HBV infection

Christiana Moigboi1, Mark Anderson2, Gavin Cloherty2, Rosh Agarwal1, Ivana Carey1. 1King’s College Hospital, Institute of Liver Studies, London, United Kingdom; 2Abbott Diagnostics, Department of Infectious Diseases, North Chicago, United States Email: christiana.moigboi@nhs.net

Background and aims: Perinatally acquired chronic hepatitis B (CHB) has often indolent course in childhood, but persistent viral infection leads to progressive liver disease in 40% of patients in adulthood. The combination of non-invasive serological (HBeAg, HBsAg levels) and virological (HBV DNA) markers together with liver enzyme activity (ALT) and liver damage scores (APRI or FIB-4) aids in monitoring disease stages and progression. Novel serological markers of cccDNA transcriptional activity-HBV pgRNA and HBcrAg—have been identified in HBV-infected populations. We aimed to investigate whether markers of cccDNA transcriptional activity in serum: HBeAg and pgRNA can help to predict future disease progression (need for therapy) in patients with perinatally acquired chronic hepatitis B infection.

Method: A retrospective study was carried out with samples from 29 chronic hepatitis B (CHB) paediatric patients diagnosed in childhood (median age 12 years, 48% males, 52% HBeAg positive) with long-term follow-up in the same centre (median follow-up duration 6.5 years, range 3–16 years) with available serum samples at the time of diagnosis. HBV DNA viral load was tested by TaqMan PCR [IU/ml], HBeAg status and HBsAg plasma levels by Abbott Architect® [log10 IU/ml], HBeAg concentrations by CLIA Fujirebio [log10 IU/ml] and pgRNA concentrations by real-time PCR Abbott Molecular Diagnostic RUO assay [LLQD = 1.65 log10 IU/ml]. Only 5 patients required to be started on antiviral therapy during follow-up.

Results: At diagnosis 79% patients had detected HBV pgRNA and HBcrAg was detected in all patients. There were strong positive correlations between serum pgRNA and HBV DNA levels (r = 0.82 p < 0.01), pgRNA and HBsAg levels (r = 0.74, p < 0.01) and pgRNA and HBeAg concentrations (r = 0.859, p < 0.01). When compared untreated vs. patients who required therapy-pgRNA was detected in 100% of untreated patients vs. 80% of patients needing therapy, but patients who needed therapy had higher pgRNA levels than untreated cohort (median: 3.02 log10 IU/ml vs. 1.94 log10 IU/ml, p < 0.05). In contrast, HBeAg was detected in all patients irrespective of therapy status, but patients who required therapy had lower HBeAg concentrations than untreated patients (median: 3.84 log10 IU/ml vs. 5.15 log10 IU/ml, p < 0.05) likely reflecting higher proportion of HBeAg negative patients in patients needing therapy (80% vs. 29%, p < 0.05).

Conclusion: The markers of cccDNA transcriptional activity-pgRNA and HBeAg—combined with the traditional serological/virological markers (HBeAg, HBsAg and HBV DNA levels) were helpful to predict at diagnosis patients who might require antiviral therapy in future and represent a valuable tool to be applied in regular diagnostics. Studies in larger paediatric cohorts to further assess this are needed.

THU388

Presence of liver inflammation and fibrosis in Asian patients with chronic hepatitis B in the grey zone

Jiacheng Liu1, Jan Wang2, Yiguang Li2, Li Zhu3, Wei Mao Ding4, Chuanwu Zhu4, Yuanwang Qiu5, Jie Li2, Rui Huang2, Chao Wu2, Nanjing Drum Tower Hospital Clinical College of Traditional Chinese and Western Medicine, Nanjing University of Chinese Medicine, Department of Infectious Diseases, Nanjing, China; 2Nanjing Drum Tower Hospital, The Affiliated Hospital of Nanjing University Medical School, Department of Infectious Diseases, Nanjing, China; 3The Fifth People’s Hospital of Wuxi, Department of Infectious Diseases, Wuxi, China; 4The Affiliated Infectious Diseases Hospital of Soochow University, Department of Infectious Diseases, Suzhou, China; 5Huai’an No. 4 People’s Hospital, Department of Hepatology, Huai’an, China Email: dr.wu@nju.edu.cn

Background and aims: Over a quarter of chronic hepatitis B (CHB) patients did not meet criteria of the traditional natural phases and hence classified as grey zone (GZ). However, few studies reported the liver inflammation and fibrosis of Asian CHB patients in the GZ.

Method: This multicenter, retrospective study included 1, 064 CHB patients underwent liver biopsy (LB). Phases of natural history were determined according the AASLD 2018 Guidance. GZ patients were divided into four categories: HBeAg-positive, normal ALT and HBV-DNA ≤ 10^4 IU/ml (GZ-A); HBeAg-positive, elevated ALT and HBV-DNA < 2 × 10^4 IU/ml (GZ-B); HBeAg-negative, normal ALT and HBV-DNA ≥ 2 × 10^3 IU/ml (GZ-C); HBeAg-negative, elevated ALT and HBV-DNA < 2 × 10^4 IU/ml (GZ-D).

Results: 263 (24.7%) patients were in the GZ with the median age of 41.5 years and male of 67.2%. Among the GZ patients, GZ-D (44.1%) was the dominate category, followed by GZ-C (37.6%); GZ-A (9.5%) and GZ-B (8.4%). Surprisingly, as high as 60.4% of GZ patients had significant inflammation (≥ G2) and 89.7% GZ patients had significant fibrosis (≥ S2), which were higher than that of patients with immune-tolerant and inactive phases. Over half of patients had significant inflammation or fibrosis in each GZ category. GZ-B patients had the highest proportions of significant inflammation (95.5%) and fibrosis (81.9%) compared to other GZ categories (GZ-A: 76.9% and 69.3%; GZ-C: 53.5% and 52.5%; GZ-D: 56.1% and 60.4%, respectively).
Background and aims: Chronic hepatitis B (CHB) infection has been associated with the development of chronic kidney disease. Bepirovirsen (BPV; GSK3228836) is an antisense oligonucleotide known to distribute into the kidneys and liver. Here, we aim to characterise the baseline renal parameters in patients enrolled in B-Clear and to understand any associations between renal parameters (estimated glomerular filtration rate [eGFR], creatinine (Cr), and clinical characteristics, and nucleotide (s)ide analogue (NA) treatment status and other baseline laboratory/clinical characteristics.

Method: B-Clear is an ongoing trial (NCT044449029) to assess the efficacy and safety of BPV in pts with CHB infection on stable NA treatment (+NA) or not on NA (-NA) at study start. Pts were grouped based on eGFR (in ml/min/1.73m²): low (60–<90), normal (90–<120) and high (≥120). Frequency counts, descriptive statistics and 95% confidence intervals (CI) were used for comparison.

Results: A total of 455 pts were enrolled: 225 +NA and 230 -NA (Table). Mean age and length of diagnosis was inversely related to eGFR status for both +NA and -NA. For both +NA and -NA pts, the highest proportion of pts with low eGFR were Asian (74% and 70%, respectively), and within race groups, Asians had the highest proportion of pts with low eGFR. +NA pts in the high eGFR group had higher HbsAg mean [95% CI]: 10.9, 939.4 [6264.0, 15614.8] vs pts in the low eGFR group (2723.5 [1545.9, 3901.1] IU/ml); this was not observed in -NA pts. In the -NA group, mean eGFR was lower in HBsAg negative pts (mean [95% CI]: 10.7 [105.0, 109.2]) vs HBsAg positive pts (114.4 [110.2, 118.6]). The number of pts with baseline non-steroidal anti-inflammatory drug (NSAID) or angiotensin-converting enzyme inhibitor/angiotensin receptor blocker use, or pts with diabetes or hypertension were low, but mean eGFR tended to be lower in these pt groups than in those without concomitant medication use or comorbidities, except for -NA pts with baseline NSAID use or diabetes. The most common NA used at baseline was entecavir (reported by 41% of those on NA).

Conclusion: Preliminary assessment of pts enrolled in B-Clear indicates that renal function may be associated with characteristics such as age, length of CHB diagnosis, race, HBsAg level, HBsAg status, and concomitant medications/comorbidities. [on behalf of the B-Clear study group].

Funding: GSK (209668).

THU390
Characterisation of baseline complement values in patients with chronic hepatitis B virus infection in the phase IIb B-clear study

Jennifer Cremer1, Anna Richards2, Tamara Lukic3, Seng Gee Lim3, Robert Plesniak4, Keiji Tsuji5, Harry Janssen6, Cristina Pojoga7,9, Corneliu Petru Popescu8,10, Tarik Asselah11, Diana Petrou12,13, Ewa Janczewska14, Man-Fung Yuen15, Jennifer Cremer17, Timaru Lukic18, Stuart Kendrick19, Robert Elston19, Geoff Quinn16, Punam Bharania19, Fiona Campbell10, Melanie Paff17, Dickens Theodore17.

Background and aims: The immune system plays an important role in disease pathogenesis and viral clearance of hepatitis B virus (HBV) infection, but the impact of HBV on the complement system, the inflammatory/immune state of patients (pts) and implications for treatment are poorly understood. Here we present preliminary data of pts enrolled in B-Clear to assess the efficacy and safety of bepirovirsen (BPV, GSK3228836), an antisense oligonucleotide, in pts with chronic hepatitis B virus infection.

Method: B-Clear is an ongoing phase IIb trial (NCT044449029) to assess the efficacy and safety of bepirovirsen (BPV, GSK3228836), an antisense oligonucleotide, in pts with chronic HBV. Pts on either

Figure: Liver inflammation and fibrosis in chronic hepatitis B with different phases of natural history and grey zones.

Conclusion: A substantial GZ patients had significant liver inflammation or fibrosis, especially for CHB patients with GZ-B. Using liver biopsy to assess the liver histological activity should be encouraged in GZ patients.
<table>
<thead>
<tr>
<th>Characteristic</th>
<th>+NA, N (%)</th>
<th>eGFR 60–90</th>
<th>eGFR 90–120</th>
<th>eGFR ≥120</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age, years</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Mean</td>
<td>56.1</td>
<td>45.9</td>
<td>32.3</td>
<td>46.4</td>
<td></td>
</tr>
<tr>
<td>Median</td>
<td>55.0</td>
<td>44.0</td>
<td>28.0</td>
<td>45.0</td>
<td></td>
</tr>
<tr>
<td>95% CI</td>
<td>53.1, 59.2</td>
<td>44.3, 47.4</td>
<td>26.9, 37.7</td>
<td>44.9, 48.0</td>
<td></td>
</tr>
<tr>
<td>Hepatitis B e antigen, n (%)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Positive</td>
<td>14 (33)</td>
<td>45 (28)</td>
<td>10 (43)</td>
<td>69 (31)</td>
<td></td>
</tr>
<tr>
<td>Negative</td>
<td>29 (67)</td>
<td>114 (72)</td>
<td>13 (57)</td>
<td>156 (69)</td>
<td></td>
</tr>
<tr>
<td>HBsAg, IU/mL</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Mean</td>
<td>2723.5</td>
<td>4356.6</td>
<td>10939.4</td>
<td>4717.4</td>
<td></td>
</tr>
<tr>
<td>Median</td>
<td>1740.0</td>
<td>1864.0</td>
<td>8792.0</td>
<td>2085.0</td>
<td></td>
</tr>
<tr>
<td>95% CI</td>
<td>1545.9, 3901.1</td>
<td>3284.2, 5429.1</td>
<td>6264.0, 15614.8</td>
<td>3768.9, 5665.9</td>
<td></td>
</tr>
<tr>
<td>HBV DNA level, IU/mL</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Mean (95% CI)</td>
<td>7.2 (2.9, 11.5)</td>
<td>8.0 (6.4, 9.5)</td>
<td>10.9 (6.7, 15.0)</td>
<td>8.1 (6.7, 9.5)</td>
<td></td>
</tr>
<tr>
<td>Length of diagnosis, years</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Mean (95% CI)</td>
<td>18.6 (15.0, 22.1)</td>
<td>15.3 (13.7, 16.9)</td>
<td>12.4 (7.9, 17.0)</td>
<td>15.6 (14.3, 17.0)</td>
<td></td>
</tr>
<tr>
<td>Race, n (%)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Asian</td>
<td>32 (74)</td>
<td>77 (48)</td>
<td>9 (39)</td>
<td>118 (52)</td>
<td></td>
</tr>
<tr>
<td>White</td>
<td>10 (23)</td>
<td>77 (48)</td>
<td>12 (52)</td>
<td>99 (44)</td>
<td></td>
</tr>
<tr>
<td>Black or African</td>
<td>1 (2)</td>
<td>4 (3)</td>
<td>2 (9)</td>
<td>7 (3)</td>
<td></td>
</tr>
<tr>
<td>American Indian or Alaska Native</td>
<td>0</td>
<td>1 (&lt;1)</td>
<td>0</td>
<td>1 (&lt;1)</td>
<td></td>
</tr>
<tr>
<td>Mixed race</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>-NA, N (%)</td>
<td>23 (10.0)</td>
<td>156 (67.8)</td>
<td>51 (22.2)</td>
<td>230 (100)</td>
<td></td>
</tr>
<tr>
<td>Age, years</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Mean</td>
<td>49.4</td>
<td>43.7</td>
<td>33.2</td>
<td>42.0</td>
<td></td>
</tr>
<tr>
<td>Median</td>
<td>48.0</td>
<td>43.0</td>
<td>33.0</td>
<td>41.5</td>
<td></td>
</tr>
<tr>
<td>95% CI</td>
<td>45.2, 53.7</td>
<td>42.1, 45.4</td>
<td>30.9, 35.4</td>
<td>40.6, 43.4</td>
<td></td>
</tr>
<tr>
<td>Hepatitis B e antigen, n (%)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Positive</td>
<td>4 (17)</td>
<td>35 (23)</td>
<td>21 (42)</td>
<td>60 (27)</td>
<td></td>
</tr>
<tr>
<td>Negative</td>
<td>19 (83)</td>
<td>117 (77)</td>
<td>29 (58)</td>
<td>165 (73)</td>
<td></td>
</tr>
<tr>
<td>HBsAg, IU/mL</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Mean</td>
<td>21680.1</td>
<td>15495.4</td>
<td>22556.1</td>
<td>17679.5</td>
<td></td>
</tr>
<tr>
<td>Median</td>
<td>5420.6</td>
<td>3795.8</td>
<td>8820.0</td>
<td>4784.5</td>
<td></td>
</tr>
<tr>
<td>95% CI</td>
<td>3813.1, 39547.1</td>
<td>8138.6, 22852.2</td>
<td>13083.6, 32028.6</td>
<td>12036.7, 23322.3</td>
<td></td>
</tr>
<tr>
<td>HBV DNA level, IU/mL</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Mean (95% CI)</td>
<td>5687821</td>
<td>6043390</td>
<td>15193241</td>
<td>8045383</td>
<td></td>
</tr>
<tr>
<td>(330085, 11045556)</td>
<td>(3474703, 8611974)</td>
<td>(6204777, 24181705)</td>
<td>(5343721, 10747044)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Length of diagnosis, years</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Mean (95% CI)</td>
<td>15.9 (9.9, 21.9)</td>
<td>15.0 (13.1, 16.9)</td>
<td>8.9 (6.8, 11.0)</td>
<td>13.7 (12.2, 15.3)</td>
<td></td>
</tr>
<tr>
<td>Race, n (%)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Asian</td>
<td>16 (70)</td>
<td>86 (55)</td>
<td>28 (55)</td>
<td>130 (57)</td>
<td></td>
</tr>
<tr>
<td>White</td>
<td>7 (30)</td>
<td>57 (37)</td>
<td>15 (29)</td>
<td>79 (34)</td>
<td></td>
</tr>
<tr>
<td>Black or African</td>
<td>0</td>
<td>12 (8)</td>
<td>8 (16)</td>
<td>20 (9)</td>
<td></td>
</tr>
<tr>
<td>American</td>
<td>0</td>
<td>1 (&lt;1)</td>
<td>0</td>
<td>1 (&lt;1)</td>
<td></td>
</tr>
<tr>
<td>Mixed race</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td></td>
</tr>
</tbody>
</table>

CI, confidence interval; HBsAg, hepatitis B surface antigen; HBV, hepatitis B virus; NA, nucleos(t)ide analogue.
stable NA therapy (+NA), or not receiving NA therapy (-NA) were enrolled. All pts screened for B-Clear were included in this analysis; pts were grouped based on baseline values of complement C3 ([in g/L] low <0.9; normal 0.9–1.8; high >1.8) and C4 ([in g/L] low <0.1; normal 0.1–0.4; high >0.4) at screening. Descriptive statistics and 95% confidence intervals were used for comparison.

Results: Of the 725 screened pts with data (N = 718 [+NA: n = 286; -NA: n = 432]): 83 had low C3 (+NA: n = 25; -NA: n = 58), 23 had low C4 (+NA: n = 4; -NA: n = 19), and 17 had both low C3 and C4 (+NA: n = 2; -NA: n = 15) (Table). A greater proportion of females had low C3 in the -NA group versus the +NA group (18%, versus 9%, respectively). Most pts with low C3 were Asian (+NA: 68%; -NA: 72%). In the +NA low C3 group, the mean hepatitis B virus surface antigen (HBsAg; 5911 IU/ml) and hepatitis B virus e-antigen (HBeAg; 41.5 U/ml) was higher vs the normal C3 mean HBsAg (4624 IU/ml) and HBeAg (11.9 U/ml). In the -NA low C3 group, the mean HBV DNA (12, 276, 923 IU/ml) and HBeAg (473 U/ml) was higher vs the normal C3 group (HBV DNA 7, 345, 220 IU/ml; HBeAg 483 IU/ml), while HBsAg was lower (low C3 group 15735 IU/ml; high C3 group 18048 IU/ml).

The complement split product C5a and factor Bb were similar, and mostly in the normal range, in pts with low, normal or high C3 in both the +NA and -NA groups.

Conclusion: Preliminary findings indicate that gender, race, HBsAg, HBV DNA, and HBeAg level may all contribute to low C3 among pts with HBV. Observed differences may be due to different stages of disease or level of immune status for pts +NA, versus -NA. Due to low numbers of pts with low C4, no conclusions could be made regarding associations with baseline characteristics. [on behalf of the B-Clear study group].

Funding: GSK (209668).

THU391
Estimations of the global prevalence and clinical burden of occult hepatitis B infection (OBI): a systematic review and meta-analysis
Yu Ri Im1, Rukmini Jagdish1, Damien Leith2, Jin Un Kim1, Gibril Ndow3, Kyoko Yoshida1, Amir Majid4, Yueqi Ge5, Yusuke Shimakawa6, Maud Lemoine1.

1Imperial College London, Section of Hepatology, Division of Digestive Diseases, Department of Metabolism, Digestion and Reproduction, London, United Kingdom; 2Glasgow Royal Infirmary, Department of Gastroenterology, Glasgow, United Kingdom; 3London School of Hygiene and Tropical Medicine, MRC Unit The Gambia, Fajara, Gambia; 4West Middlesex University Hospital, Department of Anaesthetics, Isleworth, United Kingdom; 5Chelsea and Westminster Hospital, Department of Gastroenterology, London, United Kingdom; 6Institut Pasteur, Unité d’Épidémiologie des Maladies Émergentes, Paris, France

Email: yuri.im@doctors.org.uk

Background and aims: Occult hepatitis B infection (OBI) is defined as the presence of replication-competent hepatitis B virus (HBV) DNA in the blood or liver tissue of individuals who test negative for the hepatitis B surface antigen (HBsAg). Previous studies have suggested that individuals with OBI could transmit the virus and may be at higher risk of hepatocellular carcinoma (HCC). Despite possible implications for both affected individuals and global HBV elimination goals, the prevalence of OBI is not known. Therefore, we performed a meta-analysis to estimate the global prevalence of OBI.

Method: We systematically searched the MEDLINE, Embase, Global Health and Web of Science databases for articles published between Jan 1, 2010, and August 14, 2019. We included studies on adult populations from which the prevalence of OBI could be calculated, regardless of anti-hepatitis B core (anti-HBc) status or viral load. We excluded studies on individuals <18 years of age and those on antiviral therapy active against HBV. The prevalence was pooled to
determine effect estimates and 95%CI weighted by study size for blood donors, low-risk populations, high-risk populations due to increased HBV exposure risk, and patients with advanced liver disease. We also assessed the effects of study design, HBV serology, HBV endemcity and presence of advanced liver disease on OBI prevalence.

**Results:** Our meta-analysis included 400 studies and 143,980,492 individuals. Amongst anti-HBc-positive individuals (n = 7,863), OBI prevalence was 7.9% (5.3–10.8) in blood samples (n = 7,345) and 55.2% (42.9–67.3) in liver samples (n = 367). Amongst anti-HBc-negative individuals (n = 45,853), OBI prevalence was 1.1% (0.6–1.8) in blood samples (n = 44,637) and 17.9% (5.1–35.2) in liver samples (n = 302). When assessing studies that included all individuals negative for HBsAg regardless of anti-HBc status and tested OBI in the blood, OBI prevalence was lowest in blood donors (0.2% [0.2–0.4]), followed by low-risk populations (2.5% [1.0–4.5]), high-risk populations due to increased HBV exposure risk (6.4% [4.2–9.0]) and patients with advanced liver disease (15.8% [8.1–25.2]). Endemcity of the country of study was predictive of OBI prevalence in blood donors. The presence of advanced liver disease was associated with an increased prevalence of OBI across case-control studies of patients with cirrhosis or HCC compared to healthy controls (p < 0.001).

**Conclusion:** OBI is common, clinically significant, and underestimated. Our study reports a consistently high prevalence of OBI in HBV-endemic areas and, globally, across high-risk groups. Screening of blood samples with both nucleic acid testing (NAT) and anti-HBc might be necessary to eradicate this reservoir of HBV infection globally. OBI should no longer be overlooked in regional and global hepatitis B screening, prevention, and elimination programmes.

**THU392**

Time for universal screening for hepatitis D? A study describing screening patterns, characteristics and outcomes of hepatitis D virus infection

Rohit Nathani1, Bo Hyung Yoon2, Carolina Villarrol3, Sidra Salman4, Dewan Giri5, Amreen Dinani6, Ilan Weisberg7, Icahn School of Medicine at Mount Sinai Morningside-West, Department of Medicine, New York, United States; 2Icahn School of Medicine at Mount Sinai Beth Israel-Morningside-West, Division of Gastroenterology, Department of Medicine, New York, United States; 3Icahn School of Medicine at Mount Sinai Beth Israel, Department of Medicine, New York, United States; 4Icahn School of Medicine at Mount Sinai Beth Israel, Division of Gastroenterology, Department of Medicine, New York, United States; 5Icahn School of Medicine at Mount Sinai Beth Israel, Division of hepatology, Department of Medicine, New York, United States

**Email:** rohit.nathani@mountsinai.org

**Background and aims:** The prevalence of hepatitis D virus (HDV) is as high as 10% in patients with hepatitis B virus (HBV) infection. Asian and European guidelines recommend universal testing for HDV in all HBV surface antigen positive persons. However, the AASLD guidelines recommend testing only those at increased ‘risk.’ The aim of our study was to identify patterns of screening for HDV and to understand the characteristics and outcomes of those infected with HDV.

**Method:** A retrospective cohort of patients with chronic hepatitis B (CHB) infection was identified using electronic medical record data in a tertiary health system from 01/2016 to 10/2021. We also identified those who were screened with an HDV antibody test. For this submission, detailed chart review of patients with a confirmed diagnosis of HDV infection was performed. Baseline demographic data, comorbidities, and markers of severity of liver disease (determined by FIB 4 score) and cirrhosis status (based on imaging and clinical criteria) at the time of diagnosis was recorded. We also recorded the type of screening test and the type of clinician performing the screening. Primary outcome was mortality and secondary outcomes included liver decompensation (LD), development of hepatocellular carcinoma (HCC), and need for liver transplant (LT).

**Results:** Over 6 years 11,110 patients were diagnosed with CHB and 1390 (12.5%) of them had been screened for HDV infection. A detailed chart review was performed of 86/1390 patients (6.1%) who were positive for HDV infection and had complete data. More than half (58.14%) were male, mean body mass index was 27.88 (SD ± 5.5) units. After CHB, most common co-existing condition was hepatitis C virus (HCV) infection (11.62%). Median FIB-4 score was 1.8 (11.4–2.2) and 53.48% had cirrhosis at the time of HDV diagnosis. Majority (81.4%) of screening tests were ordered at attending clinics by gastroenterologists (90.7%). Among patients with cirrhosis 17 (37%) developed LD with ascites and esophageal varices (82% each) being the most common decompensating events. 12 (13.95%) patients developed HCC and 16 (18.6%) patients needed LT. No patients died during follow-up.

**Conclusion:** Our study demonstrates that people with HBV who are infected with HDV have high morbidity and increased risk for HCC, LD, and LT. A small proportion of HBV infected persons are screened for HDV and many of them develop liver cirrhosis by the time of diagnosis. Contrary to AASLD guidelines, we found a sizable number of HDV-positive people who do not have co-existing high-risk conditions like Human Immunodeficiency Virus and HCV. Most of the screening for HDV occurred in attending clinics vs trainee/midlevel provider clinics, identifying an area for improving knowledge around HDV. We describe a significant liver-related disease burden in those with HDV and thus universal screening for HDV in people with HBV infection may be reasonable.

**THU393**

Distribution of patients by guideline-defined disease phase and/or grey zones in B-Clear, an international multcentre clinical trial

Seng Gee Lim1, Cristina Pujoga2,3, Harry Janssen4, Michio Imamura5, Ewa Janczewska6, Robert Plesniak7, Keiji Tsuji8, Corneliu Petru Popescu9, Diana Petrowa10, Adrian Gadano11, Alexander Wong12, Tarik Asselah13, Hyung Joon Yim14, Jeong Heo15, Man-Fung Yuen16, Gheorghe Diaconescu17, Giuliano Rizzardini18, Jennifer Cremer19, Robert Elston20, Stuart Kendrick21, Geoff Quinn22, Fiona Campbell20, Melanie Patt21, Dickens Theodore19, 1National University Health System, Singapore, Singapore; 2Institut Regional de Gastroenterologie si Hepatologie prof dr O Fodor, Cluj-Napoca, Romania; 3Babes-Bolyai University, International Institute for Advanced Study of Psychotherapy and Applied Mental Health, Cluj-Napoca, Romania; 4Toronto General Hospital, Toronto, Canada; 5Hiroshima University Hospital, Hiroshima, Japan; 6ID Clinic, Myslowice, Poland; 7University of Rzeszow Centrum Medyczne w Lancut Sp. z o.o., Lancut, Poland; 8Hiroshima Red Cross Hospital, Hiroshima, Japan; 9Dr Victor Babes Clinical Hospital of Infectious and Tropical Diseases, Carol Davila University of Medicine and Pharmacy, Bucharest, Romania; 10Diagnostic Consultative Centre, Varna, Bulgaria; 11Hospital Italiano de Buenos Aires, Buenos Aires, Argentina; 12University of Saskatchewan, Regina, Canada; 13Hôpital Beaujon, Clichy, France; 14Korea University Ansan Hospital, Ansan, Korea, Rep. of South; 15Pusan National University Hospital, Busan, Korea, Rep. of South; 16Queen Mary Hospital, Hong Kong, China; 17Spatialul Clinic de Boli Infectioase si Pneumoftiziologie, Craiova, Romania; 18Luigi Sacco Hospital, Milan, Italy; 19GlaxoSmithKline, Durham, United States; 20GlaxoSmithKline, Stevenage, United Kingdom; 21GlaxoSmithKline, Collegeville, United States

**Email:** jennifer.x.cremer@gsk.com

**Background and aims:** Many patients (pts) with chronic hepatitis B virus (CHB) lie in a grey zone (GZ) (i.e. they do not fit into a guideline-defined disease phase). We evaluated the distribution and characteristics of CHB pts enrolled in B-Clear, who were not on nucleos (t)ide analog (NA) therapy, by guideline-defined disease phase and GZ.

**Method:** B-Clear is an ongoing trial (NCT04449029) to assess the efficacy and safety of bepirovirsen (GSK3228836, BPV)-an antisense oligonucleotide- in pts with CHB. Pts not on NA (N = 230) were categorised as HBeAg positive (eAg+) chronic infection, eAg+ chronic hepatitis, HBeAg negative (eAg-) chronic infection, and eAg- chronic hepatitis, based on HBV DNA, alanine aminotransferase (ALT) and eAg status at baseline as per EASL 2017, AASLD 2018 and APASL 2015 CHB guidelines (90.7%). Among patients with cirrhosis 17 (37%) developed LD with ascites and esophageal varices (82% each) being the most common decompensating events. 12 (13.95%) patients developed HCC and 16 (18.6%) patients needed LT. No patients died during follow-up.

**Conclusion:** Our study demonstrates that people with HBV who are infected with HDV have high morbidity and increased risk for HCC, LD, and LT. A small proportion of HBV infected persons are screened for HDV and many of them develop liver cirrhosis by the time of diagnosis. Contrary to AASLD guidelines, we found a sizable number of HDV-positive people who do not have co-existing high-risk conditions like Human Immunodeficiency Virus and HCV. Most of the screening for HDV occurred in attending clinics vs trainee/midlevel provider clinics, identifying an area for improving knowledge around HDV. We describe a significant liver-related disease burden in those with HDV and thus universal screening for HDV in people with HBV infection may be reasonable.
guidelines. In addition, ‘Strict’ or ‘Common’ criteria were applied based upon eAg status and ALT cut-offs of 35/25 IU/ml [males/females] or 40/35 IU/ml [males/females], respectively. Pts in the GZ were categorised into four groups: A (eAg+, normal ALT), B (eAg+; high ALT), C (eAg-, normal ALT), D (eAg-, high ALT).

**Results:** Of the four guideline-defined disease phases, the highest proportion of pts were eAg+ chronic hepatitis (EASL 16.2%; AASLD 18.8%) or eAg- chronic hepatitis (EASL 16.2%; APASL 8.7%) (Figure); however, the majority of patients (55.5%, 65.9% and 81.2%) fell in the GZ using EASL, AASLD and APASL guidelines, respectively. Most pts in the GZ were eAg-. GZ C was the most common GZ group: 48.5% (EASL), 36.2% (AASLD) and 48.5% (APASL); however, the proportion of pts in other GZ groups differed by guideline. The EASL guidelines had the lowest proportion of pts in the GZ for Asian (48.8%), Black (75%) and White (60.8%) pts. The APASL guidelines had the highest proportion in the GZ for Asian (86%) and Black (95%) pts, while AASLD guidelines had the highest proportion of pts in the GZ for White pts (74.7%). When the criterion for HBV DNA was removed, the highest proportion of GZ pts fell into the eAg-, normal ALT category (52.2% ‘Common’; 40.4% ‘Strict’) and eAg-, high ALT category (21.7% ‘Common’; 33.5% ‘Strict’).

**Background and aims:** Direct-acting antivirals (DAA) carry a potential risk of inducing hepatitis B virus (HBV) reactivations in HBV-HCV co-infected patients (pts). However, dynamics and outcomes may be different according to the phase of HBV infection. Our aim was to investigate HBsAg and HBV-DNA kinetics across DAA therapy in untreated carriers with HBeAg Negative Infection (eni) and in HBV-eAg negative Chronic Hepatitis B (CHB) pts receiving Nucleos (t)ide Analogs (NA).

**Method:** We prospectively enrolled 15 (F/M: 4/11, median age: 62.1y) ENI with HBV-DNA persistently < 2,000 IU/ml, and 8 CHB (F/M: 3/6, median age: 54.8y) pts under NA (entecavir: 6; tenofovir: 3) with concomitant HCV infection (genotype 1a:4; 1b:7; 2a/c:3; 3a:7; 4d:2) who received DAAAs with Sofosbuvir (SOF:13) or without (NO-SOF:10) for 8 (4), 12 (12) or 24 (7) weeks (w). HBsAg (Abbott) and HBV-DNA (Roche) were measured at: -12w, DAAAs baseline (BL), 4w, End of Therapy (EOT), EOT + 12w (24w), EOT + 24w (36w) and EOT + 48w (60w).

**Results:** No significant difference between ENI and CHB were observed in BL Liver Stiffness (10.5 vs 15.7 kPa; p = 0.495), ALT (51 vs 44 U/l; p = 0.495) and HCV-RNA (6.2 vs 6.0 Log IU/ml; p = 0.561), whereas HBsAg levels were lower in ENI than in CHB (0.88 vs 2.42 Log IU/ml; p = 0.035). At BL HBV-DNA was undetectable or <10 IU/ml in 5 and 3 ENI; it was undetectable in all NA treated CHB and remained so thereafter. All pts achieved SVR for HCV and normalized ALT. During DAAAs, HBV-DNA increased >1 Log or became detectable >100 IU/ml in 5 and 2 ENI, respectively (overall: 46.7%); however, a trend for higher mean Log values at 4w (p = 0.100) and at EOT (p = 0.104) as compared to BL (Figure). Mean Log HBsAg levels significantly decreased in ENI from >12w to BL (p = 0.002), but not in CHB (p = 0.564). During DAAAs a significant decline occurred at 4w in both ENI (p = 0.020) and CHB (0.015), followed by a rebound at EOT in ENI only. After DAAs, HBsAg returned progressively to pre-DAAs levels in CHB, whereas continued to decline in ENI (6 cleared HBsAg). Among factors associated to a greater HBsAg decline during DAAs, there was a trend for SOF in the schedule (p = 0.083).

**Conclusion:** In ENI co-infected with HCV, reactivations of HBV during DAAs led to moderate increases of HBV-DNA, without clinically relevant events. DAAAs caused a significant HBsAg decline during therapy, however, such effect did not appear able to modify the pre-treatment individual profile, which was more favorable in untreated ENI than in CHB under NAs.

**THU395**

Predictors of advanced liver fibrosis in chronic hepatitis B patients in the daily clinical practice

Fadi Abu Baker1, Saif Mahmoud Abu Mouch2, Yael Kopelman2, Yana Davidov3, Ziv Ben Ari 3.

**Background and aims:** Staging liver disease severity using liver biopsy or, more recently, non-invasive tests such as elastography are important in guiding surveillance and assisting with treatment decisions in chronic hepatitis B (CHB) patients. The use of these tests, however, is not widely implemented as they are costly, used in limited centers, and not always covered by health insurances. Thus,
we aimed to elucidate simple clinical predictors of advanced liver fibrosis in patients with CHB in daily practice.

**Method:** We conducted a two-center, prospective study, recruiting CHB patients presenting to regular clinic visits in our hepatology units. A detailed medical history, including age, gender, ethnicity, BMI, medical background and medications, HBV infection status and treatment, as well as smoking and alcohol drinking habits were documented. Laboratory results performed within 1 month before or after the clinic visit were documented. During the clinic visit, all patients were referred for abdominal ultrasounds and all of them underwent two-dimensional shear wave elastography (2D SWE) to assess hepatic fibrosis. Univariate and multivariable logistic regression analyses were used to determine predictors of advanced fibrosis (F2≥ 7.2KPa<). 

**Results:** Of the 173 patients included in the final analysis, 40 (22%) had evidence of advanced fibrosis on 2D SWE. Age > 50 (OR 3.88, CI 1.49–9.73; p = 0.005), ALT > 40 (OR 7.41, CI 2.44–22.4; p = 0.001), HBV DNA > 2000 (OR 11.44, CI 3.19–41.02; P < 0.001), moderate to severe steatosis on US (OR 5.35, CI 1.82–15.8; P = 0.002) as well as moderate-excessive alcohol consumption and heavy smoking (>20 pack-years) were all independent predictors of advanced fibrosis.

**Conclusion:** We outlined clinical and laboratory variables that may were all independent predictors of advanced fibrosis. Excessive alcohol consumption and heavy smoking (>20 pack-years) are associated with MAFLD and sedentary life. In the multivariate analysis, low ALSTI were positively associated with MAFLD, sedentarism and high ABSI. Low HGS BMI was associated with MAFLD and high ABSI. After adjusting for confounders, in male patients, cirrhosis was independently associated with age >50 yrs., high ABSI and hepatic steatosis.

**THU397**
The course of COVID-19 infection in patients with chronic hepatitis B and Delta

Yavuz Emre Parlar1, Onur Keskin1, Beril Kirmizigüzel2, Genco Gencdal3, Mujdat Zeybel4, Mesut Gumussoy5, Ramazan Idilman6, Cihan Yurdaydın7.

1Hacettepe University School of Medicine, Gastroenterology, Turkey; 2Hacettepe University School of Medicine, Internal Medicine, Turkey; 3Koc University School of Medicine, Turkey; 4Ankara University School of Medicine, Gastroenterology, Turkey.

Email: onurkeskin81@gmail.com

**Background and aims:** SARS CoV–2-induced COVID-19 disease has caused as of November 2021 more than 5 Million deaths. Older age and co-morbidities such as liver cirrhosis have been associated with mortality (Bajaj et al, Hepatology 2020, Hamid et al JCG 2021). Among etiologies of liver disease only alcoholic liver disease was associated with mortality by multivariate analysis. Chronic hepatitis delta (CHD) had not been studied in this context. In the current study the course of COVID–19 disease in chronic hepatitis B (CHB) and CHD patients was explored in 2 academic hospitals.

**Method:** CHB and CHD patients followed in the gastroenterology departments of Hacettepe and Koc University Medical School Hospitals in Ankara and Istanbul were included in the study (n:551; 302M/249F). Median age was 47. While 479 of the patients had CHB, 77 patients had CHD. 372 of 479 CHB patients were receiving nucleos (t)ide analogs (NAs (TDF:221, ETV:107, LMV-TAF:37), 107 patients had not been studied in this context. In the current study the course of COVID–19 disease in chronic hepatitis B (CHB) and CHD patients was explored in 2 academic hospitals.

**Results:** In the CHB group (n:479), 43 patients (5 of them had cirrhosis) were diagnosed with COVID-19 infection. CHB patients with and without COVID-19 infection did not differ in terms of age, gender and laboratory parameters. No patient had a COVID-related death. ALT-AST reactivation, defined as an increase of ALT to more than 3x ULN, occurred in 3 patients (6.9%) including hepatic decompensation in 1 cirrhotic patient after COVID-19. None of the patients were followed up in the intensive care unit. In CHD patients (n:77; 37 cirrhotic), 8 patients developed COVID-19 infection and 4 had documented hepatic reactivation. None were receiving treatment for CHD. COVID–19 infection developed in 3 cirrhotic patients, of whom one died and one developed hepatic decompensation.

**Conclusion:** The course of COVID–19 infection is not severe in CHB patients but maybe so in CHD. This may be due to effective antiviral treatment in CHB but lack of it in CHD.
Background and aims: Soluble programmed cell death 1 (sPD-1) is a novel immunological marker which has been reported to be correlated to hepatocellular carcinoma in chronic hepatitis B in a case-cohort study. Although it has strong correlations with some viral markers such as qHBsAg, whether it is a predictor of HCC independent of other known host and viral risk factors remains to be explored. We aimed to investigate the association between sPD-1 levels and HCC development.

Method: Baseline serum samples from 3408 chronic hepatitis B subjects in the REVEAL-HBV cohort were assayed for sPD-1 level. Among them, 2934 with available follow-up serum samples were longitudinally analyzed. The ascertainment of HCC was done through the data linkage with the Taiwan Cancer Registry. Multivariate Cox regression analysis was used to estimate the adjusted hazard ratio (aHR) and 95% confidence interval (CI), adjusted for host and viral factors.

Results: By end of 2017, 344 HCC cases were newly developed. Both the baseline and follow-up sPD-1 level were higher in the HCC versus non-HCC patients. Despite there exists linear correlation between sPD-1 and HBsAg level (r = 0.59, P < 0.001), a dose-dependent increase of adjusted hazard ratio for sPD-1 and HBsAg level (r = 0.92, P < 0.001) or HBV DNA level (r = 0.59, P < 0.001) was marked when limited to subjects with low HBV DNA levels (<2000 IU/ml). By repeat measurement, those with sPD-1 level <944 pg/ml (Q1) at baseline or subsequent follow-up had minimal or decreased risk of HCC.

Conclusion: sPD-1 is another useful immunological marker in addition to the current markers used to predict HCC development in untreated CHB patients.
the absence of hepatitis B virus (HBV) when other co-infecting
viruses are present, such as hepatitis C virus (HCV), clinical evidence
for such unconventional HDV infections has not yet confirmed they
occur naturally in patients. As conventional HDV infection affects
the severity and progression of liver disease, it may also have the same
effects in a potential unconventional co-infection.

Method: To determine the prevalence of HDV unconventional HDV/
HCV infections, a series of HBV surface antigen negative (HBsAg-),
anti-HCV positive specimens were from Cameroon (≥87), Vietnam
(N = 100), and Uganda (N = 368) were screened for HDV antibodies
among patients (n = 284).

Results: 23 specimens were positive with both anti-HDV assays and 1
with 1 anti-HDV assay, indicating that the prevalence of potential unconventional HDV infections is 3% (11/368) in Uganda, 13.8% (12/
87) in Cameroon, and 2% (2/100) in Vietnam, consistent with the higher prevalence of conventional HDV infections in Cameroon and
Uganda compared to Vietnam. Notably, the reported dual anti-HDV
positives identified were also negative for HBV core antigen antibodies (anti-Hbc-), evidence that these individuals had not had a
past history of HBV infection. However, HDV RNA was not detectable
in these specimens, confirming that active HDV viremia had been
cleared in these patients despite detection of active HCV viremia
(HCV RNA+).

Conclusion: These data serve as the first clinical evidence of
unconventional HDV infections and indicate that unconventional
infections can be cleared even in the continued presence of chronic
HCV infection. This study also highlights the need for additional
screening for unconventional HDV infections to evaluate their
potential impact to patient health.

THU401

Rapid point-of-care test for hepatitis B core-related antigen
(HBcrAg) to identify HBV-infected patients eligible for antiviral
therapy.

Yusuke Shimakawa1,2, Gibril Ndow3,4, Théo Cerceau1, Amie Ceesay3,
Akira Hasegawa2, Atsushi Kaneko2, Katsumi Aoyagi3,
Jeanne Perpétue Vincent1, Takehisa Watanabe5, Masaya Baba2,
Bakary Sanneh2, Ignatius Baldeh2, Ramou Njie2,9,
Umberto D’Alessandro3, Maimuna Mendy10, Isabelle Chemin11,
Mark Thursz4, Maud Lemoine4, Yasuhito Tanaka6, Institut Pasteur;
2International Research Center for Medical Sciences (IRCMS), Kumamoto
University; 3Medical Research Council (MRC) Unit The Gambia at the
London School of Hygiene and Tropical Medicine; 4Department of
Metabolism, Digestion and Reproduction, Imperial College London;
5Fujirebio Inc.; 6Kumamoto University; 7National Public Health
Laboratories, Ministry of Health, The Gambia; 8Edward Francis Small
Teaching Hospital, Banjul, The Gambia; 9School of Medicine and Allied
Health Sciences, University of The Gambia; 10International Agency for
Research on Cancer (IARC), Lyon, France; 11Centre de Recherche en
Cancerologie, Université Claude Bernard, Lyon, France

Email: yusuke.shimakawa@pasteur.fr

Background and aims: To eliminate hepatitis B virus (HBV) infection,
it is vital to scale up testing services. However, conventional tools
to evaluate treatment eligibility, particularly real-time polymerase
chain reaction assays (RT-PCR) to quantify HBV DNA, are hardly
available and affordable in resource-limited settings. We developed a
simple, low-cost, lateral flow rapid diagnostic test to detect hepatitis
B core-related antigen (HBcrAg-RDT) and evaluated its performance
to diagnose clinically important HBV DNA thresholds (≥2, 000; ≥20,
000; and ≥200, 000 IU/ml) and select patients for antiviral therapy in
African patients.

Method: Analytical validation was performed using chemilumines-
cent enzyme immunoassay (CLEIA, LUMIPULSE G1200, Fujirebio,
Japan) as a reference. Clinical validation was conducted using sera
from 284 treatment-naïve patients with chronic HBV infection and 75
control participants negative for HBV surface antigen (HBsAg)
participated in the PROLIFICA (Prevention of Liver Fibrosis and
Cancer in Africa) programme in The Gambia.

Results: Using HBcrAg-CLEIA as a reference, the limit of detection of
HBcrAg-RDT was 4.3 log U/ml for serum and plasma, and 4.9 log U/ml
for whole blood. None (0/75) of HBsAg-negative samples was detected
by HBcrAg-RDT. In 284 treatment-naïve HBsAg-positive patients
(median age 36 years, interquartile range: 30–45, 66% were men), hepatitis B e antigen (HBeAg), HBcrAg-RDT, HBcrAg-CLEIA, and
HBV DNA were positive in 13%, 23%, 53%, and 58% of the participants,
respectively. HBV genotypes were E in 84% and A in 16%. The clinical
sensitivity and specificity of HBcrAg-RDT to identify highly viremic
individuals were: 72.7% and 91.7% to diagnose HBV DNA levels of ≥2,
000 IU/ml; 86.7% and 88.7% for ≥20,000 IU/ml, and 91.4% and 86.3%
for ≥200,000 IU/ml, respectively. A simplified HBV DNA-free
treatment algorithm using HBcrAg-RDT had a sensitivity of 96.6% and
specificity of 83.2% to identify HBV-infected patients eligible for
antiviral therapy by the European Association for the Study of the
Liver (EASL) criteria using the reference tests.

Table: Performance of HBcrAg-RDT, HBcrAg-CLEIA, and HBeAg-EIA to
discriminate clinically important HBV DNA levels in HBsAg-positive
patients (n = 284).

<table>
<thead>
<tr>
<th>HBV DNA levels</th>
<th>HBcrAg-RDT</th>
<th>HBcrAg-CLEIA</th>
<th>HBeAg-EIA</th>
</tr>
</thead>
<tbody>
<tr>
<td>≥20,000 IU/ml</td>
<td>72.7%</td>
<td>83.3%</td>
<td>91.7%</td>
</tr>
<tr>
<td>≥200,000 IU/ml</td>
<td>86.7%</td>
<td>88.7%</td>
<td>91.4%</td>
</tr>
<tr>
<td>≥2,000,000 IU/ml</td>
<td>91.4%</td>
<td>86.3%</td>
<td>93.2%</td>
</tr>
</tbody>
</table>

Conclusion: HBcrAg-RDT is a rapid (45 minutes), robust (operating
temperature up to 39 °C), and inexpensive alternative to HBV DNA
quantification potentially allowing the decentralisation of hepatitis
care in areas with limited access to laboratory services.

THU402

Prevalence of HBV infection and receiving antiviral treatment for
eligible patients in blood relatives from clustering families of HBV
infection with unfavorable prognoses and cascading of care
linked to treatment in West China

Yuan Yang1.1 The First Affiliated Hospital of Xi’an Jiaotong University,
Department of Infectious Disease, Xi’an, China

Email: yaxyangyuan@mail.xjtu.edu.cn

Background and aims: Accumulating evidence had shown that HBV
infection had the characteristic of family clustering, and higher risk of
progression to cirrhosis or HCC. Although many of the professional
organizations provide guidelines related to the prevention and
treatment of HBV infection, the cascade of care is still poor.

Method: First- and second-blood relatives from clustering families of
HBV infection with unfavorable prognoses, which were defined as
those families in which HBV infection patients occurred in three
successive generations, and there was more than one patient with
HBV-associated cirrhosis of liver or HCC in two generations, were
enrolled in the study, and general information and serum samples
were collected. Biochemical examinations were performed by the
Department of Laboratory, the First Affiliated of Hospital, Xi’an Jiaotong University. Virologic assessments included, HBV DNA (Roche), HBsAg, anti-HBs, HBeAg, anti-HBe, anti-HBc (Abbott Architect quantitative).

**Results:** Collected the liver function and virological features of the 1,568 participants from families with clusters of HBV infection and unfavorable prognoses included in this study. The patients with positive of HBsAg were 1033, and there were 351 (33.98%) patients receiving antiviral therapies. There were 451 (43.66%) patients with HBsAg-positive have not received antiviral treatment who should receive the antiviral treatment according to the 2019 Chronic hepatitis B Guideline of China, with age over 30 years with family with cirrhosis or HCC, or less than 30 years and ALT were elevated over upper limit normal (ULN). Patients were lack of awareness of screening before suggesting by the cascading of care linked to treatment for the blood relatives from clustering families of HBV infection with unfavorable prognoses. There were 535 participants with negative of HBsAg, and there were 278 (51.96%) participants with positive anti-HBc and 160 (29.91%) participants with only anti-HBs positive.

**Conclusion:** There were high prevalence of HBV infection in the families with clusters of HBV infection and unfavorable prognoses, and low prevalence of receiving antiviral therapies for patients eligible for treatment by professional practice guidelines. Cascading of care linked to treatment in families with clusters of HBV infection, could improve the treatment initiation rate.

**Background and aims:** Upper limits of normal (ULN) for alanine aminotransferase (ALT) are different among international guidelines or recommendations for chronic hepatitis B (CHB). We investigated the proportion of significant inflammation in Asian CHB patients with detectable HBV-DNA under diverse ALT ULNs.

**Method:** CHB patients with detectable HBV-DNA underwent liver biopsy were included from four hospitals. Liver inflammation and fibrosis were assessed by Scheuer’s classification. ULN was defined as 40 U/L in EASL 2017 and APASL 2015, 35/25 U/L (male/female) in AASLD 2018, and 30/19 U/L (male/female) in East Asia recommendations 2020. The definitions of significant inflammation and fibrosis were G ≥ 2 and S ≥ 2, respectively.

**Results:** Of 921 patients included, 640 (69.5%) patients had significant inflammation, while 577 (62.6%) had significant fibrosis. 85.6% of patients with significant fibrosis and 42.4% of patients without significant fibrosis had significant inflammation. Among CHB patients with detectable HBV-DNA and normal ALT, the proportions of those with significant inflammation was 43.8% according to the ALT ULN of 30/19 U/L (male/female), while the corresponding proportions were 53.1% and 48.1% according to the ULNs of 40U/L and 35/25U/L (male/female), respectively. In patients with detectable HBV-DNA and normal ALT levels in absence of significant fibrosis, the proportions of significant inflammation were comparable among different ULNs of ALT by 40 U/L (30.7%), 35/25U/L (27.3%) and 30/19 U/L (25.0%).
THU404
Diversity of circulating HBV genomes and impact on viral infection
Jules Sotty1, Aurélie Schnuriger1, Pierre Bablon1, Bouchra Lekbay1, Jeremy Augustin1, Morgane Girier-Dufournier1, Lucas Langlois1, Celine Dovival2, Fabrice Carrat2, Stanislas Pol1, Helene Fontaine1, Nazim Sarica4, Christine Nuveut2, Chantal Housset1, Dina Kremsdorf1, Patrick Soussan1. 1Inserm Sorbonne Université, CRSA Inserm U938, Paris, France; 2Inserm Sorbonne Université; 2Cochin, France; 3Institut de génétique humaine, Montpellier, UMR 9002, France

Background and aim: Besides the prototype of HBV infectious particle containing a 3.2 kb partially double-stranded DNA (wtDNA), additional circulating virus-like particles containing pregenomic RNA (pgRNA), spliced-RNA (spRNA) or spliced-derived DNA (defDNA) genomes have been described. Independently, detection of these circulating viral genomes may contribute to the clinical management of HBV infection and/or as a predictive marker of therapy response. Here, the diversity of circulating viral genomes was investigated in chronic infected patients then, its impact on viral lifecycle was explored.

Method: 335 chronic HBV infected patients treated (n = 158) or not (n = 177) were selected from the Hepather French Cohort. Pangenomic qPCRs were set up to quantify the four forms of circulating viral genomes from the same nucleic extract. Principal component analysis and hierarchical clustering were performed to characterize the circulating HBV genome diversity. Viral infection of differentiated HepG2-NTCP cells using blood samples from untreated patients was achieved to study its impacts on viral replication.

Results: Hierarchical clustering of circulating viral genome diversity in bloodstream divided untreated patients in 2 clusters. The cluster 1 (C1) was defined by the predominance (>50% of circulating genomes) of wtDNA while the cluster 2 (C2) contained various amount of the four viral genomes with a majority of pgRNA, wtDNA and defDNA in 77%, 18% and 5% of cases, respectively. Genomic diversity in C2 was associated with a higher level of viral load (7.1 ± 7.3 Log10 copies/ml of wtDNA), compared with C1 (6.6 ± 7.1 Log10 copies/ml of wtDNA; p < 0.001). The greatest proportion of circulating pgRNA forms was preferentially observed in high replicative patients in C1 and unexpectedly, in low replicative patients in C2. Analysis of treated patients reinforced the contribution of HBV replication in the genome diversity occurrence. In vitro infection with untreated patient samples from both clusters showed that viral diversity in inoculum modulated the intracellular viral cycle. Before infection, inoculum enrichment with pgRNA particles demonstrated their ability to interfere on viral cycle.

Conclusion: Our data provide evidences for the main role of viral replication in circulating HBV genomes diversity. Novel biomarker of HBV infection, circulating pgRNA genomes may also contribute to modulate the viral cycle in an unconventional process.

THU405
Chronic hepatitis delta with normal ALT and hepatitis D viremia
Sena Arici1, Adriana Palom2, Mesut Gumussoy3, Ramazan Idilman3, Genco Gencdal3, Rafael Esteban5, Mujdat Zeybel4, Maria Buti2, Cihan Yurdaydin4. 1Gulhane Training and Research Hospital, Internal Medicine, ANKARA, Turkey; 2Hospital Universitario Valle Hebron, Department of Gastroenterology, Barcelona, Spain; 3Ankara University, School of Medicine, Department of Gastroenterology, Ankara, Turkey; 4Koç University, School of Medicine, Department of Gastroenterology, ZEYTINBURNU, Turkey; 5Universitat Autònoma de Barcelona (UAB), Department of Gastroenterology, Barcelona, Spain

Background and aims: Chronic hepatitis delta (CHD) represents the most severe form of chronic viral hepatitis and the main cause of liver-related mortality due to suboptimal therapy. However, there is data to suggest that CHD runs a less severe course than in the past.

Conclusion: A quarter of CHB patients with detectable HBV-DNA and normal ALT without significant fibrosis had significant inflammation irrespective of the ALT ULNs. The optimal ULNs of ALT for CHB patients deserve further investigation and novel biomarkers for liver inflammation are urgently needed.
(Rosina et al, Gastro 1999, Wranke et al, JHV 2021). Patients with persistent normal ALT and hepatitis D viremia (PNAV) have been described for chronic hepatitis C and B but not for CHD.

**Method:** PNAV were arbitrarily defined as patients with normal ALT and hepatitis D viremia on at least four determinations, 3 to 6 months apart within a duration of 2 years among patients who had never received interferon-based treatment for CHD. Such patients have been collected between January 2005 to 2021 in 2 academic hospitals in Turkey and one in Spain. A total of 19 patients were found out of a cohort comprising around 420 patients. The 19 patients with PNAV were compared with sex and age-matched control patients with CHD at a 1 to 1.5 ratio. Follow-up of patients ranged from 18 months to 12 years.

**Results:** ALT, AST and GGT levels were lower and platelets were higher in PNAVs vs control CHD patients (29 IU/L [18–39] vs. 45 [23–178], 30 IU/L [24–43] vs. 52 [21–99] and 18 IU/L [13–48] vs. 57 [14–328], 240 x10^9/L [88–420] vs.114 [52–309], respectively, p < 0.05 for all comparisons). HDVRNA levels were similar (3.60 ± 1.11 vs 4.23 ± 1.43 IU/mL). Liver biopsy was available in 10 patients. Histologic activity index and fibrosis stage were lower in PNAVs vs controls (8[3–13] vs 10 [8–14] and 2 [0–4] vs 3 [2–6], p = 0.05 and p = 0.014, respectively). In the PNAV group, 2 patients had fibrosis stage 3 and 4 according to Ishak et al and one patient had cirrhosis on biopsy. Three additional patients had clinical or radiologic evidence of cirrhosis. On long-term follow-up patients normal ALT persisted. HDV RNA became undetectable in one patient.

**Conclusion:** This study suggests that a small subgroup of CHD patients may present with normal ALT and HD viremia and milder liver disease. However, underestimation due to referral bias is also likely. PNAV patients had compared to CHD patients lower ALT and GGT and higher platelet counts indicative of milder liver disease. Liver biopsy data confirm the latter. However, 3 out of 19 PNAV had clinical or histologic cirrhosis and 2 patients had moderate to severe fibrosis (Ishak score 3 to 4), suggesting that these patients may also need to be considered for treatment. Thus CHD patients with PNAV represent a heterogenous group and need careful assessment.

**THU406 Hepatitis B core related antigen, not as good as it seems: a critique and systematic review**

Yong Chuan Tan1,2, Celina Adraneda1, Ee Jin Yeo1, Guan Sen Kew2, Yeow Lua Lin School of Medicine, National University of Singapore, Department of Medicine, Singapore; 2National University Hospital, Division of Gastroenterology and Hepatology, Singapore

**Email:** mdcv341@nus.edu.sg

**Background and aims:** Hepatitis B core-related antigen (HBcrAg) is a new biomarker for chronic Hepatitis B (CHB) but its performance has not been critically or systematically appraised.

**Method:** We reviewed the biological pathway of HBcrAg. We also performed a systematic review of PubMed for studies that evaluated the role of HBcrAg in predicting important HBV specific clinical events and/or examined the strength of correlation of HBcrAg against other HBV biomarkers. Area under the receiver operating characteristic (AUROC) curve values and correlational coefficients were consolidated to appraise the predictive accuracy and correlational strength of HBcrAg. Median values from the pooled data were used as estimates and reported.

**Results:** HBcrAg consists of Hepatitis B core antigen (HBcAg), e antigen (HBeAg), and 22 kDa precore protein (p22cr). Individual contribution of HBeAg, HBcAg, and p22cr to HBcrAg in HBeAg positive CHB patients is 72 ± 10%, 17 ± 8%, and 15 ± 9% respectively. The constituent contribution to HBcrAg in HBeAg negative CHB patients is unknown. HBcrAg has a false positive rate of 9.3% and false negative rate of 12–35%. The new iTACT-HBcrAg assay is more sensitive but does not solve the false positive performance. PubMed search found 58 of 248 papers on HBcrAg suitable for analysis. Median AUROC for use of HBcrAg in predicting HBeAg seroconversion, HBsAg loss, treatment response, and relapse after stopping therapy is 0.794, 0.6445, 0.706 and 0.688 respectively. Median correlation coefficient (r) of HBcrAg with HBV DNA, qHBsAg, HBV RNA and cccDNA is 0.660, 0.4755, 0.698, and 0.590 respectively. Strength of correlation weakens after antiviral therapy.

**Conclusion:** HBcrAg is a suboptimal biomarker and performs best as a predictor of HBeAg seroconversion. Otherwise, its performance is moderate at best, and has poor correlation with HBsAg loss and antiviral therapy.

**THU407 Utilizing phenotyping algorithms as tools for increasing linkage to guideline-concordant care in patients at risk for hepatitis B**

Brooke Wyatt1, Anna Magera1,2, Stephanie Zhang1, Mark Miller1, Douglas T Dieterich1, Andrea Branch1. 1Icahn School of Medicine at Mount Sinai, New York, United States; 2Icahn School of Medicine at Mount Sinai, Liver Diseases, New York, United States

**Email:** brooke.wyatt@msm.edu

**Background and aims:** An estimated 241,000 (2.9%) NYC residents are living with chronic hepatitis B virus (HBV) infection. Management of HBV with antiviral drugs can slow disease progression and increase longevity. However, in the United States, only ~40–60% of patients with chronic HBV receive guideline-concordant care, and only ~3% of Americans with HBV receive antiviral treatment. There is a significant need to improve methods for identifying treatment-eligible patients and linking them to care. The Mount Sinai Health System (MSHS) serves the greater NYC area. Through this study, we aim to develop and validate an HBV case-finding algorithm that identifies diagnosed HBV-infected MSHS patients who are not receiving guideline-concordant antiviral treatment or monitoring, as defined by EASL or AASLD. This project builds on our previous success developing an algorithm to identify HCV treatment candidates performing with a sensitivity of 90.0%, specificity of 97.1%, positive predictive value of 85.7%, and negative predictive value of 98.1%.

**Method:** We will develop an algorithm to search ~2.5 million EPIC electronic medical records (EMRs; data entered 1/2003 to 12/2021). Death record data will be utilized to identify deceased patients. To enhance impact and portability, the algorithm will be written in SQL a versatile, widely used programming language. The algorithm will automate the interpretation of HBV serological data, ALT values, demographic information, and data about antiviral medications; and it will estimate fibrosis stage by calculating the FIB-4 score. It will categorize patients as a) receiving AASLD/EASL guideline-concordant treatment, b) not receiving guideline-concordant treatment and in need of follow-up, c) HBV negative, or d) deceased. Results will be stratified by treatment site. The algorithm is being developed iteratively, assessing each iteration by performing manual chart review at planned stages.

**Results:** The first iteration of the algorithm identified approximately 1,000 MSHS patients with an HBV DNA viral load >2,000 IU/ml and no record of a prescription for any HBV medication. Manual review of a random selection of 100 of these patients’ charts revealed that three patients had died, two were children, and four cleared HBV.
Conclusion: Our preliminary results are highly promising. Once refined and validated, the algorithm will allow us to identify patients in need of HBV outreach and care leading to evaluation for hepatitis D as well. It will also help to highlight clinical settings with suboptimal HBV care in our healthcare system. Applicable to other health systems utilizing EPIC EMR, our algorithm will be vital in streamlining case finding, freeing up resources for patient engagement and care, and advancing viral hepatitis elimination.

THU408 Hepatitis B virus antigen reduction effect of RO7049389 plus NUC with/without Peg-IFN in chronic hepatitis B patients

Jinlin Hou1, Edward J Gane2, Wenhong Zhang3, Jiming Zhang3, Man-Fung Yuen4, Tien Huey Lim5, Rozalina Balabanska6, Qing Xie7, Piyawat Komolmit8, Xieer Liang9, Wen Zhang2, Xue Zhou9, Zenghui Xue10, Miriam Triyatni11, Ethan Chen10, Yuchen Zhang9, Qingyan Bo10.

Background and aims: RO7049389 is a Class I HBV core protein allosteric modulator. In addition to potent suppression of HBV replication, in mouse model studies, RO7049389 also induced HBsAg and HBeAg reduction alongside transient and controlled immune responses. Here we report on HBV antigens reduction with RO7049389+NUC ± Peg-IFN in chronic hepatitis B patients.

Method: NUC-suppressed patients received RO7049389+NUC (Cohort A, n = 32); treatment-naïve patients received RO7049389+NUC without (Cohort B, n = 10) or with (Cohort C, n = 30) Peg-IFN-alpha for 48 weeks. At Week 48, all patients except those who met NUC stopping criteria (HBV DNA <LLOQ and HBsAg <100 IU/ml) entered a 24-week NUC-alone follow-up period.

Results: In Cohort A, 30 NUC-suppressed patients completed the study; no obvious changes in HBsAg, HBeAg or HBeAb were observed. In treatment naïve patients, no HBsAg loss occurred among 10 Cohort B and 27 Cohort C patients who completed the study. In Cohort B, at Week 48, HBsAg, HBeAg and HBeAb showed mean changes from baseline of +0.1 – 1.5 log10 IU/ml and –1.2 log10 IU/ml, respectively; 2/6 HBeAg+ patients achieved HBeAg loss without anti-HBe serocconversion. Two HBeAg+ patients had maximal HBsAg declines of 0.4–0.45 log10 IU/ml, both occurring after Grade 3 ALT flare.

Conclusion: RO7049389 did not induce obvious HBV antigen reduction in NUC-suppressed patients. RO7049389+Peg-IFN+NUC led to larger HBsAg declines, especially in difficult-to-treat Genotype C patients. HBeAg positivity and high HBsAg baseline levels seemed to positively modulate the ability of RO7049389+Peg-IFN+NUC to reduce HBsAg. Positive correlation between graded TEAFs and categorical maximal HBsAg declines may be consistent with the concept of a “good” ALT flare during RO7049389+Peg-IFN treatment.

THU409 Presence of HbeAg, HBV DNA in cord blood and down regulation of TLR9 may act as predictive marker for HBV mother to child transmission

Simanta Kalita1, Manash Jyoti Kalita1, Gautam Hazarika1, Partha Pratim Das2, Sangit Dutta2, Anjan Jyoti Talukdar2, Panchanan Das2, Subhash Medhi2,1, Gauhati University, Bioengineering and Technology, Guwahati, India; 2Gauhati Medical College and Hospital, Guwahati, India; 3Gauhati University, Guwahati, India Email: subhashmedhi@gauhati.ac.in

Background and aims: Hepatitis B virus infection is a global health problem which needs special attention mainly due to mother to child transmission of HBV. Expression pattern of TLR9 was analysed in venous cum cord blood samples collected from 25 HBsAg+ve mother during delivery from Gauhati Medical College and Hospital, Guwahati, Assam.

Method: HBsAg, HbeAg and HbeAb were detected using ELISA and TLR9 mRNA expression is performed by Real time PCR.

Results: Serological analysis of the venous blood (N = 25) showed the presence of HbeAg in 10 (40%) samples and HBV DNA+ve in 9 (36%) samples. Further, in cord blood samples (N = 25) HBsAg was positive in 17 (68%) and HbeAg was positive in 13 (52%) of the sample. HBV DNA was found to be positive in 13 (52%) of the sample. Among 25 samples, 10 samples (40%) with HbeAg positive status exhibit...
Patients with CHD coinfection have greater comorbidities, higher healthcare resource use and costs than CHB monoinfection—results from a Spanish national hospital database

Maria Buti, Ankita Kaushik, Mertxell Ascanio, Josep Darba, Nandita Kachru, 1Hospital Universitario Valle Hebron; 2Gilead Sciences, Inc.; 3BCN Health Economics and Outcomes Research SL; 4University of Barcelona

Email: Nandita.Kachru@gilead.com

Background and aims: Chronic hepatitis delta (CHD) coinfection among chronic hepatitis B (CHB) patients is associated with higher morbidity and mortality, given its relatively rapid progression to cirrhosis and liver-related complications. This retrospective study aims to compare baseline comorbidities, healthcare resource use (HRU) and costs in a matched cohort of adult patients with CHD coinfection versus (vs.) CHB monoinfection in a national hospital database in Spain.

Method: The study included subjects ≥18 years having ≥1 ICD-9-10-CM diagnosis code for CHD or CHB in the Spanish National Health System’s Hospital Discharge Records Database that covers 192 private and 313 public hospitals, with >40 million patients during the study period (Jan 1, 2000 to Dec 31, 2019). CHD and CHB cohorts were identified from Jan 1, 2001 to Dec 31, 2018 (identification period) with their first diagnosis defined as the diagnosis date, having ≥12 months of continuous enrollment before and after the diagnosis date. CHD and CHB patients were age- and gender-matched (1:3) to evaluate incremental differences in HRU and costs.

Results: The study reported 12,317 patients diagnosed with CHD or CHB, of which 3,079 (159 CHD; 2,920 CHB) met the inclusion criteria; matching yielded 125 CHD and 312 CHB patients. The male to female ratio was significantly higher in CHB vs CHD (roughly 10:1 vs. 5:1; p = 0.028). CHD patients were significantly more likely to have decompensated (50.4% vs. 20.51%; p < 0.0001) and compensated cirrhosis (24.80% vs. 9.62%; p < 0.0001) than CHB patients; hepatocellular carcinoma and liver transplant rates were at 6.40% vs. 2.56% and 5.60% vs. 1.52%, respectively. Charlson Comorbidity Index score was significantly higher for CHD than CHB (0.84 vs. 0.36; p < 0.0001). CHD patients also reported significantly higher rates of smoking (27.20% vs. 9.94%; p < 0.0001), HCV (11.20% vs. 5.45%; p = 0.0403), HIV (15.20% vs. 5.13%; p = 0.0013), substance abuse (23.20% vs. 5.77%; p < 0.0001) and alcohol abuse (20% vs. 7.37%; p = 0.0095) significant alteration in favour of downregulation of TLR-9 among the study cohort.

Conclusion: In the study, presence of HbeAg and HBV DNA in cord blood and down regulation of TLR9 may be an indication of vertical transmission of HBV.

Acknowledgements: The presenting author acknowledges Department of Science and Technology, Govt. of India, Ministry of Science and Technology, New Delhi-110016, for providing DST INSPIRE Fellowship vide sanction number: No. DST/INSPIRE Fellowship/2019/IF190163.

THU411 Clinical features predictive of cirrhosis in a large cohort of patients with chronic hepatitis delta infection—Insights from the D-LIVR trial

Ohad Etzion, Maria Buti, David Yardeni, Anat Nevo-Shor, Daniella Munteanu, Ingrid Choong, Lisa Weissfeld, Naim Abu-Freha, Rob Howard, Tarik Asselah, Pietro Lampertico, Ozana Tzanev, Ozana Tzanev.

Background and aims: Chronic hepatitis delta (CHD) infection is the most rapidly progressive form of chronic viral hepatitis. Data regarding predictors of cirrhosis in chronic HDV is fairly limited especially in those of younger age. The aim of the current analysis was to assess the predictive value of demographic and laboratory variables as well as non-invasive test scores of liver fibrosis for diagnosis of biopsy proven cirrhosis in a large cohort of patients CHD.

Method: We prospectively evaluated 407 patients with compensated liver disease who enrolled in the on-going Phase 3 HDV D-LIVR trial (NCT03719313). At baseline, demographic data and anthropometric measurements were collected. Liver stiffness measurement (LSM) and/or Fibrotest were performed, and blood tests were obtained for complete blood count, biochemical panel, and HBV and HDV serologic and viral markers. All patients underwent liver biopsy within 45 days from non-invasive testing. Descriptive statistics were used to summarize demographic and clinical baseline patient characteristics, and chi-square test was used for univariate and multivariate analysis. A series of logistic regression models was fit to the data including cirrhosis status as the outcome, and LSM results, AST, ALT, platelets, albumin, bilirubin, Fibrotest score, HbsAg, and BMI as potential covariates.

Conclusion: CHD coinfected patients had significantly greater comorbidities, HRU and costs than CHB monoinfected patients within an age- and gender-matched cohort of Spanish patients from a hospital database study over 19 years of duration. These findings further confirm the need for early linkage to care to alleviate future disease progression.
Results: Of the 407 patients enrolled to the study, median age of 42.7 (SE 0.55), 69.4% male, with 108 (26.5%) patients showing biopsy confirmed cirrhosis. Of those, 48 (44.4%) were ≤45 years of age. In patients ≥45 years of age (146), 60 (41%) were cirrhotic at baseline. In univariate analysis, the following variables were statistically significantly associated with cirrhosis: older age (p < 0.001), BMI (p = 0.02), AST (p < 0.001), but not ALT, platelet count (p > 0.001), albumin (p = 0.002), INR (p = 0.006), HBsAg levels (p = 0.03) by both LSM and Fibrotest (p < 0.001 for both). In multivariate logistic regression, the model that best fit the data included age, platelets, and Fibrotest result as covariates (p = 0.04, 0.007 and 0.008, for age, platelets and Fibrotest, respectively). Odds ratio was 1.032 (CI 1.001–1.064) for age, 0.98 (CI 0.98–0.99) for platelet count and 7.168 (CI 1.647–31.911) for Fibrotest. In the subgroup of patients ≤45 years of age, the model that best fit the data included LSM results, platelets, and INR (p = 0.04 for all). Odds ratio was 1.079 (CI 1.002–1.162) for LSM, 0.99 (CI 0.98–1.0) for platelet count and 66.9 (CI 1.176–999.999) for INR.

Conclusion: In a large cohort of patients with CHD, alarmingly high rates of cirrhosis were seen among younger patients with compensated liver disease. A high index of suspicion for cirrhosis should be maintained in this population especially as it ages, and in those showing subtle changes in markers of synthetic liver function and portal hypertension.

THU412
Establishment of a new diagnostic model for significant liver tissue damage in patients with chronic hepatitis B virus infection in the immune tolerance phase

Aijong Hu1, Suwen Jiang1, Xiaojun Shi2, Dedong Zhu1, Zheyun He2, Chenqian Zhu3, Lukan Zhang4, HwaMei Hospital, University of Chinese Academy of Sciences, Ningbo Institute of Liver Diseases, Ningbo, China; 1HwaMei Hospital, University of Chinese Academy of Sciences, Liver Disease Department, Ningbo, China; 2HwaMei Hospital, University of Chinese Academy of Sciences, Liver Oncology Department, Ningbo, China; 3Medical School of Ningbo University, Graduate School, Ningbo, China

Email: huaiyong@ucas.edu.cn

Background and aims: To establish a new diagnostic model for judging significant liver tissue damage in patients with chronic hepatitis B virus (HBV) infection in the immune tolerance (IT) phase.

Method: The clinicopathological data of 275 patients in the IT phase who underwent liver biopsy from January 2015 to November 2020 were included. According to the liver pathological changes, patients were divided into <G2 group and ≥G2 group, <S2 group and ≥S2 group, non-significant liver pathological damage group (G0 group, <G2 + <S2) and significant liver pathological damage group (G1 group, ≥G2 and/or ≥S2). The liver pathological changes and clinical features, the diagnostic models and their evaluation values for significant liver pathological damage were analyzed.

Results: Among 275 patients, 43 cases (15.64%) with liver histologic activity ≥G2, 30 cases (10.91%) with liver fibrosis ≥S2, and 55 cases (20.00%) met the liver pathological damage (G1, ≥G2 and/or ≥S2). The correlated independent risk factors affecting significant liver pathological damage were age, levels of hepatitis B e antigen, γ-glutamyltransferase, platelet, alkaline phosphatase and alanine aminotransferase (p < 0.05). The established diagnostic models included YG (≥G2), YS (≥S2), and YG/S (G1). The diagnostic values of YG/S were the highest for ≥G2 and GS1, the diagnostic values of YG and YS were the highest for ≥S2. The threshold of YG/S was 0.18, the sensitivity, specificity and negative predictive value were 78.18%, 73.64% and 93.10%, respectively. When YG/S <0.05, the sensitivity, negative predictive value and negative likelihood ratio were 98.18%, 97.96% and 0.08, respectively. When YG/S ≥0.25, the specificity and positive likelihood ratio were 90.45% and 5.14, respectively. When YG/S ≥0.30, the specificity and positive likelihood ratio were 95.91% and 9.33, respectively.

Conclusion: Approximately 20% of patients with chronic HBV infection in IT phase have significant liver pathological damage. The diagnostic model of YG/S (<0.05 or ≥0.30) has certain evaluation value for significant liver pathological damage and can avoid liver biopsy to a certain extent.

THU413
Provider factors shaping hepatitis delta screening

Dewan Giri1, Rohit Nathani2, Randy Leibowitz2, Carolina Villarreal2, Sidra Salman2, Gres Karim3, Bo Hyung Yoon4, Amreen Dinani5, Ilan Weisberg6, 1Cahn School of Medicine at Mount Sinai Beth Israel, Department of Medicine, New York, United States; 2Mount Sinai Morningside/West, Medicine; 3Mount Sinai Beth Israel, New York, United States; 4Mount Sinai Beth Israel/Morningside/West; 5Cahn School of Medicine at Mount Sinai; 6New York Presbyterian Brooklyn Methodist Hospital, United States

Email: dewan.giri@mountsinai.org

Background and aims: Hepatitis Delta is a defective RNA Virus that requires Hepatitis B Virus to propagate. Infection results in the most severe form of viral hepatitis and is associated with a high risk of cirrhosis and hepatocellular carcinoma. The global burden remains undefined despite its discovery almost 40 years ago. Increased public health measures saw a decrease in the incidence of HDV in the 1990s leading to under-testing and a complacent view of the HDV public health problem. Despite the resurgence of interest seen in the last few years, it continues to remain unrecognized, especially in the primary care setting. The objective of our study is to assess physician knowledge, attitudes, and behaviors toward hepatitis delta screening.

Method: An anonymous 6-question internet-based survey assessing knowledge, attitudes, and behavior around HDV was sent to internal medicine residents, primary care providers (PCP), gastroenterologists, and Gastroenterology Fellows at tertiary care hospital systems, New York, USA from 2/1/2022 through 03/20/2022.

Results: Approximately 200 surveys were sent, and a total of 121 (60%) responses were completed. There were 75 responses from PCP and 46 responses from Specialty Care Providers. Gastroenterologists and fellows were more likely to order HDV antibody than HDV RNA as a screening test than PCP (66% and 61% vs 18% and 22%). A substantial portion of PCPs (50%) and residents (33%) were unsure about appropriate screening tests for HDV. Less than one-third of PCPs (26%), residents (24%), and fellows (28%) identified chronic hepatitis B (CHB) in combination with additional risk factors (CHB +RF) as a criterion for HDV screening. Gastroenterologists were evenly divided between all CHB and CHB +RF patients (48% vs 44%) for screening. Majority (97%) of the participants acknowledged that HDV infection contributed to disease progression, 78% agreed that patients who have cleared HDV are at risk for re-infection and 63% agreed with the statement that the majority of the patients with HDV cleared the infection with treatment. Lack of knowledge of screening guidelines and lack of comfort interpreting results were the two most commonly cited barriers to HDV screening.
THU414
Changes of enhanced liver fibrosis score predict hepatocellular carcinoma in chronic hepatitis B patients receiving antiviral treatment
Yan Liang1, Terry Cheuk-Fung Yip1, Che To Lai1, Shuk Man Lam1, Yee-Kit Tse1, Vicki Wing-Ki Hui1, Henry IV Chan2, Vincent Wai-Sun Wong1, Grace Wong1.

Background and aims: Enhanced liver fibrosis (ELF) score is a widely used non-invasive assessment for liver fibrosis. We aimed to derive and evaluate an algorithm based on ELF score changes at three years apart to predict hepatocellular carcinoma (HCC).

Method: Antiviral treated chronic hepatitis B (CHB) patients who had two stored serum samples at about three years apart were included. ELF score was assessed by retrieving the two stored serum samples. Baseline was defined as the date of the first ELF results. The primary end point was the cumulative incidence of HCC.

Results: There were 445 CHB patients (mean age: 51.6 ± 10.3 years; male: 73.9%) included, among whom 57 (12.8%) patients developed HCC during the mean follow-up of 158 months. At baseline, 171 (38.4%) and 274 (61.6%) patients had mild/moderate and severe fibrosis respectively by ELF score (cutoff: 9.8). About three years later, 35.7%, 59.6% and 4.7% of patients had ELF score improved, stable and deteriorated, respectively. 150 patients with continuous low ELF score had lowest risk of HCC (4.0%). 21 patients with deteriorated ELF score had HCC risk increased from 5.8% to 19.0%. 159 patients with ELF score improved had HCC incidence reduced from 17.2% to 10.7%. 115 patients with continuous high ELF score had highest HCC risk (26.1%).

Conclusion: The algorithm based on ELF score changes at three years apart is a good predictor of HCC in CHB patients receiving antiviral treatment.

THU415
Trends in decompensated cirrhosis and hepatocellular carcinoma diagnosis among people with a hepatitis B notification in New South Wales: a population-based data linkage study
Syed Hassan Bin Usman Shah1, Maryam Alavi2, Behzad Hajari-zadeh1, Gail Matthews3, Marianne Martinello1, Mark Danta2, Janaki Amin4, Matthew Law3, Jacob George4, Gregory Dore1.1The Kirby Institute, UNSW Sydney, Viral Hepatitis Clinical Research Program, Sydney, Australia; 2The Kirby Institute, UNSW Sydney, Viral Hepatitis Clinical Research Program, Sydney, Australia; 3St Vincent’s Hospital Sydney, Darlinghurst, Australia; 4Macquarie University, Department of Health Systems and Populations, Macquarie Park, Australia; 5Kirby Institute, Kensington, Australia; 6Westmead Hospital, Westmead, Australia

Background and aims: Population-level trends and factors associated with hepatitis B virus (HBV)-related decompensated cirrhosis (DC), hepatocellular carcinoma (HCC), and liver mortality are crucial to evaluate therapeutic intervention impacts.

Method: Trends in HBV-DC and -HCC diagnoses and liver-related mortality in New South Wales, Australia, were determined through linkage of HBV notifications (1993–2017) to hospital admissions (2001–2018), mortality (1993–2018), and cancer registry (1994–2014) databases. Late HBV notification was defined as notification at or within two years of DC and HCC diagnosis. Cox proportional hazards regression and multivariable logistic regression analyses were performed to evaluate factors associated.

Results: Among 59,911 people with HBV notification, 1,196 (2.0%) DC and 1,001 (1.7%) HCC diagnoses, and 1,158 (1.9%) liver-related deaths were documented. Since early 2000s, DC and HCC diagnoses numbers increased; however, age-standardised incidence decreased from 2.58 and 1.99 in 2003 to 0.96 and 0.95 per 1,000 person-years (PYs) in 2017. Similarly, age-standardised liver mortality decreased from 2.64 in 2003 to 0.97 per 1,000 PYs in 2017. Among people with DC and HCC diagnoses, late HBV notification declined from 41% and 40% during 2001–2009 to 28% and 26% in 2010–2018, respectively.

Conclusion: In an era of improved antiviral therapies, HBV liver morbidity and mortality risk has declined. HCV co-infection and alcohol-use disorder are key modifiable risk factors to HBV disease burden.
Background and aims: In low endemic countries, screening for hepatitis B surface antigen (HBsAg) in migrants is cost-effective to reduce the disease burden of hepatitis B virus (HBV) infections, but linkage to care (ICT) remains a challenge. We previously found outreach screenings for HBV using point of care tests (POCT) to result in a 2.5 times higher ICT compared to venepunctures in an Asian migrant population. In the current study we compared ICT between different ethnic groups screened for HBsAg with POCT in an outreach setting. A secondary objective, was to compare the estimated HBsAg seroprevalence for ethnic minorities to the established prevalence in the general population in order to guide future screening initiatives.

Method: Opportunistic outreach screenings using finger prick Vikia HBsAg tests were performed at municipal integration classes between 11/2017 and 03/2021. If tested positive, an appointment was given immediately at the outpatient hepatology clinic for follow-up and confirmation of HBsAg positivity in blood. A dedicated nurse contacted identified patients via phone, social media or home visits to motivate them for further linkage to care. The latter was defined as having received medical care from a hepatologist, a blood test and an abdominal ultrasound.

Results: A total of 521 persons with different ethnicities (Asia, Middle-East and Africa) were serologically screened using POCT tests. The seroprevalence for HBsAg was 3.45% (18/521) and was significantly higher compared to that of the general population (i.e. 0.66% in 2003 (p < 0.0001)). All HBsAg-positive patients were linked to care and assessed by a hepatologist. ICT for all ethnicities combined (p < 0.0001), for Sub-Saharan African patients (p = 0.023) and Middle-Eastern patients (p < 0.0001) was significantly higher compared to the previously observed rate of 34.38% (11/32 patients) using venepunctures as a screening method, but without the commitment of a dedicated nurse. Among the HBV infected patients, 22.22% (4/18), 83.33% (15/18) and 22.22% (4/18) met criteria for treatment indication, intrafamilial transmission risk and HCC surveillance respectively. Despite COVID-19 pandemic, linkage to care remains high using POCT and through the commitment of a dedicated nurse. However, the time frame between screening and the first hospital visit is significantly higher (p = 0.0049) during the COVID-19 pandemic than in the pre-pandemic period.

Conclusion: HBsAg seroprevalence in ethnic minorities is higher than the general population and warrants targeted screening. Most of the identified patients meet the indication for treatment, counseling to prevent intrafamilial transmission or HCC surveillance. In addition, the use of POCT and commitment of a dedicated nurse can overcome previously identified barriers for linkage to care.
year, 10-year, and 15-year CI were 2.8%, 6.7%, and 9.7%, respectively, with greater than 259 ml in spleen volume, compared with 1.9%, 3.2%, and 5.0% with less than 259 ml of spleen volume (p=0.001). In DM development, the estimated 5-year, 10-year, and 15-year CI were 1.0%, 2.6%, and 5.8% with more than 7604 mm² in abdominal VFA, significantly different from 0.6%, 1.4%, and 2.5% respectively below 7604 mm² of abdominal VFA (p=0.001).

Conclusion: A larger spleen volume was significantly associated with HCC occurrence and hepatic decompensation, and a higher abdominal VFA was strongly correlated with DM development in patients with CHB. Automatically measured spleen volume and abdominal VFA might be used as relevant prognostic biomarkers in CHB patients.

THU418
Analysis on the normal threshold of alanine aminotransferase level based on liver pathology in patients with chronic hepatitis B
Airong Hu¹, Suwen Jiang¹, Xiaojun Shi¹, Dedong Zhu², Zheyun He³, Tukan Zhang⁴, Chenqian Zhu⁴.
¹Hwamei Hospital, University of Chinese Academy of Sciences, Ningbo Institute of Liver Diseases, Ningbo, China; ²Hwamei Hospital, University of Chinese Academy of Sciences, Liver Oncology Department, Ningbo, China; ³Hwamei Hospital, University of Chinese Academy of Sciences, Liver Disease Department, Ningbo, China; ⁴Medical School of Ningbo University, Graduate School, Ningbo, China
Email: huairong@ucas.edu.cn

Background and aims: To comparatively analyze the liver pathology and clinical characteristics in chronic hepatitis B virus (HBV) infected patients with normal alanine aminotransferase (ALT) of different upper limits of normal (ULN), and to explore the normal threshold of ALT for initiating treatment.

Method: The clinical data of 667 chronic HBV infected patients who underwent liver biopsy from January 2014 to December 2020 were included in this study. The inclusion criteria were ALT <ULN and HBV DNA positive (>30 IU/ml). According to the ULNs of ALT, the enrolled patients were divided into ALT I group (male for <30 IU/L, female for <19 IU/L), ALT II group (30 IU/L ≤ male <35 IU/L, 19 IU/L ≤ female ≤25 IU/L) and ALT III group (35 IU/L ≤ male ≤40 IU/L, 25 IU/L ≤ female ≤40 IU/L). The clinicopathological characteristics and their correlation, and the ALT cut-off value for significant liver pathological damage were analyzed.

Results: The constituent ratios of GS II (G ≥2 and/or S ≥2) in the three groups were 26.05% (99/380), 32.03% (41/128) and 46.54% (74/159), respectively. And there were significant differences in the mean R idol values of G and S and the constituent ratios of G II (G≥2), S II (G≥2 and/or S≥2) and GS II among the three groups (p<0.001). There were significant differences in the constituent ratios in gender and HBsAg staining positivity, and the levels of ALT, aspartate aminotransferase (AST), A/PL, I/F, S among the three groups (p<0.01). The positively correlated factor that affect the liver tissue damage was γ-glutamyl-transferase level, and the negatively correlated factors were PLT, albumin/globulin and HBV DNA levels. The ALT thresholds for G I (G≥2) and G II, S I (G≥2 and/or S≥2) and GS II in total patients were 21.5 IU/L, 22.5 IU/L, and 25.6 IU/L, respectively. And those of male patients were 25.6 IU/L, 23.5 IU/L, and 25.6 IU/L, respectively. Those of female patients were 17.5 IU/L, 22.5 IU/L, and 25.5 IU/L, respectively.

Conclusion: There are statistically significant differences in the significant liver pathological damage in chronic HBV infected patients with normal ALT of different ULN. The normal threshold (diagnostic cut-off value) of ALT for judging significant liver pathological damage is recommended to be adjusted to 25 IU/L.

THU419
Prevalence rates and eligibility for antiviral treatment against hepatitis B in Casamance, Senegal
Victor Arendt¹, Maame Aisie Thioyebou², Kalilou Diallo³, Henri Goedertz², Daouda Diouf⁴, Benjamin Samboub⁴, Chabi Bindia⁴, Ousseynou Cisse⁵, Salimata Camara⁶, Noel Manga⁷, Esther CalvoLassoDeVeiga⁸, Boubacar Diouf⁹, ¹Centre Hospitalier de Luxembourg, Infectious Diseases, Luxembourg, Luxembourg; ²Hôpital de la Paix, Gastroenterology, Ziguinchor, Senegal; ³SANACCESS, Psychology, Luxembourg, Luxembourg; ⁴Enda Santé, Epidemiology, Ziguinchor, Senegal; ⁵Centre de Sante Silence, Medicine, Ziguinchor, Senegal
Email: vic_arendt@yahoo.fr

Background and aims: HBV infection is a major public health problem in Casamance, southern Senegal. A cohort of HBV carriers has been set up within the framework of the CARES program. The objective of this study was to assess the prevalence of HBV in the region and the antiviral treatment needs of patients in this cohort based on current recommendations.

Method: Descriptive multicenter cohort study of patients followed in four health facilities in the region (Bignona and Ziguinchor health centers, Regional and La Paix hospitals), carried out as part of the CARES program from January 01, 2019 to December 31, 2021. Screening for HBsAg was performed with kits from Rapid Signal TM HBsAg Serum/Plasma Dipstrip (Orgenics Ltd Israel). Treatment eligibility was assessed based on age, family history of severe HBV-related disease, degree of fibrosis, HBe antigen, viral load and transaminase levels according to WHO, EASL and the TREAT-B score.

Results: HBV prevalence rates were: 8% in blood donors, 9,7% in bus drivers, 7,7% in fishermen; 8,5% in health care workers, 6% in women living with HIV (WLHIV), 5, 5% in pregnant women, 0% (0/88) in children born to WLHIV. We included 1449 HBsAg positive patients. The mean age was 35.6 years with a sex ratio (M/F) of 1, 37. The predominant circumstances of screening were: blood donation (368 cases), symptoms or medical consultation (306 cases), antenatal screening (167 cases), routine or occupational health visit (148 cases) and a screening campaign (151 cases). To assess the need for treatment we analyzed the available results of the following tests: viral load (969/1449); transaminases and GGT (1153/1449); HBe antigen assay (846/1449), Fibroscan (830/1449), AST-platelet ratio index (609/1449), Fib-4 score (608/1449), history of cirrhosis or hepatocellular carcinoma in first degree relatives (8/463). The complete panel of parameters was available in only 315 patients. The proportion of eligible patients according to the different recommendations was 6,3% (WHO 2015), 8,9% (WHO simplified), 7,6% (EASL 2017), 8% (TREAT-B).

Conclusion: The prevalence of HBV in Casamance remains high. The proportion of HBV patients eligible for antiviral treatment ranges from 6, 3 to 8, 9% with only small differences according to the different consensus recommendations (WHO 2015, EASL 2017, TREAT-B).

THU420
Comorbidity, and not viral load, are predictors of cirrhosis in AgHBe-negative chronic infection
Sara Archer¹, Luis Maia¹, Catarina Afonso², José Manuel Ferreira¹, Teresa Moreira¹, Marta Rocha¹, Tiago Pereira Guedes¹, Isabel Pedroto¹, ¹Centro Hospitalar Universitário do Porto, Portugal; ²Instituto de Ciências Biomédicas Abel Salazar, Portugal; ³Instituto de Ciências Biomédicas Abel Salazar, Porto, Portugal
Email: u13418@chporto.min-saude.pt

Background and aims: There is an ongoing debate about the heterogeneity of the definition of HBeAg-negative chronic HBV infection (formerly inactive carriers, IC), which patients to treat, and how comorbidities can influence its natural course. The aim of our study is to assess risk factors, including higher viral load (VL) and increased ALT, for cirrhosis.
Method: This is a retrospective cohort of chronic HBV hepatitis patients with at least 2 consultations between 2010–2020 in a western center Mediterranean tertiary centre. Demographic and clinical data were retrieved. Individuals with less than 1 year of follow-up, HCV or HIV co-infection and with insufficient data were excluded. Statistical analysis was performed using SPSS. As per EASL guidelines, upper limit of normal (ULN) of 40U/L for ALT was considered.

Results: 635 patients were included, of which 340 as IC. From these, 53.5% were men with mean current age 56.16 ± 13.4 years, mean follow-up of 10.14 ± 8 years, during which 4.1% developed cirrhosis. Liver-related mortality was 0.9%. 14.5% patients had excessive alcohol consumption; 12.4% diabetes, 15.9% arterial hypertension and 18.2% dyslipidemia.

Risk factors for cirrhosis: diabetes (OR 4.8, p = 0.002), arterial hypertension (OR 7.3, p = 0.000), dyslipidemia (OR 4.4, p = 0.004), alcohol (OR 4.91, p = 0.002), ALT > ULN or VL > 2000 IU/ml (OR 5.32, p = 0.005). On multivariate analysis including age and follow-up time, none was an independent predictor.

When analysed separately, alcohol (OR 18.31, p = 0.031) predicted cirrhosis in patients with both ALT < ULN and VL < 2000 IU/ml, while in the others diabetes (OR 4.4, p = 0.028) and arterial hypertension (OR 5.4, p = 0.012) were the main predictors. This may be justified as alcohol abuse has less influence in ALT values.

The cut-off of 2000 IU/ml for VL did not predict development of cirrhosis in any group of patients.

Conclusion: In our cohort, comorbidities, and not VL, are predictors of cirrhosis in IC. Treating HBV in these patients may not be as relevant as controlling comorbidities. Our results support EASL current guidelines.

THU422

A systematic literature review and meta-analysis of primary sources reporting health state preference values in chronic hepatitis B, C, and D

Ankita Kaushik1, Sarah Hofmann2, Marijãoango Janeiro2, Geoffrey Dushielvo3,4, Andrew Lloyd1, Filipa Aragão2,6, Gilead Sciences, Inc., Foster City, California, United States; 2Maple Health Group, New York, United States; 3University College London, Medical School, London, United Kingdom; 4King’s College Hospital, London, United Kingdom; 5Acaster Lloyd Consulting Ltd, London, United Kingdom; 6Universidade NOVA de Lisboa, NOVA National School of Public Health, Public Health Research Centre, Lisbon, Portugal

Email: ankita.kaushik@gilead.com

Background and aims: Chronic viral hepatitis is associated with severe patient impairment and reduction in health-related quality of life (HRQoL). This is also reflected in low patient health state preference values (utilities) for severe health states. Utilities for health states are essential variables for cost effectiveness analyses for treatments. This study aimed to derive utilities for health states in chronic hepatitis B (cHBV), C (cHCV) and D (cHDV) through a systematic literature review (SLR) and meta-analyses (MA).

Method: Electronic literature databases (EMBASE and MEDLINE) were searched for primary articles that reported health state utilities for cHBV, cHCV or cHDV. Health states evaluated include Metavir fibrosis stages F0 to F4, compensated cirrhosis (DC), hepatocellular carcinoma (HCC), post-liver transplant (LT), post-LT in year (Y1), and post-LT in year 2 and beyond (Y2). 47 studies were included. Utilities were derived using four preference elicitation methods: EQ-5D, HUI-3, HUI-2, and SF-6D. This is the first meta-analysis of health state utilities, likely due to the variation in the methods used and health states considered. The most comprehensive set of health state utility estimates were derived using EQ-5D for cHCV and from a combination of instruments for cHBV. This is the first meta-analysis of utilities in chronic viral hepatitis which could be used in future economic evaluations.

Immune-mediated and cholestatic disease: Clinical aspects

THU422

Hepatitis B transmission in early life in very remote Aboriginal communities in northern Australia

Richard Sullivan1,2,3, Jane Davies1,2, Paula Binks3, Melita McKinnon1, Roslyn Dhurrray1, Kelly Hosking1,4, Sarah Bukulatji5, Stephen Locarnini1, Margaret Littlejohn6, Steven YC Tong7, 8, Joshua Saul Davis1,8, Menzies School of Health Research, Charles Darwin University, Darwin, Australia; 8Department of Infectious Diseases, Royal Darwin Hospital, Darwin, Australia; 1Department of Infectious Diseases, Immunology and Sexual Health, St George and Sutherland Clinical School UNSW, Kogarah, Australia; 9Population and Primary Health Care, Top End Health Service Northern Territory, Darwin, Australia; 2Miwajt Health Aboriginal Corporation, Northern Territory, Australia; 3Victorian Infectious Diseases Reference Laboratory, Peter Doherty Institute for Infection and Immunity, Royal Melbourne Hospital and University of Melbourne, Melbourne, Australia; 4Department of Infectious Disease Service, The Royal Melbourne Hospital and Doherty Department University of Melbourne at the Peter Doherty Institute for Infection and Immunity, Melbourne, Australia; 5John Hunter Hospital, New Lambton Heights, Australia

Email: richie.sullivan@menzies.edu.au

Background and aims: Chronic hepatitis B is a public health concern in Aboriginal communities of northern Australia with prevalence almost four times the non-Aboriginal population in the Northern Territory. Infection is suspected to occur in early life, however, the mode of transmission and vaccine effectiveness is not known in this population. WHO has set a target for hepatitis B elimination by 2030; elimination in this disproportionately affected population will require understanding of transmission and vaccine effectiveness.
Method: We conducted the study at four very remote communities. We approached mothers who were Hepatitis B surface antigen (HBsAg) positive and gave birth between 1988 and 2013. We obtained hepatitis B serology, immunisation and birth details. If both mother and child had hepatitis B viral DNA detected, we performed viral whole genome sequencing.

Results: We included 20 mothers and 38 of their children. The median age of the children was 8.8 years (IQR 5.7–13.0). Of 33 children with results available, 8 (24.2%, 95%CI 11.1–42.3) were anti-HBsAg positive, 3 (9.1%, 95%CI 1.9–24.3) of whom were also HBsAg positive. Hepatitis B immunoglobulin (HBIG) had been given at birth in 29 (76.3%, 95%CI 59.8 – 88.6) children and 26 children (68.4%, 95%CI 51.3–82.5) were fully vaccinated. Of the 3 children who were HBsAg positive, all had received HBIG at birth and two were fully vaccinated. Of the 5 who were anti-HBc positive and HBsAg negative, 4 had received HBIG at birth and one was fully vaccinated. Whole genome sequencing revealed one episode of mother to child transmission.

Conclusion: Although uncommon, there is ongoing transmission of hepatitis B in Aboriginal communities of northern Australia despite vaccination, and is likely occurring by both vertical and horizontal routes. Prevention will require ongoing investment to overcome the many barriers experienced by this population in accessing care.

THU423
the changing scenario of HBV chronic related disease in the transplant setting
Sara Battistella1, Martina Gambato1, Umberto Cillo1, Alberto Zanetto1, Alessandro Vifica1, Enrico Gringeri1, Marco Senzolo1, Patrizia Burra1, Francesco Paolo Russo1, 1University of Padova, Department of Surgery, Oncology and Gastroenterology, Italy Email: sarabattistella93@gmail.com

Background and aims: Hepatitis B virus (HBV) related chronic liver disease is one of the most common indication for liver transplantation (LT), for both decompensated cirrhosis and hepatocellular carcinoma (HCC). Introduction of nucleotide analogues (NA) significantly modified the natural history of the disease in the pre- and post-transplant setting, preventing decompensation of liver disease, disease recurrence and increasing post- LT patient and graft survival. This study aimed to assess the evolution of admission and management of patients affected by HBV-related liver disease in the WL for LT relatively to the introduction and spreading of high barrier NA and to evaluate overall long-term graft and patient survival after LT.

Method: All adults with HBV listed for LT at Padua University Hospital between 01.2006 to 12.2020 were retrospectively evaluated. Patients were divided in two groups according to their indication to inclusion in the WL (decompensated cirrhosis group: patients listed with MELD >15 with or without HCC; HCC group: patients with MELD <15 and presence of HCC). Patients were further divided according to the time of inclusion in the WL (2006–2013 and 2014–2020). For each patient, we evaluated the antiviral treatment and HBV DNA at the time of inclusion in WL and the type of prophylaxis after LT. Patient survival were calculated using Kaplan Meier curves and comparison between different groups were performed using Log-Rank test.

Results: From 01.2006 to 12.2020 a total of 1502 patients included in the WL for LT, among them 186 patients were HBV infected. One fourth of patients had HBV DNA detectable at the time of inclusion in the WL and 86% were on antiviral treatment. Almost 60% of patients were wait-listed for compensated disease, 30% of them had HCC as well. Eventually 31 patients were excluded from the waiting list: 17 for HCC progression, 3 for not liver related causes and 11 for stability of the disease, principally after the introduction of high barrier NA treatment. A total of 29 patients died in the waiting list, mainly during the first period of the study, and 126 patients underwent LT with a median waiting time of 6 months. The overall survival after LT was 90% at 1 year and 80% at 5 years. No significant difference in survival were observed between HBV patients transplanted for decompensated cirrhosis and those for HCC. Almost all HBV patients were treated with a combination therapy of HBIG and NA after LT and we recorded only 2 cases of transitory HBV reactivation, with no consequences on liver function.

Conclusion: HBV still remains one of the most common indication to LT, both for end stage liver disease and hepatocellular carcinoma. Thanks to high barrier NA the mortality in the waiting list is decreased during the last years.

THU431
Outcomes of pregnancy in patients with autoimmune hepatitis in the Netherlands
Susan Fischer1, Elsemieke de Vries1, Ynto de Boer2, Adriaan Van der Meer3, Robert De Man4, Johan Kuyvenhoven4, Michael Klemt-Kropp5, Tom Gevers6, E.T.T.L. Tywa7, Edith Kuiper8, Marc A.M.T. Verhagen9, Philip W. Friederich10, Bart Van Hoek1, 1Leiden University Medical Center (LUMC), Gastroenterology and Hepatology, Leiden, Netherlands; 2Academic Hospital Maastricht, Gastroenterology and Hepatology, Maastricht, Netherlands; 3Radboud University Medical Center, Gastroenterology and Hepatology, Nijmegen, Netherlands; 4Maassstad Hospital, Gastroenterology and Hepatology, Rotterdam, Netherlands; 5Erasmus MC, Gastroenterology and Hepatology, Rotterdam, Netherlands; 6Sparna Hospital Hoofddorp, Gastroenterology and Hepatology, Hoofddorp, Netherlands; 7Noordwest Ziekenhuisgroep locatie Alkmaar, Gastroenterology and Hepatology, Alkmaar, Netherlands; 8Academic Hospital Maastricht, Gastroenterology and Hepatology, Maastricht, Netherlands; 9Radboud University Medical Center, Gastroenterology and Hepatology, Nijmegen, Netherlands; 10Meander Medical Center, Gastroenterology and Hepatology, Amersfoort, Netherlands Email: s.e.fischer@lumc.nl

Background and aims: Data regarding the outcomes of pregnancy in patients with autoimmune hepatitis (AIH) are limited. This study focuses on the effects of pregnancy in AIH patients and neonatal outcomes.

Method: A retrospective multicenter cohort study was performed at the Leiden University Medical Centre (LUMC) in collaboration with nine participating hospitals from the Dutch Autoimmune Hepatitis Study Group in the Netherlands. Data concerning maternal and neonatal outcomes during and after pregnancy were collected from medical records in AIH patients with pregnancy. Risk factors were identified using logistic regression analysis to examine the association of defined risk variables with adverse maternal and neonatal outcomes.

Results: 93 pregnancies in 47 women resulted in 66 deliveries (71%) with a live birth rate of 98.5%. Preterm birth was mentioned in 20% and 19% of the children were born dysmature. 34% of the neonates were admitted to the hospital after birth. Flares of disease activity occurred in
4.5% during pregnancy, and in 26% of the postpartum episodes. The absence of biochemical remission at conception was identified as a risk factor for the occurrence of postpartum flares (Odds ratio (OR) 6.8, 95% Confidence Interval (CI) 1.6–7.65). Flares in the year before conception were identified as a risk factor for the occurrence of gestational flares (OR 21.6, CI 1.7–282.0) and were associated with the occurrence of postpartum flares (p = 0.01). Maternal hypertensive disorders during pregnancy occurred in 15%. Women who were partially in remission were at higher risk for loss of biochemical remission after delivery (OR 10.0, CI 1.5–67.0) and to develop hypertensive disorders during pregnancy (OR 10.3, CI 1.5–68.6). No risk factors were found for the occurrence of adverse neonatal outcomes. Cirrhosis was found a risk factor for miscarriages (OR 3.4, CI 1.1–10.8). No other correlations between the presence of cirrhosis and adverse outcomes for both mother and child were observed.

**Conclusion:** Pregnancy in women with AIH ended in childbirth in 71%. There was a high incidence of spontaneous abortion, prematurity, dysmaturity compared to the general population. The rate of postpartum flares of AIH was similar to previous literature. Absence of biochemical remission at conception and a flare in the year prior to conception increases the risk of maternal complications during and after pregnancy. Lastly, cirrhosis was found a risk factor for miscarriages.

**THU432 Cholangiopathy after severe COVID-19: what do we know so far?**

Valéria Ferreira de Almeida e Borges1, Helma Pinchemel Cotrim2, Marcelo Simão Ferreira3, José Humberto Caetano Marins4, Haroldo Luis Oliva Gomes Rocha1, Leonardo Augusto Dias Nascimento1, Mayra Machado Fleury Guedes1, Julia Esteves Guerra1, Universidade Federal de Uberlândia, Uberlândia, Brazil;2Universidade Federal de Uberlândia, Medicine School, Brazil;3Universidade Federal de Uberlândia, Medicine School, Brazil

Email: valeriafborges@gmail.com

**Background and aims:** From 2001 to 2018, before the Covid-19 pandemic, at least 16 studies described a type of secondary sclerosing cholangitis (SSC) in critically ill patients. During the pandemic, similar cases of cholangiopathy were observed in patients with severe Covid-19. The hypotheses suggested to explain this disease will be a liver ischemia related to microthrombosis associated with SARS-CoV-2 or direct biliary epithelial infection. To describe the clinical characteristics of cholangiopathy in patients who survived the ICU period with severe Covid-19.

**Method:** Adult patients diagnosed with Covid-19, who presented severe cholestasis were included. All of them had prolonged stay in the ICU, needed for mechanical ventilation, high doses of vasopressors, ketamine use, and prone positioning. Criteria for SSC were elevated levels of alkaline phosphatase (ALP) and bilirubin; no previous history of liver disease; magnetic resonance cholangiopancreatography (MRCP) or endoscopic retrograde cholangiopancreatography (ERCP), and or liver biopsy, which showed the biliary tract alterations. The diagnosis of Covid-19 was with a positive PCR test in all cases.

**Results:** A total of 24 patients were include. Mean age was 57 ± 10 years and 66% were male. All developed cholestasis, after a mean of 20 days. The peak mean level of ALP was 1541 U/L, gamma-glutamyl transferase 2366U/L, aspartateaminotransferase 248, alanine aminotransferase was 276 U/L, and total bilirubin 10 mg/dL. MRCP were performed in 75% of cases, ERCP in 37% and cholangioscopy in one. The most relevant finding was rarefaction of the intrahepatic bile ducts in all, and biliary cholangitis in two cases. Biliary casts were removed in seven of nine cases who underwent ERCP. All patients presented elevated levels of ALP, GGT and bilirubin after discharge, regardless of the ursodiol used. During the mean follow-up of 205 days, 6 patients progressed to cirrhosis and 7 (29%) to death. At follow-up, the most recent bilirubin dosage was on average 19 mg/dL in the group that died and 3.7 mg/dL in the group that survived (p < 0.001).

**Conclusion:** In this simple of 24 cases, patients with Covid-19 presented a severe cholestatic disease and with rapid progression to cirrhosis or obit. The role of SARS-CoV-2 seems relevant, however other factors associated should be considered: mechanical ventilation for a long time; high doses of vasopressors and possible severe hemodynamic instability; prolonged stay in the intensive care unit and the ketamine used.

**THU433 Enhanced liver fibrosis score correlates with transient elastography in patients with treated autoimmune hepatitis**

Anna Stoelinga1, Elseemieke de Vries1, Maarten Tushuijen1, Albert Stättermayer2, Xavier Verhelst3, Bart Van Hoek1, Leiden University Medical Center (LUMC), Gastroenterology and Hepatology, Leiden, Netherlands;2Medical University of Vienna, Wien, Austria;3Ghent University Hospital, Gent, Belgium

Email: b.van_hoek@lumc.nl

**Background and aims:** Cirrhosis is an important prognostic factor for long-term survival of patients with autoimmune hepatitis (AIH). Little is known about progression of fibrosis during adequate therapy. The Enhanced Liver Fibrosis score (ELF-score) has not been validated in patients with AIH. The aim of this study is to evaluate the diagnostic accuracy of the ELF test for fibrosis compared to transient elastography (TE).

**Method:** Patients with AIH or AIH-variant syndrome, treated for a minimum of 6 months at baseline (BL) were eligible for inclusion. Serum samples of all patients were taken and TE was done simultaneously at BL and after one year. Patients were divided into two groups: complete biochemical remission (CR) (group 1) and incomplete remission (group 2) at BL. ELF-scores and its components were calculated from the collected serum. We investigated if there is a correlation between the ELF score and liver elastography for severe fibrosis. Cut-off for cirrhosis (=F4 fibrosis) at TE was >16 kPa. A cut-off for the ELF score was determined for cirrhosis in a receiver operator characteristics (ROC) curve analysis.

**Results:** A total of 66 patients in three academic hospitals in the Netherlands, Belgium and Austria were included. 68.2% were female, mean age at inclusion was 51.20 years (±17.24), median treatment duration at inclusion was 6.50 years (IQR: 2.00–11.00). During follow-up, two patients died (3%), two patients were lost-to-follow-up (3%). Group 1 consisted of 35 patients (53.0%), of whom 16 (45.7%) had moderate-severe fibrosis. Group 2 consisted of 31 patients (47.0%). 24 patients (77.4%) had none-mild fibrosis. ELF-score (9.46 vs 9.27, p = 0.58) and liver stiffness (8.70 vs 7.10 kPa, p = 0.078) at BL did not differ significantly between the groups. Liver stiffness did not change after one year irrespective of remission status.

There was a positive correlation between ELF-score and liver stiffness (rho = 0.48, p < 0.001). For F4 fibrosis, the area under the curve was calculated as 0.83. The cut-off value was determined at 9.68. Sensitivity, specificity, positive and negative predictive value were 86.4%, 71.7%, 40.4% and 95.9%, respectively.

![ROC Curve](image-url)
Background and aims: Transforming growth factor beta (TGF-beta) signalling is a key driver of liver fibrosis. In primary sclerosing cholangitis (PSC), integrins over-expressed on injured cholangiocytes (alpha-v/beta-6) and myofibroblasts (alpha-v/beta-1) regulate TGF-beta activity. PLN-74809 is an oral, once-daily, dual-selective inhibitor of integrins alpha-v/beta-6 and alpha-v/beta-1 in development for the treatment of PSC and idiopathic pulmonary fibrosis. It has shown favourable tolerability in over 280 healthy participants, reduced TGF-beta signalling and achieved high target engagement in human lungs. Pre-clinical evaluation of antifibrotic activity resulting from dual integrin inhibition was performed to support clinical evaluation.

Method: PLN-74809 was administered orally for 6 weeks in BALBc.Mdr2-/- mice with established fibrosis. A tool alpha-v/beta-6 and alpha-v/beta-1 inhibitor compound, PLN-75068, was tested therapeutically in a diet-induced mouse model of biliary fibrosis using 3,5-diethoxycarbonyl-1,4-dihydrocollidine (DDC). Hepatic collagen was quantified by hydroxyproline (OHP) and collagen proportionate area (CPA) and TGF-beta signalling by phosphorylated SMAD3 (pSMAD3) levels. An ex vivo study evaluated the effects of 2-day treatment with PLN-74809 on the expression of profibrotic genes, COL1A1 and COL1A2, in precision-cut liver slices (PCLivS) from tissue explants of participants with biliary fibrosis (n = 2 PSC; n = 2 primary biliary cholangiitis [PBC]). A review of available blinded safety data from the enrolling Phase 2a study in participants with PSC was performed (NCT04480840).

Results: PLN-74809 dose-dependently reduced OHP (up to ~30%, p < 0.05), CPA (up to ~50%, p < 0.05) and pSMAD3 (up to ~40%, p < 0.001) in the BALBc.Mdr2-/- mouse model, as well as COL1A1 and COL1A2 gene expression (up to ~30%, p = 0.0789) in PCLivS from tissue explants of participants with biliary fibrosis and with PBC. PLN-75068 reduced OHP (up to ~20%, p < 0.05) in DDC-injured mice in a dose-dependent manner. PLN-74809 was well tolerated in participants with PSC. Most adverse events (AEs) were mild; none were severe. The most common AE was mild headache. One participant experienced serious AEs at least 20 days after the last dose of study drug, deemed not related by the investigator. One participant prematurely discontinued due to COVID-19. PLN-74809 pharmacokinetics in participants with PSC were consistent with those of healthy participants.

Conclusion: Pharmacological inhibition of integrins alpha-v/beta-6 and alpha-v/beta-1 demonstrated antifibrotic activity in two models of biliary fibrosis and in PCLivS from participants with PSC or PBC. Available safety findings from participants with PSC enrolled in the ongoing Phase 2a INTEGRIS-PSC study, continue to support the favourable tolerability profile of PLN-74809.
35/42 patients were treated with immunosuppressive drugs; 33 steroids, 1 azathioprine, 1 azathioprine + steroids; all but one being still on treatment. Mean follow-up is 5 months; one patient died of extrahepatic cause 7 months after the diagnosis of hepatitis. All treated patients responded satisfactorily.

**Conclusion:** acute hepatitis arising after COVID-19 appears to be a heterogeneous condition: long-term follow-up will help understanding if in some cases the vaccine triggers autoimmune hepatitis or if it is a novel drug-induced nosological entity.

**THU436**

Scheduled endoscopic program for patients with primary sclerosing cholangitis improves transplant-free survival and enables early risk stratification

Burcin Özdirik1, Wilfried Veltzke-Schlieker1, Jule-Marie Nicklas1, Hilmar Berger1, Daniel Schmidt1, Silke Leonhardt1, Andreas Adler1, Tobias Müller1, Alexander Wree1, Frank Tacke1, Michael Sigal1, 2Charité Universitätsmedizin Berlin, Department of Hepatology and Gastroenterology, Campus Virchow Klinikum (CVK) and Campus Charité Mitte (CCM), Berlin, Germany

Email: michael.sigal@charite.de

**Background and aims:** Primary sclerosing cholangitis (PSC) is associated with biliary obstructions that can require endoscopic retrograde cholangiopancreatography (ERCP). While beneficial short-term effects of ERCP are well documented, follow-up interventional strategies are less defined and their long-term impact is debated. Here, we evaluated the outcome of a scheduled program that has been implemented at our tertiary liver center for over more than 20 years.

**Method:** Within our program, ERCPs were performed at regular and pre-defined intervals to follow-up or treat previously detected biliary stenosis and/or to remove concrements. In this retrospective cohort study, we evaluated the outcomes of this scheduled programmed ERCP approach in comparison to patients, who received endoscopic interventions only on clinical demand. The primary end point was transplant-free survival. The secondary endpoints were occurrence of hepatic decompensation, recurrent cholangitis episodes, development of hepatobiliary malignancies and endoscopy-related adverse events.

**Results:** We included 268 consecutive patients with diagnosed PSC, 135 receiving scheduled ERCP and 133 receiving on demand ERCP. The rates of transplant-free survival since initial diagnosis (median 27 vs. 19 years; p = 0.027) and initial presentation (median 16 vs. 12 years; p = 0.001) were significantly higher in patients receiving scheduled vs. on demand ERCP. Subgroup analysis revealed that progression in cholangiographic findings between the 1st and 2nd ERCP (progression cohort) was associated with a poorer outcome compared to patients without progression (non-progression cohort) (median transplant-free survival: 17 years vs. undefined; p = 0.021).

**Conclusion:** Our data indicate that implementation of a scheduled ERCP program with interventions performed in predefined intervals improves transplant-free survival in patients with PSC. Furthermore, we reveal that a progression in cholangiographic findings after the first ERCP procedure enables a prediction of the future disease activity and outcome.

**THU437**

Immune response and safety in standard and third dose SARS-CoV-2 vaccination in patients with autoimmune hepatitis on immunosuppressive therapy, a prospective cohort study

Kristin Jørgensen1,2, Adity Chopra3, Joseph Sexton4, Anne T Tveter4, Johannes R. Hoy5,6,7, Ingrid Jyssum3,7, Lise Sofie H. Nissen-Meyer1, John T Vaage3,7, Silje W Syversen5, Guro I Goll4, Fridtjof Lund-Johansen5, Jørgen Jahnsen1,7, 1Akershus University Hospital, Dept. of Gastroenterology, Norway; 2Oslo University Hospital, Norwegian PSC Research Centre; 3Oslo University Hospital, Department of Immunology, Norway; 4Diakonhjemmet Hospital, Division of Rheumatology and Research, Norway; 5Oslo University Hospital, Section of Gastroenterology, Department of Transplantation Medicine; 6University of Oslo, Institute of Clinical Medicine, Norway; 7University of Oslo, Immunologio Convergence Center

Email: kristin.kaaen.jorgensen@outlook.com

**Background and aims:** Vaccines against SARS-COV-2 are proven efficacious and safe in the general population. Data on vaccine response in patients with autoimmune hepatitis (AIH) are currently lacking. The aim of this study was to evaluate immunogenicity and safety following standard and three dose SARS-CoV-2 vaccination in patients with AIH on immunosuppressive therapy.

**Method:** This prospective, observational study included adult AIH patients and healthy controls, both groups receiving standard two-dose SARS-CoV-2 vaccination. The patients were voluntarily allotted a third vaccine dose according to the national vaccine strategy. Antibodies to the receptor-binding domain (RBD) of SARS-CoV-2 spike proteins were analyzed in serum samples collected prior to, and after vaccination, and serologic response was defined as >70 AU/ml. **Results:** A total of 46 patients (median age 56 years [IQR 47–63], 32 [70%] women), and 114 healthy controls (median age 43 years [IQR 32–55], 854 [77%] women) were included in the study. All patients had compensated liver disease (Child Pugh A), the median disease duration was 6.2 years (IQR 4.2–9) and 80% received BNT 162b2 as standard two-dose vaccine. After standard vaccination, 89% of patients compared to 99% of healthy controls were serologic responders, p = 0.005. Anti-RBD levels were significantly lower in patients (median 2184 AU/ml [IQR 245–8763]) than controls (3355 AU/ml [IQR 896–7849]), p = 0.005. Prednisolone and
azathioprine combination therapy demonstrated the lowest response rate (80%), compared to azathioprine (94%) and prednisolone (100%) monotherapy (figure). The patients received the third vaccine dose median 112 days (IQR 88–133) after the second dose. The serologic response rate increased from 81% at time of receiving the third dose, to 91%, measured 3–5 weeks post third vaccination. Likewise, the overall anti-RBD levels increased from median 264 AU/ml (IQR 115–6485) to 6383 AU/ml (IQR 1480–9412). After standard vaccination, adverse events (AE) were reported in 30 (71%) of patients and in 191 (78%) of 244 healthy controls with a comparable safety profile. Following the third dose, 74% of patients reported AEs, without new safety issues emerging. No serious AEs were reported.

Conclusion: response rates as well as anti-RBD levels were lower in AIH patients than healthy controls following standard vaccination, with an attenuated serologic response in particular in patients on combination therapy with azathioprine and prednisolone. Third dose vaccination was safe without new safety issues emerging and resulted in an overall increased serologic response.

THU438
Analyses of obeticholic acid treatment retention in UK patients based on medicine delivery data
Carl Gibbons1, Subash Srinavasan1, Jayнал Bodhani2, Jing Li3, Li Chen3, Palak Trivedi4. 1Intercept Pharmaceuticals, United Kingdom; 2Intercept Pharmaceuticals, Level 6, United Kingdom; 3Intercept Pharmaceuticals Inc, New York, United States; 4University of Birmingham, NIHR Birmingham Biomedical Research Centre, Birmingham, United Kingdom
Email: carl.gibbons@interceptpharma.com

Background and aims: Between 30–40% of patients with primary biliary cholangitis (PBC) inadequately respond to Ursodeoxycholic acid (UDCA) and are candidates for second-line therapy. Obeticholic acid (OCA) is the only licensed second-line treatment in the UK, however, compliance, treatment adherence and rates of drug discontinuation have not been quantified at scale.

Method: 6, 857 orders for OCA were examined, which were delivered to 744 patients with PBC between 1 May 2017 and 1 Sept 2021. We constructed longitudinal datasets allowing study of patient dose order histories. Dropout status was assigned to patients against which there had been no new orders for ≥6 months after the date covered by their most recent medicine delivery. Kaplan-Meier estimates were then generated based on the cohort of 744 patients. Additionally, to examine potential relationships between drop-out and dose order history, patients were classified into one of 4 categories: 1) 5 mg doses ordered only; 2) up-titrated to and remained on 10 mg doses; 3) up-titrated to 10 mg but later returned to 5 mg doses; and 4) mixed 5 mg and 10 mg dosing patterns.

Separate Kaplan-Meier curves were generated for each of these categories and analysed using Cox regression.

Results: 744 patient order histories yielded 1138 person-years of ordering data and 204 drop-out events, with an estimated 87%, 78% and 69% of patients who continued to receive OCA deliveries at 6, 12 and 24 months respectively. Only 51% of patients had order histories indicating successful titration to 10 mg OCA daily, with 43% never increasing beyond 5 mg. The remaining 6% had orders suggesting either mixed dosing, or 10 mg dosing for a period before returning to 5 mg doses. We observed marked separation between some dose order groups in terms of drop-out, with the 5 mg only group most likely to drop out (69%, 56%, and 49% remaining on treatment at 6, 12 and 24 months respectively). By contrast, those who received 10 mg dosing (at any point) remained on OCA at a rate of 99%, 93%, and 82% at 6, 12 and 24 months respectively. The difference in retention was statistically significant (hazard ratio of 10 mg vs 5 mg only dosing: 0.22, 95% CI 0.17, 0.30, p < 0.001). See Figure. Moreover, these differences in retention rate remained statistically significant on restricted analysis of those receiving OCA for ≥6 months.

Figure: Proportion of patients continuing to receive OCA orders by time since first Homecare order, separated by dose order history categories

Conclusion: Our findings suggest an association between dose order history category and retention on treatment, prompting further study into optimal systems of management and support for patients on OCA. Conclusions about drop-out should be made with caution, as the analyses only consider product orders, disconnected from clinical characteristics.

THU439
Real-world prevalence of pruritus with obeticholic acid: a systematic literature review and meta-analysis
Patrick Horne1, Christina Hanson2, Tracy Mayne2, Leighton Feinman3. 1University of Florida, Gainesville, United States; 2South Denver Gastroenterology, Englewood, United States; 3Intercept Pharmaceuticals Inc, New York, United States
Email: patrick.horne@medicine.ufl.edu

Background and aims: Obeticholic acid (OCA) is the only approved 2nd line therapy for patients with primary biliary cholangitis (PBC) with an inadequate response or intolerant to ursodeoxycholic acid (UDCA). High rates of pruritus observed in OCA trials have not been observed in real-world studies. We performed a systematic review and meta-analysis to estimate real-world prevalence of pruritus and associated OCA discontinuation compared to the POISE phase 3 clinical trial.

Method: Systematic review and meta-analysis. We searched Embase and MEDLINE for English-language publications and conference abstracts from real-world settings in patients with PBC treated with OCA monotherapy or combined with UDCA. A fixed- or random-effects pooled estimate was performed based on heterogeneity. POISE. We analyzed data from 209 patients with 1 year follow-up on OCA in the double-blind and open-label phase of POISE. Patients were
censored if they exceeded the approved 10 mg dose. Pruritus was assessed via visual-analogue scale, 5-D pruritus scale, Itch domain of the PBC-40 scale, and standard adverse event assessment. We compared prevalence of pruritus and discontinuations due to pruritus in POISE to the real-world meta-analysis estimates via a chi-square goodness of fit test.

Results: Eleven studies were included in the meta-analysis (total patients = 1192). The random-effects pooled estimate of pruritus prevalence was 29% (95% CI, 24%–33%; Figure 1A); the fixed-effects pooled estimate of treatment discontinuation due to pruritus was 9% (95% CI, 8%–11%; Figure 1B). Real-world pruritus prevalence was significantly lower than in POISE (29% vs 62% in POISE; \( \chi^2 = 108.69; p < 0.001 \)); real-world treatment discontinuation was significantly higher than in POISE (9% vs. 4%; \( \chi^2 = 5.62; p < 0.02 \)).

Conclusion: The prevalence of pruritus in real-world data was significantly lower than observed in POISE. Experience with other drugs indicates discontinuation can be higher in real-world settings, in the absence of mechanisms and motivation in clinical trials to maintain patients on therapy. Our observation of significantly lower pruritus prevalence in the real-world vs clinical trial setting may help providers calibrate treatment expectations when considering OCA treatment.

THU440

Cognitive symptoms in non-cirrhotic primary biliary cholangitis
Naw April Phaw 1, Aaron Wetten 2,3, David Jones 4,5, Jessica Dyson 3, Amardeep Khanna 6.
1 Newcastel University, Translational and Clinical Research Institute, Newcastle upon Tyne, United Kingdom; 2 Newcastel University, Translational and Clinical Research Institute; 3 Freeman Hospital, The Newcastle upon Tyne Hospitals NHS Foundation Trust, Hepatology, Newcastle upon Tyne, United Kingdom; 4 Newcastle University, Liver Immunology, Newcastle upon Tyne, United Kingdom; 5 The Newcastle upon Tyne Hospitals NHS Foundation Trust, Hepatology, Newcastle upon Tyne, United Kingdom; 6 Nottingham University Hospitals NHS TRUST, Hepatology Department, Nottingham, United Kingdom
Email: mail2april@gmail.com

Background and aims: There is emerging evidence of cognitive symptoms, such as memory loss and poor concentration even in early stage Primary Biliary Cholangitis (PBC), with functional imaging studies demonstrating abnormalities of the central nervous system. The aim of this study was to objectively assess performance in cognitive tasks, using CANTAB Neuropsychological Battery in PBC patients and the differences between those with and without cognitive symptoms.

Method: Non-cirrhotic PBC patients were recruited from a single tertiary hospital; those with significant additional medical conditions were excluded. Participants completed PBC-40 questionnaires and CANTAB tasks (PAL, OTS, SWM, ERT, RVP) assessing working memory, executive function, emotional cognition, attention and psychomotor speed. Analysis was performed against a normal population, with a z score of <-1.5 standard deviations considered a significant deficit.

Results: 38 PBC patients were recruited. Nearly a third of PBC patients demonstrated significant cognitive deficits in memory tasks (PAL) with more errors and fewer correct first attempt responses along with reduced correct hits and slower response times in the emotional cognition domain (ERT). PBC patients underperformed in 2 out of 3 executive function tasks (OTS; \( p = 0.00 \), SWM; \( p = 0.00 \), MTT; \( p = 0.42 \)), with fewer correct responses in the attention domain (RVP) and slower responses to stimuli however they outperformed the normative population in psychomotor speed domain (RTI). There was, however, no significant difference in CANTAB performance between cognitively symptomatic (n = 16) and asymptomatic (n = 22) PBC patients when stratified by the PBC-40 cognitive domain.

Conclusion: Objective cognitive dysfunction was frequent in PBC patients, with pronounced deficits observed in memory and emotional domains. No significant differences in CANTAB performance was observed between cognitive symptomatic and non-symptomatic patients suggesting behavioral adaption/variation may influence the symptoms exhibited in PBC patients. The patterns of abnormality integrated with functional imaging may shed light on the anatomical abnormality.
Background and aims: PSC is characterised with chronic inflammation of biliary epithelium leading to strictures in bile ducts and secondarily to cirrhosis. Chronic inflammation is associated with the increased risk for biliary dysplasia (BD) and cholangiocarcinoma (CCA), with lifetime risk 10%. CCA is the most common cause of death among PSC patients and up to half of CCAs are detected at the time of dg or within one year after. The current guidelines for surveillance for CCA in PSC are contradictory and the evidence for efficacy of surveillance is scarce. AGA guidelines recommend US, CT or MRI, with or without Ca19-9 for surveillance of CCA, none of which are suitable for early detection of biliary neoplasia. We aimed to evaluate the role ERC with brush cytology (BC) in screening and surveillance of BD and to assess its prevalence and its impact on patient outcome.

Method: In total 989 patients were retrieved from Helsinki University Hospital registry referred for ERC: documentation of dg, MRCP/liver histology suggestive for PSC or surveillance of PSC progression and/or BD. We excluded 98 patients: age <18 years (n = 69) or >65 y (n = 19), CCA detected at time of diagnosis or within one year (n = 7), serious concomitant disease or malignancy, liver transplantation (LTx) before f/u, n = 3. BC was systematically collected from intra- and extrahepatic bile ducts, regardless of the presence of dominant strictures for detection of BD. Cytological evaluation from cytospin and cell-block slides was performed, using three-tiered criteria as benign, suspicious, or malignant (CCA). Suspicous cytology: any of the following: biphasic cell population, lack of polarity, nuclear moulding, nuclear membrane irregularities, high nuclear-cytoplasm ratio, hyper/hypo-chromacy and lack of cohesion. The screening and surveillance strategy is presented in fig.

Results: Prevalence of BD and risk for CCA: Suspicous of dysplasia was detected ≥1 times in 91 patients (10%) during median f/u of 10 years, CCA in 25. If dysplasia was documented ≥3 times, the patient was referred for evaluation for LTx.

LiverTx: 22 patients were transplanted for suspicion of malignancy, 58 for other indications. Out of the 58 patients with suspicion of dysplasia (≤2 times), but not transplanted, 11 (19%) developed CCA. 800 patients without dysplasia, only 7 (0.9%) were diagnosed with CCA. In patients transplanted for dysplasia, 91% were found to have dysplasia in explant, in 3 CCA was detected at LTx. The sensitivity of BC with suspicion of malignancy at least once to detect histologically confirmed biliary neoplasia (transplantation/surgery) was 65% (52–76%) and specificity 94% (93–96%) with OR 30. If patient had BC with suspicion of malignancy ≥3 times the sensitivity to detect histologically confirmed CCA was 100% (48% to 100%) and specificity 98% (97–99%).
Conclusion: Itch related to PSC has a major adverse impact on QoL (eg, sleep, mood, fatigue), interferes with daily activities in a substantial proportion of patients but remains inadequately treated in most patients. These data highlight a major unmet need for the development of safe and effective therapies for treatment of cholestatic itch in patients with PSC.

THU443
A dynamic approach to modelling baseline disease status and ALT elevation over follow-up on clinical-event free survival in autoimmune hepatitis: a Canadian multicentre cohort
Christina Plagiannakos1, 2, Gideon Hirschfield 1, 2, Ellina Lytvyak 3, Christina Plagiannakos1, 2, Gideon Hirschfield 1, 2, Ellina Lytvyak 3, Harry Jansen 1, 5, Aliya Gulamhusein 1, 2, Aldo J Montano-Loza 2, Bettina Hansen 1, 2, 1 University Health Network, Toronto Centre for Liver Disease, Toronto Western and General Hospital, Toronto, Canada; 2University of Toronto, Institute of Health Policy, Management and Evaluation, Toronto, Canada; 3University of Alberta, Department of Medicine-Division of Gastroenterology and Liver, Edmonton, Canada; 4Unity Health Toronto, St. Michael's Hospital, Toronto, Canada; 5University of Toronto-St. George Campus, Department of Medicine, Toronto, Canada
Email: christina.plagiannakos@uhn.ca

Background and aims: Current and future treatments for autoimmune hepatitis (AIH) target ALT as a biomarker of efficacy. In patients with AIH, we sought to model ALT response dynamically over long-term follow-up, to understand clinical associations with cholestatic itch in patients with PSC.

Method: Patients diagnosed with AIH (simplified score ≥6) who initiated treatment were included from the Canadian Network for Autoimmune Liver Disease. AASLD sex-specific upper limits of normal (ULN) defined ALT normalization and site-specific ULN were used for other biochemical markers. CEFS included the absence of a decomposition event, liver transplant, or death. Kaplan-Meier estimates and Cox proportional hazards dynamic time-varying models adjusted for age at diagnosis, sex, cirrhosis at diagnosis, baseline total bilirubin, and stratified by site were used; alpha = 0.05.

Results: 579 patients with AIH initiated treatment between November 1987 and June 2020, with a median follow-up time of 59.4 years [IQR 2.70–11.6] and an average of 9 visits [4.0–21]. Median age at diagnosis was 48 years [31.0–59.4], 75.5% of patients were female (n = 437) and 71.2% reported white ethnicity (n = 412). Median baseline ALT was 15.7xULN [5.84–34.2], AST 10.5xULN [3.36–23.8], IgG 1.48xULN [1.12–193], total bilirubin 1.8xULN [0.68–6.25] and INR 1.17 [1.05–1.34]. Among the 21.2% (n = 123) of patients with cirrhosis at diagnosis, 40 had an event during follow-up, and of the 456 without, cirrhosis (Figure 1a). The survival probability at 5 years for patients with elevated and normal bilirubin values were 83% (CI 0.78–0.87) and 94% (CI 0.91–0.98), respectively. In univariate analysis AST (HR 1.58, CI 1.02–2.45), and IgG (HR 3.05, CI 1.1–8.4) were significantly related to long-term outcomes in patients without cirrhosis. In the multivariable model, cirrhosis at diagnosis (HR 4.39, CI 2.73–7.07), baseline bilirubin (HR 2.41, CI 1.34–4.33), and older age (HR 1.20, CI 1.04–1.38, unit = 10 years) were all independently associated with poorer outcomes. The predicted cumulative impact of time spent with elevated ALT during follow-up was significant (HR 1.29, CI 1.11–1.50, unit = 10% of time, Figure 1b. Patients that spent a greater amount of follow-up time with elevated ALT values had an increased risk of experiencing an event, and this was most marked in patients with cirrhosis.

Conclusion: Patients with AIH are at increased risk of a clinical event as the time spent with abnormal ALT values increases, especially those with cirrhosis at baseline. Persistent improvement in ALT values is a logical treatment goal in AIH.

THU444
Secondary sclerosing cholangitis following COVID-19 disease: a multicenter retrospective study
Peter Hunyady1, Lea Streller1, Darius Ruether1, Sara Reinartz Groba2, Dominik Bettinger3, Daniel Fitting3, Karim Hamesch1, Jens Marquardt3, Victoria Mück1, Fabian Finkelmeier1, Asieb Sekandarzad3, Tobias Wengenmayer3, Ayoub Boundiane1, Felicitas Weiss7, Kai-Henrick Peiffer1, Bernhard Schlevogt8, Stefan Zeuzem1, Oliver Waidmann1, Marcus Helenbach9, Martha M Kirstein8, Johannes Kluwe3, Fabian Kütting2, Marcus Mücke1, 1University Hospital Frankfurt; 2University Hospital Cologne; 3University Hospital Hamburg Eppendorf; 4University Hospital Münster; 5University Hospital Freiburg; 6University Hospital Würzburg; 7University Hospital Schleswig-Holstein Campus Lübeck; 8University Hospital Leipzig
Email: marcus.m.muecke@gmail.com

Background and aims: Secondary sclerosing cholangitis (SSC) is a rare disease with poor prognosis. Cases of SSC have been reported following coronavirus disease 2019 (COVID-19), COVID-SSC. Aim of this study was to compare COVID-SSC to SSC in critically ill patients (SSC-CIP) and to assess factors influencing transplant-free survival.

Method: In this retrospective, multicenter study involving 127 patients with SSC from 9 tertiary care centers in Germany, COVID-SSC was compared to SSC-CIP and logistic regression analyses were performed investigating factors impacting transplant-free survival.

Results: Twenty-four patients had COVID-SSC, 77 patients SSC-CIP and 26 patients had other forms of SSC. COVID-SSC developed after a median of 91 days following COVID-19 diagnosis. All patients had median of 91 days following COVID-19 diagnosis. All patients had received extensive intensive care treatment (median days of mechanical ventilation 48). Patients with COVID-SSC and SSC-CIP were comparable in most of the clinical parameters and transplant-free survival was not different from other forms of SSC (p = 0.443 in log-rank test). In the overall cohort, the use of ursodeoxycholic acid (UDCA, OR 0.36, 95%-CI 0.16–0.80, P = 0.013; P < 0.001 in log-rank test) and high serum albumin levels (OR 0.40, 95%-CI 0.17–0.96, P = 0.040) were independently associated with an increased transplant-free survival, while the presence of liver cirrhosis (OR 2.52, 95%-CI
Method: The Japanese PBC cohort is established by the nation-wide surveys, initiated in 1980 and updated every 3 years by the Intractable Hepato-Biliary Diseases Study Group (Japan PBC Study Group). To date, 9,919 patients with PBC have been registered. Baseline covariates included age, sex, presence of symptoms, serum levels of bilirubin, alkaline phosphatase (ALP), and albumin. Primary outcome (liver-related death or LT) was assessed using multivariable adjusted Cox proportional hazard models.

Results: Our study included 2479 patients with AIH of whom 23.1% had one or more extrahepatic autoimmune diseases. The adjusted 10-year cumulative mortality was 27.3% (95% confidence interval [CI]: 25.3–29.4) in patients with extrahepatic autoimmune diseases and 21.6% (95% CI: 19.9–23.6) in patients without. The adjusted mortality hazard ratio was 1.28 (95% CI: 1.10–1.49) in AIH patients with vs. without concurrent extrahepatic autoimmune diseases; it was 1.22 (95% CI: 1.03–1.44) for patients with one extrahepatic autoimmune disease, and 1.59 (95% CI: 1.19–2.12) for those with more than one.

Conclusion: Extrahepatic autoimmune diseases increased the mortality in patients with AIH. Moreover, patients with multiple extrahepatic autoimmune diseases had higher mortality than patients with just one extrahepatic autoimmune disease.
Background and aims: Patients with autoimmune liver diseases (AILDs) have been reported to have an impaired health-related quality of life (HRQoL) in studies based on small sample sizes. The aim of this project was to investigate HRQoL in a large transnational cohort of patients with AILDs and to identify potentially modifiable factors in the context of impaired HRQoL.

Method: A cross-sectional online survey was conducted in patients with a diagnosis of autoimmune hepatitis (AIH), primary biliary cholangitis (PBC) or primary sclerosing cholangitis (PSC) from 15 European countries. HRQoL was measured with EQ-5D-5L and EQ visual analogue scale (EQ VAS) and analysed in relationship to demographic, psychosocial, disease- and treatment-related factors. A PHQ-2 score larger than two indicated clinically relevant depression. Multivariable linear regression analyses were used to identify potentially modifiable factors associated with HRQoL and confidence in treatment while adjusting for known confounders.

Results: A group of 1,178 European patients (470 with AIH, 368 with PBC and 317 with PSC, 79% female, mean age 48 ± 14 years) participated in the study. HRQoL was markedly impaired in all three liver diseases (mean EQ-5D-5L = 0.75, mean EQ VAS = 68.9), particularly in patients with PBC (mean EQ-5D-5L = 0.73, mean EQ VAS = 66.2). Clinically relevant depression was reported in 17% of the total sample. Depression, gender, age and advanced disease stage were expectedly associated with HRQoL. Confidence in treatment was identified as a modifiable factor strongly contributing to EQ-5D-5L in the entire cohort (reg. coeff: 0.12, 95%CI: 0.07 to 0.18, p < 0.001). PSC or PBC diagnosis, advanced disease stage, treatment in non-transplant center and depression were negatively associated with patients' confidence in their treatment (Figure).

Conclusion: Our analysis detects confidence in treatment as a novel central determinant of HRQoL in patients with AILDs. This modifiable and so far underecognised factor should be further investigated in order to improve care for patients with AILDs.

THU444
A pilot study of PBC symptom management with melatonin and fenofibrate: the PIMBLE study
Beverly Rodrigues 1, Steven Nicolaides 1, Rohit Sawhney 1,2, Amanda Nicoll 1,2, Stephen Bloom 1,2.

Background and aims: Primary biliary cholangitis (PBC) disease progression is usually well controlled with ursodeoxycholic or obeticholic acid. Bezafibrate has shown benefits in refractory disease but is not available in Australia, and it is unknown if fenofibrate is similarly effective. Despite good biochemical response, the symptoms of pruritus, fatigue and altered sleep often remain. Melatonin may improve fatigue as demonstrated in animal models. We studied the short-term symptomatic and biochemical responses of PBC patients to melatonin and fenofibrate therapy.

Method: A randomised, cross-over 12-week intervention study examining symptoms and biochemistry in response to melatonin and fenofibrate between 20th July 2020–15th November 2021 inclusive.

Results: The interim results of 10 patients are shown in Table 1. Six out of 10 patients completed both trial arms, patient 10 only completed the melatonin arm only, and the remaining 3 are soon to complete arm 2 (n = 1 fenofibrate, n = 2 melatonin). Both agents were well tolerated overall; 3 patients had a mild rise in transaminases (<5x upper limit of normal) post commencement of fenofibrate. ALP improvement was seen in 6/8 on fenofibrate and 3/8 on melatonin, with degree of improvement meeting Paris II criteria in all trialled arms. Symptom improvement was seen in 6/8 on fenofibrate and 6/8 on melatonin.

Table 1: Descriptive analyses of clinical and biochemical responses to each trial arm

<table>
<thead>
<tr>
<th>Patient</th>
<th>Age (years)</th>
<th>Gender</th>
<th>Abnormal ALP (baseline)</th>
<th>Improved symptoms Y/N</th>
<th>MFIS SF36 VAS</th>
<th>Improved symptoms Y/N</th>
<th>MFIS SF36 VAS</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>54.6</td>
<td>F</td>
<td>N</td>
<td>N</td>
<td>N/A</td>
<td>Y</td>
<td>N/A</td>
</tr>
<tr>
<td>2</td>
<td>56.6</td>
<td>F</td>
<td>N</td>
<td>N</td>
<td>N/A</td>
<td>N</td>
<td>N/A</td>
</tr>
<tr>
<td>3</td>
<td>65.9</td>
<td>F</td>
<td>N</td>
<td>Y</td>
<td>N/A</td>
<td>Y</td>
<td>Y</td>
</tr>
<tr>
<td>4</td>
<td>57.8</td>
<td>F</td>
<td>N</td>
<td>N</td>
<td>N/A</td>
<td>Y</td>
<td>Y</td>
</tr>
<tr>
<td>5</td>
<td>72.7</td>
<td>M</td>
<td>N</td>
<td>N</td>
<td>N/A</td>
<td>N</td>
<td>N/A</td>
</tr>
<tr>
<td>6</td>
<td>60.6</td>
<td>F</td>
<td>N</td>
<td>P</td>
<td>P</td>
<td>P</td>
<td>P</td>
</tr>
<tr>
<td>7</td>
<td>61.3</td>
<td>F</td>
<td>Y</td>
<td>Y</td>
<td>Y</td>
<td>Y</td>
<td>Y</td>
</tr>
<tr>
<td>8</td>
<td>55.1</td>
<td>M</td>
<td>Y</td>
<td>P</td>
<td>P</td>
<td>P</td>
<td>P</td>
</tr>
<tr>
<td>9</td>
<td>52.9</td>
<td>M</td>
<td>N</td>
<td>N</td>
<td>N/A</td>
<td>P</td>
<td>P</td>
</tr>
<tr>
<td>10</td>
<td>45.2</td>
<td>F</td>
<td>Y</td>
<td>Y</td>
<td>N/A</td>
<td>N</td>
<td>N/A</td>
</tr>
</tbody>
</table>

Y = (Yes); N = (No); N/A = (not applicable or available); p = (pending)

Conclusion: This pilot study suggests that there is potential benefit in these therapies for PBC and further studies evaluating their efficacy is required.

THU449
Portal hypertension-associated clinical features in patients with primary biliary cholangitis are of distinct prognostic value
Lucas Burghart 1, Emina Halilbasic 1, Philipp Schwabl 1, Benedikt Simbrunner 1, Albert Stättermayer 1, Oleksandr Petrenko 1, Bernhard Scheiner 1, David JM Bauer 1, Matthias Pinter 1, Kaan Boztug 1, Mattias Mandorfer 1, Michael Trauner 1, Thomas Reiberger 1.

Background and aims: Primary biliary cholangitis (PBC) may progress to cirrhosis and clinically significant portal hypertension.
Results: A total of 333 PBC patients (mean age: 54.3 years, 86.8% female, median follow-up: 5.8 years) were retrospectively assessed. Overall, 127 (38.1%) showed features of CSPH: 63 (18.9%) developed varices, 98 (29.4%) splenomegaly, 62 (18.6%) ascites and 20 (15.7%) experienced acute variceal bleeding.

Spleno-megaly, portosystemic collaterals and esophageal varices were associated with an increased 5-year (5Y) risk of decompensation (15.0%, 17.8% and 20.9%, respectively). Patients without advanced chronic liver disease (ACLD) had a similar 5Y-transplant free survival (TFS) (96.6%) compared to patients with compensated ACLD (cACLD) but without CSPH (96.9%). On the contrary, PBC patients with cACLD and CSPH (57.4%) or decompensated ACLD (dACLD) (36.4%) had significantly decreased 5Y survival rates.

During a subanalysis, the combination of LSM <15 kPa and platelets ≥150 G/L indicated a negligible risk for decompensation (5Y 0.0%) and for mortality (5Y 0.0%). Overall, 44 (13.2%) patients died, with 18 (40.9%) deaths attributed to CSPH-related complications.

Conclusion: In PBC, features of CSPH may occur early and indicate an increased risk for subsequent decompensation and mortality. Hence, regular screening and on-time treatment for CSPH is crucial. Combining LSM and platelets serves as a valuable preliminary assessment, as LSM <15 kPa and platelets ≥150 G/L indicate an excellent long-term outcome.
**THU451**

The ABCB4 variant c.711 increases liver injury in PBC but not in PSC: prospective analysis with a median follow-up of 7 years in 331 patients

Beata Kruk1, Małgorzata Milkiewicz2, Piotr Milkiewicz3,4, Marcin Krawczyk1,5

1Laboratory of Metabolic Liver Diseases, Department of General, Transplant and Liver Surgery, Medical University of Warsaw, Warsaw, Poland; 2Department of Medical Biology, Pomeranian Medical University in Szczecin, Szczecin, Poland; 3Liver and Internal Medicine Unit, Medical University of Warsaw, Warsaw, Poland; 4Translational Medicine Group, Pomeranian Medical University in Szczecin, Szczecin, Poland; 5Department of Medicine II, Saarland University Medical Center, Saarland University, Homburg, Germany

**Background and aims:** Primary biliary cholangitis (PBC) and primary sclerosing cholangitis (PSC) are two progressive chronic cholestatic liver diseases. The ABCB4 gene encodes the hepatobiliary phospholipid transporter. Defects in the ABCB4 gene cause several cholestatic diseases (Städtlermaier et al., J Hepatol. 2020). Here we aim to investigate role of the ABCB4 genetic variant in patients with PBC and PSC.

**Method:** We genotyped the ABCB4 c.711 polymorphism in a total of 331 patients with PBC and PSC who were prospectively recruited in our center from year 2005. The PBC cohort was composed of 196 patients (173 females, median age 59 years, 49% with cirrhosis). The PSC cohort was composed of 135 patients (96 males, median age 35 years, 39% with cirrhosis). Clinical data were collected at least at two time points: The follow-up ranged from 2 to 20 years (median: 7 years) The PBC-40 and Short Form (SF-36) questionnaires were used for assessment health related quality of life.

**Results:** Allele and genotype distributions of the ABCB4 variant in patients with PBC and PSC cohort were consistent with Hardy-Weinberg equilibrium (p > 0.05). At baseline, the ABCB4 c.711 variant was associated with an increased cirrhosis risk (OR = 1.84, p = 0.02) in the PBC cohort, the risk of cirrhosis was also modulated by patients gender (p < 0.01). Carriers of heterozygote genotype showed significantly increased serum AST (p = 0.02), GGTP (p < 0.01) and ALP (p < 0.01). Although we detected significant improvements in laboratory findings (i.e., AST, ALT, ALP and GGTP) during the follow-up, a total of 22 patients developed new cirrhosis and this risk was significantly modulated by the ABCB4 polymorphism (OR = 5.65, p = 0.04). On the other hand, the ABCB4 genotype did not affect life quality in either of the cohorts, did not modulate liver injury in patients with PSC did not increase the odds of requiring transplantation (all p > 0.05).

**Conclusion:** The ABCB4 c.711 polymorphism might represent a common risk genetic factors for progressive liver injury in PBC. Carriers of the c.711 ABCB4 might require more aggressive therapy to lower the progression of liver scarring.

**THU452**

A multicentric study to estimate mortality and graft loss risk after liver transplantation (LT) in patients with recurrent primary biliary cholangitis (PBC)

Aldo J Montano-Loza1, Thierry Benney2, Christian Tos03, Giulia Magini4, Gideon Hirschfield5, Bettina Hansen6, Andrew L. Mason7, Maryam Ebad1, Frederik Nevens4, Natalie Van den Ende4, Debora Raquel Terrabuio5, Pablo Ruiz7, Alan Bonder8, Elina Lytvyak9, Adriaan Van der Meer9, Rozanne de Veer9, Annarosa Floreani10, Nora Cazzagon10, Stefania Casu11, Francesco Paolo Russo10, Mark Pedersen12, Marilyn J. Mayo12, Michael P. Manns13, Richard Taubert14, Theresa Kirchner15, Thomas Schiano15, Brandy Haydel16, Xavier Verhelst16, Mercedes Robles-Díaz17, Miguel Jiménez-Pérez18, Jérôme Dumortier15, Ansgar Lohse19, Christoph Schramm20, Darius Ruetther20, Benedetta Terzilli Beretta-Piccoli21, Maria Francesca Donato20, Christophe Corpechot21,1 University of Alberta, Canada; 2Geneva University Hospitals, Switzerland; 3Toronto Center for Liver Disease, Canada; 4Division Liver and Biliary Diseases, Belgium; 5University of São Paulo School of Medicine, Brazil; 6University of Barcelona, Spain; 7Liver Unit, Hospital Clinic, Spain; 8Beth Israel Deaconess Medical Center, United States; 9Erasmus MC, Netherlands; 10University of Padova, Italy; 11Universitatsspitzen Bern, Switzerland; 12Southwestern University, United States; 13Hanover Medical School, Germany; 14Dept. Gastroenterology, Hepatology and Endocrinology, Hannover Medical School, Germany; 15Mount Sinai Medical Center, United States; 16Chent Hospital University, Belgium; 17University Hospital Virgen de la Victoria, Spain; 18Málaga Regional Hospital, Spain; 19Croix Rouge Hospital and Edward Herriot Hospital, France; 20University Medical Center Hamburg-Eppendorf, Germany; 21Epatocteno Ticino, Switzerland; 22Fondazione IRCCS Maggiore Hospital Policlinico Milan, Italy; 23Saint-Antoine Hospital, France

**Background and aims:** Recurrent PBC (rPBC) developed in approximately 30% of patients, and negatively impacts graft and patient survival after LT. Liver function tests and scores to evaluate response to ursodeoxycholic acid (UDCA) have been developed to monitor disease progression and evaluate the addition of second-line treatments before LT. We aimed to evaluate the utility of serum liver function tests and the GLOBE and UK-PBC scores to predict graft and overall survival after LT in patients with rPBC.

**Method:** A total of 231 patients who had a liver biopsy-proven diagnosis of rPBC after LT from 18 centers across Europe, North and South America, were evaluated. The mean age at the time of rPBC was 58 ± 10 years, and 206 patients (89%) were women. At the time of rPBC, 145 patients (63%) were receiving tacrolimus, and 78 (34%) with cyclosporine. The biochemical response was measured with alkaline phosphatase (ALP) and bilirubin, and continuous prognostic (GLOBE and UK-PBC scores) at 1-year after UDCA was started. Graft loss was defined using a death-censored definition of graft failure and therefore, graft loss did not include patients who died with a functioning graft. Cox regression analysis was performed to determine associations between biochemical markers, scores and graft loss and mortality.

**Results:** A total of 219 patients (95%) received treatment with UDCA after rPBC diagnosis. During a median follow-up 9.16 ± 5.47 years, 47 patients (20%) had lost graft and 76 (33%) died. Graft survival after rPBC was 92% and 85%, and overall survival was 87% and 76%, at 5-, and 10-years, respectively. Use of tacrolimus or cyclosporine was not associated with graft or overall survival. Serum ALP (HR 1.002, 95% CI 1.001–1.004, p = 0.01), and bilirubin (HR 1.009, 95% CI 1.004–1.015, p = 0.001) at 1-year after UDCA were associated with graft survival. The GLOBE (HR 2.45, 95% CI 1.45–4.16, p < 0.001) and UK-score 5-year formula (2.99, 95% CI 0.48–18.77, p < 0.001) at 1-year after UDCA initiation were associated with graft survival. In addition, serum ALP (HR 1.31, 95% CI 1.10–1.55, p = 0.002), and bilirubin (HR 1.008, 95% CI 1.004–1.012, p < 0.001) at 1-year after UDCA initiation were
associated with overall survival. The GLOBE (HR 2.04, 95% CI 1.38–3.01, p < 0.001) and UK-score 5-year formula (1.94, 95% CI 0.37–10.05, p < 0.001) at 1-year after UDCA were associated with overall survival. Patients with an Alp > 2 × ULN (Figures 1a–b) and bilirubin >1 × ULN (Figures 1c–d) at 1-year of UDCA treatment had worse graft and overall survival. Only two (1%) and 10 patients (4%) started second-line treatment with obeticholic acid and fibrates, respectively.

Conclusion: Patients with rPBC and disease activity as indicated by standard PBC risk scores have impaired outcomes, supporting efforts to treat recurrent disease in similar ways to pre-transplant PBC.

THU453
Associations between novel serum biomarkers chitinase-2-like protein (YKL-40), type IV collagen, and thrombospondin-2 (TSP-2) with fibrosis stage and clinical outcomes in patients with primary sclerosing cholangitis (PSC)

Michael Trauner1, Andrew Muir2, Jun Xu3, Mina Khoshdeli2, Bryan Downie2, Andrew Billin2, Chuhan Chung1, Robert Myers1, Zachary Goodman4, Mitchell Shiffman3, Bryan Downie3, Andrew Billin3, Chuhan Chung3, Robert Myers3, Zachary Goodman4, Mitchell Shiffman3, Harry Janssen5, Aldo J Montano-Loza6, Stephen Caldwell7, Velimir Luketic8, Michael P. Manns9, Cynthia Levy10, Christopher Bowlus11. 1Medical University of Vienna, Vienna, Austria; 2Duke Clinical Research Institute, Durham, United States; 3Gilead Sciences, Inc., Foster City, United States; 4Inova Fairfax Hospital, Falls Church, United States; 5Bon Secours Mercy Health, Liver Institute of Virginia, United States; 6University of Alberta, Edmonton, Canada; 7University of Virginia, Charlottesville, United States; 8VCU Medical Center, Richmond, United States; 9University of Miami, Hannover, Germany; 10University of Miami, Miami, United States; 11University of California Davis, Davis, United States Email: jun.xu@gilead.com

Background and aims: Primary sclerosing cholangitis (PSC) is a chronic and progressive fibrotic liver disease associated with an increased risk of liver-related complications and mortality. Non-invasive biomarkers of fibrosis are needed for risk stratification and monitoring of PSC patients. YKL-40, TSP-2, and type IV collagens (α-subunit) are biomarkers of liver injury, inflammation, or extracellular matrix turnover during hepatic fibrogenesis. Our study aimed to evaluate associations between these biomarkers with fibrosis stage and PSC-related clinical events in a longitudinal study.

Method: Serum biomarkers YKL-40, TSP-2, and COL4A1 were measured via ELISA at baseline (BL) and Week 96 (W96) in PSC patients enrolled in a 96-week, phase 2 trial of simtuzumab (NCT01672853). Since simtuzumab was ineffective in this trial, data from the treatment and placebo groups were combined. Fibrosis was staged according to the Ishak classification and biomarker values were log-transformed. Odds ratios (OR) for associations between BL biomarker values with progression to cirrhosis (Ishak 5–6) at W96 among non-cirrhotic patients (Ishak 0–4) at BL were calculated using logistic regression models.

Results: At BL, serum COL4A1 and TSP-2 were moderately correlated with other serum markers, including ELF score, AST, ALP, and GGT (Spearman correlations ρ = 0.36–0.74, all p < 0.001). YKL-40 demonstrated weaker but significant correlations to ALP, AST and ELF score (ρ = 0.24–0.54, p < 0.05). TSP-2 and COL4A1 were increased with fibrosis stage in PSC patients (both p < 0.001), but YKL-40 was increased mainly in patients with cirrhosis (Figure). By W96, 44 patients (20%) developed a PSC-related clinical event (hepatic decompensation, cholangiocarcinoma, ascending cholangitis, or jaundice). Compared with patients without events (n = 175), those with events had higher YKL-40 (median 42.5 vs 29.0 ng/ml, p = 0.001), COL4A1 (168.4 vs 121.1 ng/ml, p < 0.001) and TSP-2 (85.0 vs 50.4 pg/ml, p < 0.001) at BL. Among 176 non-cirrhotic patients at BL, 27 progressed to cirrhosis at W96. Compared with patients without progression to cirrhosis (n = 149), those with progression had higher BL levels of YKL-40 (OR = 1.91, p = 0.002), TSP-2 (OR = 4.24, p < 0.001), and COL4A1 (OR = 8.24, p < 0.001). In addition, patients with progression to cirrhosis had greater relative increases from BL to W96 in YKL-40 (median 45.8% vs 3.4%, p = 0.0025) and TSP-2 (24.7% vs 0.1%, p < 0.001).

Conclusion: Serum levels of the novel biomarkers YKL-40, TSP-2, and COL4A1 are associated with fibrosis stage, progression to cirrhosis, and liver-related clinical events in patients with PSC. The utility of these biomarkers for the staging of fibrosis, risk stratification, and disease monitoring in PSC will be explored in additional studies.
THU454
MRCP+™-derived biliary metrics are associated with disease severity and clinical outcomes in patients with primary sclerosing cholangitis
Nora Cazzagon1,2, Sanaa El Mouhadi3, Quentin Vanderbeck3, Carlos Ferreira4, Sara Lemoinne3, Christophe Corpechot1, Olivier Chazouillères1, Lionel Arrive3, Assistance Publique-Hôpitaux de Paris, Sorbonne University, INSERM, Reference Center for Inflammatory Biliary Diseases and Autoimmune Hepatitis and Saint-Antoine Research Center (CRMRI MVH-B, ERN RARE-LIVER), Saint-Antoine Hospital, Paris, France, Paris, France; 2Department of Surgery, Oncology and Gastroenterology, University of Padova, European Reference Network on Hepatological Diseases (ERN RARE-LIVER), Azienda Ospedaliero-Universitaria Padova, Padova, Italy, Padova, Italy; 3Assistance Publique-Hôpitaux de Paris, Sorbonne University, Department of Radiology, Saint-Antoine Hospital, Paris, France, Paris, France; 4Perspectum Ltd, Oxford UK, Oxford, United Kingdom

Email: nora.cazzagon@gmail.com

Background and aims: Patients with primary sclerosing cholangitis (PSC) have a variable, and often progressive disease course which is associated with biliary and parenchymal changes. These changes are typically assessed by magnetic resonance imaging (MRI), including magnetic resonance cholangiopancreatography (MRCP). Our aim was to study the association of novel quantitative MRCP metrics with prognostic scores and patient outcomes.

Method: We performed a retrospective study including 77 large-duct PSC patients with baseline MRCP images, which were post-processed to obtain quantitative measures of bile ducts and biliary volume using MRCP+™ (Perspectum Ltd, Oxford). The participants’ ANALI scores, liver stiffness (measured by vibration controlled transient elastography) and biochemical indices were collected at baseline. Adverse outcome-free survival was measured as the absence of decompensated cirrhosis and liver transplantation. The prognostic value of MRCP+™ derived metrics was assessed by univariate analysis and multivariable Cox regression modelling.

Results: During a total 386 patients-years, we recorded 16 cases of decompensated cirrhosis, 2 liver transplantations and 5 liver-related deaths. At baseline, ~50% of the patients were classified as being at risk of developing disease complications based on radiological, elastographic, and biochemical prognostic scores. MRCP+™ metrics, particularly those describing the severity of bile duct dilatations, were correlated with all prognostic factors. Univariate analysis showed that MRCP+ metrics representing duct diameter, dilatations, and the percentage of ducts with strictures and/or dilatations were associated with survival. According to the multivariable Cox regression model, the median duct diameter was independently associated with adverse outcome-free survival over 5 years (HR 10.9, 95% CI 1.3–90.3, p = 0.027) (Figure). Biliary tree volume was significantly higher in patients with advanced disease as defined by the ANALI scores.

Conclusion: MRCP+™ metrics demonstrated a significant correlation with biochemical, elastographic and radiological prognostic scores and were predictive of patients’ outcomes highlighting its prognostic utility in PSC.

THU455
Safety and efficacy of the farnesoid X receptor (FXR) agonist cilofexor in a proof-of-concept study in patients with compensated cirrhosis due to primary sclerosing cholangitis (PSC)
Cynthia Levy1, Stephen Caldwell2, Parvez Mantry3, Yelimir Luketic4, Charles Landis1, Jonathan Huang5, Edward Mena6, Rahul Maheshwari7, Kevin Rank8, Jun Xu9, Xiangyu Lu4, Xiaomin Lu10, Chuanhun Chung11, Robert Myers9, Kris Kowdle11. 1University of Miami Miller School, Miami, United States; 2University of Virginia School of Medicine, Charlottesville, United States; 3The Liver Institute At Methodist Dallas, Dallas, United States; 4VCU School of Medicine, Richmond, United States; 5University of Washington School of Medicine, Seattle, United States; 6University of Rochester School of Medicine and Dentistry, Rochester, United States; 7Pasadena Liver Center, Pasadena, United States; 8Piedmont Transplant Institute, Atlanta, United States; 9MNGI Digestive Health-Northeast Minneapolis Clinic, Minneapolis, United States; 10Gilead Sciences, Inc., Foster City, United States; 11Liver Institute Northwest, Seattle, United States
Email: clevy@med.miami.edu

Background and aims: Cilofexor (CILO) is a nonsteroidal FXR agonist being evaluated in the phase 3 PRIMIS trial of non-cirrhotic patients with PSC. The safety and efficacy of CILO in patients with cirrhosis is unknown. This proof-of-concept, open-label study evaluated the safety and efficacy of escalating doses of CILO in patients with PSC and cirrhosis.

Method: Subjects with PSC and compensated cirrhosis were treated with escalating doses of CILO for 12 weeks (30, 60, and 100 mg daily for 4-week intervals). Safety, liver biochemistry, and serum markers of fibrosis, cellular injury, and pharmacodynamic effects of CILO (bile acids [BAs]) were evaluated.

Results: Among 19 subjects screened, 11 were enrolled and 10 (91%) completed the study. The median age was 48 years, 55% were male, 55% had IBD, and 46% were on ursodeoxycholic acid. At baseline (BL), median (IQR) laboratory parameters were: total bilirubin 1.1 mg/dL (0.8, 1.5), albumin 4.0 g/dL (3.9, 4.6), INR 1.0 (0.9, 1.1), platelets 201 × 109/µL (113, 218), ALP 510 U/L (269, 592), and GGT 344 U/L (208, 455). BL ELF and liver stiffness by transient elastography were 10.4 (9.5, 12.6) and 18.0 kPa (8.5, 67.6), respectively. At week 12 (W12), liver biochemistry tests improved relative to BL values including serum ALP (median: -13% [IQR: -22%, -9%]; p = 0.006), GGT (-43% [-52, -31]; p = 0.002), ALT (-25% [-36, -7]; p = 0.012), and AST (-12% [-29, 7]; p = 0.32), and rebounded after 4 weeks of untreated follow-up (Figure). Total bilirubin decreased at W12 relative to BL (-13% [-25, 0]; p = 0.13), while albumin and INR remained stable. Among 10 subjects with detectable serum BAs at baseline (26.1 µM/L [19.7, 52.9]), median change in BAs at W12 was -18% (-23, 12; p = 0.73). One patient discontinued treatment prematurely (subject decision). While no treatment-emergent (TE) serious adverse events (AEs) or deaths occurred in the study, Grade 2 or higher TEAEs occurred in 5 subjects (45%). Pruritus was reported by 8 subjects (73%), the majority (7 of 8) being Grade 1 or 2.
Conclusion: In this proof-of-concept study of patients with compensated cirrhosis due to PSC, escalating doses of CILO over 12 weeks were well tolerated and improved markers of cholestasis and liver biochemistry.

THU456
Association between patient-reported outcome measures and surrogate markers of liver fibrosis in large-duct primary sclerosing cholangitis

Emmanuel Selvaraj1,2,3, Jane D. Collier2, Emma Culver2, J Michael Brady2,**, Adam Bailey2, Michael Pavlides1,2,3, 1University of Oxford, Oxford Centre for Clinical Magnetic Resonance Research, Radcliffe Department of Medicine, Oxford, United Kingdom; 2University of Oxford, Translational Gastroenterology Unit, Nuffield Department of Medicine, Oxford, United Kingdom; 3NIHR Oxford Biomedical Research Centre, Oxford University Hospitals NHS Foundation Trust, Oxford, United Kingdom; 4University of Oxford, Department of Oncology, Oxford, United Kingdom; 5Perspectum Ltd., Oxford, United Kingdom

Email: emmanuel.selvaraj@cardiov.ox.ac.uk

Background and aims: Liver fibrosis is the main driver of disease progression in primary sclerosing cholangitis (PSC). Patient-reported outcome measures (PROMs) are increasingly used as exploratory end points in clinical trials. The aim of this study was to investigate the impact of liver fibrosis on health-related quality of life (HRQoL) using generic (SF-36) and disease-specific (PSC-PRO) tools.

Method: Patients with large-duct PSC were invited to complete HRQoL questionnaires in an outpatient setting. SF-36 and PSC-PROM domains were scored out of a maximum of 100% and 5, respectively. Mean scores were calculated for each health domain with lower SF-36 and higher PSC-PRO scores representing poorer quality of life. Transient elastography liver stiffness (LS; Echosens, France), enhanced liver fibrosis (ELF; Siemens Healthineers, Germany) and LiverMultisCan-derived iron-corrected T1 (cT1; Perspectum, Oxford, UK) were obtained on the same day. Advanced fibrosis was defined as LS > 9.6 kPa and ELF > 9.8 according to published cut-offs in PSC.

Results: Eighty patients (68% male) with median age 42 years (range: 18–76) and median PSC duration 8 years (range: 1–25) completed both HRQoL questionnaires. Median cT1 was 760 ms (range: 640–1053), median LS was 6.9 kPa (range: 3.7–45.5) and median ELF was 9.4 (range: 8.0–13.7). For the SF-36, median cT1 correlated with all health domains. Mental health (rho =−0.37, p < 0.01), bodily pain (rho =−0.31, p < 0.01) and physical functioning (rho =−0.31, p < 0.01) showed the strongest correlations. LS also correlated with all domains of SF-36 with bodily pain (rho =−0.28, p = 0.02), social functioning (rho =−0.27, p = 0.02) and physical functioning (rho =−0.25, p = 0.03) showing the strongest correlations, albeit weaker than median cT1. ELF did not correlate with any of the SF-36 domains. SF-36 scores were lower in patients with advanced fibrosis defined by LS cut-off, particularly for role physical (67% vs 85%, p < 0.01) and general health (40% vs 54%, p < 0.01) domains (Figure 1). For the PSC-PRO, median cT1 did not correlate with any of the domains. Physical function correlated with LS (rho =0.30, p <0.01) and ELF (rho <0.26, p =0.02) with higher scores in those with advanced fibrosis (LS: 1.5 vs 1.2, ELF: 1.5 vs 1.2, p = 0.01; ELF: 1.5 vs 1.2, p = 0.02). Activities of daily living correlated with LS (rho =0.26, p = 0.02) and ELF (rho =0.25, p = 0.03) with higher scores in those with advanced fibrosis (LS: 1.5 vs 1.2, p = 0.01; ELF: 1.5 vs 1.3, p = 0.03).

Conclusion: SF-36 and PSC-PRO health domains showed significant correlations with surrogate markers of liver fibrosis. Advanced fibrosis appears to have a greater impact on the physical than mental components of both PROMs. Future antifibrotic drug trials in PSC should consider assessing the impact of drug on physical well-being as one of the secondary end points.

THU457
Association between patient-reported outcome measures and severity of cholangiopathy in large-duct primary sclerosing cholangitis

Emmanuel Selvaraj1,2,3, Ahmed Ba-Ssalamah4, Sarah Poetter-Lang4, Jane D. Collier2, Emma Culver2, J Michael Brady5,6, Adam Bailey2,3, Michael Pavlides1,2,3, 1University of Oxford, Oxford Centre for Clinical Magnetic Resonance Research, Radcliffe Department of Medicine, Oxford, United Kingdom; 2University of Oxford, Translational Gastroenterology Unit, Nuffield Department of Medicine, Oxford, United Kingdom; 3NIHR Oxford Biomedical Research Centre, Oxford University Hospitals NHS Foundation Trust, Oxford, United Kingdom; 4University of Oxford, Department of Oncology, Oxford, United Kingdom; 5University of Vienna, Department of Biomedical Imaging and Image-Guided Therapy, Vienna, Austria; 6University of Oxford, Department of Oncology, Oxford, United Kingdom; 7Perspectum Ltd., Oxford, United Kingdom

Background and aims: Magnetic resonance cholangiopancreatography (MRCP) is used alongside serum alkaline phosphatase (ALP) to assess the severity of cholangiopathy in primary sclerosing cholangitis (PSC). Patient-reported outcome measures (PROMs) are increasingly used as exploratory end points in clinical trials. The aim of this study was to investigate the impact of ALP and the severity of cholangiopathy on MRCP on health-related quality of life (HRQoL) using generic (SF-36) and disease-specific (PSC-PRO) tools.

Method: Patients with large-duct PSC were invited to complete HRQoL questionnaires in an outpatient setting. SF-36 and PSC-PROM domains were scored out of a maximum of 100% and 5, respectively. Mean scores were calculated for each health domain with lower SF-36 and higher PSC-PRO scores representing poorer quality of life. 3D MRCP and serum ALP were acquired on the same day. Two radiologists reviewed MRCP images for the presence of dominant stricture (DS) and measured the maximum intrahepatic bile duct dilatation (IHBD) for Analí score. Images were analysed using a quantitative biliary tool, MRCP (Perspectum, Oxford, UK) to compute...
the intrahepatic sum of relative severity of dilatations (SumRelSevDilat). Patients were classified into high or low risk group for disease progression using ALP cut-off 1.5x upper limit normal (ULN) and the presence of DS.

Results: Eighty patients (68% male) with median age 42 years (range: 18–76) and median PSC duration 8 years (range: 1–25) completed both questionnaires. Median ALP was 150 IU/ml (range: 48–1180). DS was reported in 25 (31%) patients. Maximum IHBD was ≤3 mm in 26 (33%), 4 mm in 19 (23%) and ≥5 mm in 35 (44%) patients. Median MRCPP−derived SumRelSevDilat was 7.0m−1 (range: 0.0–19.8). The mean score for each health domain is shown in Figure 1 below. DS correlated with SF-36 bodily pain (rho = 0.28, p = 0.02). Maximum IHBD correlated with PSC-PRO physical function domain (rho 0.36, p < 0.01). SumRelSevDilat correlated with physical functioning (rho = 0.25, p = 0.04) and bodily pain (rho = 0.26, p = 0.03) domains of SF-36, and the physical function (rho 0.26, p = 0.03) and activities of daily living (rho 0.29, p = 0.01) domains of PSC-PRO. ALP correlated with bodily pain (rho = 0.37, p = 0.01), general health (rho = 0.26, p = 0.03), and energy/fatigue (rho = 0.29, p = 0.01) domains of SF-36, and the physical function (rho 0.30, p < 0.01) and emotional impact (rho 0.38, p < 0.01) domains of PSC-PRO. Bodily pain score was lower in those with DS compared to those without (74% vs 87%, p = 0.02). Both physical functioning (80% vs 92%, p = 0.04) and bodily pain (78% vs 85%, p = 0.03) scores were lower in patients with ALP greater than 1.5x ULN.

Conclusion: The presence of DS, severity of intrahepatic biliary dilatations, and ALP >1.5x ULN have a significant impact on both physical and mental health of patients with large-duct PSC.

THU458 Ultrasound for the diagnosis of gallbladder polyps in PSC: polyps greater than 8 mm indicate malignancy
Johannes Altenmüller1, Marcial Sebode2,3, Christina Weiler-Normann2,4, Christiane Wiegard2, Ansgar Lohse2,3, Christoph Schramm2,3,4,5, University Medical Center Hamburg-Eppendorf, Hamburg, Germany; 2University Medical Center Hamburg-Eppendorf, Ist Department of Medicine, Hamburg, Germany; 3European Reference Network on Hepatological Diseases (ERN RARE-LIVER); 4University Medical Center Hamburg-Eppendorf, Martin Zeitz Centre for Rare Diseases, Hamburg, Germany; 5University Medical Center Hamburg-Eppendorf, Hamburg Center for Translational Immunology, Hamburg, Germany. Email: 6817657@stud.uke.uni-hamburg.de

Background and aims: The risk of gallbladder carcinoma is increased in primary sclerosing cholangitis (PSC). Surveillance imaging every 6–12 months is used for early diagnosis. The aim of the study is to assess the reliability of ultrasound and MRI in detecting gallbladder polyps in people with PSC.

Method: All patients with PSC and a history of cholecystectomy were included for the evaluation and comparison of the two imaging methods, ultrasound and MRI for the detection of gallbladder polyps. Data including gallbladder histology were gathered retrospectively from the electronic medical records. Polyps with high-grade dysplasia were assigned to the malignancy group. We determined a cut-off for detecting malignant polyps in ultrasound using a receiver operating characteristics curve.

Results: From a cohort of 596 people with PSC at the University Medical Center Hamburg-Eppendorf, 139 patients underwent cholecystectomy. 77 patients underwent cholecystectomy for a suspected underlying gallbladder pathology. In 37 of those patients (21 m, 16 f) the detection of a polyp on imaging was the indication for surgery. Additionally, 62 patients had their gallbladder removed in the context of other interventions such as liver transplantation. Looking at all 139 cholecystectomy patients, ultrasound (sensitivity = 100%) was significantly more sensitive than MRI in detecting gallbladder polyps (sensitivity = 35%) (p < 0.001). MRI missed 3 of the 8 polyps with malignant histology. In ultrasound, malignant polyps (n = 8, median size = 13 mm) were found to be significantly larger than non-malignant polyps (n = 26, median size = 6.6 mm) (p < 0.001). Ultrasound was able to reliably detect a malignant polyp (area under the curve = 0.92, p < 0.001). At a cut-off value of 8 mm, sensitivity was 100% and specificity was 81%.

Conclusion: In people with PSC, ultrasound is more sensitive in the detection of gallbladder polyps than MRI. Based on the size of polyps, a reliable distinction can be made between malignant and benign findings: no malignant polyp was smaller than 8 mm. This validates previously published data from the Mayo Clinic. Cholecystectomy needs to be offered if a polyp of 8 mm or more is detected. Therefore, ultrasound and MRI may be complementary methods for hepatobiliary malignancy surveillance in people with PSC. A multicentre validation of the data is ongoing.

THU459 Temporal changes in patient-reported outcome measures stratified by liver fibrosis severity in large-duct primary sclerosing cholangitis
Emmanuel Selvaraj1,2,3, Jane D. Collier2, Emma Culver2, J Michael Brady4,5, Adam Bailey2,3, Michael Pavlides1,2,3, University of Oxford, Oxford Centre for Clinical Magnetic Resonance Research, Radcliffe Department of Medicine, Oxford, United Kingdom; 4University of Oxford, Translational Haematology Unit, Nuffield Department of Medicine, Oxford, United Kingdom; 5NIHR Oxford Biomedical Research Centre, Oxford University Hospitals NHS Foundation Trust, Oxford, United Kingdom. Email: emmanuel.selvaraj@cardiov.ox.ac.uk

Background and aims: Patient-reported outcome measures (PROMs) are increasingly used as exploratory end points in clinical trials. The aim of this study was to evaluate the temporal relationship between health-related quality of life (HRQoL) and liver fibrosis using generic (SF-36) and disease-specific (PSC-PRO) tools.

Method: Patients with large-duct PSC were invited to complete HRQol questionnaires in an outpatient setting at baseline (V1) and
follow-up (V2) visits at least 12 months apart. Transient elastography liver stiffness (LS; Echosens, France) measurements were recorded on the same day. SF-36 and PSC-PRO health domains were scored out of a maximum of 100 and 5, respectively. Mean scores were calculated for each domain with lower SF-36 and higher PSC-PRO scores representing poorer quality of life. Advanced fibrosis (F3-6) was defined based on published cutoff of LS >9.6 kPa in PSC.

Results: Fifty-five patients (64% male) with median age 45 years (range: 20–77) and median PSC duration 11 years (range: 2–26) attended both study visits. The median time between visits was 417 days (range: 362–582). The mean scores were numerically lower at V2 than V1 in all the SF-36 domains but only three domains showed statistically significant difference: bodily pain (74% vs 83%, p < 0.01), energy/fatigue (47% vs 57%, p < 0.001), and mental summary score (66% vs 71%, p < 0.001). There were no differences in any of the PSC-PRO domains between the visits. When stratified by baseline LS >9.6 kPa threshold (Figure 1), SF-36 physical functioning mean score dropped in the F3-6 group but increased slightly in the F0-2 group (−9.0 ± 17% vs 0.4 ± 21%, p = 0.01). In the PSC-PRO, the emotional impact mean score increased in the F3-6 group but decreased in the F0-2 group (0.6 ± 0.7 vs −0.1 ± 0.5, p < 0.01). There were no significant differences in mean scores in the other domains between the visits.

Conclusion: There was worsening of bodily pain, levels of energy and mental health even within a year in patients with large-duct PSC. Patients with advanced fibrosis reported lower physical functioning and higher emotional impact of their disease compared to those without advanced fibrosis. Changes in PROMs are related to liver fibrosis and need to be considered in future antifibrotic drug trials. These findings, however, need to be interpreted in the context of imposed restrictions during the Covid-19 pandemic which may have had a significant psycho-social impact on patients.

THU460 Temporal increase in interquartile range iron-corrected T1 in high-risk patients with large-duct primary sclerosing cholangitis
Emmanuel Selvaraj1,2,3, Jane D. Collier2, Emma Culver2, Michael Brady1,2,3, Adam Bailey2,3, Michael Pavlides1,2,3
1University of Oxford, Oxford Centre for Clinical Magnetic Resonance Research, Radcliffe Department of Medicine, Oxford, United Kingdom; 2University of Oxford, Translational Gastroenterology Unit, Nuffield Department of Medicine, Oxford, United Kingdom; 3NIHR Oxford Biomedical Research Centre, Oxford University Hospitals NHS Foundation Trust, Oxford, United Kingdom

Background and aims: Median iron-corrected T1 (tC1T) derived from LiverMultiScan (Perspectum, Oxford, UK) correlates well with histological liver fibrosis. Interquartile range (IQR) tC1T has been proposed to better reflect the patchy liver fibrosis in primary sclerosing cholangitis (PSC). The aim of this study was to investigate the temporal changes in IQR tC1T in large-duct PSC.

Method: Patients with large-duct PSC attended study visits at baseline (V1) and follow-up (V2). Standardised liver T1 and T2* maps, transient elastography liver stiffness (LS; Echosens, France), enhanced liver fibrosis (ELF; Siemens Healthineers, Germany), and blood tests were performed on the same day at each visit. MRI data were analysed using LiverMultiScan to derive liver IQR tC1T. The Amsterdam-Oxford model (AOM) score was also calculated. Patients were classified into high-risk or low-risk groups for disease progression using baseline data according to published cut-offs in PSC: AOM >2, ELF >9.8 and LS >9.6 kPa. Mixed ANOVA models were used to examine the within-subject effect (time), between-subject effect (high-risk or low-risk), and interaction between the two on changes in IQR tC1T. The magnitude of effects (partial-ETA squared) was defined as: 0.01 (small), 0.06 (medium), and 0.14 (large). Receiver operating characteristic curve (ROC) analyses were conducted to assess the diagnostic performance of V1 and delta V1–V2 measurements to identify the high-risk groups.

Results: Fifty-five patients (64% male) with median age 45 years (range: 20–77) and median PSC duration 11 years (range: 2–26) attended both study visits. The median time between visits was 417 days (range: 362–582). IQR tC1T was higher in the high-risk groups compared to low-risk groups at either time points (AOM: p < 0.001; ELF: p = 0.001; LS: p < 0.001). IQR tC1T increased over time in the high-risk group and not in the low-risk group (AOM: p = 0.03; ELF: p = 0.04; LS: p = 0.07). There was a significant interaction between time and risk grouping on IQR tC1T when stratified by AOM (F = 15.3, p < 0.001; partial-ETA squared = 0.23), ELF (F = 9.1, p < 0.01; partial-ETA squared = 0.15) and LS (F = 7.2, p = 0.01; partial-ETA squared = 0.12). Delta V1–V2 (AUC = 0.78, 95% CI: 0.61–0.95) numerically had a higher diagnostic performance than V1 IQR tC1T (AUC = 0.75, 95% CI: 0.61–0.89; p < 0.001) to detect the AOM >2 group but was no better when stratified by ELF and LS.

Conclusion: Patients who are at higher risk of death and/or liver transplantation (AOM >2) or with advanced fibrosis (ELF >9.8, LS >9.6 kPa) are likely to have a progressively higher IQR tC1T over time. Single baseline measurements alone outperformed dynamic measurements over two time points in detecting the high-risk group. Further follow-up data points with repeated-measures analysis and correlation with clinical outcomes are needed.

THU461 Seladelpar treatment of patients with primary biliary cholangitis (PBC) for 2 years improves the GLOBE PBC score and predicts improved transplant-free survival
Bettina Hansen1,2, Elaine Watkins3, Ke Yang3, Yun-Jung Choi3, Charles McWherter3, Gideon Hirschfield4, 1Toronto Centre for Liver Disease, Toronto General Hospital, University Health Network, Toronto, Canada; 2Institute of Health Policy, Management and Evaluation (IHPME), University of Toronto, Toronto, Canada; 3CymaBay Therapeutics, Inc, Newark, United States; 4Toronto Centre for Liver Disease, University of Toronto, Toronto, Canada

Background and aims: The GLOBE score is a validated risk assessment tool providing an estimate of transplant-free survival for patients with PBC. Seladelpar is a PPAR-delta agonist with anti-cholestatic, anti-inflammatory and anti-pruritic activity in PBC...
patients. Our aim was to evaluate change in GLOBE score in patients with PBC treated with seladelpar for 2 years.

Method: Eligible patients with PBC and an inadequate response or intolerance to UDCA (alkaline phosphatase (ALP) ≥1.67xULN) were enrolled into an open-label one-year phase 2 study (EudraCT: 2016-002996-91) receiving daily oral 5 or 10 mg seladelpar. After 1 year, patients were eligible for an open label long-term study (EudraCT: 2017-003910-16). The change in GLOBE score following seladelpar treatment over 2 years and the resulting predictions of transplant-free survival were assessed. The contributions of alkaline phosphatase, total bilirubin, albumin, and platelets to changes in GLOBE score were examined.

Results: 101 patients entered the long-term study with available GLOBE score and were evaluated: 94% female, mean (SD) age 57 (9.0) years, duration of PBC 10 (6.6) years, and UDCA dose of 15 (3.7) mg/kg/day. Mean baseline values were ALP 321 (165) U/L, bilirubin 0.8 (0.3) mg/dL, albumin 4.1 (0.3) mg/dL, platelets 237 (82) × 10^9/L, and GLOBE score 0.390 (0.656). After treatment with seladelpar for 3 months, 1 year and 2 years the mean (SD) change from baseline in GLOBE score was −0.330 (0.321), −0.324 (0.281), and −0.417 (0.269), respectively. The observed early fall of GLOBE score within 3 months was followed by a gradual decline through 2 years (Fig. 1A). The improvements in GLOBE score for all patients and those completing two years were comparable. The greatest changes in GLOBE score were attributable to changes in alkaline phosphatase values followed by those of total bilirubin (Fig. 1B). Seladelpar treatment led to improvements in GLOBE score for all patients and those completing 2 years treatment (47 of 50, Fig. 1D).

Conclusion: Seladelpar treatment over 2 years resulted in a sustained decrease in GLOBE score for patients with PBC that is associated with a predicted improvement in transplant-free survival.

THU462 Validation of a novel method of identifying patients with Primary Sclerosing Cholangitis (PSC) in a Canadian population

Harshil Patel1, Fengjuan Yang1, Mark G Swain1, Gideon Hirschfield2, Gilaaad Kaplan1, Bettina Hansen1, Abdel-Aziz Shaheen1. 1University of Calgary, Calgary, Canada; 2University Health Network, Toronto, Canada Email: az.shaheen@ucalgary.ca

Background and aims: Studies describing the epidemiology of primary sclerosing cholangitis (PSC) have been limited due to suboptimal case-finding and case-ascertainment. Using administrative databases to identify PSC in the population is not reliable. Guidelines recommend PSC patients should undergo a colonoscopy to rule out inflammatory bowel disease (IBD). Therefore, we aimed to evaluate the role of using an endoscopy database to improve PSC patient identification.

Method: We used the Pentax medical endoscopy endoPRO iq® database to identify adult (≥18 years) patients who had undergone a colonoscopy in the Calgary Health Zone [(CHZ) population ~1.5 million]. We searched the endoscopy report database for one of the following predefined texts: primary sclerosing cholangitis, PSC, sclerosing cholangitis, between 2005 and 2019. The CHZ is a one-payer system providing medical care to all residents in the zone. All endoscopies performed in the CHZ are captured within a secure Pentax medical database. We used the International Classifications of Diseases (ICD) codes to identify patients with PSC in the following administrative databases: inpatient, ambulatory, and physician claims. Finally, for case-ascertainment, we conducted a validation study using medical charts on all PSC patients identified in the endoscopy database and a systematic random sample of patients identified by the administrative databases but not by the endoscopy database (sample size = 207). In our validation study, we identified patients with ulcerative colitis (UC), Crohn’s disease (CD), and indeterminate colitis.

Results: During our study period, we identified 535 patients using the endoscopy database and 4, 544 patients in administrative databases with a potential PSC diagnosis. Within the endoscopy database, we identified 406 PSC patients (male sex 59.4%) who had a confirmed PSC diagnosis using radiological modalities and/or a liver biopsy. In this cohort, 1.5% (n = 6) patients were not identified in the administrative databases. IBD was prevalent at 81.5% (n = 331) in our cohort (UC 149 [36.7%], CD 146 [36.0%], and 36 [8.9%] indeterminate colitis). In our validation study (n = 742 charts), 412 patients had a confirmed PSC diagnosis using the endoscopy database alone to identify PSC patients had sensitivity 98.5% (406/412), specificity 60.9% (201/330), positive predictive value (PPV) 75.9% (406/535), and negative predictive value (NPV) 97.1% (201/207). Using multiple previously recommended algorithms in the administrative databases to identify PSC patients had a maximum PPV of 62% and sensitivity of 54%.

Conclusion: Using endoscopy databases to identify PSC patients is a reliable, accurate and feasible method compared to using administrative databases. Our proposed method would lead to better case-ascertainment and should improve the quality of future studies evaluating the natural history of PSC.

THU463 The prevalence of primary biliary cholangitis (PBC) is on the rise: a Canadian population-based study

Bryce Tkachuk1, Fengjuan Yang2, Gideon Hirschfield3, Mark G Swain2, Abdel-Aziz Shaheen2. 1University of Calgary, Medicine, Calgary, Canada; 2University of Calgary, Calgary, Canada; 3University Health Network, Toronto, Canada Email: az.shaheen@ucalgary.ca

Background and aims: Canada has one of the highest rates of primary biliary cholangitis (PBC) incidence and prevalence worldwide. Our group reported the natural history of PBC in Calgary (population ~1.5 million) more than a decade ago. Significant awareness and recent advancement of PBC management were reported. Therefore, we aimed to study the impact of these factors on the natural history of PBC in a well-defined Canadian population and evaluate the temporal trends of PBC incidence and prevalence.

Method: We used population-based administrative data (inpatient, ambulatory care, and physician claims) and a previously validated International Classification of Diseases coding algorithm to identify PBC patients in the Calgary Health Zone between 2003 and 2018. We applied the same validated methods that we implemented in our
original study (Myers et al., 2009, study period: 1996–2002). We conducted a validation study on incident cases to confirm the performance of the used algorithm in order to identify definite PBC patients (those who had at least two of the following criteria: positive anti-mitochondrial antibody, cholestatic liver enzymes, and a compatible liver biopsy). The positive predictive value (PPV) was 78.2%, while PPV of the original algorithm was 73.1%. We used a washout period of 2 years (2003–2004) to identify incident PBC cases. We chose March 31st of each year as point prevalence. Temporal trends were evaluated using generalized linear models assuming a Poisson distribution or a negative binomial distribution if over-dispersion is present. Rates were adjusted to the Canadian population census of 2016.

**Results:** Between 2005 and 2018, the overall age/sex annual incidence of PBC was 39.4 cases per million. Age-adjusted incidence rates were 60.7 per million in women versus 16.7 per million in men (incidence rate ratio [IRR] 3.68; 95% CI 2.98–4.54). The highest adjusted incidence was observed among the age group 60–79 years (74.0 case per million). Age/sex-adjusted point prevalence rates of PBC increased from 295.8 to 500.0 per million between 2005 and 2018, p < 0.001. As expected, adjusted point prevalence rates were much higher among women than men (799.8 versus 169.0 per million). We identified 520 incident cases during our study time (female 78.7% [n = 409]). After a median follow-up of 6.8 years (IQR 3.9–10.6), 29 patients underwent transplantation (5.6%) and 81 patients died (15.6%). The annual mortality rate was 8.1% (95% CI 9.8–14.0%). The estimated 5- and 10-year survival rates were 90.7% (87.5%–93.0%) and 77.4% (72.2%–81.7%), respectively. Survival was not significantly different between men and women, p = 0.50.

**Conclusion:** In this well-defined cohort, we reported a significant increase in the prevalence of PBC in a Canadian population. Prevalence of PBC is higher among the older age group which could reflect better case-identification and management.

**THU464**

Rituximab is a safe and effective treatment for patients with autoimmune hepatitis: results from the Spanish registry for cholestatic and autoimmune hepatitis

Ana Barreira1,2, Maria Carlota Londoño3,4, Carmen Álvarez-Navascués5, Carlos Ferre Aracil6, Indhira Perez Medrano1, Juan Turnes1,2, Diana Horta2, Álvaro Díaz-González7, Fernando Díaz Fontela8, Magdalena Salcedo1,2, Mar Riveiro Barciela1,9,10

Hospital Vall Hebron, Liver Unit, Barcelona; 2Centro de Investigación Biomédica en red de enfermedades hepáticas y digestivas; 3Hospital Clinic, Liver Unit, Barcelona; 4Hospital Universitario Central de Asturias. Digestive Department, Oviedo; 5Hospital Universitario Puerta de Hierro Majadahonda. Digestive Department, Madrid; 6Complejo Hospitalario Universitario de Pontevedra. Digestive Department, Pontevedra; 7Hospital Universitari Mutua de Terrassa. Digestive Department, Barcelona; 8Hospital Universitario Marqués de Valdecilla. Instituto de Investigación Sanitaria Valdecilla. Digestive Department, Santander; 9Hospital General Universitario Gregorio Marañón. Digestive Department, Madrid; 10Hospital Vall Hebron, Liver Unit, Barcelona

Email: mar.riveiro@gmail.com

**Background and aims:** The evidence of second-line therapy for autoimmune hepatitis (AIH) is relatively scarce, especially concerning biological agents such as rituximab. This study aims to evaluate the efficacy and safety of rituximab in patients with autoimmune hepatitis (AIH).

**Method:** Multicenter retrospective study of all patients with AIH from the ColHai registry who received rituximab from January 2015 to September 2021. Efficacy was assessed by improvement in transaminases and immunoglobulin (Ig) G or normalization (biochemical response) and later development of flares; safety in terms of adverse reactions, infectious and tumoral complications.

**Results:** 2763 AIH patients were included in the ColHai registry (Spanish registry for cholestatic and autoimmune disorders). Out of them, 13 patients with type 1-AIH were treated with rituximab in 8 different hospitals. The majority were women (10/13), median age 43 years. At diagnosis 1 presented an acute severe hepatitis and 2 had liver cirrhosis. Time from diagnosis to beginning of rituximab was 20 months and to last follow-up 5 years. The reasons for biological therapy were: 4 difficult-to-manage AIH and 9 due to indication for other comitant autoimmune disorder (4 multiple sclerosis, 3 vasculitis and 2 rheumatoid arthritis). The majority (11/13) received a 2-dose induction course followed by a new dose every 6 months. After rituximab, at the 1-month follow-up an improvement of IgG levels was observed (p = 0.018) and a tendency towards decrease of AST/ALT. At month 6, the reduction in AST/ALT was statistically significant (p = 0.012 and p = 0.008). Eight out of 13 presented increased transaminases and IgG levels at the start of rituximab, and 5/8 achieved biochemical response after rituximab therapy. Treatment was well tolerated, without infusion reactions, though 3 patients developed non-severe infectious complications. All patients but one were on corticoids at the beginning of rituximab and in 8/12 they could be tapered or discontinued. Moreover, in five of these patients other immunosuppressants could be stopped due to the positive impact of rituximab as shown in the figure. Despite initial improvement, four patients presented flares of AIH during follow-up that were successfully managed with new doses of rituximab.

<table>
<thead>
<tr>
<th>Patient</th>
<th>Corticoids</th>
<th>Azathioprine</th>
<th>MMF</th>
<th>Tacrolimus</th>
<th>Everolimus</th>
</tr>
</thead>
<tbody>
<tr>
<td>Patient 1</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Patient 2</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Patient 3</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Patient 4</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Patient 5</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Patient 6</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Patient 7</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Patient 8</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Patient 9</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Patient 10</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Patient 11</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Patient 12</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Patient 13</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Figure: Individual therapy at the beginning of rituximab (grey squares) and drugs that were reduced or discontinued during follow-up (striped squares).

**Conclusion:** Rituximab is a safe and effective treatment for AIH, leading to reduction of immunosuppression in a high proportion of patients and improvement of transaminases and IgG levels.
Autoimmune hepatitis diagnosed after COVID-19 vaccination. Results from the spanish registry for autoimmune and cholestatic hepatitis

Ana Barreira1,2, Mar Riveiro Barciela1,3, Agustin Castiella3, Álvaro Díaz-González4, María Carola Londoño5,6, Indhira Perez Medrano6,7, Judith Gómez-Camaredo2,7, Marta Casado6, Carmen Del Pozo-Calzada7,8, María Dolores Antón Conejero2,9,10, Magdalena Salcedo1,2,11, Hospital Universitario Vall de Hebrón, Liver Unit; 2Instituto de Salud Carlos III, Centro de Investigación Biomédica en Red de Enfermedades Hepáticas y Digestivas (CIBEREhd); 3Hospital Universitario de Torrecárdenas, Servicio de Aparato Digestivo; 4Hospital General Universitario Gregorio Marañón, Madrid, Hepatology and Liver Transplantation Unit; 5Hospital Universitario Vall de Hebrón, Liver Unit; 6Complejo Hospitalario Universitario de Pontevedra, Servicio de Aparato Digestivo; 7Hospital Universitario de A Coruña, Servicio de Aparato Digestivo; 8Hospital Universitario Marqués de Valdecilla. Instituto de Investigación Sanitaria Valdecilla (DIVVAL), Servicio de Aparato Digestivo; 9Hospital Universitario Donostia, Liver Unit; 10Hospital Universitario Marqués de Valdecilla. Instituto de Investigación Sanitaria Valdecilla (DIVVAL), Servicio de Aparato Digestivo; 11Hospital Universitario de Donostia, Liver Unit; 12Hospital Universitario Universitario de Murcia, Servicio de Aparato Digestivo; 13Hospital Universitario Universitario de Murcia, Servicio de Aparato Digestivo; 14Hospital General Universitario Gregorio Marañón, Madrid, Hepatology and Liver Transplantation Unit
Email: magdalena.salcedo@salud.madrid.org

Background and aims: Universal vaccination has become the main strategy against the COVID-19 pandemic. The SARS-CoV-2 spike protein used in the vaccines is believed to be responsible for stimulating the immune system, thus suggesting a possible association between COVID-19 vaccines and the development of auto-immune diseases. To date, different events of probable autoimmune origin have been reported in association with the COVID-19 vaccine, including few cases of autoimmune hepatitis (AIH). The aim of this study was to describe the clinical and epidemiological characteristics of a number of patients with AIH debut or reactivation after COVID-19 vaccination.

Method: Multicenter, retrospective-prospective study, that included subjects who have received one or two doses of any of the approved COVID-19 vaccines and later presented increased transaminases values due to AIH within the 90 days after vaccination.

Results: 23 patients from 9 Spanish academic hospitals were included. 17/23 were female, mean age 51 (±15) years. 19/23 patients were biopsied and four were not. 3 of them had a previous diagnosis of AIH. Seven patients had another prior autoimmune disorder, including few cases of autoimmune hepatitis (AIH). All but one of the biopsied patients showed histological findings compatible with AIH. Simplified AIH Score (≥4 points) in 16/23 patients. All patients received treatment with corticosteroids and in 19 patients immunosuppressive treatment with azathioprine was initiated.

Conclusion: An increase in transaminases values after administration of COVID-19 vaccine should be evaluated given the possibility of diagnosing autoimmune hepatitis.

A prospective trial of a gluten free diet in primary sclerosing cholangitis with associated colitis

Timur Liwinski1, Sina Hübener1, Lara Henze1, Peter Huebener1, Melina Heinemann1, Bettina Jagemann1, Marcus Tetzlaff1, Guido Schachtschal1, Thomas Rösch1, Erikia Monguzzi2, Corinna Bang3, Andre Franke3, Ansgar W. Loshe4, Detlef Schuppan4, Christoph Schramm1, University Medical Center Hamburg-Eppendorf, Hamburg, Germany; 5Universitätsmedizin der Johannes Gutenberg-Universität Mainz, Mainz, Germany; 6University of Kiel, Kiel, Germany
Email: liwinskt@gmail.com

Background and aims: Primary sclerosing cholangitis (PSC) is a progressive autoimmune disease of the bile ducts associated with inflammatory bowel disease. Several studies indicated that gluten restriction might ameliorate autoimmune liver disease and inflammatory bowel disease (IBD) symptoms. We investigated whether patients with PSC associated IBD can benefit from a diet free of wheat and gluten (GFD) using a prospective multi-omics approach.

Method: We performed a prospective clinical pilot study administering an eight-week GFD to PSC patients with non-advanced liver disease and associated colitis without overt clinical activity. A clinical dietitian trained patients and controlled adherence to the intervention by validated questionnaires and measuring gluten peptides in urine. The patients were evaluated at several time points, including endoscopy before and after the GFD period. We recorded multiple clinical parameters, dietary information, and biologically relevant parameters, including intestinal mucosal cytokine levels, intestinal bulk RNA-Seq transcriptomics. The enteric fecal and mucosal microbiota were analyzed by sequencing the variable region V1/V2 of the 16S rRNA gene and shotgun metagenomics.

Results: In total, fifteen patients were enrolled and completed the study. A decreased expression of proinflammatory mucosal cytokines and chemokines such as IL6 (p < 0.001), IL8 (p < 0.001), CCL2 (p = 0.042), and TNF-alpha (p < 0.001) was observed after GFD. Moreover, the intestinal transcriptome indicated improvement of the gut barrier, with an increase of pathways related to “adhesers junction” (p = 0.0471), “cell-substrate junction” (p = 0.0262), “cell-substrate adherers junction” (p = 0.0233), and “focal junction” (p = 0.0217). We found mild to moderate changes in luminal microbiota composition after GFD, including a decrease of Romboutsia ilealis (FC = −9.02, FDR < 0.001). As expected from the short intervention period and the low disease activities, no statistically significant response was observed regarding clinical parameters such as the endoscopic score (p = 0.398) and patient-reported outcome measures. According to the food frequency questionnaire, the macronutrient composition (other than gluten) did not change during eight weeks of diet.

Conclusion: This is the first study to demonstrate that GFD may improve intestinal inflammation and barrier function in patients with PSC-IBD. This effect was linked to changes in the enteric microbiota composition. This pilot study justifies subsequent studies in patients with more severe disease activity.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Median (IQR)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Aspartate aminotransferase (AST)</td>
<td>915 (622-1448)</td>
</tr>
<tr>
<td>Alanine aminotransferase (ALT)</td>
<td>568 (704-1498)</td>
</tr>
<tr>
<td>Alkaline phosphatase (AP)</td>
<td>135 (131-239)</td>
</tr>
<tr>
<td>Gamma-glutamyl transferase (GGT)</td>
<td>183 (120-266)</td>
</tr>
<tr>
<td>Total bilirubin, mg/dl</td>
<td>2.96 (1.8-10.3)</td>
</tr>
<tr>
<td>Direct bilirubin, mg/dl</td>
<td>2.3 (1.3-11)</td>
</tr>
<tr>
<td>International Normalized Ratio (INR)</td>
<td>1.09 (0.98-1.28)</td>
</tr>
<tr>
<td>Immunoglobulin G (IgG), mg/dl</td>
<td>1684 (1262-2240)</td>
</tr>
<tr>
<td>Total proteins, mg/dl</td>
<td>7.4 (6.6-7.9)</td>
</tr>
</tbody>
</table>

Figure: Analytical data of the patients at the time of hepatitis
**THU467**

The international autoimmune hepatitis group retrospective registry: quality assessment and analysis of clinical characteristics and liver-related outcome

Charlotte Slooter, Floris van den Brand, Ana Lleo, Francesca Colapietro, Marco Lenzi, Paolo Muratori, Nanda Kerkar, Málaga, Spain; Hospital of Larissa, Greece; Vírgen de Victoria University Hospital, University of Málaga, Spain; University of Alberta Hospital, Edmonton, Canada; University of Bologna, Italy; Golisano Children's Hospital, University of Rochester Medical Center, Rochester, United States; University Hospital of Larissa, Greece; Virgen de Victoria University Hospital, University of Málaga, Spain; University of Alberta Hospital, Edmonton, Canada; Centro Hospitalar Sao Joao, Porto, Portugal; King's College, United Kingdom

**Background and aims:** The International Autoimmune Hepatitis (AIH) Group retrospective registry (IAIHG-RR) is a web-based platform for large scale aetiological and therapeutic studies in paediatric and adult subjects enrolled with a diagnosis of AIH. This study aimed to ascertain data quality and describe the clinical characteristics and outcomes of this cohort.

**Method:** This retrospective analysis included all patients with a clinical diagnosis of AIH (n = 2278) from the IAIHG-RR entered between December 2018 and September 2021. This registry contains data on clinical characteristics and liver-related outcomes from 37 centers in 7 countries. Quality assessment included cohort completeness for 31 pre-defined variables, consistency and data was externally validated.

**Results:** Completeness of individual data was 75.8% (range 3.0–100). Per center, completeness varied between 69.5% and 99.9%. Consistency of inclusion criteria and outlier analysis was nearly 100%. Among patients for whom a simplified AIH score was available, diagnosis was classified as possible in 27.5%, probable in 25.0% and in 47.5% as definite. At diagnosis, 21.9% showed signs of cirrhosis and median Model for End-Stage Liver Disease (MELD) score was 11 [range 6–40]. Primary biliary cholangitis and primary sclerosing cholangitis were reported in 10.0% and 7.0%, respectively. Other associated diseases were reported in 26.3%. For 1191 patients follow-up and outcome data was available. With a median follow-up period of 12 [range 0–49] years 36.8% demonstrated signs of cirrhosis, 2.2% were diagnosed with hepatocellular carcinoma and 10.6% underwent liver transplantation. 172 patients died during the follow-up period at a median age of 65 (range 15–94). In 49.7%, the cause of death was reported liver-related. Liver transplantation and liver related death were both associated with signs of cirrhosis at baseline (hazard ratio [HR] 1.90; p < 0.001), the MELD score at baseline (HR 1.09; p < 0.001) and with persistence of elevated aminotransferases at 6 months (HR 2.75; p < 0.001).

**Conclusion:** The IAIHG-RR represents world’s largest patient cohort with moderate-to-good quality of baseline and follow-up data with relevant number of liver-related adverse events. This study showed that cirrhosis and MELD score at baseline and persistence of elevated aminotransferases at 6 months are associated with liver transplantation and liver-related death. This registry is a suitable platform, which allows for patient selection for future therapeutic and aetiological studies.

**THU468**

Liver inflammation activity in autoimmune hepatitis patients with normal ALT and IgG levels

Chuanwu Zhu, Jiacheng Liu, Jian Wang, Huali Wang, Yilin Liu, Viguang Li, Li Zhu, Weimao Ding, Yuanwang Qiu, Yongfeng Yang, Jie Li, Rui Huang, Chao Wu, The Affiliated Infectious Diseases Hospital of Soochow University, Department of Infectious Diseases, Suzhou, China; Nanjing Drum Tower Hospital Clinical College of Traditional Chinese and Western Medicine, Nanjing University of Chinese Medicine, Department of Infectious Diseases, Nanjing, China; Nanjing Drum Tower Hospital, The Affiliated Hospital of Nanjing University Medical School, Department of Infectious Diseases, Nanjing, China; Nanjing Second Hospital, Nanjing University of Chinese Medicine, Department of Hepatology, Nanjing, China; The Fifth People's Hospital of Wuxi, Department of Infectious Diseases, Wuxi, China; Huai'an No. 4 People's Hospital, Department of Hepatology, Huai'an, China

**Background and aims:** Serum alanine transaminase (ALT) and IgG levels are considered as surrogate markers for histological activity in autoimmune hepatitis (AIH). We assessed the inflammatory activity in AIH patients with normal ALT and IgG levels.

**Method:** 257 AIH patients underwent liver biopsy (LB) were retrospectively included from four medical centers. Liver inflammation and fibrosis were estimated by Scheuer scores. The definitions of advanced inflammation and fibrosis were G ≥ 3 and S ≥ 3, respectively.

**Results:** 163 (63.3%) AIH patients had advanced inflammation, while 125 (48.6%) patients had advanced fibrosis. The proportion of advanced inflammation was 62.1% in patients with normal ALT and 55.6% in patients despite normal ALT and IgG. The proportion of advanced inflammation was 44.0% in patients without advanced fibrosis and was 81.8% in those with advanced fibrosis. Of patients with advanced fibrosis, 78.6% (33/42) of patients with normal ALT presented advanced inflammation, which was 75.0% in patients with normal ALT and IgG. Among patients without advanced fibrosis, the proportion of advanced inflammation was as high as 33.3% in those with normal ALT and 31.3% in those despite normal ALT and IgG. Red cell distribution width was independently associated with advanced inflammation (OR: 1.521, 95% CI: 1.193–1.938, P = 0.001) in entire patients.

**Figure:** Data captured in absolute numbers for a pre-defined set of 31 variables in the IAIHG-RR (n = 2278).
THU469
Novel screening test for primary sclerosing cholangitis: the role of serology, liver function tests, histology and radiology
Nina Barner-Rasmussen1, Nelli Sjöblom2, Hannu Kautiainen3, Johanna Arola2, Martti Farkkila1. 1University of Helsinki and Helsinki University Hospital, Departement of Gastroenterology, Helsinki, Finland; 2University of Helsinki and Helsinki University Hospital, Department of Pathology, Helsinki, Finland; 3University of Eastern Finland, Institute of Public Health and Clinical Nutrition, Kuopio, Finland
Email: nina.barner-rasmussen@hus.fi

Background and aims: Primary sclerosing cholangitis (PSC) is a chronic cholestatic liver disease. There is no specific laboratory test for surveillance or screening in PSC unlike in primary biliary cholangitis. At present, the screening of PSC is mainly based on elevated alkaline phosphatase (ALP) in patients with inflammatory bowel disease (IBD). However, ALP and gamma-glutamyl transferase (GT) may be normal, even in advanced bile duct disease. The diagnosis is made by magnetic resonance cholangiopancreatography (MRCP) or by endoscopic retrograde cholangiography (ERC). The latest guidelines from Europe and America do not recommend liver biopsy, apart from small-duct PSC or a suspicion of an overlap condition. Patients with or without advanced fibrosis

Methods: We retrieved 395 PSC patients from the PSC registry of Helsinki University Hospital who came for their 1st ERC to confirm the diagnosis. 69 patients with suspicion of PSC who underwent ERC, liver biopsy and MRCP excluding PSC, served as controls (non-PSC patients). Liver histology was scored according to the Nakanuma classification from Herovici stained core needle biopsy specimens. MRCP before diagnosis was scored from the existing radiology report as negative for PSC, finding suggestive for PSC, and clear findings for PSC. We included demographics and eleven different laboratory tests in the analysis. Area under the curve (AUC), positive prediction value, likelihood ratio, sensitivity, specificity, and odds ratio (OR) were calculated. Variables with highest OR were selected for multivariate logistic regression, which was used to create the novel scoring system.

Results: IBD, perinuclear anti-neutrophil cytoplasmic antibodies (P-ANCA) and ALP had the best predictive value. A score was assigned to each statistically significant predictor. Presence of IBD and P-ANCA gives 2 points each and ALP >UNL 1 point. The optimal cut-off point for the score was ≥3, with AUC of 0.83 (95%CI 0.78–0.88). If a patient got a score of 3 or higher, the probability of a true PSC diagnosis was >90%. Adding liver histology or MRCP to the score did not add predictive value.

Conclusion: High proportion of advanced inflammation was found in PSC patients despite normal ALT and IgG levels even for those without advanced fibrosis. Though fibrosis can be ruled out by non-invasive methods in PSC patients with normal ALT and IgG, LB is encouraged to assess inflammatory activity.

THU470
More than just an itch: impact of cholestatic pruritus in primary biliary cholangitis (PBC) on health-related quality of life (HRQoL)
Helen Smith1, James Fettiplace1, Robyn von Maltzahn1, Sugato Das2, Megan McLaughlin3, David Jones1,1GlaxoSmithKline, India; 2GlaxoSmithKline, United States; 4Newcastle University, United Kingdom
Email: helen.t.smith@gsk.com

Background and aims: Pruritus associated with PBC affects sleep and social and emotional wellbeing. Limited data exist on the impact of pruritus on health utility in patients with PBC. The impact of itch severity on health utility (a single value between 0 [death] and 1 [perfect health]), commonly used in health technology assessments to calculate quality-adjusted life years and compare different conditions. A recent UK study explored EQ-5D utilities in a broad PBC population (Rice et al. Clin Gastroenterol Hepatol 2021;19:769–76). Here, using data from the Phase 2b GLIMMER study (post hoc) investigating lirilixibat for the treatment of pruritus in PBC (NCT02966834), the impact of itch severity on health utility in PBC is explored and quantified for the first time.

Methods: Patients in GLIMMER recorded itch twice daily on a 0–10 numeric rating scale (NRS) and completed the EQ-5D-5L at study entry, baseline (BL) and end of treatment. BL followed a 4-week single-blind placebo run-in. Patients were classed as having mild (<4), moderate (4 to <7) or severe pruritus (≥7 to 10) based on mean Worst Daily Itch NRS score in the 7 days prior to BL.

Results: The GLIMMER population (N = 147) was 94% female with a mean (SD) age at BL of 55.8 (11.04) years. Most patients had moderate pruritus (n = 76), with similar numbers with mild (n = 35) and severe (n = 36) pruritus. At BL, alkaline phosphatase levels were higher with greater itch severity: mean (SD) 177 (115.4) and 249 (190.8) IU/L in patients with mild and severe itch, respectively. Overall, mean (SD) BL utility was 0.69 (0.23), lower than the general PBC population (Figure) and with a clear and notable impact of pruritus severity on health utility. Thus, patients with mild or moderate pruritus at BL had similar utilities (0.75 [0.17] and 0.76 [0.17], respectively), marginally lower than the general UK population

Figure: Prognostic performance of HelPSCreening-score

Conclusion: We have created a novel scoring system to screen the probability of PSC using non-invasive tests. The HelPSCreening-score may help target further investigations in patients with suspicion of PSC.
Isolated IgG elevation is not associated with worse outcome in patients with autoimmune hepatitis

Alvaro Diaz Gonzalez2, Lorena Carballo-Folgoso2, Carmen Alvarez-Navascues2, Judith Gómez-Camaraero1, Diana Horta4, Beatriz Mateos Muñoz3, Ma María Del Barrio1, Marina Cobreros1, Sergio Rodríguez-Tajes2, Olivas Ignasi6, Indhira Perez Medrano7, Sergio Rodriguez-Tajes6, Olivas Ignasi6, Indhira Perez Medrano7, Beatriz Mateos Muñoz3, María Carlota Londoño6.

Conclusion: Pruritus (particularly severe pruritus) has a significant negative impact on HRQoL and health utility. Presence and severity of itch should be evaluated in PBC and prioritised in treatment plans.

Funding: GSK (201000).

THU471

Continuous variables are presented as median and IQR.

<table>
<thead>
<tr>
<th>Age</th>
<th>Total (n = 266)</th>
<th>IgG (n = 78)</th>
<th>IgGn (n = 160)</th>
<th>IgGf (n = 28)</th>
</tr>
</thead>
<tbody>
<tr>
<td>67.1 (59–75)</td>
<td>26.7 (24–32)</td>
<td>27.0 (24–32)</td>
<td>26.2 (24–32)</td>
<td>27.0 (24–32)</td>
</tr>
<tr>
<td>68.2 (63–76)</td>
<td>26.7 (24–32)</td>
<td>27.0 (24–32)</td>
<td>26.2 (24–32)</td>
<td>27.0 (24–32)</td>
</tr>
<tr>
<td>70.6 (65–75)</td>
<td>26.7 (24–32)</td>
<td>27.0 (24–32)</td>
<td>26.2 (24–32)</td>
<td>27.0 (24–32)</td>
</tr>
<tr>
<td>72.9 (67–75)</td>
<td>26.7 (24–32)</td>
<td>27.0 (24–32)</td>
<td>26.2 (24–32)</td>
<td>27.0 (24–32)</td>
</tr>
<tr>
<td>75.0 (70–80)</td>
<td>26.7 (24–32)</td>
<td>27.0 (24–32)</td>
<td>26.2 (24–32)</td>
<td>27.0 (24–32)</td>
</tr>
</tbody>
</table>

Conclusion: Isolated IgG elevation in patients with persistently normal transaminase levels, did not impact the outcome of patients with AIH.

THU472

Linerixibat dose-response analysis of C4 concentrations as a quantitative approach to predict gastrointestinal tolerability

Fernando Carreño1, Rashmi Mehta2, Andrea Ribeiro3, Jon Collins2, Brandon Swift2.

Background and aims: Linerixibat is an ileal bile acid transporter (IBAT) inhibitor in Phase 3 development for the treatment of cholestatic pruritus in primary biliary cholangitis (PBC). IBAT inhibition reduces bile acid (BA) reabsorption from the intestine, reducing circulating systemic BA concentrations and pruritus but leading to excess BA in the colon with potential to cause diarrhoea. Linerixibat increases concentrations of 7-alpha-hydroxy-4-cholestene-3-one (C4), a prognostic biomarker for BA-induced diarrhoea. Here we evaluate the relationships between (1) linerixibat and serum C4 concentrations; and (2) effect of C4 on probability of diarrhoea using the gastrointestinal symptoms rating scale (GSRS).

Method: Serum C4 data were included from healthy subjects in three Phase 1 studies (114985, 116511, 205808) and from patients with PBC in two Phase 2 studies (177213, 201000 (GLIMMER)). C4 concentrations over time were described by a K-PD indirect-response model with a stimulatory effect of linerixibat on C4 production. Weekly GSRS data were collected in GLIMMER, which evaluated the impact of five linerixibat treatment regimens in patients with PBC.

Results: The K-PD model showed a saturable dose-response relationship with C4 concentrations. The two BID linerixibat
regimens led to a 24% increase in C4 compared with the change from baseline for a similar daily QD dose (i.e. 90 mg BID vs 180 mg QD). Increased C4 concentrations trended with increased diarrhoea scores in the GSRS tool. C4 concentrations >52 ng/ml were associated with a 62% increased probability of moderate-to-severe diarrhoea scores compared with C4 concentrations <14 ng/ml, as observed in participants in the placebo arm. Simulations showed increases of 9%, 17%, 20%, 19% and 23% in moderate-to-severe diarrhoea scores for the 20 mg, 90 mg and 180 mg QD, and 40 mg and 90 mg BID doses, respectively, after the first week of linezolid treatment. This was consistent with the rate of on-treatment diarrhoea adverse events by treatment arm in GLIMMER (placebo: 11%; 20 mg QD: 38%; 90 mg QD: 65%; 180 mg QD: 67%; 40 mg BID: 52%; 90 mg BID: 68%).

Conclusion: Linezolid led to dose-dependent increases in serum C4 concentrations that predicted an increased probability of moderate-to-severe diarrhoea. The increase in diarrhoea scores highlights the trade-off between maximising the pharmacodynamic effect of linezolid on pruritus and increase in GSRS scores, which guided dose selection for Phase 3.

Funding: GSK (114985, 116511, 205808, 177213, 201000)

THU473
Urinary sulfated progesterone metabolites are diagnostic markers for cholestatic pregnancy and markers of treatment response to ursodeoxycholic acid

Luiza Borges Manna1, Caroline Ovadia1, Jenna Sajous1, Anita Lovgren-Sandblom2, Hanns-Ulrich Marschall3, Catherine Williamson1, 1King’s College London, Women and Children’s Health, London, United Kingdom, 2Karolinska University Hospital Huddinge, Stockholm, Sweden, 3University of Gothenburg, Department of Molecular and Clinical Medicine, Gothenburg, Sweden

Background and aims: Serum concentrations of sulfated metabolites of progesterone are elevated in intrahepatic cholestasis of pregnancy (ICP), and have been proposed as predictive and diagnostic biomarkers. Ursodeoxycholic acid (UDCA) treatment can alter urinary excretion of progesterone sulfates. We aimed to determine whether urinary progesterone sulfate excretion is predictive or diagnostic of ICP, and whether their levels are associated with UDCA treatment response.

Method: Urine was obtained from women with cholestatic and uncomplicated pregnancies throughout pregnancy and postpartum, including matched samples before and 1–2 weeks after commencing UDCA treatment. Urinary progesterone sulfates were measured by ultra performance liquid chromatography-mass spectrometry, and normalised according to creatinine levels (measured by colorimetric assay). Results were compared in Graphpad Prism by multiple t tests with Benjamini-Hochberg correction for multiple testing, Fisher’s exact test and logistic regression.

Results: Urinary 5α-pregnan-3α, 20α-diol-3, 20α-hydroxyprogesterone (PM2DIS), 5α-pregnan-3α, 20α-diol-3, sulfato (PM3DS), 5β-pregnan-3α, 20α-diol-3-sulfato (PM3S), 5α-pregnan-3α-sulfato, 20-one (PM4S) and 5α-pregnan-3α, 20α-diol-3-sulfato (PM8S) were higher in women with cholestatic than uncomplicated pregnancies; PM8S differentiated well between the two groups (AUC 0.86, figure 1). UDCA treatment was associated with significantly reduced PM2DIS and PM3DIS (from 19.10 to 12.22, p = 0.032). Symptomatic response (pruritus improvement) with UDCA was predicted by the total sulfated progesterone metabolites (area under curve (AUC) = 0.80), whilst biochemical response (fall in total serum bile acid concentration) was predicted by urinary 5α-pregnan-3β-ol-20-one-sulfato (PM5S) and 5β-pregnan-3β-ol-20-one-sulfato (PM7S) (AUC = 0.81).

Conclusion: Linezolid is beneficial, and may contribute to the variable clinical response to UDCA treatment that complicates trials of its use in ICP.

THU474
COVID-19 vaccine induced autoimmune hepatitis—a first case series from India

Sowmya Iyengar1, Anand Kulkarni1, Goutham Reddy Katukuri2, Mithun Sharma3, Nageshwar Reddy2, Nagaraja Rao Padaki1, 1AIG Hospital, Hepatology, Hyderabad, India; 2AIG Hospital, Gastroenterology, Hyderabad, India
Email: sowmya.iyengar.18@gmail.com

Background and aims: Liver injury is common in patients with coronavirus disease-2019 (COVID-19) infection. Recently, few studies have reported the development of autoimmune hepatitis (AIH) following COVID-19 vaccination. However, there is a lack of studies reporting the outcomes of AIH following ChAdOx1 (vector-based) and BBV152 (inactivated virus) from India. Here we aimed to describe the clinical profile of patients who developed AIH following COVID-19 vaccination. The causal association is attributed based on the temporal relationship in patients with no prior liver diseases.

Method: Patients presenting with deranged liver functions following COVID-19 vaccination to hepatology clinic were included. Virus infections were ruled out in all patients either by serology or viral quantification methods. We aimed to assess the demographics, clinical profile, and outcome of patients with vaccine-induced AIH (V-AIH) in the absence of known liver disease.

Results: A total of 31 patients presented with altered liver chemistries following vaccination. Seventeen patients were diagnosed with V-AIH (age-39.8 ± 11.4 years; males-70.4%). None of the patient had history of alcohol overconsumption. Seventy six percent of patients had received ChAdOx1 and 23.53% had received BBV152 vaccine (Table). Seventy six percent of patients following first dose of vaccine and 23.5% following second dose of vaccine were diagnosed as V-AIH. Mean duration for development of symptoms after first dose was 25.7 days. Common symptom at presentation was jaundice in 82.3% of patients. Antinuclear antibody was positive in 71% of patients and 17% patients were negative for all serological markers of autoimmune hepatitis but had elevated IgG levels. Fifty-nine percent of patients required immunosuppression of which 41% percent of patients received oral steroids, 17% patients received intravenous steroids for 3 days followed by oral steroid, 12% patients received azathioprine. One patient succumbed to pneumonia with multiorgan failure by day 30. At 3 months, it was observed that only 17% patients needed prolonged immunosuppression and had deranged liver functions until last follow-up. Mean duration of recovery amongst rest of 76.4% patients was 5.15 ± 3.1 weeks.
Conclusion: COVID-19 vaccine can trigger autoimmune hepatitis.

antibody type 1, AMA-Anti mitochondrial antibody.

ASMA- anti smooth muscle antibody, Anti-LKM1- liver-kidney microsomal amino transferase, ALP- alkaline phosphatase, ANA-anti-nuclear antibody, alcoholic fatty liver disease, ALT- alanine amino transferase, AST- aspartate aminotransferase.

SD-standard deviation, CKD- chronic kidney disease, NAFLD- Non-alcoholic fatty liver disease, ALT- alanine amino transferase, AST- aspartate aminotransferase, ALP- alkaline phosphatase, ANA-anti-nuclear antibody, AMA-Anti mitochondrial antibody.

Conclusion: COVID-19 vaccine can trigger autoimmune hepatitis. Males are affected more often than females. Treatment with steroids has high success rate and significant proportion of patients have self-limiting disease and may not require long term immunosuppression.

**THU475**

**Lymphoma in IgG4-related disease: should we be concerned?**

Arif Hussenbux, Rory Peters, Charis Manganis, Eve Fryer, Helen Bungay, Joel David, Emma Culver. 1John Radcliffe Hospital, Gastroenterology, Oxford, United Kingdom; 2Authors contributed equally; 3John Radcliffe Hospital, Histopathology, Oxford, United Kingdom; 4John Radcliffe Hospital, Radiology, Oxford, United Kingdom; 5John Radcliffe Hospital, Rheumatology, Oxford, United Kingdom

Email: arif.hussenbux@hotmail.co.uk

**Background and aims:** Immunoglobulin G4-Related Disease (IgG4-RD) is a systemic fibroinflammatory disorder, with a predilection for the pancreas and biliary tree. We have reported an association of malignancy in our cohort of IgG4-related pancreatobiliary disease. We sought to assess the frequency and type of malignancy in our prospective cohort of IgG4-RD patients with radiological and histological evaluation through our monthly IgG4-RD multi-disciplinary meeting (MDM).

**Method:** Patients diagnosed with IgG4-RD and discussed at the MDM between November 2016 and September 2021 were included, with diagnosis based on established HISORt, CDC or Boston histopathological consensus criteria. Retrospective evaluation of presence and timing of malignancy confirmed radiologically and histologically through the MDM. UK national cancer registry data was used to determine the age and gender standardised incidence ratios (SIR) for malignancy and non-hodgkin’s lymphoma (NHL) for comparison.

**Results:** Of 105 IgG4-RD patients (median age 67; IQR 56–76 years, male:female ratio 2.4:1), 21 (20%) developed malignancy (table 1), with an SIR of 12.3 (95%CI 7.6–18.8).

**Table 1:**

<table>
<thead>
<tr>
<th>Primary Cancer</th>
<th>Observed Cases</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lymphoma</td>
<td>7</td>
</tr>
<tr>
<td>Renal</td>
<td>2</td>
</tr>
<tr>
<td>Gastric</td>
<td>1</td>
</tr>
<tr>
<td>Biliary</td>
<td>2</td>
</tr>
<tr>
<td>Breast</td>
<td>1</td>
</tr>
<tr>
<td>Oesophagus</td>
<td>1</td>
</tr>
<tr>
<td>Thyroid</td>
<td>1</td>
</tr>
<tr>
<td>Pancreas</td>
<td>1</td>
</tr>
<tr>
<td>Prostate</td>
<td>2</td>
</tr>
<tr>
<td>Colon</td>
<td>2</td>
</tr>
<tr>
<td>Ovarian</td>
<td>1</td>
</tr>
</tbody>
</table>

One-third (7/21) had lymphoma. Most (6/7) were NHL B cell lymphomas, SIR 93.6 (95%CI 34.2–203.7). 3 patients with lymphoma had IgG4-related pancreato-biliary disease, 3 had IgG4-related head and neck disease and 1 had IgG4-related renal disease. 3 lymphomas were diagnosed prior, and 4 subsequent, to their IgG4-RD diagnosis. The median time between lymphoma and IgG4-RD diagnosis was 4.4 years; (range –10.5–11.8 years). Of these, 1 had been exposed to an immunomodulator, azathioprine, prior to lymphoma. Lymphoma was successfully treated with R-CHOP chemotherapy in all cases.

**Conclusion:** We demonstrate an increased incidence of malignancy in our IgG4-RD cohort with a striking incidence of NHL, which otherwise accounts for <4% of annual UK new cancer diagnoses. There are currently no cancer surveillance guidelines in IgG4-RD, and the frequency of lymphoma makes us question the use of off-label azathioprine as relapse prevention in this older male cohort.

**References**


**THU476**

**Measurement properties of the PBC-10 in a dutch population**

Maria van Hooff, Rozanne de Veer, Maren Harms, Geraldine Da Silva, José Willemsse, Hendrik Metselaar, Elaine Utomo, Adriaan Van der Meer. 1Erasmus University Medical Center, Department of Gastroenterology and Hepatology, Rotterdam, Netherlands; 2Dutch Liver Patients Association, Hoogland, Netherlands; 3Independent Researcher, Berkel en Rodenrijs, Netherlands

Email: m.vanhooff@erasmusmc.nl

**Background and aims:** Practice guidelines advice to evaluate the Health Related Quality of life (HRQoL) of all patients with primary biliary cholangitis (PBC). The PBC-40 has proven to be an adequate PBC-specific HRQol measure. However, as this measure can be time consuming and thus less practical, the UK-PBC group developed the PBC-10 as a shorter version for screening HRQoL in clinical practice. The aim of this study was to assess the measurement properties of the items selected for the PBC-10 in a Dutch PBC population.

**Results:** Of 105 IgG4-RD patients (median age 67; IQR 56–76 years, male:female ratio 2.4:1), 21 (20%) developed malignancy (table 1), with an SIR of 12.3 (95%CI 7.6–18.8).

**Table 1:**

<table>
<thead>
<tr>
<th>Primary Cancer</th>
<th>Observed Cases</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lymphoma</td>
<td>7</td>
</tr>
<tr>
<td>Renal</td>
<td>2</td>
</tr>
<tr>
<td>Gastric</td>
<td>1</td>
</tr>
<tr>
<td>Biliary</td>
<td>2</td>
</tr>
<tr>
<td>Breast</td>
<td>1</td>
</tr>
<tr>
<td>Oesophagus</td>
<td>1</td>
</tr>
<tr>
<td>Thyroid</td>
<td>1</td>
</tr>
<tr>
<td>Pancreas</td>
<td>1</td>
</tr>
<tr>
<td>Prostate</td>
<td>2</td>
</tr>
<tr>
<td>Colon</td>
<td>2</td>
</tr>
<tr>
<td>Ovarian</td>
<td>1</td>
</tr>
</tbody>
</table>

One-third (7/21) had lymphoma. Most (6/7) were NHL B cell lymphomas, SIR 93.6 (95%CI 34.2–203.7). 3 patients with lymphoma had IgG4-related pancreato-biliary disease, 3 had IgG4-related head and neck disease and 1 had IgG4-related renal disease. 3 lymphomas were diagnosed prior, and 4 subsequent, to their IgG4-RD diagnosis. The median time between lymphoma and IgG4-RD diagnosis was 4.4 years; (range –10.5–11.8 years). Of these, 1 had been exposed to an immunomodulator, azathioprine, prior to lymphoma. Lymphoma was successfully treated with R-CHOP chemotherapy in all cases.

**Conclusion:** We demonstrate an increased incidence of malignancy in our IgG4-RD cohort with a striking incidence of NHL, which otherwise accounts for <4% of annual UK new cancer diagnoses. There are currently no cancer surveillance guidelines in IgG4-RD, and the frequency of lymphoma makes us question the use of off-label azathioprine as relapse prevention in this older male cohort.

**References**


**THU476**

**Measurement properties of the PBC-10 in a dutch population**

Maria van Hooff, Rozanne de Veer, Maren Harms, Geraldine Da Silva, José Willemsse, Hendrik Metselaar, Elaine Utomo, Adriaan Van der Meer. 1Erasmus University Medical Center, Department of Gastroenterology and Hepatology, Rotterdam, Netherlands; 2Dutch Liver Patients Association, Hoogland, Netherlands; 3Independent Researcher, Berkel en Rodenrijs, Netherlands

Email: m.vanhooff@erasmusmc.nl

**Background and aims:** Practice guidelines advice to evaluate the Health Related Quality of life (HRQoL) of all patients with primary biliary cholangitis (PBC). The PBC-40 has proven to be an adequate PBC-specific HRQol measure. However, as this measure can be time consuming and thus less practical, the UK-PBC group developed the PBC-10 as a shorter version for screening HRQoL in clinical practice. The aim of this study was to assess the measurement properties of the items selected for the PBC-10 in a Dutch PBC population.
Method: Our study group previously translated the PBC-40 into Dutch and validated it in a Dutch population. Existing data of the Dutch PBC-40 questionnaire was used to assess patients responses on the PBC-10 items. Internal consistency of the PBC-10 was assessed by Cronbach’s alpha. A value between 0.70 and 0.95 is considered as adequate. Content validity was assessed by determination of floor and ceiling effects (i.e. >15%). Each PBC-10 item was correlated with the total score of the corresponding original PBC-40 domain.

Results: In total, 177 patients with PBC were included. The mean (SD) age was 61.1 (9.9) years and the majority of patients was female (n = 164; 92.7%). Of the total 1770 items, 81 items (4.6%) were missing. The total score of the corresponding original PBC-40 domains ranged from 0.711 to 0.912, p < 0.001 for all) (Table).

The Dutch PBC-10 may be less suitable to identify PBC patients with less severe HRQoL impairment or to detect further improvement of their HRQoL following intervention.

Conclusion: In a Dutch population, the PBC-10 showed an adequate internal consistency and reflects the content of corresponding PBC-40 domains. There were, however, substantial floor effects. The PBC-10 may be considered in clinical practice as a screening tool for HRQoL following intervention.

THU477
Glucoregulatory disturbances in primary biliary cholangitis and non-alcoholic fatty liver disease compared with healthy individuals

Anne-Sofie Houlberg Jensen1,2, Henriette Ytting1,3, Josephine Grandt2,3, Andreas Møller1, Mikkel Werge1, Elias Rashu1, Liv Hetland1, Mira Thing1, Anders Junker1, Lise Hobolth1, Christian Mortensen1, Flemming Bendtsen1, Flemming Tofteng1, Mogens Vybarg2,3, Reza Serizawa1, Lise Lotte Gluud1, Nicolai J Wever Albrechtsen1,2, Hvidovre Hospital, Gastro Unit, Hvidovre, Denmark; 2Novo Nordisk Foundation Center for Protein Research, København, Denmark; 3Righospitalet, European Reference Network on Hepatological Diseases (ERN-RARE-LIVER), København, Denmark; 4The University of Copenhagen, Faculty of Health and Medical Sciences, København, Denmark; 5Hvidovre Hospital, Department of Pathology, Hvidovre, Denmark; 6Center for RNA Medicine, Aalborg, Denmark; 7Righospitalet, Department of Clinical Biochemistry, København, Denmark; 8The University of Copenhagen, Faculty of Health and Medical Sciences, Department of Biomedical Sciences, København, Denmark

Email: nicolai.albrechtsen@sund.ku.dk

Background and aims: Glucoregulatory disturbances such as hepatic insulin resistance, hyperinsulinemia and pre-diabetes are observed in individuals with non-alcoholic fatty liver disease (NAFLD). Whether autoimmune liver diseases–herein primary biliary cholangitis (PBC)—also carry glucoregulatory disturbances is unknown. We therefore investigated glucose and hormonal responses to an oral glucose tolerance test (OGTT) in patients with biopsy-verified non-cirrhotic PBC and NAFLD and healthy controls.

Method: 23 participants have been included hereof 8 healthy controls (mean age 23, mean BMI 23 kg/m2), 9 patients with PBC (mean age 55, mean BMI 31 kg/m2) and 6 patients with NAFLD (mean age 38, mean BMI 31 kg/m2). None of the included patients had diabetes. In the PBC group, 3 had NAFLD. Blood samples were obtained at baseline (fasting) and 15, 30, 45, 60, 90 and 120 minutes during the OGTT. Glucose, c-peptide and insulin concentrations were measured. A validated marker for hepatic insulin resistance (the homeostasis model assessment of insulin resistance (HOMA-IR)) and the incremental area under curve (iAUC) for glucose, c-peptide and insulin responses were calculated. Results are presented as means (95% CI).

Results: Fasting glucose, c-peptide and insulin levels were significantly increased in both PBC (glucose 5.6 mM (4.7–6.7), c-peptide 993 pM (556–1773), insulin 98 pM (33–298)) and NAFLD (glucose 5.7 mM (5.2–6.1), c-peptide 1334 pM (1036–1719), insulin 166 pM (136–267)) compared with healthy (glucose 4.7 mM (3.9–5.6), c-peptide 483 pM (268–869), insulin 43 pM (14–136)). Hepatic insulin resistance (reflected by fasting HOMA-IR) was present in PBC (4.0 (1.2–13.9)) and NAFLD (7.0 (4.1–11.9)) but not in healthy individuals (1.5 (0.4–5.4)). No significant difference in glucose levels was observed between the groups (p = 0.106). Beta-cell secretion (c-peptide) was significantly increased in PBC (p < 0.001) and NAFLD (p < 0.001) suggesting that peripheral insulin resistance was present in patients with PBC and NAFLD. Insulin responses (reflecting both beta-cell secretion and hepatic insulin extraction) were numerically higher in both PBC and NAFLD compared with healthy but only reached statistical significance in NAFLD (p = 0.002).

Conclusion: Our data suggest that patients with PBC may have glucoregulatory disturbances including both hepatic insulin resistance and altered pancreatic endocrine function. Whether these impairments reflect an obesity prone phenotype in PBC and NAFLD patients cannot be concluded from the current data. Metabolic dysfunction of PBC may be underestimated and warrant further investigation.
8.4. On – and 3.6% (N = 86) were censored at start of 2L treatment. Mean follow-up period (mean 2.5 yrs), 73.8% received ursodeoxycholic acid 2, 379 patients (85.3% female) were included. At baseline, treatment.

Patients were censored at end of follow-up or initiation of 2L Biochemistry values were carried forward until the next recorded hepatic decompensation, liver transplant, or death was conducted. Survival analysis with the proportion of time spent out-of-range, including normal values associated with adverse liver health, predict time to first occurrence of negative hepatic outcomes. Patients with autoimmune hepatitis, HIV, gastric bypass, liver disease, hepatic decompensation, or use of second line (2L) treatment (obeticholic acid or fibrates) prior to PBC diagnosis were excluded. Survival analysis with the proportion of time spent out-of-range as a time-dependent variable and a composite end point of greater divergence from normality on each liver biochemistry was associated with significantly increased risk of hepatic decompensation, liver transplant, or death in patients with PBC. These results suggest that avoiding substantial time with out-of-range liver biochemistries, potentially through greater utilization of effective first line and 2L therapies, may improve hepatic outcomes for patients with PBC.

**Background and aims:** Previous research has demonstrated a significant association between abnormal liver biochemistries at one point in time and the risk of death and liver transplant in patients with primary biliary cholangitis (PBC). We hypothesized that both the proportion of time and degree to which liver biochemistries are out-of-range, including normal values associated with adverse liver health, predict time to first occurrence of negative hepatic outcomes.

**Method:** Patients in the Optum Clinformatics database between July 1, 2016 and December 31, 2020 were included if they were diagnosed with PBC by either ≥ 1 inpatient discharge claim with a PBC diagnosis or ≥ 2 outpatient claims with a primary PBC diagnosis on separate days and had ≥ 1 of each liver biochemistry available (ALP, TB, AST, ALT, and ALB). Patients with autoimmune hepatitis, HIV, gastric bypass, liver disease, hepatic decompensation, or use of second line (2L) treatment (obeticholic acid or fibrates) prior to PBC diagnosis were excluded. Survival analysis with the proportion of time spent out-of-range as a time-dependent variable and a composite end point of hepatic decompensation, liver transplant, or death was conducted. Biochemistry values were carried forward until the next recorded value. Patients were censored at end of follow-up or initiation of 2L treatment.

**Results:** 2, 379 patients (85.3% female) were included. At baseline, mean age was 63 years; 11% had cirrhosis; 7% had DASH. During the follow-up period (mean 2.5 yrs), 73.8% received ursodeoxycholic acid and 3.6% (N = 86) were censored at start of 2L treatment. Mean number of measures per biochemistry ranged from 7.2–8.4. On average patients spent 52.5%, 8.5%, 37.5%, and 20.7% of the follow-up period over ULN for ALP, TB, AST, and ALB, respectively, and 19.1% under LLN for ALB. For each individual biochemistry the risk of negative hepatic events increased significantly with greater proportion of time out-of-range and greater divergence from desired values (Figure). For example, for a patient with all 5 years follow-up (i.e., 100% time) with ALB ≤ 0.9xLLN, the risk of an event was 271% higher than that of a patient with ALB > 0.9xLLN all 5 years (i.e., 0% time); 104% higher for ALP > 1.5xULN; 124% for AST > 2xULN; 145% higher for TB > 1xULN.

**Conclusion:** Greater proportion of time spent out-of-range and greater divergence from normality on each liver biochemistry was associated with significantly increased risk of hepatic decompensation, liver transplant, or death in patients with PBC. These results suggest that avoiding substantial time with out-of-range liver biochemistries, potentially through greater utilization of effective first line and 2L therapies, may improve hepatic outcomes for patients with PBC.

**THU479**

Outcomes following immune checkpoint inhibitor re-challenge in patients who developed grade 3 and 4 hepatotoxicity

Amy Hicks1, Ramu Chimakurthi1, 2Leeds Teaching Hospitals NHS Trust, Hepatology, Leeds, United Kingdom

Email: amy.hicks@nhs.net

**Background and aims:** Immune checkpoint inhibitors (ICI) are used to treat a variety of cancers. Immune-related adverse events (irAEs) are not uncommon, with Grade 3 hepatitis in 1–2% of those treated with single agents and ~15% in those treated with Ipitumumab and Nivolumab combination (ESMO guidelines 2017). European and American society guidelines recommend discontinuation of ICI after development of Grade 3 or 4 hepatitis. Re-challenge with single ICI can be considered in those who developed Grade 3 hepatitis on combination therapy. We reviewed our outcomes following re-challenge in those who developed Grade 3 and 4 hepatitis in our regional oncology center.

**Method:** Patients who received ICI from January 2018 to January 2022 were reviewed. Those who developed Grade 3 and 4 hepatotoxicity were identified by accessing their electronic health record. We assessed the following outcomes in these patients: a) those who had re-challenge with ICI b) choice of ICI in re-challenged c) whether they developed further hepatitis d) outcomes in those who were not re-challenged.

**Results:** 1045 patients received ICIs over a 4-year period (807 single agent and 238 Ipitumumab-Nivolumab combination), 54 patients developed Grade 3 or 4 hepatitis. Of these, 22 (40.7%) were re-challenged and their outcomes are shown in Table 1. All patients were off immunosuppression at the time of re-challenge. Contrary to existing guideline recommendations, 3 patients with Grade 4 hepatitis and 7 patients with Grade 3 hepatitis on single agent were re-challenged with ICIs. 4 out of 11 (36%) developed further hepatitis (Grade ≥ 3) on re-challenge. Of note, all patients with recurrent hepatotoxicity developed this after only 1 cycle of retreatment. ICI were discontinued permanently in the remaining 32 patients. 15 had complete response to treatment, 8 had disease progression and were switched to an alternative treatment, 6 patients deteriorated and died (1 from irAE and 5 from disease progression), 1 is due for re-challenge soon, and 2 patients changed to an alternative regimen due to the hepatitis.

**Table 1:** ICI re-challenge outcomes.

<table>
<thead>
<tr>
<th>Initial hepatitis grade (n= no. patients)</th>
<th>Initial ICI</th>
<th>Re-challenge ICI</th>
<th>Recurrence of hepatitis and cycle number (Cx)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gr 3 = 19</td>
<td>Ipi and Nivo = 12</td>
<td>Nivo = 12</td>
<td>- 2 pts (17%); - Gr 3 (C2)</td>
</tr>
<tr>
<td></td>
<td>Nivo = 3</td>
<td>Nivo = 3</td>
<td>- 1 pt (33%); - Gr 4 (C1)</td>
</tr>
<tr>
<td></td>
<td>Pembro = 4</td>
<td>Pembro = 3</td>
<td>None</td>
</tr>
<tr>
<td></td>
<td>Pembro = 2</td>
<td>Pembro = 2</td>
<td>- 1 pt (100%); - Gr 3 (C1)</td>
</tr>
<tr>
<td></td>
<td>Ipi and Nivo = 1</td>
<td>Nivo = 1</td>
<td>- 2 pts (100%); - Gr 3 (C1)</td>
</tr>
</tbody>
</table>

**Conclusion:** Re-challenge with ICI following Grade 4 hepatitis resulted in early irAE recurrence in our group. However, the vast majority (>70%) re-challenged with ICIs after Grade 3 hepatitis on
single agent did not develop hepatitis recurrence. Nearly 50% of patients are in remission and alive to this day despite cessation of ICI following Grade 3 and 4 hepatitis. Our numbers are small but will add to a growing body of evidence in this field.

THU480
Development of a novel MRCP-score for patients with primary sclerosing cholangitis, and assessment of agreement and prognostic value
Aristeidis Grigoriadis1,2, Kristina Ringe3, Johan Bengtsson4,5, Erik Frithd Baubeta6, Cecilia Forsman7, Nafsika Korsavidou-Hult8, Fredrik Rorsman9, Emma Nilsson9, Nikolaos Kartalis2,11, Annika Bergquist1,12.
1Karolinska Institutet, Medicine, Stockholm, Sweden; 2Karolinska University Hospital, Radiology, Stockholm, Sweden; 3Hannover Medical School, Diagnostic and Interventional Radiology, Hannover, Germany; 4Lund University, Department of Clinical Sciences/Division of Radiology, Lund, Sweden; 5Skåne University Hospital, Center for Medical Imaging and Physiology, Lund, Sweden; 6Skåne University Hospital, Diagnostic Radiology, Department of Translational Medicine, Lund, Sweden; 7Uppsala University Hospital, Medical Imaging Centre, Sweden; 8Uppsala University, Radiology and Nuclear Medicine, Sweden; 9Uppsala University Hospital, Gastroenterology and Hepatology, Sweden; 10Skåne University Hospital, Department of Clinical Sciences, Lund, Sweden; 11Karolinska Institutet, Department of Clinical Science, Intervention and Technology (CLINTEC), Stockholm, Sweden; 12Karolinska University Hospital, Hepatology, Stockholm, Sweden
Email: aristeidis.grigoriadis@ki.se

Background and aims: MRCp is used for diagnosis and follow-up of patients with primary sclerosing cholangitis (PSC). Interest in the prognostic value of MRCP is increasing. Aim of our study is to develop a score associated to outcomes and assess its reproducibility and prognostic value of MRCP.

Method: We identified all patients with autoimmune hepatitis (AIH), primary biliary cholangitis (PBC), primary sclerosing cholangitis (PSC) or variant syndromes (AIH/PBC and AIH/PSC), who underwent a double biopsy of both liver lobes during minilaparoscopy between 01/2016–12/2020 in our prospectively maintained database. Differences in fibrosis stage and disease activity between liver lobes were assessed by an experienced hepatopathologist.

Results: A total of 111 patients with AIH received a biopsy of both liver lobes (AIH: N = 83, AIH/PBC: N = 24, AIH/PSC: N = 4). Differences in inflammatory activity as assessed by Ishak's modified activity index (mHAI) were observed in 69 (62%) patients. In 41 (38%) patients the difference was ≥2 points. For 12 patients (11%) ≥3 points. According to current EASL guidelines, starting/intensification of immunosuppression should be discussed in patients with a mHAI of 4–5, as it was reported to be associated with excess mortality, a mHAI ≥ 6 prompts intensified immunosuppression in most cases. Thus, a mHAI 4–6 represents a more relevant range for guiding treatment decisions. 48% of the AIH patients had a mHAI within this range. Importantly, in 21 patients (20%) a mHAI ≥ 4 was only observed in one liver lobe. Also, 17 (15%) patients demonstrated a mHAI ≥ 6 in only in one liver lobe. Based on these observations, the number needed to double-biopsy to identify clinically relevant differences in inflammatory activity was only 5 patients. Differences of fibrosis stage were identified in 31/111 (28%) AIH patients. In 3/18 (17%) cirrhotic patients, histological changes consistent with cirrhosis were only observed in one liver lobe.

A biopsy of both liver lobes was performed in 16 PSC and 13 PBC patients. Differences of fibrosis stage were observed in 11/16 and 3/13 patients, and differences in mHAI in 8/16 and 5/13 patients, respectively. However, no treatment relevant difference was identified.

Conclusion: Obtaining a biopsy of the right and left liver lobe is a safe procedure during minilaparoscopy that results in more accurate staging and grading with direct therapeutic consequences in patients with AIH.
THU482
Should we seek complete liver tests normalization in primary biliary cholangitis? Data from the ColHai registry
Álvaro Díaz-González1, Sergio Rodríguez-Tajes2, Mercedes Vergara Gómez3, Emilio Fabrega4, Manuel Romero Gómez4, Agustín Albillos5, Judith Gómez-Camareno6, Diana Horta7, Adolfo Gallego8, Montserrat Garcia-Retortillo9, Raul J. Andrade10, Moises Diago11, Rosa M Morillas12, Manuel Hernández Guerra13, Carlos Ferre Aracil4, Margarita Sala15, Elena Gómez Domínguez16, Marina Berenguer17, Maria Carlota Londoño18, Grupo del Registro Col-Hai Enfermedades Autoinmunes y colestásicas19, Hospital Marqués de Valdecilla20, Hospital Clinic Barcelona21, Hospital Universitario Parc Taulí22, Hospital Universitario Ramón y Cajal23, Hospital Universitario de Burgos24, Hospital Mutua de Terrassa25, Hospital de la Santa Creu i Sant Pau26, Hospital del Mar27, Universidad de Málaga28, Hospital Universitario General de Valencia29, Hospital Germans Trias i Pujol30, Hospital Universitario Puerta del Hierro31, Hospital Josep Trueta32, Hospital Universitario Doctor de October33, Hospital La Fe34, Hospital Clinic Barcelona, Liver Unit, Barcelona, Spain; 19.AEEH, CIBEREHd

Background and aims: Response criteria to ursodeoxycholic acid (UDCA) treatment in patients with primary biliary cholangitis (PBC) are based on the reduction of alkaline phosphatase (ALP), total bilirubin (TB), and aspartate aminotransferase (AST). However, recent studies suggest that complete normalization of these tests result in better clinical outcomes. More studies are necessary to validate these data and to determine the need for increasing the strictness of UDCA treatment-response criteria. Therefore, we sought to investigate the impact of TB, AST, ALP and gamma-glutamyl transferase (GGT) normalization after 12 months of UDCA treatment on patients’ survival.

Method: Retrospective analysis of 1154 patients with PBC patients included in the ColHai registry (Spanish registry for patients with autoimmune and cholestatic liver disease). Liver tests were categorized according to the upper limit of normal (ULN) for each center: 1) AST: <1, 1–1.5, >1.5; 2) ALP: <1, 1–1.5, 1.5–1.67, >1.67; 3) GGT: <1, 1–3, 3–5, >5; 4) TB: <0.6, 0.6–1.2, >1.2.

Results: Most of the patients were female (90%), with a median age of 53 years (range 46–63). 116 (10%) died during a median follow-up period of 10 years (6.7–15.7). In the univariate analysis AST < ULN (HR 0.45; 95%CI 0.35–0.65), ALP < ULN (HR 0.51; 95%CI 0.34–0.78), GGT < ULN (HR 0.69; 95%CI 0.53–0.94) and TB <0.6 × ULN (HR 0.35; 95%CI 0.24–0.52) were associated with a significantly lower mortality rate. There were no significant differences in survival between patients with ALP < ULN vs. <1.5 × ULN or those with GGT < ULN vs. <3 × ULN (Figure). In the multivariate analysis, only TB < 0.6 × ULN and ALP < 1.5 × ULN were independently associated with lower mortality (HR 0.42; p < 0.01 and HR 0.57; p = 0.01, respectively).

Conclusion: ALP normalization was not better than the usual cut-off of 1.5 × ULN to predict survival but decreasing TB to better than normal levels (0.6 × ULN) significantly improved patients’ survival.

THU483
Home-based exercise in patients with refractory fatigue associated primary biliary cholangitis: final results from the EXExercise Intervention in cholesTatic Liver Disease (EXCITED) clinical trial
Alice Freer1, Felicity Williams1,2, Simon Durman1, Jennifer Hayden1, Matthew Armstrong1, Palak Trivedi1,3,4, University Hospital Birmingham NHS Foundation Trust, Liver Department, Birmingham, United Kingdom; 2University of Birmingham, Institute of Inflammation and Ageing, Birmingham; 3University of Birmingham, NIHR Birmingham Centre for Liver and Gastrointestinal Research, Birmingham, United Kingdom

Background and aims: Debilitating, refractory fatigue is the most commonly reported symptom of primary biliary cholangitis (PBC), affecting 40–80% of patients (pts). The pathogenesis is unknown, but muscle bioenergetic abnormalities are proposed to contribute. Herein, we present the results of a single-arm, open-label clinical trial, to assess the efficacy and safety of a novel home-based exercise program (HBEP) in pts with PBC and severe fatigue (NCT04265235).

Method: A remotely-monitored, 12-week (wk) HBEP was delivered to patients with PBC and moderate-severe fatigue (PBC40 fatigue score >33; other causes excluded). This consisted of individualised body weight resistance exercises completed at moderate intensity and weekly telephone health calls (first 6 wks only). Adherence was monitored using GeneActiv wrist monitors. The primary efficacy outcome measure was the proportion of individuals attaining at least a 5-point reduction in the PBC40 fatigue domain at wk 12. Key secondary outcomes included assessment of the Fatigue Impact Scale (FIS), other domains of the PBC-40, the Chronic Liver Disease Questionnaire, (CLDQ), the Epworth Sleep Score (ESS), the Hospital Anxiety and Depression Scale (HADS), aerobic exercise capacity (incremental shuttle walk test [ISWT]; Duke Activity Status Index [DASI]; metabolic equivalent of task [MET]), and functional capacity (short physical performance battery [SPPB]) at 6 and 12wks. Full study protocol is available at BMJ Open Gastro (PMID33707216).

Results: In all, 31 pts were recruited. One individual withdrew prior to wk12 due to unforeseen personal issues. The remaining thirty participants (29 women, 1 man) completed the 12-wk HBEP: median age 53yrs, ALP 1.9xULN, bilirubin 17 μmol/L, MELD 7, and baseline PBC40 fatigue score 41. The primary outcome was met by 26 pts (87%); the median reduction in PBC40 fatigue score at wk12 was 11 points (interquartile range –9 to –13 (Fig)). Significant reductions were also observed in the FIS, score, ESS, HADS and the composite PBC40 score (Fig), alongside individual symptom, cognition, emotion and social domains, and the CLDQ (data not shown). Significant changes were seen in METs (+0.46, p < 0.001) and SPPB (+1 point, p < 0.001), with 28 pts (93%) achieving the maximum SPPB score at 12 wks (vs. 43% at baseline; p < 0.001). No significant differences in ALP values or MELD score were observed from baseline to 12wks. No significant adverse events were observed during the course of the study.

Conclusion: A 12-wk individualised HBEP, incorporating resistance and aerobic exercise, is safe, feasible, and significantly improves fatigue, quality of life, and exercise/functional capacity in patients with refractory fatigue associated with PBC. These findings warrant validation through a longer duration randomised control trial.
Background and aims: The POISE randomized double-blind (DB) placebo-controlled trial and open label extension (OLE) demonstrated that obeticholic acid (OCA) reduced biomarkers associated with adverse clinical outcomes in patients with primary biliary cholangitis (PBC). The objective of this analysis was to evaluate event-free survival in OCA-treated patients in POISE (DB + OLE) compared to non-OCA treated external controls.

Method: The treatment arm included patients in the POISE study. External controls were OCA-naive patients from the GLOBAL PBC registry who were diagnosed with PBC, treated or untreated with ursodeoxycholic acid (UDCA), with >1 year of follow-up. Study end point was time to first occurrence of hepatic decompensation, liver transplant (LT) or death. As treatment was not assigned randomly, baseline variables could influence both the chances of a clinical event and of receiving treatment. To ensure a fair and balanced comparison, inverse probability of treatment weighting (IPTW) was used to balance groups. Logistic regression model was used to create weights for the following key baseline confounders: age, sex, calendar year of diagnosis, PBC duration, UDCA use, ALP, bilirubin and AST or ALT. Weights were assigned to each patient. Cox-proportional hazards models were run to establish the hazard ratio (HR) and 95% confidence. A secondary analysis examined the impact of adding cirrhosis to the model.

Results: Over the 6.3 years of follow-up, there were 16 events of hepatic decompensation, liver transplant or death in 209 subjects in the POISE arm (Incidence rate (IR) 18.0 per 1,000 person-years; 95% CI 10.7–28.6) and 212 events in 1381 patients (IR 35.5 per 1,000 person-years; 95% CI 31.0–40.5) in the GLOBAL PBC external control group. The IPTW HR = 0.42 (95% CI 0.21, 0.85; p = 0.02), indicating that patients treated with OCA in a trial setting had significantly greater event-free survival than patients in the GLOBAL PBC control group. The Kaplan-Meier curve is shown in Figure. When cirrhosis was added to the model, it was a significant predictor (HR = 0.26; 95% CI 0.21–0.43, p < 0.01), and increased the effect size of treatment (HR = 0.35; 95% CI 0.17–0.71, p < 0.01). For patients with cirrhosis, HR = 0.38 (95% CI 0.12, 1.20) versus Global PBC controls; for patients without cirrhosis, HR = 0.34 (95% CI 0.14, 0.82). With widely overlapping confidence intervals, while cirrhosis significantly predicts time to events, it does not significantly affect treatment response.

Conclusion: Patients treated with OCA in a trial setting demonstrated a statistically significant and clinically meaningful 58% reduction in relative risk of hepatic decompensation, LT or death compared to non-OCA treated patients in the GLOBAL PBC registry. Reduction in risk was independent of cirrhosis. These results support the continued use of long-term OCA therapy to optimize prognosis of patients with PBC.

THU485
Investigation of linerixibat 40mg BID for cholestatic pruritus of primary biliary cholangitis (PBC); further data from the phase 2 GLIMMER study to support the phase 3 GLISTEN study
James Fettiplace1, Brandon Swift2, Shu Zhang3, Robyn von Maltzahn3, Megan McLaughlin2, 1GlaxoSmithKline, United Kingdom; 2GlaxoSmithKline, United States; 3GlaxoSmithKline, United States

Background and aims: Reduction of pruritic bile acids in circulation is under investigation for the treatment of cholestatic pruritus in PBC. Due to lack of previously approved therapies, what constitutes a meaningful within-patient change in itch has not been determined. The phase 2b GLIMMER study was a randomized, double-blind, placebo-controlled, dose response study of linerixibat, a minimally
absorbed ileal bile acid transporter inhibitor, in PBC patients with moderate to severe pruritus; 12 weeks of treatment followed a 4-week placebo run-in (N = 147). Data from GLIMMER was reanalyzed to look at multiple potential itch responder definitions for the linerixibat 40mg BID group, the phase 3 dose. Consistent with the mechanism of action, changes in total serum bile acids (TSBA) are also reported.

**Method:** Participants assessed itch daily using a 0–10 numeric rating scale. Proportion of responders were assessed using reductions in monthly itch scores (MIS) at week 16 compared to baseline. An empirical cumulative distribution function (eCDF) graph was generated for the proportion of participants with change from baseline in MIS for the linerixibat 40mg BID (N = 23) and placebo (N = 36) groups. Bile acid samples from GLIMMER were reanalyzed using an enzymatic assay that quantifies TSBA consistent with the Phase 2a study method (the original analysis summed specific bile acids utilizing a liquid chromatography tandem mass spectrometry method). Change from baseline in TSBA were analyzed using a mixed model repeated measures analysis (MMRM).

**Results:** The eCDF curves showed clear separation of linerixibat 40mg BID group, the phase 3 dose. Consistent with inhibition of reuptake of bile acids, 40 mg BID linerixibat resulted in significant reductions in total serum bile acids. The proportion of participants with change from baseline in MIS at week 16 was greater in the linerixibat 40mg BID group than placebo group for a wide range of responder threshold values. The largest differences between the curves were observed between thresholds of −3 to −2, where the cumulative percentages were more than 20% greater in the linerixibat group than the placebo group.

Linerixibat 40mg BID (N = 22) reduced mean TSBA from a baseline of 18.6 μM (21.8) by −6.94 μM (17.5) [Mean (SD)] on average after 12-weeks of treatment. A MMRM analysis resulted in a significant decrease of 39% (p = 0.0001) from baseline and 37% (p = 0.0030) from placebo (n = 36) over the 12-week double-blind treatment period.

**Conclusion:** Consistent with inhibition of reuptake of bile acids, 40 mg BID linerixibat resulted in significant reductions in total serum bile acids. The proportion of participants with change from baseline in MIS at week 16 was greater in the linerixibat 40mg BID group than placebo over a range of responder threshold values. Linerixibat 40 mg BID is being studied in the ongoing confirmatory phase 3 GLISTEN study (NCT04950127). Responder thresholds of 2, 3 and 4-point improvements in MIS compared to baseline are key secondary end points of this phase 3 study.

**Funding:** GSK (study 2010000)
Conclusion: The present findings are akin to those described in the CHP of CIP. Only Covid-19 patients requiring intensive care develop CHP. This suggests that the virus does not have a direct role in the CHP. It is more likely that, as with CIP, hypoxemia due to arterial hypotension and lung damage associated with vasoconstrictor and other drugs cause damage to the biliary tree.

THU488
Examining the role of thiopurine metabolite testing in the management of patients with autoimmune hepatitis
Andrew Roberts¹, Declan Connolley¹, Ryan Hirsch¹, Gauri Mishra¹, Marcus Robinson¹, Sally Bell¹, Dilip Ratnam¹, ¹Monash Health, Department of Gastroenterology and Hepatology, Clayton, Australia
Email: atr444@gmail.com

Background and aims: Thiopurines (TP) are widely used to maintain steroid-free remission in autoimmune hepatitis (AIH), however there is a lack of data examining the role of metabolite testing in the management of AIH. We evaluated whether metabolite monitoring affected steroid-free remission and TP-attributed adverse event (AE) rates in our AIH patients.

Method: We conducted a retrospective cohort study of adult patients with AIH treated with TP at a metropolitan health network over a 10-year period (2011–2021). Baseline demographic and clinical data were recorded. Patients were stratified by metabolite testing status. Time of censor was last clinical review. The primary outcome was steroid-free remission, improvements in AIH disease activity, reduction in AIH flares or reduction in thiopurine-related adverse events. Aiming for therapeutic metabolite levels did not improve steroid-free remission rates. Metabolite testing may provide little utility in the management of AIH patients on TP and may result in increased patient testing and healthcare resource burden.

THU489
Patient reported symptom burden in primary biliary cholangitis and how to inform trial design
Aaron Wetten¹,², Claire Johnstone-hume², Kathryn Houghton¹, Chris Mitchell¹,², David Jones¹,², Jessica Dyson¹,², ¹Newcastle Freeman Hospital, Liver unit, High Heaton, United Kingdom; ²Newcastle University, Translational and Clinical Research Institute, United Kingdom; ²PBC Foundation, United Kingdom
Email: aaron.wetten@nhs.net

Background and aims: Primary Biliary Cholangitis (PBC) is a chronic, cholestatic autoimmune liver disease. Symptoms of pruritus, fatigue and ‘brain fog’ are common, and significantly impact quality of life. Current pruritus treatments are effective for some patients, but no therapies address fatigue or cognitive symptoms. This remains an area of significant unmet need, reflected by the recent increase in clinical trials to identify new agents. This study explored the prevalence of PBC symptoms, patients’ priorities for their management, what they consider a meaningful improvement in their symptoms and how we should collect symptom data. These are crucial questions to inform trial design in this area where patient-reported outcomes are key metrics for success.

Method: An electronic survey was sent to members of the PBC Foundation (an international patient support group) in February 2022 with responses collected over 6 weeks. The survey comprised 9 questions regarding: current/past symptom burden; nature/degree of symptoms and how we should collect symptom data. These are crucial questions to inform trial design

Results: 599 surveys were completed. Symptom prevalence was high: 64% reporting current/past itch, 93% fatigue and 78% brain fog. ‘Any improvement being significant’ was the commonest category for each symptom: brain fog 54%, fatigue 53% and itch 48% (Figure 1). When asked how a treatment should help reduce symptoms, patients considered a meaningful improvement in their symptoms and how to inform trial design

Conclusion: TP metabolite testing was not associated with improved steroid-free remission, improvements in AIH disease activity, reduction in AIH flares or reduction in thiopurine-related adverse events. Aiming for therapeutic metabolite levels did not improve steroid-free remission rates. Metabolite testing may provide little utility in the management of AIH patients on TP and may result in increased patient testing and healthcare resource burden.

THU489
Patient reported symptom burden in primary biliary cholangitis and how to inform trial design

Email: atr444@gmail.com
**THU490**

**A randomized control trial evaluating the impact of a web-based mind-body wellness intervention for patients with primary biliary cholangitis**

Makayla Watt¹, Ashley Hyde¹, John Spence¹, Gail Wright², Shauna Vander Well², Emily Johnson¹, Andrew L. Mason¹, Hin Hln Ko³, Edward Tam³, Puneeta Tandon¹.

**Background and aims:** People with primary biliary cholangitis (PBC) experience significantly higher rates of mental distress, fatigue and impaired health related quality of life (HRQoL) as compared to the general population. Online mind-body wellness programming has improved mental wellness and decreased fatigue in a variety of chronic disease populations, but limited data is available in PBC. We previously conducted a pilot study of a novel online mind-body wellness intervention in PBC that demonstrated high feasibility and acceptability, as well as promising exploratory efficacy. After refining the intervention using feedback from the pilot study, the current study aimed to assess the efficacy of the online intervention.

**Method:** This was a sequential mixed-methods randomized control trial (RCT). Adult participants with PBC were randomized to receive either standard of care (SOC) or SOC alongside a 12-week online mind-body intervention involving mindful movement, breathwork, meditation, an acceptance and commitment therapy chronic disease skills program, and tips from PBC physicians. The primary outcome was changes in the Hospital Anxiety and Depression Scale (HADS). Secondary outcomes evaluated fatigue, perceived stress, resilience, HRQoL through the PBC-40, and physical functioning. ANCOVA was used to determine between group differences. A qualitative descriptive approach with semi-structured interviews was used to evaluate study experiences.

**Results:** Of the 123 patients screened for the study, 87 were randomized to the control (n = 44) and intervention (n = 43) groups (mean age 59.8 ± 10.6 years; 98% female). The between-group HADS total score improved by 20.0% (95% CI 4.7, 35.2, p = 0.011) and the HADS depression score improved by 25.8% (95% CI 4.8, 46.8, p = 0.017). Significant improvements were seen in the PSS (15.2%), and two PBC-40 domains (emotional symptoms by 16.3%, and social symptoms by 11.8%) with a mean satisfaction score of 82/100. No significant improvements were observed in fatigue, interviews revealed improved ability to cope with fatigue. In the 36/43 participants who completed the intervention, 25 (69%) adhered to the program goal of completing the program at least 3x per week. Enhancing group support was highlighted as a way to improve adherence.

**Conclusion:** This 12-week intervention improved measures of mental wellness and quality of life. High satisfaction and adherence rates were observed. Future online mind-body online wellness studies could explore strategies to optimize adherence and increase the physical activity intervention, which may in turn result in a greater impact on fatigue.
Table linear mixed-effects model SF-36. The intercept indicates the reference value of the physical component summary (PCS) and mental component summary (MCS) score for all patients without or before II conditional on the reference value of the other variables included. The estimate of the listed factors indicates the particular effect of each factor.

<table>
<thead>
<tr>
<th></th>
<th>PCS Estimate</th>
<th>PCS 95% CI</th>
<th>MCS Estimate</th>
<th>MCS 95% CI</th>
</tr>
</thead>
<tbody>
<tr>
<td>Intercept</td>
<td>50.6</td>
<td>-48.2 - 103.0</td>
<td>48.9</td>
<td>46.9 - 50.7</td>
</tr>
<tr>
<td>Female</td>
<td>-2.8</td>
<td>-5.0 - -0.7</td>
<td>-0.7</td>
<td>-0.7 - -0.7</td>
</tr>
<tr>
<td>Age per 10 years</td>
<td>-0.1</td>
<td>-0.2 - 0.0</td>
<td>-0.0</td>
<td>-0.0 - 0.0</td>
</tr>
<tr>
<td>End-stage liver disease</td>
<td>-4.3</td>
<td>-7.8 - -0.9</td>
<td>3.5</td>
<td>-0.0 - 6.7</td>
</tr>
<tr>
<td>ACH Overlap</td>
<td>2.7</td>
<td>7.4 - -0.1</td>
<td>6.7</td>
<td>6.7 - -0.1</td>
</tr>
<tr>
<td>IBSD None</td>
<td>[reference]</td>
<td>[reference]</td>
<td>[reference]</td>
<td>[reference]</td>
</tr>
<tr>
<td>Oral Crohn's Disease</td>
<td>2.4</td>
<td>-0.1 - 4.8</td>
<td>2.5</td>
<td>-2.0 - 4.8</td>
</tr>
<tr>
<td>IBD activity</td>
<td>3.3</td>
<td>0.2 - 6.4</td>
<td>-0.3</td>
<td>-3.8 - 2.8</td>
</tr>
<tr>
<td>ITCH</td>
<td>-12.2</td>
<td>-16.7 - -7.6</td>
<td>-12.0</td>
<td>-18.9 - -5.9</td>
</tr>
</tbody>
</table>

**Conclusion:** PSC patients report impaired HRQoL compared to the general population. After liver transplantation, HRQoL scores of PSC patients are at comparable levels as in the general population. HRQoL scores are associated with potentially modifiable factors such as itch and IBD activity, emphasizing the importance of adequate treatment.

### Cirrhosis and its complications: ACLF and Critical illness

**THU493 COVID-19 in patients with cirrhosis: insights from the multinational LE OSS registry**

Jonathan Frederik Brozat¹, Frank Hanses², Martina Haselberger³, Melanie Stecher¹, Michael Dreher¹, Lukas Tometten¹, Maria Madeleine Rüthrich⁷, Johannes Wesling Hospital Minden, Ruhr University Bochum, Germany; ¹Jena University Hospital, Department of Internal Medicine, Jena, Germany; ²University of Cologne, Department of Internal Medicine I, Cologne, Germany; ³University of Bonn, Department of Internal Medicine I, Bonn, Germany; ⁴University Hospital RWTH Aachen, Department of Gastroenterology, Digestive Diseases and Medical Intensive Care, Internal Medicine III, Aachen, Germany; ⁵University Hospital Regensburg, Germany; ⁶Department of Internal Medicine, Faculty of Medicine and University Hospital Cologne, Cologne, Germany; ⁷University Hospital RWTH Aachen, Department of Pneumology and Intensive Care Medicine, Internal Medicine V, Aachen, Germany; ⁸Hospital Ernst von Bergmann, Potsdam, Germany; ⁹Jena University Hospital, Department of Internal Medicine II, Jena, Germany; ¹⁰Goethe University Frankfurt, Department II of Internal Medicine, Hematology/Oncology, Frankfurt, Germany; ¹¹Hospital Ingolstadt, Department of Infectious Diseases and Infection Control, Ingolstadt, Germany; ¹²Goethe University Frankfurt, Department of Internal Medicine, Infectious Diseases, Frankfurt, Germany; ¹³Jena University Hospital, Department of Internal Medicine IV, Jena, Germany; ¹⁴Johannes Wedling Hospital Minden, Ruhr University Bochum, University Clinic for Haematology, Oncology, Haematosanology and Palliative Care, Minden, Germany; ¹⁵Catholic Hospital Bochum (St. Josef Hospital), Ruhr University Bochum, Department of Neurology, Bochum, Germany; ¹⁶University Hospital Würzburg, Department of Internal Medicine II, Würzburg, Germany; ¹⁷Klinikum rechts der Isar der Technischen Universität München, Department of Internal Medicine II, München, Germany; ¹⁸UKB University of Bonn, Department of Internal Medicine I, Bonn, Germany

**Background and aims:** International registries have reported high mortality rates in patients with liver disease and coronavirus disease 2019 (COVID-19). However, the paucity and heterogeneity of data leaves the extent to which comorbidities contribute to excess COVID-19 mortality in cirrhosis as controversial. This study thus aimed to control the influence of comorbidities through propensity score matching, enabling a controlled comparison of symptomatic presentation, disease progression and mortality of patients with COVID-19 and underlying cirrhosis to those without chronic liver disease.

**Method:** We used the multinational Lean European Open Survey on SARS-CoV-2-infected patients (LEOSS) to identify patients with cirrhosis. We compared symptoms, disease progression and mortality after propensity score matching (PSM) for age, sex, obesity, smoking status, and concomitant diseases. Mortality was further compared with that of patients with another significant precipitator of acute-on-chronic liver failure, spontaneous bacterial peritonitis (SBP).

**Results:** Among 7096 patients with SARS-CoV-2 infection eligible for analysis, 70 (0.99%) had cirrhosis, and all were hospitalized. Risk factors for severe COVID-19, such as diabetes, renal disease and cardiovascular disease were more frequent in patients with cirrhosis. Case fatality rate in patients with cirrhosis was 31.4% with the highest odds of death in patients older than 65 years (43.6% mortality; odds ratio [OR] 4.02; p = 0.018), Child-Pugh class C (57.1%; OR 4.00; p = 0.026), and failure of two or more organs (81.8%; OR 19.93; p = 0.001). After PSM for demographics and comorbidity, the COVID-19 case fatality of patients with cirrhosis was comparable to that of patients without (28.8% vs. 26.1%, p = 0.644) and similar to 28-day mortality in a comparison group of patients with cirrhosis and SBP (33.3% vs. 31.5%; p = 1.000). In contrast, the number of patients that initially reported no symptoms of COVID-19 was significantly higher in patients with cirrhosis (37.5% vs. 10.5%; p < 0.001), yet more than half progressed into complicated or critical disease phases.

**Conclusion:** Although patients with cirrhosis and SARS-CoV-2 infection regularly present without any specific symptoms, the mortality in hospitalized SARS-CoV-2-infected patients with cirrhosis is high. Propensity score matching suggests this can be largely attributed to pre-existing comorbid conditions and extrahepatic organ failure.

**THU494 Serum metabolites on admission associate with the development of nosocomial infections in patients with cirrhosis**

Jasmohan S Bajaj¹, Jacqueline O’Leary², Puneeta Tandon³, Guadalupe Garcia-Tsao⁴, Patrick S. Kamath⁵, Ram Subramanian⁶, Hugo E. Vargas⁷, Sara McGeorge¹, Andrew Fagan¹, Florence Wong², Jennifer Lai¹, Leroy Thacker³, Rajender Reddy⁴, Virginia Commonwealth University and Richmond VAMC, GL Richmond, United States; ²Dallas VAMC; ³University of Alberta; ⁴Yale University; ⁵Mayo Clinic, Rochester; ⁶Mercy Medical Center; ⁷Emory university; ⁸Mayo Clinic, Arizona; ⁹University of Toronto; ¹⁰UCSF; ¹¹University of Pennsylvania

**Email:** jasmohan.bajaj@vcuhealth.org

**Background and aims:** The inpatient course of patients with cirrhosis is complicated by a high rate of nosocomial infections (NI). These infections increase the need for intensive care, often lead to acute on chronic liver failure (ACLF), and death and are challenging to predict using clinical biomarkers. Better determination of a group that develops NI on admission could prevent one of the leading causes of ACLF and death in cirrhosis. Aim: Determine predictors of NI using serum metabolomics on admission in large cohort of inpatients with cirrhosis.
Method: We enrolled inpatients with cirrhosis admitted non-electively across 7 centres in North America and collected clinical data and infection status on admission. Serum was collected on admission and analysed for LC/MS metabolomics. Hospital course, including NI development, ICU, ACLF and death were analysed. Metabolomic analysis using ANCOVA adjusted for age, sex, admission MELD, WBC, and albumin, rifaximin, infection status was performed. Also, we performed random forest analyses (RFA) for NI development. Finally logistic regression with clinical variables and then additional metabolites to predict NI was performed.

Results: 602 patients (376 men, 231 admission infection) were included. 101 (17%) developed NI 5 ± 2 days after admission. NI patients had more frequent admission infections and longer LOS. NIs resulted in worse inpatient outcomes including ICU transfer, death, and organ failures. Infection details: Most common initial infections were SSB followed by UTI and respiratory tract from bacterial causes. On the other hand, NIs were more likely to be fungal (n = 39, p < 0.0001 vs admission infections); rest were bacterial.

Metabolomics: 247 metabolites were significantly different between patients with vs. without a NI using ANCOVA with a AUC of 0.83 (metabolites alone). The top 25 metabolites on RFA are shown in Table 1 and according to mean decrease accuracy (Figure). Logistic regression: Higher MELD (OR 1.05, CI 1.02–1.09, p < 0.0001), admission infection (OR 3.54, CI 2.18–5.76, p < 0.0001) and admission WBC (OR 1.05, CI 1.00–1.09, p = 0.04) were significant predictors with AUC of 0.74. Of the metabolites, ↑ 1-linolenoyl-GPC, 1-stearoyl-GPC and and ↑ N-acetyltryptophan and N-acetyl isoputrein added significantly to the clinical model (AUC 0.77, p = 0.05).

Conclusion: NIs are seen in almost a fifth of hospitalized patients with cirrhosis and are associated with poor outcomes. Admission metabolites focused on spermidine, tryptophan, and phospholipid metabolism were independently associated with NI prediction with significant contribution over clinical factors.

THU495
Association of impaired neutrophil migration with adverse outcomes in patients with liver cirrhosis
Mona-May Langer1,2, Stefanie Sichelschmidt1, Alina Bauschen1, Sabrina Guckenbiel1, Lea Bornemann1, Matthias Gunzer1, Christian M. Lange1,2. 1Essex University Hospital, Department for Gastroenterology and Hepatology, Essen, Germany; 2Hospital of the Ludwig Maximilian University (LMU), Medical Clinic and Polyclinic II, Munich, Germany; 3University Duisburg-Essen, Institute for Experimental Immunology and Imaging, Essen, Germany
Email: monamay.langer@med.uni-muenchen.de

Background and aims: Neutrophil granulocytes are important cells of the first line defense against bacterial and fungal infections. In the present study, we aimed to determine associations between neutrophil migration capacity and clinical outcome of patients with liver cirrhosis and acute-on-chronic liver failure.

Method: Patients with compensated (n = 11) or acutely decompensated liver cirrhosis (n = 84) or ACLF (n = 29) were recruited from a prospective, monocentric cohort study. Neutrophils were isolated of peripheral blood by magnetic beads. Neutrophil migration was tracked during steady-state-, fMLP-, CXCL1-, or CXCL8-stimulated conditions using time-lapse video microscopy and automated cell tracking. Proportion of migrating cells as well as average migration speed was quantified. Regression analyses were used to determine associations between neutrophil migration and clinical end points.

Results: The percentage of migrating neutrophils was significantly lower in patients with acute decompensation (81.32 ± 1.65%, P = 0.01) or ACLF (76.63 ± 3.4%, P = 0.003) after fMLP-stimulation compared to healthy individuals (89.04 ± 0.8%). Moreover, CXCL8-stimulation was less effective in neutrophils of patients with ACLF (75.56 ± 3.2%) compared to healthy individuals (87.14 ± 2.0%, P = 0.04). Average migration speed of neutrophils was reduced after both fMLP- and CXCL8-stimulation in patients with acute decompensation (fMLP 15.23 ± 3.3 μm/min, P = 0.001; CXCL8 14.42 ± 0.3 μm/min, P = 0.048) or ACLF (fMLP 14.91 ± 0.7 μm/min, P = 0.005; CXCL8 13.82 ± 0.4 μm/ min, P = 0.008) compared to healthy individuals (fMLP 17.8 ± 0.5 μm/min, CXCL8 15.78 ± 0.5 μm/min). A low proportion of migrating neutrophils under steady-state or stimulated conditions was associated with the development of ACLF (p < 0.05), sepsis (p < 0.05), or the composite of ACLF; sepsis and death (p < 0.01) within 7 days.

Conclusion: Defective neutrophil migration under ex vivo steady-state conditions or after stimulation with fMLP or CXCL8 is associated with adverse outcomes in liver cirrhosis such as the development of sepsis and ACLF. Hence, neutrophil migration analysis might provide as a novel early warning sign for the development of serious complications in liver cirrhosis patients.
invasive tool for assessing the cardiocirculatory effects of terlipressin; however, additional studies with larger sample sizes are needed to confirm these results.

THU497
SARS-CoV-2 infection in patients with underlying chronic liver disease is associated with significantly greater risks of inpatient hospitalization, intensive care unit admission, and overall mortality

Robert Wong1, Yi Zhang2, Mae Thamer2, 1Stanford University School of Medicine, United States; 2Medical Technology and Practice Patterns Institute, Bethesda, United States
Email: rwong123@stanford.edu

Background and aims: Patients with chronic liver disease (CLD) are hypothesized to have greater risk of developing liver decompensation following COVID-19. However, it is unclear whether the increased risks of liver decompensation result in higher overall mortality in CLD patients with COVID-19 (CLD+COVID-19). We aim to evaluate whether CLD+COVID-19 patients have higher rates of inpatient hospitalization, intensive care unit (ICU) admission, and overall mortality compared to CLD patients without COVID-19 among one of the largest U.S. cohorts evaluating COVID-19 outcomes.

Method: Using the Common Data Schema from COVID-19 Research Database, a large U.S. database containing over 72 million linked patients with both electronic health records and claims data, we identified patients with CLD (hepatitis C, hepatitis B, alcoholic liver disease, and non-alcoholic fatty liver disease/steatohepatitis) with COVID-19 (CLD+COVID-19) and without COVID-19. Patients were followed for at least 6 months until a censoring event (i.e. death) or end of the study period (August 31, 2021). Outcomes assessed included need for inpatient hospitalization, ICU admission, and overall mortality, and outcomes were compared between groups with chi-square testing. Multivariate regression models evaluated whether COVID-19 was independently associated with greater risk of hospitalization, ICU admission, and overall mortality in CLD patients.

Results: Among 973, 634 adult patients with CLD (55.2% men, 44.8% women, 28.5% age >65y, 40.4% age 45–64y, 30.7% age 18–44, 12.0% with cirrhosis), 3.5% had CLD+COVID-19 and 96.5% had CLD without COVID-19. CLD+COVID-19 patients had significantly higher rates of hospitalization (25.7% vs. 9.2%, p < 0.01), ICU admission (15.5% vs. 4.9%, p < 0.01), and overall mortality (5.6% vs. 3.8%, p < 0.01). On adjusted multivariate regression, when compared to CLD patients without COVID-19, patients with CLD+COVID-19 had significantly greater risk of hospitalization (OR 3.27, 95% CI 3.19–3.35, p < 0.01), ICU admission (OR 3.36, 95% CI 3.26–3.47), and overall mortality (OR 1.36, 95% CI 1.29–1.42). These findings were likely mediated by increased risks liver decompensation (HR 1.23, 95% CI 1.15–1.32, p < 0.01) and acute on chronic liver failure (ACLF) (HR 7.32, 95% CI 6.40–8.38, p < 0.01) due to acute SARS-CoV-2 infection observed in CLD+COVID-19 compared to CLD without COVID-19 patients.

Conclusion: Among one of the largest cohorts evaluating COVID-19 outcomes in patients with underlying CLD, we observed that SARS-CoV-2 infection was associated with significantly greater risks of inpatient hospitalization, ICU admission, and overall mortality in patients with CLD. The increased mortality observed in CLD patients with COVID-19 is likely a result of the increased risks of liver decompensation and ACLF due to COVID-19.

THU498
Low FT3 levels are associated with acute decompensation and acute-on-chronic liver failure

Mona-May Langer1,2, Alina Bauschen1, Sabrina Guckenbühl1, C. Sebastian Hones1, Denise Zwanziger1, Lars Christian Möller3, Christian M. Lange1,2, 1University Hospital Essen, Department for Gastroenterology and Hepatology, Essen, Germany; 2Hospital of the Ludwig Maximilian University (LMU), Medical Clinic and Polyclinic II, Munich, Germany; 3University Hospital Essen, Department of Endocrinology, Diabetes and Metabolism and Division of Laboratory Research, Essen, Germany
Email: monamay.langer@med.uni-muenchen.de

Background and aims: Thyroid hormones (TH) are important for regulation of hepatic lipolysis, gluconeogenesis, and immune-metabolism, and may thereby impact the pathogenesis and severity of liver cirrhosis and acute-on-chronic liver failure (ACLF). Therefore, we determined associations between TH, clinical stages of liver cirrhosis including ACLF and TH targets in immune cells.

Method: From a prospective cohort study, patients with compensated liver cirrhosis (n = 163) or acute decompensation (n = 169) or ACLF (n = 36) were recruited. Thyroid-stimulating hormone (TSH), free T3 (FT3) and free T4 (FT4) levels were determined by immunoassays. Associations between TH and clinical parameters were assessed by regression analyses. T cells of healthy donors and patients were isolated from peripheral blood and characterized for expression of TH target genes by RT-PCR.

Results: TSH concentration in patients with acute decompensation (2.81 ± 0.2 mU/l) was increased compared to patients with compensated liver cirrhosis (2.01 ± 0.1 mU/l, P = 0.03) and ACLF (2.18 ± 0.34 mU/l, P = 0.42). Contrariwise FT3 levels were significantly lower already in patients with acute decompensation (3.80 ± 0.06 pmol/l) compared to compensated liver cirrhosis (4.79 ± 0.06 pmol/l, P < 0.0001), and even lower in those with ACLF (3.24 ± 0.15 pmol/l, P < 0.0001; compensated vs. ACLF P = 0.0001; acute decompensation vs. ACLF P < 0.01). Decreased FT3 concentrations were associated with infections in acute decompensated patients (3.45 ± 0.10 pmol/l/without infection vs. 3.90 ± 0.07 pmol/l/with infection, P = 0.0009), while FT3 concentrations were not different in ACLF with (3.23 ± 0.24 pmol/l) or without infections (3.25 ± 0.16 pmol/l, P = 0.8). FT3 concentrations correlated inversely with CLIF-OF-, CLIF-C-AD/ACLF- and MELD-scores (p < 0.0001). Furthermore, low FT3 levels (p < 0.001) as well as a low FT3/FT4 ratio (p < 0.001) were associated with mortality of liver cirrhosis patients. RT-PCR showed that T cells derived from healthy donors and patients with liver cirrhosis or ACLF did not express TH receptor β, but TH receptor α. Compared to T cells of healthy donors, expression of TH receptor α was significantly decreased in T cells derived from patients with compensated liver cirrhosis (p = 0.02) and even more in T cells of patients with acute decompensation (p = 0.001) or ACLF (p < 0.0009).

Conclusion: Acute decompensation complicated with infections as well as ACLF with or without infections is associated with profound alterations in the TH balance resembling low T3 syndrome. Strikingly, low FT3 level and decreased FT3/FT4 ratio are associated with elevated mortality in patients with liver cirrhosis. Reduced TH receptor α expression suggests impaired TH signaling in T cells of patients with liver cirrhosis possibly contributing to reduced survival. Mechanism and functional consequences of these findings will be further explored in the new SFB-CRC/TR 296.
Background and aims: Acute decompensation (AD) and acute-on-chronic Liver failure (ACLF) are characterised by increased systemic inflammation and immunosuppression. There are data supporting gender differences in the inflammatory response in health and differences in outcomes between genders in AD/ACLF. Post-hoc subgroup analyses of the neutral ATTIRE trial (Albumin To Prevent Infection in Chronic Liver Failure) suggested a differential effect of targeted albumin infusions according to gender and so we investigated this in greater detail.

Method: ATTIRE was a randomized, multicenter, open-label trial involving 777 patients including 227 women, hospitalized with decompensated cirrhosis and serum albumin <30 g/L. Patients received standard of care or targeted albumin therapy (aiming for serum albumin >30 g/L) for up to 14 days or discharge. Baseline clinical characteristics and patient outcomes were analysed using appropriate statistical tests in RStudio software.

Results: Baseline characteristics, including MELD (Model for End-Stage Liver Disease) score, age and cirrhosis aetiology were similar between genders apart from an elevated creatinine in men (70 (57–94) vs 60 (48–77) μmol/L, p < 0.001). The volume of albumin infused did not differ between genders but resulting serum albumin values in the targeted albumin group were higher in women throughout the trial treatment period (p < 0.001). Women also had higher white cell counts (WCC) throughout the trial independent of treatment group (p < 0.001) but not C-reactive protein values. Overall outcomes did not differ between genders, although fewer events of renal dysfunction were seen in women (but not men) in the albumin treatment group compared to standard care (Chi-squared test (X²(1) = 6.85, p = 0.009). The incidence of serious adverse events with pulmonary oedema or fluid overload was similar between treatment groups in women, in contrast to men in which these were four times as common.

Conclusion: Higher WCC levels in women irrespective of treatment group might suggest a difference in the inflammatory response but infection rates and overall outcomes were similar. The improved renal function in albumin-treated women without evidence of increased adverse events may relate to their increased rate of serum albumin increment, however, there was no mortality benefit according to gender. These findings may warrant further investigation.

Table: Outcomes and serious adverse events in ATTIRE according to gender and treatment group

<table>
<thead>
<tr>
<th>Treatment group (%)</th>
<th>MALE</th>
<th>FEMALE</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Albumin (257)</td>
<td>Standard care (293)</td>
</tr>
<tr>
<td>Outcome = n (%)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>New infection</td>
<td>55 (21.4)</td>
<td>48 (16.3)</td>
</tr>
<tr>
<td>Renal dysfunction</td>
<td>30 (11.7)</td>
<td>35 (11.9)</td>
</tr>
<tr>
<td>Death during 48 h</td>
<td>20 (7.8)</td>
<td>23 (7.8)</td>
</tr>
<tr>
<td>Death at 28 days</td>
<td>37 (14.4)</td>
<td>47 (16)</td>
</tr>
<tr>
<td>Death at 90 days</td>
<td>85 (52.3)</td>
<td>70 (23.9)</td>
</tr>
<tr>
<td>Death at 180 days</td>
<td>94 (56.8)</td>
<td>87 (29.7)</td>
</tr>
<tr>
<td>Severe adverse event</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Pulmonary oedema/</td>
<td>63</td>
<td>52</td>
</tr>
<tr>
<td>Fluid overload</td>
<td>19</td>
<td>4</td>
</tr>
<tr>
<td>GI bleed</td>
<td>8</td>
<td>9</td>
</tr>
</tbody>
</table>

Conclusion: Among tested machine learning models, SVM seems to have the highest accuracy in predicting liver decompensation. In addition to classical laboratory parameters, genetic factors and infections were critical parameters for individual predictions by SVM.
LivR Well is a multidisciplinary intervention aimed at reducing mortality and readmission through a home-based, liver optimisation program after an ACLF episode. We assessed feasibility, safety, patient acceptability and clinical impact.

**Method:** A prospective, feasibility study was conducted at an Australian tertiary hospital from March to October 2021. ACLF was defined as an acute hepatic insult with serum bilirubin ≥50 umol/L and International Normalized Ratio ≥1.5, complicated within 4 weeks by ascites and/or encephalopathy. Exclusions included end-of-life care, heart failure management and aged care residents. Participants received weekly medical review and oral nutritional supplementation. Home nursing, dietitian, physiotherapist, pharmacist, social worker, and neuropsychiatrist consultations were provided (Fig 1). The primary outcomes were adverse events/death. Secondary outcomes were attrition, liver disease severity, healthcare utilization, and patient-reported outcomes.

**Results:** We enrolled 32 patients: 31 patients completed the program. The median age was 53 years (Interquartile range (IQR) 49–60); 75% were male. The median Charlson Co-Morbidity Index score was 4 (IQR 3–5.5). Excess alcohol was the most common etiology (72%). Baseline median Model for End-Stage Liver Disease (MELD) score was 17 (IQR 13–21). Baseline handgrip strength in 11/27 (41%) patients met sex-specific criteria for sarcopenia. Two patients died at 16 and 148 days from enrolment. The 28-day mortality was 3% and the 30-day readmission rate was 16%. LivR Well cost $4,947 AUD compared to $16,197 AUD for an inpatient ACLF admission. Median MELD score improved at 28 days (17 vs. 15, p = 0.31). The Chronic Liver Disease Questionnaire showed improvement in ‘fatigue’ (p = 0.03) and ‘worry’ (p = 0.05), at 28 days compared to baseline. Qualitative interviews were undertaken in 24 participants with all reporting positive experience pertaining to interactions with clinicians. The importance of health literacy (22/24) and patient autonomy (20/24) were emphasized in >80% of interviews.

**Conclusion:** LivR Well was safe, feasible, acceptable, and cost-efficient with a reduction in 28-day mortality and 30-day readmission rates. We plan to conduct a randomized controlled trial of LivR Well compared to standard care to evaluate cost-effectiveness and patient acceptability and clinical impact on re-admission and mortality.

**Background and aims:** Severe alcohol-associated hepatitis (SAH) without response to medical therapy is associated with unacceptably high mortality, particularly with concomitant acute-on-chronic liver failure (ACLF). Only a minority of these SAH-ACLF patients are eligible for early liver transplantation (eLT) and the outcomes of declined candidates are unknown. The aim of our study was to determine the outcomes of declined eLT for SAH candidates and to examine variables associated with outcomes in SAH-ACLF.

**Method:** We analysed a prospectively maintained database of SAH patients (probable or definite per NIAAA guidelines, MELD >20) hospitalized at a LT centre from 1/2012–7/2021. All non-responders to corticosteroids were presented at our transplant selection meeting. Patients declined for eLT for SAH and those accepted who died prior to eLT were identified. The U.S. centralised National Death Index (NDI) was used to determine outcomes of patients lacking follow-up at our centre.

**Results:** Over 9.5 years, a total of 234 SAH patients were either declined for eLT (n = 207) or accepted and died prior to eLT (n = 27). Median time to eLT decision was 5 days (3–11). The cohort was young and diverse: median age 44 years (35–53), nearly half were women (108/234, 46%) with significant racial minority representation: 55% White, 26% Hispanic, 8% Black, 7% Asian, 3% unknown. Most of the cohort met EASL-CLIF criteria for ACLF (62%); 71% had ACLF grade 2 or 3. Mean MELD score at the time of waitlisting decision was 33 (±8), mean Maddrey’s discriminant function was 96 (±79), median CLIF-C Organ Failure score (CLIF-C OFs) was 10 (9–12) and median CLIF-C ACLF score was 49 (43–55). Over a median follow-up of 494 days (17–1291), 145/234 died (62%) Of patients with ACLF-3, 38/45 (84%) died and median time to death was 8 days (3–18) versus 17 days (9–59) in ACLF-2, 78.5 days (22.5–228) in ACLF-1 and 71 days (19.5–210) in patients without ACLF (p = 0.001) (figure).

**Background and aims:** Severe alcohol-associated hepatitis with acute-on-chronic liver failure in a diverse cohort: lung and circulatory organ failures along with MELD 35 are predictive of mortality

**Method:** We analysed a prospectively maintained database of SAH patients (probable or definite per NIAAA guidelines, MELD >20) hospitalized at a LT centre from 1/2012–7/2021. All non-responders to corticosteroids were presented at our transplant selection meeting. Patients declined for eLT for SAH and those accepted who died prior to eLT were identified. The U.S. centralised National Death Index (NDI) was used to determine outcomes of patients lacking follow-up at our centre.

**Results:** Over 9.5 years, a total of 234 SAH patients were either declined for eLT (n = 207) or accepted and died prior to eLT (n = 27). Median time to eLT decision was 5 days (3–11). The cohort was young and diverse: median age 44 years (35–53), nearly half were women (108/234, 46%) with significant racial minority representation: 55% White, 26% Hispanic, 8% Black, 7% Asian, 3% unknown. Most of the cohort met EASL-CLIF criteria for ACLF (62%); 71% had ACLF grade 2 or 3. Mean MELD score at the time of waitlisting decision was 33 (±8), mean Maddrey’s discriminant function was 96 (±79), median CLIF-C Organ Failure score (CLIF-C OFs) was 10 (9–12) and median CLIF-C ACLF score was 49 (43–55). Over a median follow-up of 494 days (17–1291), 145/234 died (62%) Of patients with ACLF-3, 38/45 (84%) died and median time to death was 8 days (3–18) versus 17 days (9–59) in ACLF-2, 78.5 days (22.5–228) in ACLF-1 and 71 days (19.5–210) in patients without ACLF (p = 0.001) (figure).

**Figure:** Kaplan-Meier survival by ACLF grade

---

Of the components of CLIF-C OFs, lung (HR 2.5, 95% CI 1.4–4.6), brain (HR 2.4, 95% CI 1.5–3.8) and coagulation scores (HR 1.4, 95% CI 1.03–1.97) were also significantly associated. MELD >35 was determined as the optimal threshold for predicting mortality (HR 3.1, 95% CI 1.7–5.6). Compared with a “static” bilirubin during admission, a 10% bilirubin decrease had 66% lower mortality risk (p = 0.01) and a 20% increase was associated with 200% higher mortality (p = 0.05).

Conclusion: In a diverse, real-world cohort of patients with sAH declined for eLT, we identified a high prevalence of ACLF with very high short-term mortality. Lung and circulatory components of CLIF-C OFs and MELD >35 at the time of waitlisting decision were most predictive of mortality and may help guide clinical decision-making.

THU503 Bilirubin and its dynamics are independently associated with mortality in patients with acute decompensation of cirrhosis
Konstantin Kazankov1,2, Peter Holland-Fischer1,2,
Karen Louise Thomsen1,2, Rajiv Jalan1, Raj Mookerjee1,1 University College London (UCL), Institute for Liver and Digestive Health, UCL Medical School, Royal Free Hospital, Liver Failure Group, United Kingdom; 2Aarhus University Hospital, Department of Hepatology and Gastroenterology, Denmark; 3Aalborg University Hospital, Department of Medical Gastroenterology, Denmark
Email: konksazaj@rm.dk

Background and aims: Patients with acute decompensation of cirrhosis (AD) are at high risk of mortality, and current practice is still devoid of accurate parameters indicating poor outcome. In our AD cohort, we assessed the value of bilirubin alone and its dynamic changes to predict mortality.

Method: We included patients with AD cirrhosis from a prospective database in which clinical and biochemical data were registered. Multivariate logistic regression and Kaplan-Meier analysis were used for statistical analysis. Odds ratios (OR) were based on bilirubin increments of 1.45 mg/dL (25 μmol/L).

Results: 519 patients were included, with alcohol (68%) as the predominant etiology. Main precipitants for AD were: harmful drinking (35%), infection (17%) and unknown (24%). 137 patients had alcoholic hepatitis. 354 patients (67%) did not have ACLF on admission or develop ACLF pre-discharge, whereas 24% had ACLF on admission, and 9% developed ACLF during hospitalization. Fifty-nine patients (11%) died within 4 weeks, and 118 (23%) within 12 weeks, with the highest mortality in patients with ACLF on admission or during hospitalization.

In multivariate analysis, admission bilirubin was associated with both 4- (OR 1.09 [CI 1.03–1.15]) and 12-week mortality (OR 1.08 [CI 1.03–1.13]) adjusted for age, sodium, creatinine, INR, white cell count, CRP and presence of alcoholic hepatitis and infection. Bilirubin levels beyond 12 mg/dL, the liver failure threshold according to the CLIF-Cortium ACLF-score, showed increasing 12-week mortality (Figure, log-rank test p < 0.001).

During admission (median 11 [IQR 7–20] days), 328 (63%) patients decreased their bilirubin, whereas it increased or was unchanged in 190 (37%) patients. Lack of reduction in bilirubin was strongly associated with death after 4 (OR 4.12 [CI 2.13–7.99]) and 12 weeks (OR 2.77 [CI 1.65–4.64]) in multivariate analysis. Accordingly, 18% of patients with a decrease in bilirubin died after 12 weeks vs. 35% in those with an increase or no change.

In patients with AD without ACLF, admission bilirubin lost its association with death at 4 weeks (OR 0.96 [CI 0.75–1.24]) but remained associated with 12-week mortality (OR 1.09 [CI 0.997–1.20]) in multivariate analysis, especially for levels >17.5 mg/dL. In patients without ACLF at admission, bilirubin was independently associated with ACLF development during hospitalization (OR 1.16 [CI 1.07–1.26]).

Figure: Kaplan-Meier 12-week survival estimates according to bilirubin at admission.

Conclusion: In AD cirrhosis patients, bilirubin at admission is a strong independent predictor of mortality. A step-wise increase in mortality arises from bilirubin levels >12 mg/dL. Failure to improve bilirubin during admission is an even stronger predictor of death. We propose a more detailed analysis of bilirubin and its dynamics in future studies, to generate new models for prognostication in AD cirrhosis.

THU504 Impact of predisposition and precipitants on the short-term prognosis among inpatients with chronic liver disease
Yan Zhang1, Guohong Deng2, Xian-Bo Wang3, Xin Zheng4, Yan Huang5, Jinjun Chen6, Zhong-Ji Meng7, Yanhang Gao8, Zhiping Qian9, Feng Liu10, Xiao-Bo Lu11,12, Yu Shi12, Yan Huadong13, Zheng Yubao14, Hai Li1,1, Ren Ji Hospital, School of Medicine, Shanghai Jiao Tong University, Department of Gastroenterology, Shanghai, China; 2Southwest Hospital, Third Military Medical University (Army Medical University), Department of Infectious Diseases, Chongqing, China; 3Beijing Ditan Hospital, Capital Medical University, Center of Integrative Medicine, Beijing, China; 4Institute of Infection and Immunology, Union Hospital, Tongji Medical College, Huazhong University of Science and Technology, Department of Infectious Diseases, Wuhan, China; 5Hunan Key Laboratory of Viral Hepatitis, Xiangya Hospital, Central South University, Department of Infectious Diseases, Changsha, China; 6Nanjing Hospital, Southern Medical University, Hepatology Unit, Department of Infectious Diseases, Guangzhou, China; 7Taihe Hospital, Hubei University of Medicine, Department of Infectious Disease, Shiyian, China; 8The First Hospital of Jilin University, Department of Hepatology, Changchun, China; 9Department of Liver Intensive Care Unit, Shanghai Public Health Clinical Centre, Fudan University, Shanghai, China; 10Tianjin Institute of Hepatology, Nankai University Second People’s Hospital, Tianjin, China; 11Infectious Disease Center, The First Affiliated Hospital of Xi’an Jiaotong University, Xi’an, China; 12The State Key Laboratory for Diagnosis and Treatment of Infectious Diseases, The First Affiliated Hospital of School of Medicine, Zhejiang University, Hangzhou, China; 13Department of Infectious Diseases, Huamei Hospital, Ningbo, China; 14Department of Infectious Diseases, The Third Affiliated Hospital of Sun Yat-sen University, Guangzhou
Email: haili_17@126.com

Background and aims: Little is known about the impact of predisposition, especially the severity of liver fibrosis, and the type of precipitants on the short-term prognosis in hospitalized patients with chronic liver disease. We aimed to evaluate the risk of predisposition and precipitants on the short-term prognosis in hospitalized patients with chronic liver disease.

Method: This study was performed in 3970 cirrhosis and other chronic liver disease patients hospitalized for acute decompensation.
or acute liver injury from two prospective large multicenter studies in high-endemic HBV areas (NCT02457637 and NCT03641872). The primary endpoint was a composite outcome comprised of death and liver transplantation. We investigated the natural history of composite outcome within 1 year and assessed the risk of predisposition, precipitants for 90-day or 365-day composite outcome.

Results: In 2826 patients with cirrhosis, 2306 admitted for classical AD (including overt ascites, hepatic encephalopathy, gastrointestinal bleeding and bacterial infection) burden with high 90-day and 365-day composite outcome rate (24.7%, 33.0%), while 291 admitted without classical AD but with jaundice (TB >5 mg/dl) showed comparable high 90-day and 365-day composite outcome rate (26.1%, 33.0%). In 1144 patients without cirrhosis, 955 patients with advanced fibrosis (FIB-4 >1.45) burdened with relatively high 90-day and 365-day composite outcome rate (8.7%, 9.9%) when compared to those with mild or none fibrosis (2.2%, 2.2%). After adjusting age, gender, TB, INR, Creatine and sodium, the severity of liver fibrosis in non-cirrhosis had no impact of 90-day (p = 0.222) and 365-day composite outcome (p = 0.581). But the occurrence of cirrhosis significantly increased the risk for 90-day (p < 0.001, OR = 2.45) and 365-day (p < 0.001, OR = 3.09) composite outcome when compared to non-cirrhosis. Moreover, in patients with cirrhosis and AD, previous decompensation independently increased the risk of 365-day adverse outcomes by 1.39-fold (p = 0.005) and 365-day composite outcome by 1.85-fold (p < 0.001), and the risk of 90-day and 365-day adverse outcomes in patients with extrahepatic precipitants was significantly higher than that in patients with intrahepatic precipitants.

Conclusion: The severity of liver fibrosis did not impact the 90-day and 365-day composite outcome in patients without cirrhosis, but the occurrence of cirrhosis significantly increased the risk for 90-day and 365-day composite outcome. In cirrhosis, jaundice should be also recognized as a kind of AD owing to its contribution to the comparable high 90-day mortality. Moreover, in patients with cirrhosis and AD, long-term surveillance monitoring in patients with previous decompensation and intensive therapy targeting extrahepatic precipitants are suggested which could enhance disease management and decrease the mortality.

THU505
A study evaluating outcomes of a virtual specialist liver cirrhosis clinic
Claudia Moore-Gillon1, Alex Cole1, Maria Bashyam1, Mathew Vithayathil1, Rooshi Nathwani1,2, David Koeckerling2, Sujit Mukherjee1,2, Benjamin H. Mullish1,2, Maud Lemoine1,2, Lucia Possamai1,2, Heather Lewis1,2, Nowlan Selvapatt1,2, Ameet Dhar1,2, 1Imperial College Healthcare NHS Trust, United Kingdom; 2Imperial College London, United Kingdom
Email: c.moore-gillon@nhs.net

Background and aims: Managing patients in a specialist cirrhosis clinic improves survival. The COVID-19 pandemic necessitated the transition to virtual clinics (VC). We aimed to evaluate the clinical impact of VC on survival, admission and decompensation rates in cirrhotic patients managed in a specialist service.

Method: We retrospectively analysed cirrhotic patients who had a specialising VC from March to June 2020. Clinical parameters were collected at baseline and 6 months and compared with a cohort of patients reviewed face to face (F2F) in the same specialist cirrhosis clinics from March to June 2019. Patients with COVID-19 were excluded.

Results: 143 patients attended for VC, 129 for F2F review. Groups were matched for age, sex, aetiology, and Child Pugh grade (CP). There was no difference at 6 months in survival, change in MELD/UKELD, decompensation or need for ambulatory review in all cirrhosis grades combined or CP BandC subgroup alone (p > 0.05) (Table 1). Fewer patients were admitted in the VC vs the F2F group (p = 0.01) but this was not validated in CP BandC subgroup (p = 0.28). Fewer blood tests were ordered for the VC group (p = 0.0001). The VC group had longer delays for ultrasound HCC surveillance (<0.0001) without an increase in new HCC cases.
Background and aims: Chronic liver failure is associated with multiple metabolic alterations that are related to its severity and pronounced in acute decompensation (AD) and more so in acute-on-chronic liver failure (ACLF). We previously showed that high-density lipoprotein cholesterol (HDL-C) levels are reduced in patients with chronic liver failure, showing similar prognostic information as the model for end-stage liver disease (MELD). In the present study we aimed to determine whether a combination of metabolite parameters altered in chronic liver failure can yield superior prognostic accuracy for short- and intermediate-term survival.

Method: We studied a multinational cohort of patients with chronic liver failure of varying severity, including compensated cirrhosis (CC), AD and ACLF. Metabolomics analysis was performed by NMR spectroscopy and revealed several metabolites that were significantly associated with survival in univariate analyses. After checking intercorrelation of prognostic parameters by variance inflation factors (VIF), multivariable competing risk analysis was performed with death as the event and liver transplantation as a competing risk to identify independent predictors of survival. The performance of the new prognostic model was compared to that of MELD using ROC analysis (DeLong test) for 3-month, 1-year and 2-year survival.

Results: We included 423 patients (median age 58 years; 70% male; CC 54%/AD 35%/ACLF 11%; etiology alcohol 55%). Thirty-nine patients received liver transplantation, 160 patients died and 224 were censored. The risk of death (HR, 95%CI) increased with age (1.03, 1.00–1.07), ln (creatinine) (1.88, 1.13–3.13), ln (bilirubin) (1.75, 1.31–2.35), ornithine (0 vs. >0) (1.69, 1.06–2.69) and lower HDL-C (0.98, 0.97–1.00). While the performance of this multivariable model was similar to that of MELD in the prediction of 3-month survival, it was superior to that of MELD for 1-year and 2-year survival (Table).

Conclusion: A metabolomics-based prognostic model including age, creatinine, bilirubin, ornithine and HDL-C showed superior accuracy for prediction of 1-year and 2-year survival as compared to MELD. External validation is warranted to confirm our findings.

THU507
Uncovering monocyte transcription, functional and metabolic signatures in recovery and non-recovery ACLF patients
Rita Furtado Feio de Azevedo1, Hannelie Korf1, Markus Boesch1, Silvia Radenkovic2,3, Marie Wallays1, Lena Smets1, Lukas Van Melkebeke1,4, Philippe Meersseman5, Hannah Van Malenstein1,4, Frederik Nevens1,4, Wim Laleman1,4, Jef Verbeek1,4, Schalk van der Merwe1,4, 1Laboratory Hepatology, KU Leuven, CHROMETA Department, Leuven, Belgium; 2VIB Center for Cancer Biology, Metabolomics Expertise Center, Center for Cancer Biology, Leuven, Belgium; 3KU Leuven, Metabolomics Expertise Center, Department of Oncology, Leuven, Belgium; 4UZ Leuven, Department of Gastroenterology and Hepatology, Leuven, Belgium;5UZ Leuven, KU Leuven, Department of Internal Medicine, Leuven, Belgium
Email: rita.azevedo@kuleuven.be

Background and aims: Cirrhosis is the end-result of a progressive chronic liver disease that may progress to the development of ascites, variceal hemorrhage, encephalopathy and hepatic decompensation. A precipitating event such as an infection can trigger a rapid deterioration of liver function and result in organ failure: acute-on-chronic liver failure (ACLF). It is a devastating clinical entity with a mortality exceeding 70% within a 28-day period in its most severe form. It is not known if these patients have infections due to a failure
Transcriptomic analysis unraveled a distinct pattern of monocytes in dampening the production of pro-inflammatory mediators, or whether they trigger a prolonged anti-inflammatory response making these patients incapable to respond to a secondary infection. Likewise, the functional and metabolic defects in ACLF are incompletely understood, and this information may be the key to restoring immune dysfunction. We aim to study the dynamics of monocyte function during the course of ACLF progression and how this associates with disease outcome.

**Method:** We performed paired transcriptional, functional and metabolic analysis of CD14+CD16- monocytes at day 0 and 7 from ACLF patients to compare profiles in recovery vs non-recovery. ACLF patients with a CLIF-SOFa score of 2/3 with underlying chronic alcoholic liver disease and no corticoid therapy were included in the study and were followed for 28 days after admission.

**Results:** Transcriptomic analysis unraveled a distinct pattern between ACLF non-recovery and recovery at baseline together with expression differences between day 0 and 7 in each group. Non-recovery monocytes showed an impaired phagocytic capacity, oxidative response and incapability of inducing CD4+ T cell proliferation and low capacity to trigger T cell activation. Conversely, ACLF patients that recovered showed an improvement in phagocytic and oxidative burst capacity from day 0 to 7, and despite being inefficient in triggering T cell proliferation they featured an intact ability to induce T cell activation. In addition, monocyte metabolic profile of recovery patients clustered separately from non-recovery ACLF patients at day 0. And, the monocyte metabolic profile clustered separately day 0 from 7 on both groups.

**Conclusion:** The immune phenotype seen in monocytes from ACLF patients that recover can effectively respond to an infectious challenge. In stark contrast monocytes from non-recovery ACLF patients showed a functional impairment, which renders these patients susceptible to new infections.

**THU508**

Early initiation of continuous renal replacement therapy improves renal outcomes and survival in patients with acute chronic liver failure-a prospective cohort study

Rakhi Mawiwal1, Ashini Hidam2, Sonia Kadayam1, Mansi Singh1, Anupam Kumar2, Rajendra Mathur3, Harshvardhan Tevethia1, Hitesh Singh3, Siva Tez Pv3, Shiv Kumar Sarin1.

**Background and aims:** Systemic inflammatory response syndrome (SIRS) is a driver of acute kidney injury (AKI) in patients with acute-on-chronic liver failure (ACLF). Early initiation of continuous renal replacement therapy (CRRT) improves outcomes in patients with acute liver failure, however there are no studies in patients with ACLF. We aimed to investigate the impact of initiation strategy of CRRT on AKI outcomes in patients with ACLF. Our primary outcome was to evaluate predictors of renal recovery. Our secondary outcomes included lactate and ammonia clearance, impact of CRRT on systemic inflammation, endothelial function and adverse effects. Early initiation group (EG) was defined as initiation of CRRT within 24 hours of initiation of vasopressors (norepinephrine or terlipressin)

**Method:** Prospective cohort of ACLF patients admitted to the intensive care unit. In all patients, urine and plasma samples were collected at baseline and 24 hours for analysing the impact of CRRT on markers of inflammation, endothelial function, renal injury and repair. Clinical, hemodynamic and lung parameters (VolumeView system, Edwards Lifesciences) and blood gas parameters were recorded.

**Results:** Thirty patients with ACLF [early group (EG, n = 15) and late group (LG, n = 15)], aged 43.33 ± 10.1; 87% males, 70% alcoholics with mean MELD 37 ± 5, AARC 10 ± 1.61 and SOFA 14 ± 2.55 score were enrolled. The median time to CRRT after onset of AKI was [44 ± 7.1 vs. 113.6 ± 4.0] hours and after initiation of vasopressors was [143.7 ± 7.56 vs. (49.7 ± 17.8)] hours in EG vs. LG respectively (p < 0.001). A significant improvement in SIRS, extravascular lung water (EVLW), pulmonary vascular permeability index, arterial lactate and ammonia was noted in dialysis-responders (DR) compared to non-responders (p < 0.05).

**Conclusion:** Only one in three patients of ACLF achieve renal recovery with CRRT. Response to CRRT is associated with improvement in hemodynamics, systemic inflammation, endothelial and renal function. Each hour delay in CRRT after onset of shock and higher SOFA score are associated with decreased chances of renal recovery and worse outcomes in patients with ACLF.

**THU509**

Different clinical courses of acutely decompensated cirrhosis in hepatitis B virus high-endemic area: data from Chinese Acute-on-Chronic Liver Failure (CATCH-LIFE) study

Tongyu Wang1, Yu Shi2, Hai Li1, 1Shanghai, China; 2Hangzhou, China

**Background and aims:** Cirrhotic patients with acute decompensation (AD) have different clinical course and pathophysiology base on the PREDICT study in a predominately alcohol-related etiologic population: pre-ACLF (acute-on-chronic liver failure), UDC (unstable decompensated cirrhosis) and SDC (stable decompensated cirrhosis) patients with different pathophysiology and prognosis. However, in hepatitis B virus (HBV) high-endemic area, the characteristics of these three subtypes are not well characterized. The aims of this study were to explore the characteristics and outcomes of different clinical courses within 1 year.

**Method:** We identified 2597 cirrhotic patients with AD from a prospective multi-center cohort with 66.85% HBV-related etiology and explored the disease dynamics and prognosis within 1 year. Clinical and biological parameters during hospitalization, 3-month re-admission and outcomes during follow-up were collected. Pre-ACLF was defined as patients developed ACLF within hospitalization. Subgroup analysis was conducted based on etiology, prognostic scores were recorded to predict outcomes in ACLF, UDC and SDC patients, respectively.

**Results:** Totally, 2188 AD without ACLF at baseline were identified. There are 184 (8.41%) pre-ACLF patients with 3-month and 1-year in-free mortality rates of 60.49% and 70.93%, respectively. 663 UDC (27.38%) patients had at least one readmission within 3 month and had no ACLF development during hospitalization, with 22.05% and 22.05% in SIRS reactivation and low capacity to trigger T cell activation. Conversely, ACLF patients that recovered showed an impaired phagocytic capacity, oxidative burst capacity from day 0 to 7, and despite being inefficient in triggering T cell proliferation they featured an intact ability to induce T cell activation. In addition, monocyte metabolic profile of recovery patients clustered separately from non-recovery ACLF patients at day 0. And, the monocyte metabolic profile clustered separately day 0 from 7 on both groups.

**Conclusion:** The immune phenotype seen in monocytes from ACLF patients that recover can effectively respond to an infectious challenge. In stark contrast monocytes from non-recovery ACLF patients showed a functional impairment, which renders these patients susceptible to new infections.

**THU508**

Early initiation of continuous renal replacement therapy improves renal outcomes and survival in patients with acute chronic liver failure-a prospective cohort study

Rakhi Mawiwal1, Ashini Hidam2, Sonia Kadayam1, Mansi Singh1, Anupam Kumar2, Rajendra Mathur3, Harshvardhan Tevethia1, Hitesh Singh3, Siva Tez Pv3, Shiv Kumar Sarin1.

**Background and aims:** Systemic inflammatory response syndrome (SIRS) is a driver of acute kidney injury (AKI) in patients with acute-on-chronic liver failure (ACLF). Early initiation of continuous renal replacement therapy (CRRT) improves outcomes in patients with acute liver failure, however there are no studies in patients with ACLF. We aimed to investigate the impact of initiation strategy of CRRT on AKI outcomes in patients with ACLF. Our primary outcome was to evaluate predictors of renal recovery. Our secondary outcomes included lactate and ammonia clearance, impact of CRRT on systemic inflammation, endothelial function and adverse effects. Early initiation group (EG) was defined as initiation of CRRT within 24 hours of initiation of vasopressors (norepinephrine or terlipressin)

**Method:** Prospective cohort of ACLF patients admitted to the intensive care unit. In all patients, urine and plasma samples were collected at baseline and 24 hours for analysing the impact of CRRT on markers of inflammation, endothelial function, renal injury and repair. Clinical, hemodynamic and lung parameters (VolumeView system, Edwards Lifesciences) and blood gas parameters were recorded.

**Results:** Thirty patients with ACLF [early group (EG, n = 15) and late group (LG, n = 15)], aged 43.33 ± 10.1; 87% males, 70% alcoholics with mean MELD 37 ± 5, AARC 10 ± 1.61 and SOFA 14 ± 2.55 score were enrolled. The median time to CRRT after onset of AKI was [44 ± 7.1 vs. 113.6 ± 4.0] hours and after initiation of vasopressors was [143.7 ± 7.56 vs. (49.7 ± 17.8)] hours in EG vs. LG respectively (p < 0.001). A significant improvement in SIRS, extravascular lung water (EVLW), pulmonary vascular permeability index, arterial lactate and ammonia was noted in dialysis-responders (DR) compared to non-responders (p < 0.05).

**Conclusion:** Only one in three patients of ACLF achieve renal recovery with CRRT. Response to CRRT is associated with improvement in hemodynamics, systemic inflammation, endothelial and renal function. Each hour delay in CRRT after onset of shock and higher SOFA score are associated with decreased chances of renal recovery and worse outcomes in patients with ACLF.

**THU509**

Different clinical courses of acutely decompensated cirrhosis in hepatitis B virus high-endemic area: data from Chinese Acute-on-Chronic Liver Failure (CATCH-LIFE) study

Tongyu Wang1, Yu Shi2, Hai Li1, 1Shanghai, China; 2Hangzhou, China

**Background and aims:** Cirrhotic patients with acute decompensation (AD) have different clinical course and pathophysiology base on the PREDICT study in a predominately alcohol-related etiologic population: pre-ACLF (acute-on-chronic liver failure), UDC (unstable decompensated cirrhosis) and SDC (stable decompensated cirrhosis) patients with different pathophysiology and prognosis. However, in hepatitis B virus (HBV) high-endemic area, the characteristics of these three subtypes are not well characterized. The aims of this study were to explore the characteristics and outcomes of different clinical courses within 1 year.

**Method:** We identified 2597 cirrhotic patients with AD from a prospective multi-center cohort with 66.85% HBV-related etiology and explored the disease dynamics and prognosis within 1 year. Clinical and biological parameters during hospitalization, 3-month re-admission and outcomes during follow-up were collected. Pre-ACLF was defined as patients developed ACLF within hospitalization. Subgroup analysis was conducted based on etiology, prognostic scores were recorded to predict outcomes in ACLF, UDC and SDC patients, respectively.

**Results:** Totally, 2188 AD without ACLF at baseline were identified. There are 184 (8.41%) pre-ACLF patients with 3-month and 1-year in-free mortality rates of 60.49% and 70.93%, respectively. 663 UDC (27.38%) patients had at least one readmission within 3 month and had no ACLF development during hospitalization, with 22.05% and
35.27% mortality rates. 1232 (49.36%) SDC patients had neither readmission within 3 months nor ACLF development, with 3.42% 1-year mortality. Systemic inflammation parameters including WBC, CRP and PCT increased markedly in pre-ACLF group, while had no significant differences between UDC and SDC group. Portal hypertension related complications including variceal haemorrhage and portal vein thrombosis proportion were significantly higher in UDC group than those in SDC group.
Conclusion: The recently proposed different courses of hospitalized decompensated cirrhosis with AD are validated in a multi-center study targets in critically ill LC.

THU511
Extracorporeal membrane oxygenation, a valuable life-saving treatment in liver transplanted patients

Benjamin Buchard1,2, Sophie-Caroline Sacleux2,3, Samir Jaber4, François Stéphan1,2,3, Alain Combes6, Elise Lemaître2,3,7, Audrey Coilly2,3,7, Faouzi Saliba2,3,7, Didier Samuel2,3,7, Armand Abergel1, Philippe Ichai2,3

Background and aims: Extracorporeal membrane oxygenation (ECMO) is a valuable salvage therapy providing circulatory and/or ventilatory assistance. Clinical illness does not augment energy demands in vLC patients. This characterisation may help to redefine nutritional targets in critically ill LC.

Table 1: Age and BMI adjusted comparison of clinical and metabolic characteristics

<table>
<thead>
<tr>
<th>Parameter</th>
<th>1 (HC) (n=20)</th>
<th>2 (sLC) (n=46)</th>
<th>3 (vLC) (n=49)</th>
<th>4 (vACLF) (n=34)</th>
<th>Overall p</th>
<th>Intergroup p</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age</td>
<td>24 ± 5.3</td>
<td>24 ± 4.8</td>
<td>26 ± 4.6</td>
<td>26 ± 5.6</td>
<td>0.01</td>
<td></td>
</tr>
<tr>
<td>BMI</td>
<td>24.4 ± 3.3</td>
<td>24.5 ± 4.4</td>
<td>26 ± 4.6</td>
<td>26 ± 5.6</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Etiology (%</td>
<td>29 (60)</td>
<td>33 (70.3)</td>
<td>28 (62.4)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>NASH</td>
<td>7 (15.2)</td>
<td>6 (13.2)</td>
<td>3 (6.8)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>others</td>
<td>16 (21.7)</td>
<td>10 (20.4)</td>
<td>3 (6.8)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CTP</td>
<td>8.4 ± 1.2</td>
<td>12.8 ± 1.4</td>
<td>13.4 ± 1.9</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MELD</td>
<td>15.3 ± 5.8</td>
<td>29 ± 8.8</td>
<td>34.1 ± 5.8</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>REE</td>
<td>1309 ± 82</td>
<td>1581 ± 47</td>
<td>1528 ± 46</td>
<td>1760 ± 54</td>
<td>0.001</td>
<td>4 vs all</td>
</tr>
<tr>
<td>VO2</td>
<td>198 ± 13</td>
<td>229 ± 7.5</td>
<td>226 ± 7.3</td>
<td>263 ± 8.5</td>
<td>0.001</td>
<td>1 vs 3 vs all</td>
</tr>
<tr>
<td>VCO2</td>
<td>180 ± 16</td>
<td>185 ± 5.6</td>
<td>164 ± 5.4</td>
<td>181 ± 6.4</td>
<td>0.039</td>
<td>2 vs 3-0.01</td>
</tr>
<tr>
<td>RQ</td>
<td>153 ± 7.9</td>
<td>277 ± 6.1</td>
<td></td>
<td>189 ± 6.4</td>
<td>0.001</td>
<td>1 vs 4 vs all</td>
</tr>
<tr>
<td>UN</td>
<td>77 ± 5.1</td>
<td></td>
<td></td>
<td>75 ± 1.1</td>
<td>0.04</td>
<td>vs all</td>
</tr>
<tr>
<td>FO</td>
<td>27 ± 8.1</td>
<td>62 ± 4.3</td>
<td></td>
<td>69 ± 6.8</td>
<td>0.001</td>
<td>vs all</td>
</tr>
<tr>
<td>PO</td>
<td>33 ± 3.4</td>
<td>115 ± 1.9</td>
<td>132 ± 2.2</td>
<td>112 ± 2.8</td>
<td>0.023</td>
<td>vs all</td>
</tr>
<tr>
<td>PO</td>
<td>33 ± 4.3</td>
<td>115 ± 1.9</td>
<td>132 ± 2.2</td>
<td>112 ± 2.8</td>
<td>0.023</td>
<td>vs all</td>
</tr>
<tr>
<td>PO</td>
<td>77 ± 5.1</td>
<td></td>
<td></td>
<td>75 ± 1.1</td>
<td>0.04</td>
<td>vs all</td>
</tr>
</tbody>
</table>

Data expressed in mean ± SD

Conclusion: Accelerated starvation is the hallmark in LC, that worsens with critically illness. vACLF have highest energy expenditure. Critical illness does not augment energy demands in vLC patients. This characterisation may help to redefine nutritional targets in critically ill LC.

Journal of Hepatology 2022 vol. 77(S1) | S119–S388
Invasive fungal infections (IFI) in ACLF. We correlated the timing of occurrence, predictors of development, diagnostic potential of biomarkers, antifungal prophylaxis with the outcome of IFI.

**Method:** The demographic, clinical and laboratory characteristics of ACLF patients, admitted to ILBS, developing IFI were studied retrospectively based on the APASL ACLF Research Consortium (AARC) data base. The diagnosis of IFI was based on revised definitions of invasive fungal disease from the European organization for research and treatment of cancer/Invasive fungal infections cooperative group and the national institute of allergy and infectious diseases mycoses study group (EORTC/MSG) consensus group. We also measured the biomarkers in bronchoalveolar lavage (BAL) and serum Galactomannan index (GMI).

**Results:** Amongst 1670 ACLF patients, 320 (19.16%) had recent history of neutropenia, prolonged use of corticosteroids or immunosuppressive therapy, and sufficient clinical evidence consistent with IFI but no mycological evidence were classified as possible IFI. Sixty (3.6%) patients who had host factors, clinical features, and mycological evidence consisting of direct test (cytology, direct microscopy, or culture) and indirect test, positive Galactomannan assay, were classified as probable IFI. Amongst the probable IFI group, the most common site of infection was urinary tract (n = 42/60, 70%) followed by respiratory (n = 12/60, 20%) and blood (n = 6/60, 10%). On univariate analysis, prior antibiotic use, high total leucocyte count (TLC), acute renal failure, hemodialysis, diabetes mellitus, multiorgan failures, were predictors for development of IFI (p < 0.05). On multivariate analysis, TLC >14.3 × 10^3/ml^3, multiorgan failure, hemodialysis and prior antibiotics use predicted the development of IFI (p < 0.05). IFI occurrence was associated with significantly high 30 and 90 day mortality (p < 0.001). 68.4% patients with IFI in the first 7 days of enrolment died as compared to 47.9% in control group (p = 0.002). BAL GMI (cut-off >1) was positive in 38/60 (63.33%) and serum GMI was positive in 11/60 (18.33%). BAL GMI above 3.25 was a better predictor of IFI (sensitivity 72.7%, specificity 51.5%).

**Conclusion:** Invasive fungal infections cause high mortality in ACLF patients. High TLC at admission, multiorgan failure, hemodialysis, prior antibiotics usage and high BAL GMI predict the development of IFI. High vigilance, early diagnosis and initiation of anti-fungal therapy is essential to prevent mortality due to IFI in ACLF.

---

**THU512**

Outcomes in patients with cirrhosis and fungal infections: a systematic review and meta-analysis with machine learning

Nipun Verma¹, Shreya Singh², Akash Roy³, Arun Valsan⁴, Pratibha Garh¹, Pranita Pradhan⁴, Meenu Singh⁵.¹Postgraduate Institute of Medical Education and Research, HEPATOLOGY, Chandigarh, India; ²Postgraduate Institute of Medical Education and Reseurch, Hepatology, Chandigarh, India; ³Postgraduate Institute of Medical Education and Reseurch, Hepatology, Chandigarh, India; ⁴Sanjay Gandhi Postgraduate Institute of Medical Sciences, HEPATOLOGY, Lucknow, India; ⁵Postgraduate Institute of Medical Education and Reseurch, Hepatology, Chandigarh, India.

Email: nipun29j@gmail.com

**Background and aims:** Fungal infections (FIs) are an emerging threat in patients with cirrhosis. Due to the lack of systematic data, we performed a comprehensive literature search to systematically evaluate the impact of FIs on mortality and contributory factors in cirrhosis patients.

**Method:** Pubmed, Embase, Ovid, and Web of Science were searched since their inception till Oct 30, 2020, for full-text articles describing mortality in cirrhosis patients with FIs. Point and relative-risk estimates of mortality were pooled on random-effects meta-analysis, and their variation (I^2) was explored on subgroups, meta-regression, and machine learning (ML). Quality of studies was evaluated with the New-castle Ottawa scale and estimate’s asymmetry with a funnel plot and Eggers regression. (CRD42019142782)
Results: Of 4345, 34 studies (2134 patients) were included (good/fair/poor quality: 12/21/59%, p = 0.03 (Figure 1). Significant variation in mortality estimates was identified on geographic dimensions and site of infection. The highest mortality was noted in pulmonary-FIs (79.4%), followed by peritoneal-FIs (68.3%) and fungemia (55%). On meta-regression, MELD of cases was identified as a predictor of mortality; adjusted estimate: 64.5% (54.5–83.9). The mortality among patients with FIs was 1.7 (1.4–2.1) and 2.9 (1.8–4.9) times higher than bacterial infections and non-infected controls. The relative risk persisted above 1.5 times in ICU-admitted and ACLF patients as well. After adjusting for the proportion of bacterial infection in controls, the relative risk was 2.16 (1.85–2.53). Asymmetry was evident in point-estimate and relative-risk estimates of FIs. Three k-means clusters, 2 DBSCAN clusters, 8 GMM clusters, and 5 outlier studies were detected on ML. On excluding these, the estimate’s heterogeneity was abolished (I²:0%, p = 0.68). Estimates did not vary as per the quality of the study.

Conclusion: About 2/3rd cirrhosis patients with FIs die with the highest risk of death among ACLF and ICU patients. FIs are more serious than bacterial infections and warrant dedicated efforts in the cirrhosis patients.

Impact of the presence of acute-on-chronic liver failure on morbimortality after liver transplantation

Carlos Benitez1, Verónica Cambindo Santana1, Jorge Arnold1,2
1Pontificia Universidad Católica, Hepatología, Santiago, Chile; 2Pontificia Universidad Católica de Chile, Gastroenterología
Email: vcambindo@gmail.com

Background and aims: Acute over chronic liver failure (ACLF) implies high short-term mortality. The impact of its presence at the time of liver transplantation (LT) has been less studied.

Objectives: To evaluate the impact of ACLF on post-LT survival.

Method: A retrospective registry of 263 liver recipients between 2013 and 2020 was evaluated: 197 patients met the inclusion criteria and their survival and complications were recorded at one year of follow-up.

Results: The average age was 57.1 ± 10.5, men 55.3%, MELD Na 23.15 ± 9.76. The main etiologies were MAFLD (35.5%), alcohol (12.7%), autoimmune hepatitis (9.6%), PBC (9.1%) and HCV (7.6%). 22.5% of the patients developed ACLF. One year survival of those transplanted without ACLF, ACLF grade 1, grade 2, and grade 3 were 89.8%, 91.7%, 66.7%, and 66.7%, respectively (p = 0.042). Survival of those without ACLF and grade 1 vs grade 2 and 3 were 90% vs 66.7% (p = 0.005) (figure). Transplant patients with grade 2–3 ACLF had more post-LT bacterial infections 59.3% vs 36.5% (p = 0.024), a higher frequency of mechanical ventilation 46.2% vs 19.4% (p = 0.003) and renal replacement therapy (RRT) (42.3% vs 11.6% (p = <0.001). In the multivariate analysis, the variables independently related to survival were the requirement for mechanical ventilation before LT (OR 4.3, p = 0.026, CI (1.19–15.62) and RRT post LT (OR 2.95, p = 0.39, CI (1.05–8.2).

Conclusion: The presence of ACLF grade 2 and 3 at the time of LT is associated with marked reduction of one year patient survival. 1530/1600 (with space)
THU516
Untargeted lipidomics differentiate ACLF precipitated by severe alcoholic hepatitis

Florent Artru1,2, Stephen Atkinson1, Ewan Forrest3, Francesca Trovato4, Nikhil Vergis1, Vishal C Patel5,6,7, Salma Mujib2, Anna Cavazza2, Alexandros Pechlivanis1, Ellen Jerome2, Marc Zentar1, Evangelos Triantafyllou1, Elaine Holmes1, Mark J W McPhail1,2, Mark Thursz1, 1Imperial College London, London, United Kingdom; 2Institute of Liver Studies, King’s College Hospital, London, United Kingdom; 3University of Glasgow, Glasgow, United Kingdom; 4The Roger Williams Institute of Hepatology London, Foundation For Liver Research, London, United Kingdom; 5Institute of Liver Sciences, King’s College London, Department of Inflammation Biology, School of Immunology and Microbial Sciences, FoLSM, London, United Kingdom
Email: florent.artru@kcl.ac.uk

Background and aims: Severe alcoholic hepatitis (SAH) is a common cause of acute on chronic liver failure (ACLF). Patients with SAH-ACLF present intense systemic inflammation and immune dysfunction. While lipids are involved in inflammatory and immune responses, lipidomics is understudied in the setting of SAH-ACLF. We evaluated whether specific changes in the blood lipidome are observed in ACLF precipitated by SAH.

Method: Untargeted serum lipidomics was performed using reversed phase ultra-performance liquid chromatography coupled to mass spectrometry in patients with SAH participating in the STOPAH trial (n = 154–46 with ACLF labelled SAH-ACLF) and with cirrhosis (n = 74–21 with ACLF labelled Cirrh-ACLF). Serum lipidome changes between patients with and without ACLF in SAH and cirrhosis groups were evaluated by principal component analysis (PCA) and orthogonal partial least squares discriminant analysis (OPLS-DA).

Results: MELD score was higher in patients with SAH without ACLF vs. cirrhotics without ACLF (20.7 vs. 11.3, p < 0.0001) but matched between patients with SAH-ACLF vs. Cirrh-ACLF (26.1 vs. 24.7, p = 0.4). PCA and OPLS-DA analyses were not able to accurately discriminate between SAH with or without ACLF (OPLS-DA in positive mode R²Y = 0.14 Q² = 0.06 CV-ANOVA p = 0.01 AUROC = 0.71 and negative mode R²Y = 0.18 Q² = 0.04 p = 0.22 AUROC = 0.62). Importantly, PCA and OPLS-DA did accurately discriminate between SAH-ACLF and Cirrh-ACLF (OPLS-DA in positive mode: R²Y = 0.78 Q² = 0.49 CV-ANOVA <0.0001 AUROC = 0.91; in negative mode: R²Y = 0.66 Q² = 0.4 p < 0.0001 AUROC = 0.88) (Figure 1). The 10 metabolites showing the greatest variable importance projection were included in multivariate analyses adjusting for age, sex and MELD score. Two lipids in positive mode (PE P-38:4, PE-P36:3) and negative mode (PC41:5, LPC14:0) disclosed independent associations with SAH-ACLF (Figure 1). Using these lipids, we derived 2 scores relating to positive and negative ionisation modes; both accurately discriminated SAH-ACLF from Cirrh-ACLF with an AUROC of 0.86 (CI95% 0.73–0.93, p < 0.0001, sensitivity 76% specificity 88%) and 0.82 (CI95% 0.68–0.90, p < 0.0001, sensitivity 71% specificity 84%).

Figure: A. OPLS-DA in positive mode. B. ROC curve of OPLS-DA model in positive mode. C. Univariate analyses of the lipids included in the 2-lipids models in positive (PE-P38:4, PE-P36:3) and negative modes (PC41:5, LPC14:0).
**Conclusion:** This lipidomic analysis of the STOPAH cohort demonstrates a specific lipidomic signature—mainly composed of species that are known to be involved in immune-modulatory functions and liver repair—in patients with SAH-ACLF. These pathways require further exploration on their diagnostic and mechanistic role in the development of SAH-ACLF compared to other cause of ACLF.

**THU517**

**Metabolomic analysis of organ failure marker compounds in blood samples of patients with decompensated liver cirrhosis after administration of the novel drug VS-01**

Frank Uschner1, Wenyi Gu1, Olaf Tyc1, Martin Schütz1, Philip Fersstl1, Katharina Katharina Staufer2, Stoffers Philipp1, Hans–Peter Erasmus1, Johannes Massel1, Kai–Henrik Peiffer1, Fabian Finkelmeier1, Anita Pathil–Warth1, Jörg Bojunga1, Stefan Zeuzem1, Meriam Kabbaj2, Jonel Trebicka1,2,1Department of Internal Medicine I, University Hospital Frankfurt, Frankfurt, Germany; 2Versantis AG, Zurich, Switzerland; 3European Foundation for the Study of Chronic Liver Failure, Barcelona, Spain

Email: jonel.trebicka@kgu.de

**Background and aims:** Acute-on-chronic liver failure (ACLF) is defined by the presence of organ dysfunctions and failures in decompensated cirrhosis and is associated with high short-term mortality. VS-01 is a novel intraperitoneal (i.p.) pH-gradient liposomal infusion drug that enhances the clearance of ammonia and other potentially harmful metabolites. This study analyzed metabolite clusters already described to be involved in organ failure (OF) of liver, brain and kidney failures in patients with liver cirrhosis (Moreau et al. 2019) in the phase 1b clinical trial of VS-01 (Eudra no.: 2018-004606-25).

**Method:** VS-01 was infused in the peritoneal cavity of the patients and removed by paracentesis after two (part A) or three hours (part B). Patients received a single dose of 15, 30 or 45 ml/kg VS-01 (Part A; n = 9) or four consecutive doses of 34–42 ml/kg VS-01 (Part B; n = 3). Metabolomic analysis was performed on plasma samples of patients with ascites and covert hepatic encephalopathy (HE) using an untargeted LC/MS analysis approach. Peak areas were extracted and peak lists containing the mass features and identified compounds were exported to MetaboAnalyst 5.0 for statistical analysis.

**Results:** In the whole dataset, 24 out of 65 highly upregulated OF metabolites were detected. In part A of the study, we were able to detect 19 OF metabolites in plasma samples, of which 11 showed a decreasing trend in the plasma samples of the patients up to 24 hours after infusion of VS-01. In part B of the study, we could detect 10 OF metabolites in plasma samples of which 7 metabolites showed a decreasing trend during the infusion of VS-01 (Figure 1).

**Conclusion:** VS-01 is a novel drug, which is able to reduce metabolites that are associated with organ failures e.g. brain, liver and kidney failure. The current metabolic results support the future development of VS-01 in patients with ACLF and organ failure.

---

**Figure:** (abstract: THU517): Heatmap of log2 (fold-change) reduced organ failure markers in plasma samples of study A shown per dosage (a) and study B shown per marker compound (b) and per patient (c) after administration of VS-01 (red = high/Blue = low). *, FDR < 0.05.
THU518
Metabolomic analysis of bacterial infection markers in blood samples of patients with decompensated liver cirrhosis infused with the novel drug VS-01
Frank Uschner1, Olaf Tyc1, Wenxi Gu1, Martin Schulz1, Philip Ferstl1, Katharina Stauffer2, Philipp Stoffers1, Hans-Peter Erasmus1, Johannes Massel1,1 Kai-Henrik Peiffer1, Fabian Finkelmeier1, Anita Pathil-Warth1, Jörg Bojunga1, Stefan Zeuzem1, Meriam Kabbaj1,2, Jonel Trebicka1,3. 1Department of Internal Medicine I, University Hospital Frankfurt, Frankfurt, Germany; 2Versantis AG, Zurich, Switzerland; 3European Foundation for the Study of Chronic Liver Failure, Barcelona, Barcelona, Spain Email: jonel.trebicka@kgu.de

Background and aims: Bacterial infections are known as one frequent precipitant event for the development of acute decompensation (AD) and its maximal-form acute-on-chronic liver failure (ACLF) (PREDICT study). VS-01 is a novel intraperitoneal (i.p.) pH-gradient liposomal infusion drug that enhances the clearance of ammonia and other metabolites associated to bacterial infection in patients with ACLF. This study analyzed metabolites described to be associated with bacterial infection in patients with liver cirrhosis (Moreau et al. 2019) in the phase 1b clinical trial of VS-01 (Eudra no.: 2018-004606-25).

Method: The novel drug VS-01 was infused in the peritoneal cavity and removed by paracentesis after two (part A) or three hours (part B). Patients received either a single dose (15, 30 or 45 ml/kg) VS-01 (Part A; n = 9) or four consecutive doses of 34–42 ml/kg VS-01 (Part B; n = 3). Metabolomic analysis was performed on blood samples of cirrhotic patients with ascites and covert hepatic encephalopathy (HE) using untargeted LC/MS analysis. Peak areas were extracted and peak lists containing the mass features and identified compounds were exported to MetaboAnalyst 5.0 for statistical analysis.

Results: Overall, 10 out of 31 metabolites included in the metabolite cluster of infection-related ACLF were identified in plasma samples of the patients. The infusion of VS-01 resulted in a decrease of several markers for bacterial infection in the blood of the patients (Figure 1). In part A of the study, 6 metabolites related to bacterial infection showed a decreasing trend in plasma up to 24 hours after infusion of VS-01. In part B of the study, 7 metabolites related to the infection-related ACLF cluster were detected in plasma samples, from which 4 showed a decreasing trend over time after infusion of VS-01 (Figure 1).

Conclusion: Single and repeated i.p. administrations of the novel drug VS-01 was able to reduce the concentration of several metabolites that are associated with the sepsis-related ACLF metabolite cluster. These results support the future investigation of VS-01 in patients with ACLF and bacterial infection.

THU519
Disturbances in sodium and chloride hemostasis predict outcome in stable and critically-ill patients with cirrhosis—not two sides of the same coin
Georg Semmler1,2, Bernhard Scheiner1,2, Rafael Paternostro1,2, Benedikt Simbrunner1,2, Lorenz Balcar1,2, Matthias Pinter1,2, Michael Trauner1, Matthias Mandorfer1,2, Christian Zauner1, Thomas Reiberger1,2, Georg-Christian Funk3,4. 1Medical University of Vienna, Division of Gastroenterology and Hepatology, Department of Internal Medicine III, Wien, Austria; 2Medical University of Vienna, Vienna Hepatic Hemodynamic Lab, Division of Gastroenterology and Hepatology, Department of Internal Medicine III, Wien, Austria; 3Klinik Ottakring, Department of Internal and Respiratory Medicine, Vienna, Austria; 4Karl-Landsteiner-Institute for Lung Research and Pulmonary Oncology, Vienna, Austria Email: georg.semmler@meduniwien.ac.at

Background and aims: Serum electrolyte disturbances are common in patients with cirrhosis. Hyponatremia has profound prognostic implications, and thus, has been incorporated in the 2016 update of...
the UNOS MELD. Changes in serum chloride (Cl) are thought to be interrelated, however, are less well studied in the context of cirrhosis. We investigated the prognostic utility of Na- and Cl-changes on hepatic decompensation/liver-related death in patients with stable advanced chronic liver disease (ACLD) as well as on ICU-mortality in critically-ill patients with cirrhosis.

**Method:** 1256 patients with stable ACLD (defined by hepatic venous pressure gradient (HVPG) ≥6 mmHg) undergoing HVPG measurement at the Vienna Hepatic Hemodynamic Lab between 2003–2020 were included in cohort I. 181 critically-ill patients with cirrhosis admitted to our ICU between 1993–2003 were recruited for cohort II. Hypo-/hyper-Na (normal: 136–145 mmol/L) and hypo-/hyper-Cl (normal: 98–107 mmol/L) were assessed.

**Results:** **Cohort I:** 68% male patients with a mean UNOS MELD (i.e., excluding Na) of 12 ± 4 were included (CPA/B/C: 53%/35%/12%). Na and Cl levels were significantly interrelated (Spearman’s ρ = 0.54, p < 0.001). Hypo-/hyper-Na was present in 25%/0% and hypo-/hyper-Cl in 15%/8%. Patients with hypo-Na (HR: 2.44 [95%CI:2.05–2.90], p < 0.001) and hypo-Cl (HR: 2.19 [95%CI: 1.74–2.77], p < 0.001) had an increased risk for hepatic decompensation/liver-related death. When incorporating both variables in a model adjusting for age, HVPG, albumin levels, and MELD score, hypo-Cl (aHR: 1.77 [95%CI:1.37–2.29], p < 0.001) but not hypo-Na (aHR:1.10 [95%CI:0.88–1.38], p = 0.40) remained independently associated with the outcome of interest. As depicted in the Figure, the presence of hypo-Na, hypo-Cl, none, or both identified patient groups with a distinct prognosis.

**Cohort II:** 70% male patients had a mean UNOS MELD of 27 ± 9 at ICU admission (92% with Child-Pugh-stage [CPS] C). Again, Na and Cl levels were strongly correlated (Spearman’s ρ = 0.81, p < 0.001). Hypo-/hyper-Na was present in 47%/7% and hypo-/hyper-Cl in 30%/25%. ICU-mortality was 50% after a median of 6 (IQR:5–7) days. While the effect of Na on ICU mortality was U-shaped in restricted cubic spline analyses, it seemed to be rather linear for chloride with a worse prognosis in patients with hypo-Cl as well as hypo- and hyper-Na. In univariable logistic regression analyses, patients with hypo-Cl (OR: 2.65 [95%CI:1.30–5.53], p = 0.008), but not hypo-Na had a significantly worse ICU survival, which was confirmed after adjusting for hypo-Na and MELD (aOR Cl: 3.24 [95%CI: 1.31–8.23], p = 0.012).

**Conclusion:** Even though Na and Cl levels are strongly interrelated in patients with stable ACLD/cirrhosis and critical illness, hypo-Cl rather than hypo-Na is associated with a worse outcome.

**THU520**

**Sarcopenia assessed via computed tomography is associated with short-term outcomes and improves prognostic scores’ performance in critically ill patients with acute on chronic liver failure**

Thomas Mangana Del Rio1, Fabio Becce1, Julien Vionnet1, Alban Denys1, Antoine Schneider1, Alexandre Wetzel1, Darius Moradpour1, Jean-Daniel Chiche1, Florent Artru1,2,1Lausanne University Hospital, Lausanne, Switzerland;2King’s College Hospital, Institute of Liver Studies, London, United Kingdom

Email: florent.artru@kcl.ac.uk

**Background and aims:** Prognostication of patients with cirrhosis and acute-on-chronic liver failure (ACLF) relies on organ failure scores. Sarcopenia is associated with poor outcomes in patients with cirrhosis but has not been investigated in critically ill patients with ACLF. We aimed to evaluate whether sarcopenia was associated with short-term outcome in this population.

**Method:** We retrospectively included all patients with cirrhosis and ACLF (as defined by EASL criteria) admitted to the intensive care unit (ICU) of Lausanne University Hospital between January 2010 and December 2019, who had a recent CT (within 15 days from admission to the ICU). L3 skeletal muscle index (L3SMI) was quantified by using a deep learning-based method from a single axial CT image at the level of lumbar vertebra 3. Sarcopenia was defined by previously published sex-specific cut-offs: 50 cm²/m² in men and 39 cm²/m² in women.

**Results:** A total of 194 patients fulfilled the inclusion criteria. Their characteristics at admission were the following: 26% were female, median age was 62 years (IQR, 54–70 years), MELD 21 (13–28), CLIF-C ACLF 79 (74–85), CLIF-C ACLF-lactate 83 (76–92). Sixty percent of patients had ACLF grade 3, 34% grade 2 and 6% grade 1. Median 28-day transplant-free survival (TFS) was 58% (95% CI, 51–65%). Median L3SMI was 43 (37–51), with 59% of patients being sarcopenic. In multivariate Cox-regression analyses at day 0 (D0), the three independent variables associated with 28-day TFS were CLIF-C ACLF-lactate (HR 1.06, 1.04–1.09, p < 0.0001), MELD score (HR 1.03, 1.01–1.07, p = 0.03) and sarcopenia (HR 2.1, 1.3–3.5, p = 0.003). At day 3 (D3), the two independent variables associated with 28-day TFS were CLIF-C ACLF-lactate (HR 1.08, 1.07–1.11, p < 0.0001) and sarcopenia (HR 1.9, 1.2–3.1, p = 0.01). Based on the results of multivariate analyses, we derived two scores (CLIF-C ACLF-lactate-sarcopenia at D0 and D3, CCLS-D0 and CCLS-D3) with the aim of improving prognostic stratification. For the prediction of 28-day TFS, CCLS-D0 had an AUROC of 0.80 and outperformed CLIF-C ACLF-lactate on day 0 (0.74, p = 0.004). Similarly, CCLS-D3 had an AUROC of 0.89 and outperformed CLIF-C ACLF-lactate on day 3 (0.86, p = 0.04) (Figure 1).
Conclusion: Sarcopenia, as assessed by CT-Scan is independently associated with 28-day TFS in critically ill patients with cirrhosis and ACLF. Adding sarcopenia to CLIF-C-ACLF-lactate score at D0 and D3 improved the performance of the scores. Sarcopenia is an important parameter related to outcomes and should be evaluated in this population.

THU521
Use of Tocilizumab in patients with stable chronic liver disease and severe COVID-19 for prevention of decompensated cirrhosis, a prospective, open-label, randomized controlled trial.
Luis Alejandro Rosales Renteria1,2, Hiram Jaramillo-Ramírez2, Francisco Calderón-Mendieta3, Jesús Camacho-Escobedo1, José Manuel Avendaño-Reyes2, Diana Laura López-Rubio1, Adrián Sáncheza1, Gisel Estefania Reyes-Higuera1, Dulce Renée Soto-González1, Erik Jesús Arzola-Renteria1, 1Mexicali General Hospital, Internal Medicine, Mexicali, Mexico; 2Faculty of Medicine UABC, Mexicali, Mexico; 3Mexicali General Hospital, Mexicali, Mexico; 4Mexicali General Hospital, Mexicali, Mexico
Email: luis.alejandro.rosales.renteria@uabc.edu.mx

Background and aims: Interleukin-6 (IL-6) is involved both in the pathogenesis of severe COVID-19 (SC) and decompensated Chronic Liver Disease (CLD). Tocilizumab, a monoclonal antibody used to block the IL-6 signal transduction pathway, has been proved to have beneficial effects in the prognosis of patients with SC. However, evidence of its effect on patients with CLD that develop SC is scarce. We aimed to evaluate the efficacy of Tocilizumab on patients with CLD and SC in a tertiary care hospital from Mexico.

Method: A single center, prospective, open-label, randomized controlled trial, which included patients with CLD with either compensated cirrhosis or stable decompensated cirrhosis (according to EASL definition) that developed SC, and were admitted to our hospital in Mexicali, Mexico, from March 1, 2020, to December 31, 2021. General characteristics were obtained. The Primary Outcome was overall mortality according to the absence or presence of Tocilizumab administration (administered in the first 12 hours of arrival according to hospital availability at an 8mg/kg single IV dose), secondary outcomes were mortality according to each stage of CTP, and development of acute decompensation (AD), defined as one or more of the following : Acute Kidney Injury (AKI), Hepatorenal syndrome-AKI (HRS-AKI), Variceal Hemorrhage (VH), West Haven (WH) grade III or IV Hepatic Encephalopathy (HE), Spontaneous Bacterial Peritonitis (SBP) or Acute on Chronic Liver Failure (ACLF). A value of p < 0.05 was significant. Exclusion criteria were age younger than 18 years and patients with unstable decompensated cirrhosis at baseline.

Results: A total of 361 patients were included. They were classified according to the Child-Turcotte-Pugh (CTP) classification, and the Model for end-stage Liver Disease-Sodium (MELD-Na). Most patients were classified as CTP B (216 patients, 59.8%). Median MELD-Na in the intervention group was 22 vs 19 in control. 77 patients were randomized to Tocilizumab, and 284 patients were not. With regards to the primary outcome, 32.4% patients in the intervention group died vs 53.8% patients in the control group, this difference was significant with a relative risk (RR) of 0.6, a 95% confidence interval [0.4–0.8], p = 0.001, and a number needed to treat (NNT) of 4.6 with a NNT 95% CI of [2.9–11.3]. Secondary outcomes were significant for mortality reduction in the CTP subgroup for all grades of severity and showed a lower risk of developing HRS- AKI (RR = 0.4, 95% CI [0.2–0.7], NNT 4.3, 95% NNT CI [2.8–9.1], p < 0.001) and WH III/IV HE (RR = 0.5, 95% CI [0.3–0.8], NNT 5.2, 95% NNT CI [3.1–14.7], p = 0.003).

Conclusion: Tocilizumab reduced mortality in CLD patients with SC, overall, in each stage of CTP classification, and reduced the risk of developing both HRS-AKI and severe HE, but not other events. Whether these results can be reproduced in patients without SC warrants further research.

THU522
Comprehensive immunophenotyping reveals profound alterations of T cell subsets in acute decompensation of liver cirrhosis
Yasmina Chouik1,2, Fabienne Venet3,4, Morgane Gossez3,4, Thibault Andrieur2, Marie-Laure Plissonnier2, Bordes Isabelle2, Teresa Antonini1, Domitille Erard1, Miroslava Subic-Levrero1, Francois Villere1,2, Wafa Khamri1, Fabien Zoulim1,2, Massimo Levrero1,2, Fanny Lebosse1,2, Hospices Civils de Lyon, Hepatology Unit, Lyon, France; 1Cancer Research Center of Lyon INSERM U1052, Lyon, France; 2Hospices Civils of Lyon, Immunology Laboratory, Lyon, France; 3International Center for Infectiology Research, Lyon, France; 4Imperial College London, Liver Immunology Laboratory, London, United Kingdom
Email: fanny.lebosse@inserm.fr

Background and aims: Bacterial infection is a frequent and life threatening event in acute decompensation (AD) of cirrhosis, with a 1-month mortality rate of 20–30%. Septic risk is notably underpinned by cirrhosis-associated immune dysfunction. Recent data suggest the potential involvement of adaptive immune responses in cirrhosis-related immune dysfunction. We conducted a detailed analysis of circulating T cells in patients with AD compared to patients with compensated cirrhosis (C) and healthy subjects (HS) in order to gain insights in circulating adaptive immune cells alterations in cirrhosis.

Method: Thirty seven patients from a monocentric prospective study (EmiC cohort, n = 97 patients) were selected for T cells phenotyping. Clinical and biological samples were collected at hospital admission and up to 6 months after inclusion. PBMC from HS were obtained from the French Blood Bank. Phenotyping of circulating T cells was conducted on frozen PBMC by spectral cytometry (26-color panel). This panel enables the analysis of effector, memory and naïve T cells, regulatory T cells (Treg), T-helper (Th)1, Th2, Th17, Th17+1, Th22 CD4+ T cells, Tc1, Tc2, Tc17, Tc22 CD8+ T cells, gamma delta T cells and NKT cells. Activation, inhibition and death markers were also studied. Unsupervised analysis was performed using Qlucore™ and Cytobank™. Plasma cytokines were measured by Simple Plex™ immunoassays on a microfluidic ProteinSimple® ELLA analyzer.

Results: Spectral cytometry analysis was performed in 7 HS, 10 C and 27 AD patients including 9 patients with Acute on Chronic Liver Failure. Principal component analysis showed clear distinct T cells features between HS, C and AD patients (Figure 1). T cell phenotyping revealed progressive imbalance between type 1 and type 2 T cell responses with a decrease of the Th1/Th2 and Th1/Treg ratios.
throughout cirrhosis progression. T cells of patients with decompensated cirrhosis displayed increased surface expression of both activation and death markers. In addition, circulating Th17 cells significantly decreased in patients with bacterial infection (n = 12) and correlated with C-reactive protein and albumin levels. Increased Th1/Th2 ratio was associated with the occurrence of nosocomial infection (n = 6), while proportion of Th17 could significantly predict 6-month survival in AD patients.

Conclusion: Alterations of circulating T cells subsets are associated with cirrhosis severity and clinical outcomes. These results underlie the role of T cells in cirrhosis-associated immune dysfunction.

THUS23 Low hemoglobin level predicts early hospital readmission in patients with cirrhosis and acute decompensation

Enrico Pompili1, Maurizio Baldassarre1,2,3, Gaetano Zacherini1,2, Manuel Tufoni2, Giulia Iannone1, Dario Pratelli1, Clara De Venuto1, Marco Domenicalli1,2, Paolo Caraceni1,2,3.

1University of Bologna, Department of Medical and Surgical Sciences, Bologna, Italy; 2University of Bologna, Center for Applied Biomedical Research, Bologna, Italy; 3IRCSS Azienda Ospedaliero-Universitaria di Bologna, Division of Medical Semiotics, Bologna, Italy; 4Maria delle Croci Hospital, AUSL della Romagna, Department of Internal Medicine, Ravenna, Italy

Email: paolo.caraceni@unibo.it

Background and aims: Patients with decompensated cirrhosis are at high risk of emergent hospitalizations leading to a very economic and social burden. This study aimed to determine the incidence of readmission up to 1 year after discharge from an index hospitalization and to identify predictors of liver-related early readmission (within 30 days).

Method: We performed a secondary analysis in a prospectively collected cohort of patients admitted to hospital for acute decompensation (AD) complicated or not by acute-on-chronic-liver-failure (ACLF). After discharge, patients were prospectively followed until death, liver transplantation or up to a maximum of 1 year for recording any emergent hospitalization and related cause. Laboratory and clinical data at admission and discharge of the index hospitalization and the occurrence of nosocomial bacterial infection and ACLF were also collected.

Results: Of the 329 patients included in the analysis, 182 patients were hospitalized during the 1-year follow-up (26% once, 15% twice, 10% three times and 6% four or more times, leading to a total of 369 readmissions). The most frequent causes of readmission were hepatic encephalopathy (36%), ascites (22%) and bacterial infection (21%). Cumulative incidence of all-cause readmission was 19% at 30 days, 36% at 90 days and 56% at 1 year. Fifty-four patients were readmitted for emergent liver-related causes within 30 days after discharge. Early readmission was associated to a higher 1-year mortality (47 vs 32%, p = 0.037). Data collected both at admission (MELD-Na score, diabetes), during hospitalization (development of ACLF, days spent in hospital) and at discharge (hemoglobin (Hb) value, MELD-Na score) were significantly associated with early readmission. Multivariable competing risk regression analysis showed that Hb lower than 8.75 g/dL (shR 2.38 [95%CI 1.22–4.64], p = 0.011), MELD-Na > 16 at discharge (shR 2.25 [95%CI 1.27–3.99], p = 0.005), and diabetes (shR 1.74 [95%CI 1.02–2.99], p = 0.044) were independent predictors of early readmission. Cumulative incidence of early readmission was 8% (95% CI 4–14) in patients without risk factors, 16% (95% CI 11–22) in those presenting one risk factor and 35% (95% CI 23–47) in those presenting 2 or more risk factors (p < 0.001). For instance, in patients with MELD-Na > 16 at discharge, the presence of Hb <8.75 g/dL doubles the risk of early re-hospitalization (42% vs 21%, p = 0.031).

Conclusion: Besides the already documented MELD-Na and diabetes, this study identifies a level of Hb <8.75 g/dL at discharge as a new independent risk factor for liver-related early readmission, thus contributing to identify the subgroup of high-risk patients to be included in programs of transitional care after discharge.

THUS24 Thrombospondin 1: an emerging key-role in the acute-on-chronic liver failure pathogenesis

Hozeifa Mohamed Hassan1, Xi Liang1, Jiaojiao Xin1,2, Dongyan Shi1,2, Keke Ren1, Qi Chen1, Jiang Li1, Peng Li3, Hui Yang1, Jinjin Luo1, Jing Jiang1,2, Jun Li1,2, Taizhou Central Hospital (Taizhou University Hospital), Precision Medicine Center, Taizhou, China; 2The First Affiliated Hospital, Zhejiang University School of Medicine, State Key Laboratory for Diagnosis and Treatment of Infectious Diseases, National Clinical Research Center for Infectious Diseases, Collaborative Innovation Center for Diagnosis and Treatment of Infectious Diseases, Hangzhou, China

Email: lijun2009@zjyu.edu.cn

Background and aims: Acute-on-chronic liver failure (ACLF) is a clinical syndrome that develops in patients with chronic liver diseases following a precipitating event and associated with a high mortality rate due to systemic multiorgan failure. In China, the most common precipitating disorder is hepatic insult due to hepatitis B virus (HBV) reactivation. Although HBV-ACLF disease progress rapidly with limited treatment options, the pathogenesis still unclear and there is a lack of effective biomarkers for early diagnosis and prognosis of HBV-ACLF. Thrombospondin 1 (THBS1) was recognized among the top significantly differentially expressed potential key molecular biomarkers associated with HBV-ACLF disease progression, but the THBS1 key-role participation in ACLF is not clear. This study aimed to evaluate the biomarker probabilities of THBS1 in ACLF pathogenesis.

Method: The biobanked peripheral blood mononuclear cells (PBMCs) from 330 subjects with HBV-related etiologies, including HBV-ACLF, liver cirrhosis (LC), chronic hepatitis B (CHB) and normal controls (NC) from the Chinese Group on the Study of Severe Hepatitis B (COSSH) prospective multicenter cohort were subjected to transcriptome analyses (ACLF = 20; LC = 10; CHB = 10; NC = 15), and the findings were validated in humans and ACLF preclinical rat model. Substantially, a THBS1 knockout mice model was developed to validate the liver protection capabilities following drugs intoxication. Results: THBS1 was identified as the top significantly differentially expressed genes (DEGs) in PBMCs transcriptome, with most significant upregulation in ACLF, and qPCR (ACLF = 110; LC = 60; CHB = 60; NC = 45) verified the consistency of THBS1 expression with the ACLF disease severity. Moreover, the precision of THBS1 prediction abilities for ACLF short-term mortality were 0.8438 and 0.7776 at 28 and 90 days, respectively (p < 0.05). THBS1 expression patterns were significantly positively correlated with inflammatory-
related cytokine gene (CCL2, IL-6, IL-10, CXCL2, etc.), and apoptosis-related genes (Bcl2 and Caspase-9). External validation in ACLF rat serum and liver tissues fortified the functional association between THBS1, immune response and cellular apoptosis. THBS1 knockout improves mice survival, showed significant repressions of major inflammatory cytokines (CCL2, IFNγ, IL-1β, etc.), enhances expression (p < 0.01) of several anti-inflammatory mediators (IL-10, IL-4, IL-13, etc.) and impedes hepatocellular apoptosis.

Conclusion: THBS1 might be considered as a new key-molecule in severity prediction of ACLF, being a disease development-related biomarker, promoting inflammatory responses and hepatocellular apoptosis, thus facilitating timely intensive clinical interventions by providing clinicians with potential new targets to improve the diagnostic and therapeutic strategies for ACLF management.

THU525
Beta-blockers can reduce mortality in patients with acute-on-chronic liver failure-a multi-center study
Anand Kulkarni1, Madhumita Premkumar2, Karan Kumar3, Juned Khan4, Baqar Gora1, Sowmya Iyengar1, Mithun Sharma1, Nageshwar Reddy1, Nagaraja Rao Padaki1, Asian Institute of Gastroenterology, Hyderabad, India; 2Post Graduate Institute of Medical Education and Research, Chandigarh, Chandigarh, India; 3Mahatma Gandhi Hospital, Jaipur, Jaipur, India; 4Hopewell Hospital, Lucknow, India
Email: anandvk90@gmail.com

Background and aims: Beta-blockers (BBs) can reduce the incidence of complications in patients with cirrhosis and prolong survival. The safety and efficacy of BBs in real-world settings in patients with ACLF identified by the Asian Pacific Association for the Study of Liver (APASL) criteria is unknown. Therefore, we aimed to assess the safety and efficacy of BB in patients with APASL defined ACLF.

Method: In this retrospective, multi-center study, patients with ACLF with complete 30 days follow-up were included. The primary objective was to compare day 30, 90, and 1-year mortality among standard of care (SOC) and BB (+SOC) groups. The secondary objectives were: to compare the incidence of infection and variceal bleed on days 30, 90, and one year among both the groups. We also assessed the time to resolution of ACLF (recompensation).

Results: A total of 346 patients were included. Only 26% (n = 89) received BBs, while 74% (n = 257) received only SOC. Age and severity scores (MELD NA-SOC: 28.4 ± 5.21 vs. 27.88 ± 4.9 in BB; p = 0.3) were similar in both groups. Alcohol was the most common cause of ACLF. Heart rate was higher and mean arterial pressure (MAP) lower in the SOC group than in the BB group. The indication for BB was large high-risk varices in 48.3% (43/89), history of acute variceal bleed in 40.4% (36/89), and 11.2% (10/89) were prophylactically started on BB to prevent further decompensation. Fifteen percent in SOC group and 12.35% in BB group were ACLF grade III patients. Though 9% of patients had a history of AVB in the BB group, CO could not be added either due to sepsis, low MAP, or kidney injury. The incidence of mortality was 21% (54/257) in SOC group compared to only 8% (7/89) in BB group at day 30 (p = 0.005). Similarly, at day 90, mortality was 37.2% (94/226) in SOC group compared to 17% (15/88) in BB group (p = 0.001). Mortality at one year was 48% (88/183) in SOC group compared to 27% (18/66) in BB group (p = 0.003). BB therapy could not reduce the incidence of infections or variceal bleed (Table). Complete resolution of ACLF (recompensation) was noted in 47% (121/257) of patients in SOC group and 73% (65/89) patients in BB group (p < 0.001). The mean time to recompensation was 2.66 ± 1.42 months in the SOC group compared to 2.3 ± 1.15 months in the BB group (p = 0.07). Four percent in SOC group and 1% in BB group underwent liver transplantation. Carvedilol was prescribed in 77.5% and propranolol in 22.5% of patients. Eight patients discontinued BB. On subgroup analysis, BB reduced mortality in ACLF grades I and II but not in grade III. Recompensation was significantly better in those with ACLF I and II but not in grade III. Furthermore, there was a significant reduction in the incidence of infection in the BB group in ACLF grade I. Conclusion: Only 1 in 4 ACLF patients are suitable for beta-blocker therapy. Beta-blocker therapy can reduce mortality and lead to early recompensation, especially in early grades of ACLF.

Cirrhosis and its complications: Experimental and pathophysiology.

THU526
Increased platelet aggregation in decompensated cirrhosis indicates higher risk of further decompensation and liver-related mortality
Alberto Zanetto1, Elena Campello2, Cristina Bulato2, Sabrina Cavassò2, Fabio Farinatti3, Patrizia Burra1, Francesco Paolo Russo1, Paolo Simioni2, Marco Senzolo1, Gastroenterology and Multivisceral Transplant Unit, Surgery, Oncology, and Gastroenterology, Padova, Italy; 2Thrombotic and Hemorrhagic Diseases Unit, General Internal Medicine, Medicine, Padova, Italy
Email: alberto.zanetto@yahoo.it

Background and aims: Studies on platelet aggregation in cirrhosis are controversial because interpretation of platelet function is challenged by thrombocytopenia. In this two-part study, we investigated platelet aggregation in cirrhosis and its correlation with development of liver-related events.

Method: Platelet aggregation was assessed by whole blood aggregometry. To overcome the influence of platelet count, we calculated a “platelet aggregation/platelet count ratio” (PLT ratio) to compare cirrhosis with thrombocytopenia and controls (60 chronic hepatitis and 45 healthy subjects) with normal platelet count (study part #1). Then, we prospectively followed patients with cirrhosis and investigated predictors of hepatic decompensation, transplantation, and death (study part #2).

Results: 203 cirrhosis patients were prospectively recruited (77% decompensated; median MELD 14). PLT ratio was significantly higher in cirrhosis than in chronic hepatitis and healthy subjects (0.44 vs. 0.25 and 0.26, respectively; p < 0.0001). Among patients with
Conclusion: Patients with cirrhosis, particularly when decompensated, have increased platelet aggregation. Among decompensated patients, those with PLT ratio >1 have an 80% probability of progressing towards further decompensation, transplantation, or liver-related death within 6 months.

THU527
Renin/angiotensin system-coagulation-inflammation axis abnormalities: a possible explanation for susceptibility to severe COVID-19 in cirrhosis

Lukas Hartl1,2, Mathias Jachs1,2, Benedikt Simbrunner1,2,3, David JM Bauer1,2, Georg Sennme1,2, Daniela Gömpelmann4, Thomas Szekeres5, Peter Quehenberger5, Michael Trauner1, Mattias Mandorfer1,2, Bernhard Scheiner1,2, Thomas Reiberger1,2,3.
1Medical University of Vienna, Division of Gastroenterology and Hepatology, Department of Medicine III, Vienna, Austria; 2Medical University of Vienna, Division of Hepatology, Department of Medicine III, Vienna, Austria; 3Medical University of Vienna, Christian Doppler Lab for Portal Hypertension and Liver Fibrosis, Vienna, Austria; 4Medical University of Vienna, Division of Pulmonology, Department of Internal Medicine II, Vienna, Austria; 5Medical University of Vienna, Department of Laboratory Medicine, Vienna, Austria
Email: thomas.reiberger@meduniwien.ac.at

Background and aims: Risk for severe coronavirus disease of 2019 (COVID-19) is increased among cirrhotic patients. Plasmin may aggravate COVID-19 by facilitation of cell entry of the virus. We investigated parameters of the renin/angiotensin system (RAS), endothelial dysfunction, coagulation/fibrinolysis and inflammation in both cirrhotic patients and COVID-19 patients.

Method: 127 prospectively characterized cirrhotic patients (CIR), as well as 9 patients with mild COVID-19 (mCOV), 11 patients with COVID-19 ARDS (aCOV) and 10 healthy subjects (HS) were included in the study. In cirrhotic patients, portal hypertension was assessed by hepatic venous pressure gradient (HVPG).

Results: With increasing liver disease severity (Child-Pugh stage A vs. B vs. C) and compared to HS, CIR patients displayed higher RAS activity (renin, angiotensin-converting enzyme [ACE], aldosterone), endothelial dysfunction (von Willebrand-factor [VWF] antigen) and inflammation (C-reactive protein [CRP], CRP, IL-6) along with a dysregulated coagulation/fibrinolysis profile (D-dimer, plasminogen activity, antiplasmin activity). Renin (i.e. RAS activity), VWF antigen (i.e. endothelial dysfunction), coagulation parameters (D-dimer, plasminogen fragment F1, 2) and parameters of inflammation (CRP, IL-6) were significantly elevated in COVID-19 patients and increased from mCOV to aCOV. In CIR patients, ACE activity was associated with IL-6 (p = 0.026; p = 0.003), independently linked to VWF antigen (ab: 0.10; p = 0.001) and was inversely correlated with plasminogen fragment F1, 2 (ab: −0.03; p = 0.023) and antiplasmin activity (ab: −0.58; p = 0.006).

Conclusion: RAS activity is considerably upregulated in Child-Pugh B/C cirrhosis and linked to endothelial dysfunction, abnormal coagulation profile and systemic inflammation. The cirrhosis-associated abnormalities of ACE (i.e. RAS activation), VWF antigen (i.e. endothelial dysfunction), antiplasmin (i.e. coagulation dysregulation and increased plasmin) and IL-6 (i.e. increased inflammation) may explain the susceptibility for severe COVID-19.

THU528
Improvement of hepatic and extrahepatic functions and anti-inflammatory effects of nitazoxanide in disease models of LPS-induced systemic inflammation and acute-on-chronic liver failure

Vanessa Legry1, Philippe Delataille1, Maryse Malyasi1, Valérie Daix1, Simon Debachecker1, Bart Steael2, Remy Hanf1, Dean Hum1,1GENFIT SA, Loos, France; 2Univ. Lille, Inserm, CHU Lille and Institut Pasteur de Lille, U1011-ECID, Lille, France
Email: vanessa.legry@genfit.com

Background and aims: Systemic inflammation (SI) is a hallmark of multiple organ failures in Acute on Chronic Liver failure (ACLF). Therefore, anti-inflammatory compounds may have the potential to alleviate ACLF, especially if they have immediate effects on the inflammatory state. The FDA approved anti-parasitic drug, nitazoxanide (NTZ), is suspected to exert direct anti-inflammatory actions. Our aim was to assess the efficacy of NTZ to rapidly counteract SI and improve hepatic and extra-hepatic functions after LPS challenge in healthy and fibrotic rats.
Method: Direct effects of NTZ on LPS-induced activation of human differentiated THP1 macrophages were assessed in vitro. Single ip LPS injection (1 mg/kg) was applied to healthy rats to induce a transient increase in circulating cytokines at 1–3 hours. A single oral dose of NTZ (100 mg/kg) was administered just before LPS injection and blood samples were collected 3 h later before sacrifice. To assess NTZ’s effects in an ACLF-model, a single ip LPS injection (0.03 mg/kg-adapted dose to limit mortality) was administered to rats with liver fibrosis induced by oral CC14 administration for 15 weeks followed by 1-week CC14 washout. Before the LPS challenge, the rats received NTZ (50 mg/kg BID) or vehicle for 3 days. Plasma samples were collected 24 h post-LPS.

Results: In THP1 macrophages, the active NTZ metabolite tizoxanide blunted LPS-induced TNFα secretion (IC50 = 6 μM, Emax = 88%). In healthy rats, NTZ reduced the LPS-induced rise in circulating cytokines (619 vs 1782 pg/ml TNFα, p = 0.01; 17.5 vs 24.8 ng/ml IL6, p = 0.06; 633 vs 834 pg/ml IL1b, p = 0.10; 4740 vs 6760 pg/ml IFNγ, p = 0.09) within 3 hours of treatment. In rats with CC14-induced fibrosis (F3–F4), NTZ treatment before LPS-induced ACLF reduced ALT (214 vs 919 U/l, p = 0.007), AST (355 vs 2072 U/l, p = 0.005) and total bilirubin (3.7 vs 13.3 μmol/l, p = 0.02), resulting in hepatoprotective effects. Moreover, NTZ treatment also prevented LPS-induced increases in creatinine (48 vs 83 μmol/l, p = 0.009), urea (46 vs 140 mg/dl, p = 0.002) and cystatin C (1471 vs 2869 ng/ml, p = 0.02).

Conclusion: These results suggest that the rapid anti-inflammatory effects of NTZ may participate in beneficial effects on hepatic and extrahepatic functions in a disease model of ACLF.
THU530
Long-chain acylcarnitines promote leukocyte mitochondrial dysfunction: role in patients with acutely decompensated cirrhosis
Ingrid Wei Zhang1,2, Cristina López-Vicario1,2-3, Mireia Casulleras1,2, Maria Duran-Guell1,2, Roger Flores-Costa1,2, Paula Segalés3,4, M. Carmen Garcia-Ruiz3,4,5, José Fernandez-Checa1,4,5, Joan Claria1,2,3,6, 1Institut d’Investigacions Biomèdiques August Pi i Sunyer (IDIBAPS), Barcelona, Spain; 2European Foundation for the study of chronic liver failure, Barcelona, Spain; 3CIBER-Center forBiomedical Research Network, Madrid, Spain; 4Institut d’Investigacions Biomèdiques deBarcelona (IIBB-CSIC), Barcelona, Spain; 5Keck School of Medicine of USC, Research center forALPD, Los Angeles, United States; 6Universitat de Barcelona, Department of Biomedical Sciences, Barcelona, Spain
Email: ingrid-wei.zhang@charite.de

Background and aims: Acute-on-chronic liver failure (ACLF) is characterized by acute decompensation (AD) of cirrhosis, organ failure(s) and high short-term mortality. The cytokinome of these patients revealed that exaggerated systemic inflammatory response is an important driver of disease progression. Recently, it has been demonstrated that the elevated circulating levels of acylcarnitines predict mortality in patients with AD and ACLF. Therefore, inflammation-associated mitochondrial dysfunction can be regarded as another major contributor to disease progression. Here, we hypothesize that acylcarnitines not only function as biomarkers of mitochondrial dysfunction but also exert biological effects on mitochondria of circulating immune cells. In addition, as organ donors are scarce, we explore whether existing treatments such as human serum albumin (HSA) might modulate the effect of acylcarnitines on mitochondrial function.

Method: Peripheral blood mononuclear leukocytes from healthy subjects were isolated by Ficoll gradient and in vitro experiments were performed to assess mitochondrial function under treatment with long- and medium-chain acylcarnitines, in the presence or absence of HSA. We assessed mitochondrial membrane potential (MMP) with the cationic dye JC-1 and mitochondrial respiration using Agilent Seahorse XF technology. This was complemented by electron microscopic evaluation of mitochondrial ultrastructure of immune cells treated with acylcarnitines and expression analysis of genes involved in mitochondrial function and biogenesis.

Results: Palmitoyl- and hexanoylcarnitine were increased in blood of patients with AD cirrhosis. In contrast to hexanoylcarnitine, the long-chain palmitoylcarnitine impaired maximal respiration of leukocyte mitochondria and reduced MMP in peripheral mononuclear leukocytes of patients with AD cirrhosis. In contrast to hexanoylcarnitine, the long-chain palmitoylcarnitine impaired maximal respiration of leukocyte mitochondria and reduced MMP in peripheral mononuclear leukocytes of patients with AD cirrhosis. In contrast to hexanoylcarnitine, the long-chain palmitoylcarnitine impaired maximal respiration of leukocyte mitochondria and reduced MMP in peripheral mononuclear leukocytes of patients with AD cirrhosis. In contrast to hexanoylcarnitine, the long-chain palmitoylcarnitine impaired maximal respiration of leukocyte mitochondria and reduced MMP in peripheral mononuclear leukocytes of patients with AD cirrhosis. In contrast to hexanoylcarnitine, the long-chain palmitoylcarnitine impaired maximal respiration of leukocyte mitochondria and reduced MMP in peripheral mononuclear leukocytes of patients with AD cirrhosis. In contrast to hexanoylcarnitine, the long-chain palmitoylcarnitine impaired maximal respiration of leukocyte mitochondria and reduced MMP in peripheral mononuclear leukocytes of patients with AD cirrhosis. In contrast to hexanoylcarnitine, the long-chain palmitoylcarnitine impaired maximal respiration of leukocyte mitochondria and reduced MMP in peripheral mononuclear leukocytes of patients with AD cirrhosis. In contrast to hexanoylcarnitine, the long-chain palmitoylcarnitine impaired maximal respiration of leukocyte mitochondria and reduced MMP in peripheral mononuclear leukocytes of patients with AD cirrhosis. In contrast to hexanoylcarnitine, the long-chain palmitoylcarnitine impaired maximal respiration of leukocyte mitochondria and reduced MMP in peripheral mononuclear leukocytes of patients with AD cirrhosis. In contrast to hexanoylcarnitine, the long-chain palmitoylcarnitine impaired maximal respiration of leukocyte mitochondria and reduced MMP in peripheral mononuclear leukocytes of patients with AD cirrhosis. In contrast to hexanoylcarnitine, the long-chain palmitoylcarnitine impaired maximal respiration of leukocyte mitochondria and reduced MMP in peripheral mononuclear leukocytes of patients with AD cirrhosis. In contrast to hexanoylcarnitine, the long-chain palmitoylcarnitine impaired maximal respiration of leukocyte mitochondria and reduced MMP in peripheral mononuclear leukocytes of patients with AD cirrhosis.

Conclusion: Our results indicate that elevated circulating long-chain acylcarnitines in patients with AD are not only an epiphenomenon but have the potential to actively promote mitochondrial dysfunction in immune cells, thereby contributing to immune dysbalance in these patients.

THU531
Reduced plasma extracellular vesicle CD5L content in patients with acute-on-chronic liver failure: interplay with specialized pro-resolving lipid mediators
M. Belén Sánchez-Rodríguez1, Érica Téllez2, Mireia Casulleras1, Francesc Borras2, Vicente Arroyo3, Joan Claria1,4,5, María-Rosa Sarrias2,6, 1Hospital Clinic-IDIBAPS, Biochemistry and Molecular Genetics Service, Spain; 2Innate Immunity Lab, IGTP, Spain; 3IVECAT, IGTP, Spain; 4European Foundation for the Study of Chronic Liver Failure, Spain; 5Universitat de Barcelona, Department of Biomedical Sciences, Spain; 6CIBERehd, Spain
Email: jclaria@clinic.cat

Background and aims: Acute-on-chronic liver failure (ACLF) is a syndrome that develops in patients with acutely decompensated cirrhosis (AD). It is characterized by a systemic hyperinflammatory state, leading to multiple organ failure. Our objective was to analyze macrophage anti-inflammatory protein CD5L in plasma extracellular vesicles (EVs) and assess its as yet unknown relationship with lipid mediators in ACLF.

Method: EVs, isolated by size exclusion chromatography from the plasma of healthy subjects (HS) (n = 9) and patients with compensated cirrhosis (CC) (n = 8), AD (n = 13) and ACLF (n = 14), were defined as positive for CD9, CD5L and CD63 and their size, number, morphology and lipid mediator content were characterized by nanoparticle tracking analysis, electron microscopy and liquid chromatography with tandem mass spectrometry, respectively. Plasma CD5L was quantified by enzyme-linked immunosorbent assay in 10 HS, 20 CC and 149 AD patients (69 with ACLF). Macrophage CD5L expression and the biosynthesis of specialized pro-resolving lipid mediators (SPMs) were characterized in vitro in primary cells.

Results: Circulating EVs were significantly suppressed in cirrhosis, regardless of severity, and showed considerable alterations in CD5L and lipid mediator content as the disease progressed. In AD patients, levels of EV CD5L correlated best with those of the SPM resolvins E1 (RvE1). Analysis of total plasma supported these data and showed that, in ACLF, low CD5L levels were associated with circulatory (p < 0.001), brain (p < 0.008) and respiratory (p < 0.05) failure (Mann-Whitney test). Functional studies in macrophages indicated a positive feedback loop between CD5L and RvE1 biosynthesis.

Conclusion: We have determined a significant alteration of circulating EV contents in ACLF, with a loss of anti-inflammatory and pro-resolving molecules involved in the control of acute inflammation in this condition.

THU532
Peptidylglycine alpha-amidating monoxygenase and adrenomedullin measurements suggest cardio-circulatory dysfunction in advanced cirrhosis
Søren Møller1, Andrei Voiosu1, Signe Wiese2, Janum Schulte2, Paul Kaufmann3, Andreas Bergmann3, Emil Bartels3, Jens Peter Goetze2, 1Hvidovre Hospital, Center of Functional and Diagnostic Imaging and Research, Department of Clinical Physiology and Nuclear Medicine 260, Hvidovre, Denmark; 2Hvidovre Hospital, Gastro Unit, Hvidovre, Denmark; 3Spartagene GmbH, Berlin, Germany; 3Rigshospitalet, Department of Clinical Biochemistry, Copenhagen, Denmark
Email: soeren.moeller@regionh.dk

Background and aims: Peptidylglycine α-amidating monoxygenase (PAM) is a processing enzyme involved in maturation of a plethora of regulatory peptides. One product of PAM activity is adrenomedullin (bio-ADM), which regulates vascular tone and endothelial integrity. In this study, we aimed to examine PAM activity and bio-ADM concentrations in patients with cirrhosis and explore the role of the liver in net release of the two markers.

Method: We enrolled 48 patients with cirrhosis and 16 control subjects. The patients were evenly distributed according to the Child-
The study was performed in Sprague-Dawley rats induced by cecal ligation and puncture (CLP) as novel experimental model mimicking extrahepatic organ failures defined in ACLF. The CCl4 + CLP model in rats reproduces the spectra of extra-hepatic organ impairments present in patients with ACLF and thus appears as an optimized experimental model to explore the pathophysiology of this disease.

### THU534

Thorbin-induced platelet activation across distinct stages of portal hypertension and cirrhosis

Ksenia Bruslowskaya1,2,3, Benedikt Hofer1,2,3, Beate Eichelberger4, Simon Panzer4, Benedikt Simbrunner1,2,3, Mattias Mandorfer1,2, Thomas Gremmel1,6,7, Thomas Reiberger1,2,3, 1Medical University of Vienna, Division of Gastroenterology and Hepatology, Department of Medicine III, Vienna, Austria; 2Medical University of Vienna, Vienna Hepatic Hemodynamic Lab (HEPEX), Division of Gastroenterology and Hepatology, Department of Medicine III, Vienna, Austria; 3Medical University of Vienna, Department of blood group serology and transfusion medicine, Vienna, Austria; 4Medical University of Vienna, Department of Internal Medicine II, Vienna, Austria; 5Landesklinikum Mistelbach-Gänserndorf, Department of Internal Medicine I, Cardiology and Intensive Care Medicine, Mistelbach, Austria; 6Karl Landsteiner society, Institute of antithrombotic therapy in cardiovascular disease, St. Poelten, Austria

**Background and aims:** Patients with advanced chronic liver disease (ACLD) often show thrombocytopenia; however, primary hemostasis seems re-balanced by higher levels of von Willebrand factor (VWF). Still, alterations in thrombin-induced platelet activation may put patients at increased risk for both bleeding and organ impairments by measuring biochemical and histological parameters (hematocrit, von Willebrand factor, and platelet count). Given the major expression of PAM in the heart, we propose that increased PAM activity in cirrhosis may reflect a cardio-circulatory dysfunction in advanced cirrhosis.

**Conclusion:** The CCl4 + CLP model in rats reproduces the spectra of extra-hepatic organ impairments present in patients with ACLF and thus appears as an optimized experimental model to explore the pathophysiology of this disease.
thromboembolic events. Therefore, we aimed to characterize platelet function in a thoroughly characterized ACLD patient cohort.

**Method:** 110 ACLD patients with portal hypertension (PH), i.e., a hepatic venous pressure gradient (HVPG) ≥6 mmHg, were prospectively included and stratified by Child-Pugh stage (CPS) and HVPG. Platelet surface P-selectin and activated glycoprotein IIb/IIIa (GPIIb/IIIa) (mean fluorescent intensity, MFI) were assessed with flow cytometry as sensitive parameters of platelet activation in unstimulated and stimulated (agonists of the protease-activated receptors, PAR-1 and PAR-4) conditions.

**Results:** The level of “baseline” platelet activation was similar across CPS stages A, B, and C (unstimulated P-selectin expression: 0.0 MFI vs. 0.0 MFI, p = ns; unstimulated GPIIb/IIIa expression: 0.0 MFI vs. 0.0 MFI, p = ns). PAR-1 mediated platelet activation was significantly impaired in CPS-B and C patients (P-selectin: CPS-A: 2261.0 MFI [1815.0–2942.0] vs. B: 1793.0 MFI [1299.0–2523.0], p = 0.02 vs. C: 1577.0 MFI [1101.0–1926], p < 0.01; GPIIb/IIIa: CPS-A: 20.6 MFI [3.4–32.8] vs. B: 1.8 MFI [0.0–16.2], p < 0.01 vs. C: 0.0 MFI [0.0–0.0], p < 0.001). Similarly, a decreased response to PAR-4 mediated platelet activation was observed with increasing CPS stages (P-selectin: CPS A: 1159.0 MFI [332.8–2721.0] vs. B: 582.3 MFI [101.3–1236.0], p = 0.03 vs. C: 464.0 MFI [1071–5471], p = 0.02; GPIIb/IIIa: CPS-A: 18.1 MFI [21.9–93.8] vs. B: 8.0 MFI [0.0–13.7], p < 0.01 vs. C: 0.0 MFI [0.0–0.0], p < 0.001). The severity of PH had no impact on “baseline” activation (all p = ns). PAR-1 mediated platelet surface expression of P-selectin was comparable across the HVPG strata 6–9 vs. 10–19 vs. ≥20 mmHg (p = ns), while activated GPIIb/IIIa was significantly reduced in HVPG ≥20 group (HVPG 6–9: 20.8 MFI [7.5–46.4] vs. HVPG ≥20: 0.5 MFI [0.0–20.8], p < 0.01). PAR-4 mediated platelet activation was also reduced in the HVPG ≥20 mmHg group (P-selectin: HVPG 6–9: 1775.0 MFI [668.6–3287.0] vs. HVPG ≥20: 20.8 MFI [0.0–6.8], p < 0.01). PAR-4 mediated platelet surface P-selectin expression of patients achieving Child stage of A and C. Moreover, high risk PH (HVPG ≥20 mmHg) is associated with impaired platelet activation upon stimulation. The impact of these alterations on the risk of bleeding or thrombotic events remains to be studied.

**Conclusion:** ACLD patients exhibit decreased thrombin-inducible platelet activation when progressing to Child stage of B and C. Therefore, we aimed to characterize platelet function in a thoroughly characterized ACLD patient cohort.

**Background and aims:** Liver fibrosis is the main determinant of clinical outcomes in advanced chronic liver disease (ACLD) of any etiology. Regression of bridging fibrosis and cirrhosis can take place after effective etiological treatment, but not in all cases, suggesting that factors other than the etiology play a role in the modulation of this important outcome. We hypothesized that thorough assessment of liver function markedly improves, suggesting that several metabolic pathways are influenced by regression of fibrosis. However, the metabolic pathways associated with fibrosis regression in ACLD have not been characterized. We hypothesize that thorough assessment of liver metabolism could provide evidence-based data for better characterization of cirrhosis patients with regression following effective etiological treatment, thus providing a rational basis for personalized interventions.

**Method:** We performed a case-control pilot study of 60 patients with ACLD of different etiologies, 30 with histological and/or clinical evidence of regression of ACLD (Regressors) and 30 without any improvement (Non-regressors) after a minimum of 24 months of successful etiological therapy. We used the combination of metabolic modelling and metabolic profiling to define metabolic pathways and associated signature that differentiate Regressors from Non-regressors. We have developed a transcriptomics-driven metabolic modeling approach to assess the regression of ACLD. We further investigated the associated metabolic signature using mass spectrometry-based metabolomics.

**Results:** Although Regressors and Non-regressors showed similar profiles at baseline, our observation is pointing to fatty acid β-oxidation and arachidonic acid metabolism (associated to inflammation and oxidative stress) as key metabolic pathways differentiating Regressors from Non-regressors after therapy, suggesting that lipid metabolism plays a central role in the modulation of the extracellular matrix in ACLD. In addition, Using Least Absolute Shrinkage and Selection Operator (LASSO) analyses, the Regressor phenotype was predicted with 80% accuracy based on the levels of identified lipid markers after etiologic therapy.
**Conclusion:** Our preliminary observations suggest several metabolic pathways that were associated with persistence or regression of ACLD after successful etiological therapy. These results allow proposing a metabolic signature of regression of fibrosis in ACLD.

**THU536**

**Exacerbated response to patterned injury in the cirrhotic liver: potential susceptibility to ischemia**

Benjamin Leaker1,2, Mozhdeh Sojoodi1, Kenneth K. Tanabe3, R. Rox Anderson2,4, Joshua Tam2,4, 1Massachusetts Institute of Technology, Harvard–MIT Health Sciences and Technology, Cambridge, United States; 2Massachusetts General Hospital, Wellman Center for Photomedicine, Boston, United States; 3Mass General Cancer Center, Division of Surgical Oncology, Boston, United States; 4Harvard Medical School, Department of Dermatology, Boston, United States

**Email:** leakerb@mit.edu

**Background and aims:** The response to injury in the cirrhotic liver is an important factor in both the pathogenesis of cirrhosis and the treatment of patients living with end stage liver disease. This study aimed to investigate the differences in the short-term tissue response to a controlled injury between the healthy and cirrhotic liver.

**Method:** Healthy and cirrhotic rats underwent a laparotomy to expose the liver followed by treatment with a tunable ablative laser to create a pattern of micro-injuries in the left lobe. The roughly 1 cm² treatment area contains over 100 uniformly spaced micro-injuries, each approximately 300 μm in diameter and 2 mm deep. Animals were euthanized at 0 hr, 2 hr, 4 hr, 6 hr, 3d, 7 d, and 14d after laser treatment. RNA samples from the 4 hr and 6 hr timepoints, resulting in enlarged and haphazardly completely healed within 7 days in the non-cirrhotic liver. In the cirrhotic liver, the treatment area contains over 100 uniformly spaced micro-injuries, notably capillarization of sinusoids and the formation of intrahepatic vascular shunts.

**Conclusion:** Our histology and transcriptomics data show that the cirrhotic liver has an exacerbated response to injury, possibly due to an increased susceptibility to ischemia which can compound with other injuries to cause far greater damage. This could be a result of the changes in the hepatic microvasculature that occur in cirrhosis, most notably capillarization of sinusoids and the formation of intrahepatic vascular shunts.

**THU537**

**The regulatory protein and gene expression profile of skeletal muscle in chronic liver disease patients**

Sophie Allen1, Jonathan Quinlan1, Amitpal Dhaliwal2, Thomas Nicholson2, Felicity Williams2, Matthew Armstrong3, Ahmed Elsharkawy4, Simon Jones2, Carolyn Greig1, Janet Lord2, Gareth Lavery4, Leigh Breen1, 1University of Birmingham, School of Sport, Exercise and Rehabilitation Sciences, Birmingham, United Kingdom; 2University of Birmingham, Institute of Inflammation and Ageing, Birmingham, United Kingdom; 3University Hospitals Birmingham, Liver Unit, Birmingham, United Kingdom; 4Nottingham Trent University, Department of Biosciences, Nottingham, United Kingdom

**Email:** s.l.allen@bham.ac.uk

**Background and aims:** The molecular pathways which may underpin sarcopenia in Chronic Liver Disease (CLD) are largely unclear. The aim of this study was to characterize the intracellular signaling pathways that may underscore sarcopenia in CLD patients of different etiologies and disease stages.

**Method:** Muscle biopsy and blood samples were obtained from 9 non-cirrhotic non-alcoholic fatty liver disease patients (NAFLD; aged 61.1 ± 9.0), 12 decompensated alcoholic related end-stage liver disease patients (ESLD; 55.7 ± 5.7) and 12 healthy, age-matched healthy controls (CON; 55.7 ± 8.7). The protein content of skeletal muscle anabolic, catabolic and mitochondrial signaling intermediates was determined via western blot. The muscle transcriptome was analyzed using RNA-sequencing. Analysis with DESeq2 was used to determine differences in gene expression between the untreated samples. Over-representation analysis and gene set enrichment analysis were then used to identify biological pathways that may underscore sarcopenia in CLD patients of different etiologies and disease stages.

**Results:** Citrate synthase activity (~43%) and the protein content of OXPHOS complex I was significantly lower (~26%) in ESLD vs. CON (p < 0.01 for both), whereas OXPHOS complex IV was significantly lower in ESLD vs. CON (71%; p < 0.01) and NAFLD (61%; p = 0.04). Total-mTOR protein was significantly lower in NAFLD (62%, p = 0.01) and ESLD (52%, p = 0.03) vs. CON. Myostatin protein content was significantly greater in NAFLD vs. CON (77%; p < 0.01) and ESLD (70%; p < 0.01). Gene pathway analysis revealed a significant enrichment in pathways related to oxidative stress in ESLD vs. CON. A significant enrichment in genes related to senescence was evident in NAFLD vs. CON.

**Conclusion:** Our preliminary observations suggest several metabolic pathways that were associated with persistence or regression of ACLD after successful etiological therapy. These results allow proposing a metabolic signature of regression of fibrosis in ACLD.
Conclusion: Collectively these findings highlight some similar but largely distinct signaling pathways that may underscore sarcopenia in CLD patients across different etiologies and disease stages.

THU538
Proteomic analysis of dysfunctional liver sinusoidal endothelial cells reveals substantial differences in the most common experimental models of chronic liver disease
Mar Gil1, Carla Fuster1, Mikel Azkargorta2,3, Imma Raurell1,2, Aurora Barbera1, Felix Elortza2,3, Joan Genesca2,3, Diana Hide1,3, Maria Martell1,3.1Liver Diseases, Vall d’Hebron Institut de Recerca (VHIR), Liver Unit, Hospital Universitari Vall d’Hebron (HU VH), Vall d’Hebron Barcelona Hospital Campus, Universitat Autònoma de Barcelona (UAB), Barcelona, Spain; 2Proteomics Platform, CIC bioGUNE, BRTA (Basque Research and Technology Alliance), ProteoRed-ISCIII, Bizkaia Science and Technology Park, Derio, Spain; 3Centro de Investigación Biomédica en Red de Enfermedades Hepáticas y Digestivas (CIBERehd), Madrid, Spain
Email: diana.hide@vhir.org

Background and aims: Therapies specifically aimed at liver sinusoidal endothelial cells (LSEC), first inducers of liver damage, could help to slow down the entire pathological process. Although physiological markers of LSEC have been described, there is lack of information regarding dysfunctional LSEC in chronic liver diseases (CLD). Here, we aimed to decipher the molecular profile of dysfunctional LSEC in different pathological situations to improve the effectiveness of potential therapeutic agents.

Method: LSEC from three experimental rat models (bile duct ligation–BDL, inhaled carbon tetrachloride–CCl4 and high fat glucose/fructose diet–HFGFD) and their controls were isolated and sorted by flow cytometry using cd11b to eliminate macrophages and cd32b to sort dysfunctional (CD32⁻) LSEC. Full proteomic profile was performed applying label free proteomics by nano–scale liquid chromatography tandem mass spectrometry on an EvoSep ONE (EVOSEP) coupled online to a TIMS ToF Pro (Bruker). Obtained data was processed and analyzed with PEAKS software.

Results: The percentage of CD32⁻ LSEC was different between groups. Of relevance is the comparison between HFGFD (early stage of CLD) with 16.9% CD32⁻ LSEC and CCl4 (advanced stage) with only 6.0%, suggesting differences in the capillarization process. Principal component analysis (PCA) revealed that CD32⁺ LSEC are more similar between models and to healthy controls than to CD32⁻ LSEC of their respective model (Fig A). Accordingly, the number of differentially expressed proteins vs. control LSEC is lower in CD32⁺ than in CD32⁻ LSEC. Nevertheless, further PCA also clusters CD32⁺ LSEC in separate groups by models (Fig B) representing protein expression differences between them. Looking for similarities in the capillarization process, we found 51 common proteins differentially expressed compared to controls in CD32⁻ LSEC from the 3 models and 354 shared by at least 2 models. Finally, heatmap representation of significantly differentially expressed proteins between models, both for CD32⁺ and CD32⁻ LSEC, evidenced specific patterns for each model being CCl4 and HFGFD more similar to each other than BDL (Fig C).

Conclusion: Substantial differences in dysfunctional LSEC from the three most common models of CLD were found, supporting the idea that in different etiologies/disease stages, LSEC may harbor different protein expression profiles. In deep analysis of deregulated proteins...
and pathways in each model will allow to better understand and use the preclinical models in translational research and will facilitate the specific targeting of experimental drugs. Funded by Instituto de Salud Carlos III and European Union EuroNanoMed III [AC18/00033].

THU539
Long-term albumin administration improves survival, reduces TLR4 mediated hepatic inflammation and reduces gut translocation in models of cirrhosis
Alexandra Phillips1, Qianwen Zhao2, Abheba Habtesion1, Fausto Andreola3, Nathan Davies1, Lindsay A Edwards3, Jane Macnaughtan1, Rajiv Jalan1. 1University College London, Institute of liver and digestive health, United Kingdom; 2Sichuan University, Department of Gastroenterology and Hepatology, West China Hospital, Chengdu Shi, China; 3Institute of Hepatology, King’s College Hospital, United Kingdom
Email: alexandra.phillips5@nhs.net

Background and aims: Long-term albumin administration reduces mortality in patients with decompensated cirrhosis. The underlying mechanisms are unknown. The aims of this study were to investigate how the absence of endogenous albumin and albumin administration impacts liver injury, toll-like receptor 4 (TLR4) signalling and gut translocation.

Method: 10 rodent groups: Naïve, cirrhosis (4-wk; bile-duct ligation (BDL)) and acute-on-chronic liver failure (ACLF) models (induced by lipopolysaccharide (LPS) 0.025 mg/kg intraperitoneal (i.p.) to BDL) ± albumin infusion (1.5 g/kg ip; 2-wk) of analbuminaemic (NAR) and wild-type (SD) rats. Plasma biochemistry and hepatic TUNEL staining. Hepatic TLR4 expression and pathways (hTLR4): qPCR and RT2 PCR profiler. Gut permeability: d-lactate and zonulin in plasma. Ileal integrity: western blot of tight junction proteins.

Results: ALT levels showed significant improvement after albumin administration in SD BDL LPS group (p = 0.01), and non-significant improvement in SD BDL and NAR BDL LPS. Significant reduction in the liver of TUNEL positive areas in LPS groups with albumin administration. hTLR4: NAR animals had greater hTLR4 expression, with all treatment groups showing a reduction of hTLR4 expression after albumin administration. hTLR4 gene array confirmed the activation of TLR4 dependent pathways in the cirrhotic NAR animals, which was abrogated by albumin infusion. Markers of gut permeability: Plasma D-lactate showed a reduction in all treatment groups with albumin (see figure). Plasma zonulin decreased after albumin in NAR BDL animals with and without LPS administration. Tight junction: ZO-1, claudin-4 and occludin in ileum showed a reduction in NAR diseased animals compared to SD groups with albumin administration increasing tight junction protein abundance in all disease groups.

Conclusion: The results of this study show for the first time that that albumindeficient animals have increased mortality, significantly increased liver injury and increased sensitivity to LPS. Chronic albumin administration partially reversed this, as well as reduces gut translocation resulting in decreased TLR4 pathway activation and improving the integrity of tight junctions. The data provide mechanistic insight into the biological effect on albumin on gut-liver interactions.

THU540
The prevalence and prognostic significance of vitamin C deficiency in patients with cirrhosis: a prospective observational cohort study
Declan Connoley1, Phil Ha1, Joseph Nim1, Elaine Koh1, Ryan Hirsch1, Marcus Robertson1. 1Monash Health, Department of Gastroenterology, Melbourne, Australia
Email: declan.connoley@gmail.com

Background and aims: Malnutrition is a common comorbidity in cirrhotic patients and confers a poorer prognosis. Vitamin C (VC) is a micronutrient essential for human health. Vitamin C deficiency (VCD) can lead to scurvy and may impair immune and liver functions. Although previously thought to be rare in developed countries, VCD is now well described in patients with pneumonia, COVID19 and upper gastrointestinal bleeding (UGIB). The prevalence and clinical significance of VCD in cirrhosis remains poorly studied.

Method: Patients with cirrhosis admitted to 3 metropolitan tertiary centres in Australia were prospectively included over a 10-month period in 2021. Fasting VC levels were collected on admission and we recorded demographic data and clinical outcomes. The primary outcomes were the prevalence of VCD (defined as VC level <23 mcg/ml) and severe VCD (SVCD), defined as <11 mcg/ml. Secondary outcomes included mortality, intensive care admission, length of stay (LOS) and rate of infection.

Results: 117 patients were included. Mean age was 57.1 ± 13.9 years, 59.0% were male and 23.9% belonged to the lowest socioeconomic decile. The most common aetiologies of cirrhosis were alcohol (62.4%), viral hepatitis (24.0%) and non-alcoholic fatty liver disease (18.8%). Median MELD score was 29 (IQR 22–36) and Child Pugh (CP) grades were 12.8% A, 46.2% B and 41.0% C. Most patients (74.4%) were hospitalised with complications of decompensated cirrhosis, including ascites (59.0%), encephalopathy (31.6%) and variceal bleeding (11.1%).

Median VC level was 34mcg/ml (IQR 16–55) and did not differ with age, gender, or aetiology of cirrhosis. Increasing CP grade correlated with significantly lower median VC levels (CP-A 46.0 mcg/ml vs. CP-B 36.5 mcg/ml and CP-C 20.5 mcg/ml, p = 0.026). The prevalence of VCD and SVCD were 39.3% and 17.1% respectively. SVCD was more prevalent in patients with a body mass index <25 (28.3% vs 13.0%, p = 0.036).

In-hospital mortality was 12.8% and did not differ by VCD status, however in the subgroup of patients presenting with UGIB, SVCD correlated with significantly higher mortality (50% vs 4.1%, p = 0.045). Bacteraemia was more frequent in patients with VCD (13.3% vs. 1.4%, p = 0.014) and SVCD (26.3% vs 2.1%, p < 0.001), which remained significant at multivariate analysis (OR for every 1mcg/ml increase in VC, 0.91 (95% CI: 0.83–0.99), p = 0.037). Overall infection rates were higher in patients with SVCD (40.0% vs. 27.8%) although this was non-significant (p = 0.279). Median hospital LOS was 10 (IQR 6–18) days and did not differ by VCD status.
Conclusions: VCD is common in hospitalised cirrhotic patients and prevalence increases with severity of liver disease. VCD increases the risk of infective complications and higher mortality was observed in patients with UGIB and SVCD. Further studies are required to assess the significance of VCD in cirrhosis and the impacts of VC replacement.

**THU541**
Wnt as activator of regeneration in cirrhosis of human liver: tissue collapse brings the Wnt source in hepatic veins to the site of the progenitor cell niche
IanR Wanless1, Ashley Stueck1. Dalhousie University, Anatomic Pathology, Halifax, Canada
Email: ian2460@gmail.com

**Background and aims:** Recent studies show that Wnt is secreted by hepatic vein endothelial cells (HV-EC). Glutamine synthetase (GS) activation in peri-venular hepatocytes (HV) of normal livers is considered a downstream event initiated by Wnt. Thus, we consider GS activation a surrogate histologic marker for Wnt and call it Wnt-GS. Hepatic regeneration is also activated by the Wnt/beta-catenin pathway. We previously showed that human cirrhotic liver is repopulated by buds of new hepatocytes derived from distal bile ducts. GS expression was a prominent feature in ducts forming buds, which is consistent with a response to local exposure to secreted Wnt. However, in normal livers, Wnt secreted from HV-EC affects a thin rim of perivenular/zone 3 hepatocytes and is then washed toward the cava. In order to reach portal tracts and activate the bud sequence in cirrhosis, we hypothesize that some Wnt is distributed to the distal bile ducts by altered circulation. The aim is to identify the anatomic basis of this pathway in human cirrhosis.

**Method:** Resected liver samples with chronic disease (n=38) were serially sectioned and stained with GS, CD34, and CK19. Wnt-GS was semi-quantitated by location.

**Results:** Perivenular Wnt-GS generally decreased with advancing stage, associated with decreased HV number but also decreased Wnt-GS per HV, likely because of damage to HV-EC and arterialization with washout. Stage 4A and 4B livers usually had occasional nodules with focal increase in Wnt-GS, likely because of retrograde flow. Active budding correlated with Wnt-GS, mostly in septal ducts and associated new hepatocytes, usually in stage 4A and 4B. Wnt-GS in HC at nodular periphery were often seen to connect with intranodular HVs but also appeared to be a response to Wnt-secreting HV remnants that were deeply embedded in adjacent septa (see fig); these HVs appear to be the main conduits allowing HV-derived Wnt to be transported to small duct regions.

**Conclusion:** In cirrhotic livers, Wnt appears to migrate in intact HV remnants to distal ductal regions, either by veno-portal approximation in collapsed tissue (PELs) or, where sinusoidal connections are intact, by reversed sinusoidal blood flow aided by focal shunt-related blood flow, as seen in other liver conditions. This explains how Wnt can be delivered from hepatic veins to the progenitor cell niche and activate regeneration. Wnt-GS is a useful surrogate marker for the location of Wnt, although confirmation with direct techniques is required. The patchy anatomic distribution of Wnt-GS suggests that Wnt concentration is focally suboptimal to support regeneration, justifying therapeutic trial options.

**THU542**
The portal vein in patients with cirrhosis is not an extensively inflammatory or hypercoagulable vascular bed
Ellen Driever1, Marta Magaz2, Jelle Adelmeyjer1, Fanny Turon3, Anna Baiges2, Pol Olivas2, Virginia Hernandez-Gea2, Annabel Blasi1, Juan Carlos Garcia Pagan2, Ton Lisman1. University Medical Center Groningen, Department of Surgery, Groningen, Netherlands; 2Barcelona Hepatic Hemodynamic Laboratory, Liver Unit, Hospital Clinic, Institut de Investigaciones Biomèdiques August Pi i Sunyer (IDIBAPS); 3Hospital Clinic, Department of Anesthesiology, Barcelona, Spain
Email: e.g.driever@umcg.nl

**Background and aims:** Portal vein thrombosis (PVT) is a common complication in patients with cirrhosis. Although we previously demonstrated that hypercoagulability is a reflection of severity of liver disease rather than a causal factor for PVT, other groups demonstrated elevated levels of markers of inflammation and activation of haemostasis in the portal vein (PV) compared to post-hepatic veins. However, many studies did not take clearance of these markers by the liver into account. We aimed to determine whether the PV in cirrhotic patients has particular proinflammatory or hypercoagulable characteristics by comparing blood sampled in the PV, in the hepatic vein (HV), and in the peripheral circulation.

**Method:** Plasma samples from 52 cirrhotic patients with clinically significant portal hypertension receiving transjugular intrahepatic portosystemic shunt, were taken from the PV, HV, and jugular vein (JV). Plasma levels of markers of inflammation, endothelial damage and haemostasis were determined and compared between the three vascular beds.

**Results:** Inflammatory markers LPS and IL-6 were slightly, but significantly higher in the PV than in the HV and JV. The neutrophil extracellular trap markers cfDNA and MPO-DNA were similar between the vascular beds. Endothelial marker VWF and markers of haemostasis were modestly elevated in the PV. Levels of multiple markers are lower in the HV compared to the PV and JV.
Table 1: Levels of markers of inflammation, endothelial damage and haemostasis, measured in plasma sampled from different vascular beds.

<table>
<thead>
<tr>
<th></th>
<th>Portal vein</th>
<th>Hepatic vein</th>
<th>Jugular vein</th>
</tr>
</thead>
<tbody>
<tr>
<td>LPS (pg/ml)</td>
<td>162 [96–259]*</td>
<td>125 [68–233]**</td>
<td>156 [66–251]**</td>
</tr>
<tr>
<td>TNF-α (pg/ml)</td>
<td>12 [6–22.5]</td>
<td>11.7 [5.1–23.9]</td>
<td>11.9 [5.2–21.5]</td>
</tr>
<tr>
<td>IL-6 (ng/ml)</td>
<td>16.5 [7–35.1]</td>
<td>8.5 [5.5–32.5]**</td>
<td>10.3 [5.4–34.7]**</td>
</tr>
<tr>
<td>cfDNA (μg/ml)</td>
<td>1 [0.9–1.2]</td>
<td>1 [0.8–1.2]</td>
<td>1 [0.8–1.2]</td>
</tr>
<tr>
<td>MPO-DNA (AU)</td>
<td>0.2 [0.1–0.4]</td>
<td>0.2 [0.1–0.4]</td>
<td>0.2 [0.1–0.4]</td>
</tr>
<tr>
<td>TAT (ng/ml)</td>
<td>479 [298–479]</td>
<td>19.5 [72–35.6]**</td>
<td>43.8 [12–17]†</td>
</tr>
<tr>
<td>PAP (ng/ml)</td>
<td>1001 [556–4045]**</td>
<td>790 [535–1581]**</td>
<td>867 [530–2425]**</td>
</tr>
<tr>
<td>D-dimers (ng/ml)</td>
<td>3670 [2237–7205]**</td>
<td>2720 [1700–3662]**</td>
<td>3040 [1827–530]**</td>
</tr>
</tbody>
</table>

* Comparison between portal vein and peripheral vein; † comparison between portal vein and hepatic vein; ‡ comparison between hepatic vein and jugular vein. *; p < 0.05; **; p < 0.01; ††; p < 0.001.

Conclusion: In contrast to published studies, we found only a slight prothrombotic environment in the PV. In previous studies, comparison of levels of markers in PV with an immediate post-hepatic vascular bed may have erroneously led to the conclusion that the portal circulation is hypercoagulable. Here we demonstrate that many markers are lowest in the HV compared to the PV and the systemic circulation, indicating that the low level of these markers in the HV, at least in part, reflect clearance of those markers in the liver.

THU543

Effect of liver stiffness on hepatocellular carcinoma phenotype in a biometric 3D model

Carlemi Calitz1, Jaafar Khaled1, Jenny Rosenquist2, Maria Kopsida1, Oliver Dergerstedt2, Hans Lennerns3, Märtten Fryknäs4, Ayan Samanta2, Femke Heindryckx1, Uppsala University, Medical Cell Biology, Uppsala, Sweden; Uppsala University, Department of Chemistry–Ångström Laboratory, Polymer Chemistry, Uppsala, Sweden; Uppsala University, Department of Pharmaceutical Biosciences, Uppsala, Sweden; Uppsala University, Department of Medical Sciences, Cancer Pharmacology and Computational Medicine, Uppsala, Sweden

Email: c.calitz@amsterdamumc.nl

Background and aims: Hepatocellular carcinoma (HCC) usually occur in patients with an underlying chronic liver disease. The tumor micro-environment (TME) is therefore characterized by an increased deposition of extracellular matrix proteins (ECM). The abundance of ECM results in physical and biomechanical changes in the TME, which could influence tumor behavior. The aim of our study was to determine how liver stiffness affects the HCC phenotype in a novel biometric 3D model to study tumor-stroma interactions.

Method: HepG2 and Huh7 cells were grown in a 3D biometric hydrogel model with tunable biomechanical properties for 21 days. Matrix stiffness, epithelial-to-mesenchymal transitions (EMT), metastatic potential, drug sensitivity and overall survival was assessed and compared to current two-dimensional (2D) models, an in vivo HCC mouse model and clinical data. Tumour nodules were collected from the culture medium and cells were extracted from the gels for subsequent RT-qPCR analyses.

Results: Cells were embedded in hydrogels mimicking the onset of a fibrotic and cirrhotic TME, as determined by patient-derived data. HepG2 and Huh7 cells grown in a stiffer matrix (resembling a cirrhotic liver) increased proliferation and protein content, compared to those grown in a less stiff matrix (resembling a fibrotic liver). HepG2 cells significantly decreased albumin synthesis in the cirrhotic TME compared to the fibrotic TME, while Huh7 cells increased albumin synthesis. While urea production in HepG2 cells decreased over time, it increased in Huh7 cells in both conditions. Tumor nodules started to form spontaneously outside the 3D gels after 11 days. The HepG2 tumour nodules appeared earlier in the medium outside the cirrhotic gels and were significantly larger in size when compared to those found in the medium outside a fibrotic gel. Cells derived from these tumour nodules showed an increased mRNA expression of αSMA and SNAIL, and decrease in E-cadherin when comparing cirrhotic to fibrotic environment, thus suggesting that increased stiffness could induce EMT in HCC cells. HepG2 cells grown in the 3D cirrhotic group were also more resistant to doxorubicin treatment compared with those grown in the 3D fibrotic group or grown in 2D. No differences were seen in drug distribution and penetrations between the two different gel compositions, thus further confirming that stiffness induced changes in the HCC phenotype that could explain a reduced response to chemotherapy. This was then confirmed by an increased expression of the drug resistance gene MDR1 in HepG2 cells grown in a cirrhotic gel, compared to those grown in a fibrotic gel.

Conclusion: Increasing the stiffness of the liver markedly increases the formation of metastatic nodules, induces several markers of EMT and reduces response to chemotherapeutics in a biomimetic 3D model of HCC.

THU545

Ascites reduction and anti-inflammatory effects after albumin infusion for the management of cirrhosis: evidence from an animal model

Raquel Horrillo1, Anna Mestre1, Estefania Alcaraz1, Guillermo Fernández Varo2, Wladimiro Jiménez-2,3, Ricardo Gonzalo1, Jordi Vidal1, Vicente Arroyo4, Joan Claria2,3,4, Todd Willis1, Montserrat Costa1,2, Grifols, Bioscience Research Group, Barcelona, Spain; Spain; 2Hospital Clinic, IDIBAPS and CIBEREhd, Barcelona, Spain; 3University of Barcelona Medical School, Department of Biomedical Sciences, Barcelona, Spain; 4EF Clínic EASL-CLIF Consortium and Grifols Chair, Barcelona, Spain

Email: montse.costa@grifols.com

Background and aims: The prevention of mortality by long-term albumin treatment in decompensated cirrhotic patients with ascites is currently under investigation (PRECIOSA phase 3 trial, NCT03451292). Albumin has non-oncotic functions such as binding, antioxidant and immunomodulatory capacities which have been postulated to be related to beneficial effects of albumin administration in cirrhotic patients. However, the specific mechanisms of action associated with albumin in liver cirrhosis are still under research. The present study was aimed at evaluating the effect of therapeutic albumin infusion in cirrhotic rats with ascites. Assessments included were albumin binding capacity, inflammation biomarkers, and a transcriptomic analysis.

Method: Male Wistar rats underwent chronic exposure to carbon tetrachloride to induce cirrhosis. Two weeks after ascites development, rats were randomized to receive intravenously therapeutic human albumin 1.5 g/Kg (Albutein®, Grifols; n = 20) or vehicle (0.9% saline; n = 16) on days 1 and 3. At day 4, ascites volume was assessed and serum and tissue samples were collected for biochemical and inflammatory markers determination (total protein, albumin, IL-2, IL-18, TNF-alpha), albumin binding capacity (using a specific fluorescent marker) and transcriptomic analysis (oxidative stress panel in liver and Toll-Like Receptors (TLR) panel in liver, heart and kidney). Results were expressed as median [IQR].

Results: Therapeutic albumin infusion increased total protein and albumin levels (32 [27–34] g/L), compared to vehicle (22 [18–26] g/L; p < 0.0001), 72 h after the initial administration. Human albumin represented 41% of total albumin. Ascites volume was significantly reduced after albumin infusion (2.0 [2.0–3.0] ml vs vehicle infused rats 13.5 [6.5–25.0] ml; p < 0.01). These changes were accompanied by an increase of albumin binding capacity (treated 49.2 [43.3–53.8%] vs vehicle 35.7 [33.3–43.4]; p < 0.01) and a decrease of serum proinflammatory cytokines IL-2 (p < 0.01), IL-18 (p < 0.01) and TNF-alpha (p < 0.05) in treated rats compared to vehicle. Furthermore, transcriptomic analysis in albumin-treated rats revealed an increase in albumin gene expression in the liver, and an attenuation of transcriptomic changes associated with TLR signaling pathways previously altered by cirrhosis induction in liver, heart and kidney.
Conclusion: Albumin infusion resulted in increased albumin binding capacity that was accompanied by ascites mobilization and reduced systemic inflammation as observed by a decrease of cytokine levels and attenuation of transcriptomic changes in TLR signaling pathways. These results using an animal model are in agreement with the role of albumin ameliorating liver disease complications.

THU546
Presence of NOD2 mutations is not associated with hepatic or systemic hemodynamic abnormalities of cirrhosis
Robin Greinert1, Alexander Zipprich2, Anna Hauptmann3, Markus Casper3, Frank Lammert2, Cristina Ripoll2, Martin-Luther University Halle Wittenberg, Internal Medicine I, Halle, Germany; University Hospital Jena, Internal Medicine IV, Jena, Germany; Saarland University Medical Center, Internal Medicine II, Homburg, Germany
Email: robin.greinert@uk-halle.de

Background and aims: Presence of NOD2 mutations has been associated to infections in cirrhosis. This association is more evident in compensated patients (pts) (PMID: 30702490). According to the systemic inflammation hypothesis, bacterial translocation is one of the main drivers of complications of end-stage liver disease. The aim was to evaluate the association of NOD2 mutations with hepatic and systemic hemodynamics.

Method: The presence of NOD2 risk variants (p.N289S, p.R702W, p.S389) was evaluated in 825 pts (screening in context of INCA trial: EudraCT 2013-001626-26). From these, 215 pts received a hepatic hemodynamic study and right heart catheterization. This cross-sectional study compared hepatic hemodynamic and systemic hemodynamics according to NOD2 status. Variables are described with median (IQR) or proportions. Mann Whitney U or Chi-square test were applied.

Results: Two-hundred-fifteen pts were included [median age 59 (IQR 53–66); male 67%; 76% alcohol associated cirrhosis]. Most pts were Child Pugh stage B (A 25%, B 64%, C 11%). Sixty-six pts (31%) carried a NOD2 risk variant, of which 64 were heterozygous pts. Although there was an increase in the proportion of NOD2 risk variants among Child Pugh stage C (p = 0.05), no differences were observed in MELD score [wild-type: 13 (10–16); NOD2 variants 13 (10–18)]. No significant differences in hepatic and systemic hemodynamics were observed when comparing patients with and without NOD2 risk variants (table 1). Analyses were repeated excluding patients who were on prophylactic or therapeutic antibiotics, and again no association between hepatic or systemic hemodynamic parameters and NOD2 risk variants could be observed.

<table>
<thead>
<tr>
<th>NOD2 wild-type</th>
<th>NOD2 Variants</th>
<th>p value</th>
</tr>
</thead>
<tbody>
<tr>
<td>HR (bpm)</td>
<td>74 (65–83)</td>
<td>78 (65–87)</td>
</tr>
<tr>
<td>MAP (mmHg)</td>
<td>83 (76–89)</td>
<td>83 (75–91)</td>
</tr>
<tr>
<td>CO (l/min)</td>
<td>5.56 (4.67–7.08)</td>
<td>5.97 (4.98–7.64)</td>
</tr>
<tr>
<td>CI (l/min/m2)</td>
<td>2.93 (2.47–3.52)</td>
<td>3.31 (2.59–3.95)</td>
</tr>
<tr>
<td>SVR (dyn·sec·cm⁻⁴)</td>
<td>1069 (840–1376)</td>
<td>1042 (747–1273)</td>
</tr>
<tr>
<td>SVRI (dyn·sec·cm⁻⁴/m²)</td>
<td>2016 (1641–2490)</td>
<td>1814 (1473–2399)</td>
</tr>
<tr>
<td>PAP (mmHg)</td>
<td>16 (13–20)</td>
<td>17 (14–20)</td>
</tr>
<tr>
<td>PCWP (mmHg)</td>
<td>11 (7–15)</td>
<td>12 (8–15)</td>
</tr>
<tr>
<td>PHT (dyn·sec·cm⁻⁴)</td>
<td>75 (43–112)</td>
<td>65 (32–112)</td>
</tr>
<tr>
<td>VCI (mmHg)</td>
<td>8 (6–12)</td>
<td>8 (5–11)</td>
</tr>
<tr>
<td>WHVP (mmHg)</td>
<td>29 (23–32)</td>
<td>28 (23–35)</td>
</tr>
<tr>
<td>FHV (mmHg)</td>
<td>12 (8–15)</td>
<td>12 (7–15)</td>
</tr>
<tr>
<td>HVPG (mmHg)</td>
<td>19 (15–22)</td>
<td>19 (15–23)</td>
</tr>
</tbody>
</table>

THU547
Demonstration of gut-barrier dysfunction and endotoxemia in patients with cirrhosis presenting with acute variceal bleeding: a proof of concept
Rajat Bansal1, Samagra Agarwal1, Sanchit Sharma1,2, Kanav Kaushal1,2, Srikanth Gopi1, Deepak Gunjan1, Anoon Saraya1, All India Institute of Medical Sciences, Gastroenterology and Human Nutrition Unit, New Delhi, India; John Radcliffe Hospital, Translational Gastroenterology Unit, Oxford, United Kingdom
Email: ansaraya@yahoo.com

Background and aims: Limited data exist on the demonstration of gut-barrier dysfunction and factors predisposing to this in patients with chronic liver disease (CLD) presenting with acute variceal bleeding (AVB). We studied the presence of this dysfunction in a prospectively recruited cohort of patients with AVB.

Method: Consecutive patients with CLD presenting with AVB were prospectively included, who underwent duodenal biopsy at the time of upper GI endoscopy. Gut-barrier dysfunction was demonstrated by semi-quantitative immunohistochemical (IHC) expression of tight junction proteins like claudin-2, claudin-4, zonulin-1, occludin and junctional adhesion molecule-A (JAM-A) in both villi and crypt of duodenal biopsies. Endotoxemia was estimated indirectly using serum IgM anti-endotoxin assay and systemic inflammation was evaluated using serum interleukin-1 (IL-1) and tumor necrosis factor alpha (TNF-alpha) levels. The expression was compared across different Child-Pugh strata of liver disease and with a control group of cirrhosis without AVB.

Results: Patients with CLD presenting with AVB (n = 71) (Child A/B/C: 25/30/16) and controls (n = 84) were recruited. Zonulin-1 protein expression was elevated [H score at crypt: AVB: 9 (9–9) vs controls: 2 (1–6), p < 0.001; H score at villi: AVB: 6 (6–9) vs controls: 2 (2–6), p < 0.001] in patients with AVB. IgM endotoxin levels (AVB: 28.5 ± 9.9 MMU/ml vs controls: 87.4 ± 20.2 MMU/ml; p < 0.001) were lower while IL-1 (AVB: 1005 ± 82 pg/ml vs controls: 49 ± 14.4 pg/ml; p < 0.001) were elevated in AVB cohort. No difference was seen in the IHC expression of any tight junction barrier proteins, IgM endotoxin, IL-1 and TNF-alpha levels across different strata of liver disease. No association was seen between the studied proteins expression with the aetiology, active alcohol consumption, hypotension at presentation, hepatic venous pressure gradient and presence of active bleeding on endoscopy.

Conclusion: The presence of NOD2 mutations is not associated with hepatic or systemic hemodynamic abnormalities in patients with cirrhosis, suggesting that other mechanisms leading to bacterial translocation predominate.
Worsening of low-grade systemic inflammation heralds compensation and severity of bleeding episode.

Conclusion: While the gut-barrier dysfunction, endotoxemia and systemic inflammation are upregulated in patients with cirrhosis with A VB, the extent of these changes may be independent of aetiology and severity of liver disease, degree of portal hypertension and severity of bleeding episode.

THU548
Worsening of low-grade systemic inflammation heralds compensation in patients with compensated cirrhosis
Rubén Sánchez-Aldehuelo1, Cándid Villanueva1, Joan Genesca2,4, Juan Carlos García Pagan3, Ana Brujats4, José Luis Calleja Panero3,6, Carlos Aracil2, Rafael Bañares3,8, Rosa M Morillas3,9, Maria Poca2,3, Beatriz Peñas1,3, Salvador Augustin3,10, Juan Abraldes3,5,11, Edilmar Alvarado-Tapias2,3, Ferran Torres12,13, Jaime Bosch3,5,14, Agustín Albillos1,3, 1Ramón y Cajal University Hospital, Ramón y Cajal Institute of Health Research (IRYCS), University of Alcalá, Madrid, Spain; 2Hospital of Santa Creu and Sant Pau, Autonomous University of Barcelona, Hospital Sant Pau Biomedical Research Institute (IIB Sant Pau) Barcelona, Spain; 3Centre for Biomedical Research in Liver and Digestive Diseases Network (CIBERHebd); 4Liver Unit, Vall d’Hebron University Hospital, Vall d’Hebron Research Institute (VHRI), Autonomous University of Barcelona, Barcelona, Spain; 5Barcelona Hepatic Haemodynamic Laboratory, Liver Unit, Institute of Digestive and Metabolic Diseases, August Pi i Sunyer Institute of Biomedical Research, Hospital Clínic, Barcelona, Spain; 6Puerta de Hierro University Hospital, Puerta de Hierro University Hospital Research Institute, Autonomous University of Madrid, Madrid, Spain; 7Institute of Biomedical Research, Arnau de Vilanova University Hospital (IRBLeida), Lleida, Spain; 8Gregorio Marañón University General Hospital, Gregorio Marañón Sanitary Research Institute, Faculty of Medicine, Complutense University of Madrid, Spain; 9Hospital University Germans Trias i Pujol, Badalona, Spain; 10Liver Unit, Vall d’Hebron University Hospital, Vall d’Hebron Research Institute (VHRI), Autonomous University of Barcelona, Barcelona, Spain; 11University of Alberta, Edmonton, Canada; 12Medical Statistics Core Facility, August Pi i Sunyer Biomedical Research Institute, Hospital Clinic, Barcelona; 13Biostatistics Unit, Faculty of Medicine, Autonomous University of Barcelona, Barcelona, Spain; 14InserMespital, Bern University, Switzerland

Email: ruben.sanchez.aldehuelo@gmail.com

Background and aims: Portal hypertension is a major driver of progression and decompensation in cirrhosis. Systemic inflammation has been recognized in decompensated cirrhosis, where it contributes to accelerate the disease course. However, less information is available regarding inflammation in patients with compensated cirrhosis. Our aims were to investigate i) whether systemic inflammation is present in patients with compensated cirrhosis, and if so, ii) whether its worsening associates with the development of complications.

Method: This is a nested cohort study within the PREDESCI trial, a double blind multicentre, RCT to evaluate the efficacy of beta-blockers to prevent decompensation in patients with compensated cirrhosis and clinically significant portal hypertension (HVPG ≥10 mmHg). Biomarkers were measured in blood at baseline and at 1-year follow-up. Development of complications of portal hypertension was registered during the study. A group of 35 healthy controls was included for the specific purposes of this study.

Results: We included 201 patients with compensated cirrhosis, most (56.2%) by chronic hepatitis C, that were followed-up for a median of 37 months (27–47). Decompensation occurred in 17.4% at a median of 24 months (13.6–31.4), being ascites the main cause of decompensation (14.4%). Low-grade systemic inflammation was present at baseline and at 1-year as shown by greater serum levels of IL-6, von Willebrand factor (vWF) and CD163 at both time points in patients compared to controls (Table). Compared to baseline, IL-6 increased (p < 0.05) at 1-year in those patients that decompensated on follow-up. Fatty acid binding protein (FABP), used as marker of intestinal barrier function, was greater in patients compared to controls. Values of TNFa, IL1b, IL8 LBP and CD14 were similar in patients and controls at all points. The macrophage activation marker, CD163, correlated (r = 0.27) and at 1-yr (r = 0.46).

Background and aims: Lipids, especially lipid mediators derived from polyunsaturated fatty acids (PUFA), play a critical role in the regulation of inflammatory and immune responses. In this investigation, we characterized the blood lipid profile in patients with...
acutely decompensated (AD) cirrhosis and explored how changes in this profile might affect the composition of circulating albumin. In addition, we investigated the effects of albumin on the release of PUFAs-derived lipid mediators by peripheral leukocytes.

Method: Lipids and lipid mediators were measured by liquid chromatography-tandem mass spectrometry in leukocyte incubations, plasma and albumin-enriched and albumin-depleted plasma fractions from 18 patients with AD and 10 healthy subjects. Lipid mediators were also measured in 41 patients with AD included in an albumin therapy trial.

Results: The plasma lipidome associated with AD cirrhosis was characterized by generalized suppression of all lipid classes except FAs. The lipid profile of circulating albumin in AD patients was dominated by reduced content of docosahexaenoic acid (DHA) (omega-3–PUFA) and anti-inflammatory/pro-resolving lipid mediators (i.e. 15-hydroxyeicosatetraenoic acid (15–HETE) and 17-hydroxydocosahexaenoic acid (17–HDHA)). In addition, albumin from AD patients was depleted in prostaglandins (PGs) (PGE2, PGD2 and PGF2α), implying dysregulated degradation and higher circulatory content of these pro-inflammatory lipid mediators. Incubation of leukocytes with exogenous albumin reduced PG production while inducing 15-lipoxygenase expression and 15–HETE and 17–HDHA release. Finally, PGE2 and PGD2 levels were lower in AD patients receiving albumin therapy whereas 15–HETE was increased after albumin treatment compared to baseline.

Conclusion: Our findings indicate that both blood and albumin lipid landscape is severely disorganized in AD cirrhosis and that exogenous albumin has potential to redirect leukocyte biosynthesis from pro-inflammatory to pro-resolving lipid mediators.

THU550
miRNA associated with systemic inflammation may have prognostic utility in predicting decomposition in patients with chronic liver disease

Oliver Tavabie1, Vishal C Patel2,3,4, Siamak Salehi1, Marilena Stamouli1, Francesca Trovato1, Savannah Rivera1, Salma Mujib1, Ane Zamalloa1, Eleanor Corcoran1, Krishna Menon1, Andreas Prachalias1, Michael Heneghan3, Kosh Agarwal1, Mark J W McPhail3, Varuna Aluvihare1, 1King’s College Hospital, United Kingdom; 2King’s College Hospital, Institute of Liver Studies and Transplantation, London, United Kingdom; 3Foundation For Liver Research, The Roger Williams Institute of Hepatology, London, United Kingdom; 4Institute of Liver Sciences, King’s College London, Department of Inflammation Biology, School of Immunology and Microbial Sciences, FoLSM, London, United Kingdom
Email: oliver.tavabie@nhs.net

Background and aims: Chronic liver disease (CLD) is associated with significant mortality and encompasses; acute-on-chronic liver failure (ACLF), acute decompensation (AD), chronic decompensation (dCLD) and compensated CLD (cCLD). Transition between these states impacts on patient (Pt) survival. Here we investigate miRNA expression across the spectrum of CLD to evaluate their prognostic utility.

Method: Plasma samples were provided by pts and healthy controls (HC). Pts sampled included ACLF, AD, dCLD, HC (each groups n = 20) and dCLD (n = 94). ACLF and AD Pts were sampled within 72 hours of admission. 90-day transplant-free survival (TxFS) across Pts with CLD was 68.8%. 6 Pts in the cCLD group decompensated in the year post-sampling. A panel of 21 miRNA developed from our previous studies were analysed. Univariate and multivariate analyses were utilized to identify miRNA associated with decompensated CLD states and 90-day TxFS.

Results: Figure 1 demonstrates significant correlations of miRNA with clinical and laboratory parameters across CLD groups. Notably, miR-24 correlated with markers of systemic inflammation (CRP), liver failure (bilirubin, INR, lactate and ascites) and CLD prognostic models (Child–Pugh r (s) = 0.25 (95%CI 0.09–0.40), MELD r (s) = 0.25 (95%CI 0.09–0.40)). miRNA expression was compared between ACLF/AD/ dCLD cohorts and HC/cCLD cohorts. Downregulation of miR-122, −24 and −29a and upregulation of miR-223, −27a and −29b was associated with decompensated CLD states. MetaCore pathway analysis demonstrated an association between these miRNA and systemic inflammation (z = 188.35, p < 0.0001). A model including miR-24 and −27a discriminated Pts with ACLF/AD/dCLD from cCLD/ HC Pts (AUC 0.77 (95%CI 0.69–0.85)). Sensitivity analyses were performed excluding each group individually. Excluding the HC cohort reduced model performance (AUC 0.69 (95%CI 0.56–0.81)). However, subsequently excluding the 6 cCLD Pts who decompensated the following year improved this (AUC 0.74 (95%CI 0.60–0.88)). Only the detection of miR-200b discriminated 90-day TxFS across CLD groups but did not remain significant when adjusted for MELD. Subgroup analysis of Pts with; dCLD, alcohol related CLD (ARLD) and ascites Pts demonstrated different miRNAs associated with 90-day TxFS (miR-24 in dCLD, miR-220b in ARLD and no miRNA in ascites Pts). Only the detection miR-200b in ARLD Pts remained significant when adjusted for MELD (aOR 0.23 (95%CI 0.06–0.82).
Liver tumours: Therapy

THU566
Systemic treatments with tyrosine kinase inhibitors and platinum-based chemotherapy in patients with unresectable or metastatic hepato-cholangiocarcinoma
Elia Gigante1,2, Christian Hobelka3, Brigitte Le Bail4, Valérie Paradis5, David Tougeron6, Marie Lequoy7, Mohamed Bouattour8, Jean-Frédéric Blanc9, Nathalie Ganne-Carrié1, Henri Tran1, Clemence Hollandie10, Manon Allaire11, Giuliana Amaddeo12, Helene Regnault12, Paul Vigneron12, Maxime Ronot13, Laure Elkrief14, Contran Verset15, Eric Trepo15, Aziz Zaan16,6, Marianne Ziol17, Massih Ningarhari18, Julien Calderaro19, Julien Edeline20, Paul Vigneron12, Maxime Ronot13, Laure Elkrief14.

Background and aims: Although there is currently no validated systemic therapy for unresectable hepatocellular carcinoma (HCC-CCA), tyrosine kinase inhibitors and platinum-based chemotherapy are frequently used in clinical practice. Our study has aimed to describe the effectiveness of first-line systemic treatments in patients with cHCC-CCA.

Method: Patients with histological diagnosis of unresectable or metastatic chCC-CCA confirmed by a centralized review (WHO classification 2019) who received systemic treatment from 2009 to 2020 were included retrospectively in 11 centers. The outcomes of patients with chCC-CCA were compared with patients with hepato-cellular carcinoma (HCC) treated by sorafenib (n = 225) and with intrahepatic cholangiocarcinoma (iCCA, n = 94) treated mainly by platinum using a frailty Cox model. The efficacy of tyrosine kinase therapy are frequently used in clinical practice. Our study has aim to describe the effectiveness of first-line systemic treatments in patients with cHCC-CCA.

Results: A total of 83 patients with chCC-CCA were included and were predominantly male (72%), 67% of patients had extrahepatic metastases and 31% macrovascular tumor invasion. Compared with iCCA (n = 94) and HCC (n = 225), chCC-CCA were more often developed on cirrhosis (55%) than iCCA (27%) but less frequently than HCC (88%) (p < 0.001). cHCC-CCA (66%) and HCC (30%) had extrahepatic metastases less frequently than iCCA (81%) (p < 0.001). Unadjusted overall survival was better in CCA (13 months) compared to chCC-CCA (12 months) and HCC (9 months) (p = 0.017). In multivariate analysis after adjustment by a Cox frailty model, patients with chCC-CCA had the same survival than HCC and iCCA (HR = 1.5; 95% CI = 0.98, 2.3; p = 0.063). ALBI score (HR = 2.15; CI0.1.13, 3.76; p = 0.09), ascites (HR = 3.45, CI95%:1.31, 9.03; p = 0.013) and tobacco (HR = 2.29; CI95%:1.08, 4.87; p = 0.032) were independently associated with OS in patients with chCC-CCA. Among patients with chCC-CCA, 25 patients treated with tyrosine kinase inhibitors were compared with 54 patients with platinum-based chemotherapies. Patients treated by tyrosine kinase inhibitors had a median overall survival of 728 months versus 12.1 months for patients treated with platinum-based chemotherapies (p = 0.86) (Figure). After a robust double adjustment on tumor number and size, vascular invasion, ALBI, MELD and cirrhosis, treatment’s regimen had no influence on overall survival (HR = 0.92, 95%CI = 0.27–3.15, P = 0.88) and progression-free survival (HR = 1.24, 95%CI = 0.44–3.49, P = 0.67).

Conclusion: Systemic treatments with tyrosine kinase inhibitors or platinum-based chemotherapies have similar efficacy in first line of patients with unresectable/metastatic chHCC-CCA. The ALBI score predicts overall survival.

THU567
The systemic inflammatory response identifies patients with adverse clinical outcome from immunotherapy in hepatocellular carcinoma
Claudia Fulgenzi1,2, Ambreen Muhammad2, Sirish Dharmapuri3, Matthias Pinter4, Lorenz Balcar4, Bernhard Scheiner4, Thomas U. Marron3, Tomi Jun4, Anwaar Saeed5, Hannah Hildebrand6, Mahvish Muzaffar7, Musharraf Nawaid8, Abdul Rafeh Naqash9, Anuhya Gampa8, Umut Ozbek7, Yinghong Wang9, Uqba Khan10, Yi-Hsiang Huang11, Dominik Bettinger12, Yehia Abugabal13, Ahmed Kasheb13, Tiziana Pressiani14, Nicola Personeni15,16, Lorenza Rimassa15, Nicolai Nishiida16, Luca Di Tommaso12, Masatoshi Kudo12, Arndt Vogel12, Francesco Mauri1, Alessio Cortellini2, Rohini Sharma2, Antonio D’Alessio17,18, Celina Ang19, David J. Pinato19, Campus Biomedico, Medical Oncology, Roma, Italy; 10University of Milan, Department of Medical Oncology, Milan, Italy; 11University of Maastricht, Department of Hematology and Oncology, Maastricht, Netherlands; 12The Mount Sinai Hospital, Department of Medicine, Division of Hematology/Oncology, New York, United States; 13Medical University of Vienna, Department of Internal Medicine III, Division of Gastroenterology and Hepatology, Wien, Austria; 14University of Kansas, Division of Medical Oncology, Department of Medicine, Westwood, United States; 15East Carolina University, Division of Hematology/Oncology, Greenville, United States; 16University of Kansas, Division of Medical Oncology, Department of Medicine, Westwood, United States; 17The University of Texas MD Anderson Cancer Center, Department of Gastroenterology, Hepatology and Nutrition, Houston, United States; 18NY-Presbyterian Hospital, Division of Hematology and Oncology, New York, United States; 19Veterans General Hospital, Division of Gastroenterology and Hepatology, Institute of Clinical Medicine, National Yang Ming Chiao
Background and aims: Systemic inflammation is a hallmark of cancer, and it has a pivotal role in HCC development and progression. The role of systemic inflammation in influencing outcomes of patients treated with immunotherapy for HCC has not been fully elucidated.

Method: We conducted a retrospective study including 362 patients receiving immune-checkpoint inhibitors (ICIs) across 3 continents, evaluating the influence of neutrophiles to lymphocytes ratio (NLR), platelet to lymphocytes ratio (PLR) and prognostic nutritional index (PNI) on overall (OS), progression free survival (PFS) and radiologic responses.

Results: In our 362 patients treated with immunotherapy, median OS and PFS were 9 and 3.5 months respectively. Amongst tested inflammatory biomarkers, patients with NLR ≥5 had shorter OS (7.7 vs 17.6 months, p < 0.0001), PLR ≥300 reported shorter OS (6.4 vs 16.5 months, p < 0.0001) and PFS (1.8 vs 3.7 months, p = 0.0006). NLR emerged as independent prognostic factors for OS in univariate and multivariate analysis (HR 1.95, 95%CI 1.11–3.49, p = 0.021). Multivariate analysis showed that low CRAFTY score (NLR <100 ng/ml or CRP <10 mg/l) and satisfactory AFP response at 6 weeks (≥75% decrease or ≤10% increase from baseline) were independent factors associated with good OS (hazard ratio [HR] = 0.263, p = 0.041 and HR = 0.102, p = 0.004), PFS (HR = 0.681, p = 0.046 and HR = 0.326, p = 0.008) and good responder (odds ratio [OR] = 4.354, p = 0.044 and OR = 6.406, p = 0.017). Patients were further divided into three classes: low CRAFTY score (0–1 points) with satisfactory AFP response at 6 weeks (class I), either high CRAFTY score (2 points) or unsatisfactory AFP response at 6 weeks (class II) and neither low CRAFTY score nor satisfactory AFP response at 6 weeks (class III).

Conclusion: Systemic inflammation measured by NLR and PLR is an independent negative prognostic factor in HCC patients undergoing ICI therapy. Further studies are required to understand the biological mechanisms underlying this association and to investigate the predictive significance of circulating inflammatory biomarkers in HCC patients treated with ICIs.
In this retrospective study, we analyzed all patients or procedure-related factors influencing TO. This study aimed to propose a uniform (MH) which remains the only curative therapy option for perihilar cholangiocarcinoma (PHC). This study investigated the effect of BMI on safety and efficacy of real-life use of atezolizumab plus bevacizumab in patients with advanced HCC and DFS (disease-free survival) did not differ significantly between the outcome groups (OS: p = 0.280, DFS: p = 0.735). However, there was a trend towards better overall survival, especially in the late course with TO. The differences in OS between the TO and no TO groups were statistically significant when analyzing patients with survival of at least 30 months (p = 0.039, Figure 1).

**Conclusion:**
Our analysis proposed a uniform definition of TO after MH for PHC. We identified left hepatectomy as an independent factor positively influencing TO. In patients where both right- and left-sided resections are feasible, this underlines the importance of a careful selection of patients who are scheduled for right hepatectomy.

**THU571 Impact of body mass index in patients receiving atezolizumab plus bevacizumab for hepatocellular carcinoma**

Mathew Vithayathil1, Antonio D’Alessio 1,2, Arndt Weinmann3, Peter Galle1, Claudia Angela Maria Fulgenzi 1,4, Petros Fessas1, Dominik Bettinger3, Bertram Bengsch3, Arndt Vogel3, Lorenz Balcar7, Bernhard Scheiner2, Mahvish Muzaffar3, Suneetha Amara4, Ambreen Muhammed7, Abdul Rafeh Nqash6, Nicola Personeni2,9, Tiziana Pressiani7, Antonella Cammarata2,8, Matthias Pinter3, Alessio Cortellini1,10, Lorenza Rimassa2,9, David J. Pinato1,11, Rohini Sharma1,1 Imperial College London, United Kingdom; 2Humanitas University, Italy; 3Universitätsmedizin der Johannes Gutenberg-Universität Mainz, Mainz, Germany; 4Bio-Medico Campus University Hospital, Roma, Italy; 5University of Freiburg, Freiburg University Medical Center, Freiburg im Breisgau, Germany; 6Hanover Medical School, Hannover, Germany; 7Medical University of Vienna, Wien, Austria; 8East Carolina University, Greenville, United States; 9Humanitas Research Hospital, Cascina Perseghetto, Italy; 10University of L’Aquila, L’Aquila, Italy; 11University of Eastern Piedmont, Vercelli, Italy

**Background and aims:** Atezolizumab plus bevacizumab is the new first-line treatment for unresectable hepatocellular carcinoma (HCC). Body mass index (BMI) has demonstrated predictive value for response to immunotherapy in non-HCC cancer types. Our study investigated the effect of BMI on safety and efficacy of real-life use of atezolizumab plus bevacizumab.

**Results:**
Of 283 patients, TO was achieved in 67 (24%) patients. Multivariate regression analysis revealed that preoperative biliary drainage was associated with a decreased (OR = 0.405, 95% CI: 0.194–0.845, p = 0.016) and left-sided-resection (OR = 1.899, 95% CI: 1.048–3.440, p = 0.035) with increased odds for TO. Overall survival (OS) and DFS (disease-free survival) did not differ significantly between the outcome groups (OS: p = 0.280, DFS: p = 0.735). However, there was a trend towards better overall survival, especially in the late course with TO. The differences in OS between the TO and no TO groups were statistically significant when analyzing patients with survival of at least 30 months (p = 0.039, Figure 1).
Method: Sixty-four consecutive patients from seven centres receiving atezolizumab plus bevacizumab were included in the retrospective study. Overall survival (OS), progression-free survival (PFS), overall response rate (ORR) and disease control rate (DCR) defined by RECIST v1.1 were measured in overweight (BMI ≥ 25) and non-overweight (BMI < 25) patients. Treatment-related adverse events (trAEs) were evaluated for each BMI cohort.

Results: Baseline Child-Pugh class, Eastern Cooperative Oncology Group performance status and Barcelona Clinic Liver Cancer stage was similar between overweight (n = 36) and non-overweight patients (n = 28). Underlying non-alcoholic fatty liver disease was more prevalent in overweight patients (27.8 vs. 7.1%; p = 0.04). Overweight patients had a longer OS compared to non-overweight (median OS 11.6 vs. 7.5 months; p = 0.045) (Figure 1). BMI did not influence median PFS (6.9 vs. 3.0 months; p = 0.34), ORR (26.7% vs. 25.0%; p = 0.90) and DCR (63.3% vs. 60.0%; p = 0.81). trAEs were comparable between the two groups (atezolizumab-related 44.4% vs. 53.6%; p = 0.47 and bevacizumab-related 18.8% vs. 12.5%; p = 0.68).

Conclusion: Higher BMI is associated with increased OS in HCC patients receiving atezolizumab plus bevacizumab for unresectable HCC, without an increase in trAEs. BMI may have a predictive role in immunotherapy treatment response in HCC.

THU572 Outcome predictors of gemcitabine-based or fluoropyrimidine-based chemotherapy for unresectable intrahepatic cholangiocarcinoma

Chen-Ta Ch1, 2, I-Cheng Lee3, Ming-Huang Chen3, Pei-Chang Lee1, Yi-Ping Hung1, Ming-Chih Hou1, Yee Chao3, Yi-Hsiang Huang1, 2.

1Taipei Veterans General Hospital, Taipei, Taiwan, Division of Gastroenterology and Hepatology, Department of Medicine; 2National Yang Ming Chiao Tung University, Taipei, Taiwan, Institute of Clinical Medicine, School of Medicine; 3Taipei Veterans General Hospital, Taipei, Taiwan, Department of Oncology.

Email: yhhuang@vghtpe.gov.tw

Background and aims: Intrahepatic cholangiocarcinoma (ICC) is a highly aggressive malignancy, and the resectability rate for curative surgical resection is low. Gemcitabine-based and fluoropyrimidine-based chemotherapy are the mainstay treatments for Unresectable ICC, even though the survival is still far from satisfaction in real-world experience. This study aimed to assess outcomes and identify the prognostic factors for patients with unresectable ICC patients receiving gemcitabine-based or fluoropyrimidine-based chemotherapy.

Method: From December 2006 to January 2020, consecutive 309 unresectable ICC patients were enrolled. Of them, 162 ICC patients received chemotherapy as first-line treatment were retrospectively reviewed, and 123 patients had evaluable images for tumour response evaluation. Objective response rate (ORR) and overall survival (OS) were assessed and factors associated with ORR and OS were analysed.

Results: Of the 162 ICC patients received chemotherapy as first-line therapy, the mean age was 62 years old. Most patients were within Child-Pugh class A (61.7%) and Albumin-bilirubin (ALBI) grade 2/3 (67.3%). Of them, 106 (65.4%) received gemcitabine-based regimen, while 56 (34.6%) patients received fluoropyrimidine-based regimen. The ORR was 26.0% and disease control rate (DCR) was 48.0% in the whole 123 ICC patients with evaluable images (including 32 partial responses, 27 stable diseases, and 64 progressive disease). HBV infection (OR, 3.223; p = 0.032), gemcitabine-based regimen (OR, 4.714; p = 0.008) were the independent predictors of ORR. In general, the median OS of the 162 ICC patients was 6.1 months. Presence of cirrhosis, Albumin < 3.5 g/dl, Child-Pugh B/C, ALBI grade 2/3, NLR ≥ 3, and CA 19-9 ≥ 300 U/ml were independent risk factors associated with OS. A novel ALBI-based scoring system to predict OS was created, the patients could be classified into 4 groups. Kaplan-Meier analysis showed that the new ALBI-based model could significantly discriminate OS between contiguous groups (p < 0.001, Figure). Noteworthily, patients without any risk factors had a promising overall survival of 21.3 months.

Conclusion: Albumin-bilirubin grade is an important factor associated with survival in unresectable ICC patients receiving chemotherapy. The new ALBI-based model can be applied to select patients who can get the best benefit from chemotherapy.

Conflict of Interest: The authors declared no conflicts of interest.

Funding: The work was partly supported by the Taipei Veterans General Hospital, Taipei, Taiwan (grant numbers V110A-004).

THU573 Transarterial radioembolisation in non resectable hepatocellular carcinoma in curative strategies: a single centre experience

Helene Regnault1, Clara Perrin2, Giuliana Amaddeo3, Sebastien Mulé1, Hicham Kobeiter1, Edouard Rezine1, Emmanuel Itti1, Christophe Duvox1, Alexis Laurent1, Vincent Leroy1, Raffaele Brustia2, Daniele Sommacale 1, Françoise Roudot-Thoraval1, Christophe Duvoux1, Alexis Laurent1, Vincent Leroy1, Raffaele Brustia2, Daniele Sommacale 1, Françoise Roudot-Thoraval1, Lerman Lionel1, Alain Luciani 1, Julien Calderaro 1, Julia Chalaye1, Hicham Kobeiter1, Edouard Rezine1, Emmanuel Itti1, Christophe Duvox1, Alexis Laurent1, Vincent Leroy1, Raffaele Brustia2, Daniele Sommacale 1, Françoise Roudot-Thoraval1, Lerman Lionel1, Alain Luciani1, Julien Calderaro1, Julia Chalaye1, Vanja Tacher1, Athena Galletto 1, 2, Henri Mondor University Hospital, Hepatology, Créteil, France; 3Antoine Beclere University Hospital, Hepatology, Clamart, France; 4Henri Mondor University Hospital, Medical Imaging, Créteil, France.

Email: heleneregnault@aphp.fr

Background and aims: Transarterial radioembolisation (TARE) has the potential to be curative either directly (radiation segmentectomy) or as neoadjuvant strategy before resection or transplantation.
POSTER PRESENTATIONS

However, its place remains largely debated. The aim of our study was to evaluate the outcome of initially non-operative patients after TARE in a single tertiary centre.

**Method:** This retrospective, observational study included all consecutive patients treated by TARE in our centre between October 2013 and June 2020. Clinical, biological and imaging data were collected at baseline and every 3 months during follow-up. Tumour response was evaluated at 6 months according to Response Evaluation Criteria in Solid Tumors (RECIST) 1.1 and modified RECIST (mRECIST). The suitability of surgical treatment after downstaging was systematically discussed in a weekly tumour board.

**Results:** 128 patients (male = 90%, mean age 64 years) were included. The majority (n = 88%) had cirrhosis (CPT A: 84%, CPT B: 16%) mainly due to viral hepatitis (21%), non-alcoholic steatohepatitis (18%) and alcohol (18%). HCC was classified as BCLC A: n = 14 (11%), BCLC B: n = 50 (39%) and BCLC C: n = 64 (50%). The majority of patients had an imaging infiltrative pattern: n = 62 (49%) classified as VP1: n = 3, VP 2: n = 22, VP3: n = 28 and VP4: n = 9. Median AFP was 115. TARE was the first-line therapy in 77 patients. TARE could be successfully applied in all patients. At 6 months, the rates of complete and partial responses were 4 and 40% respectively, according to RECIST and 23 and 28% according to mRECIST. A downstaging was obtained in 50 (39%) patients, whom 29 (23%) had access to a curative treatment (transplantation: n = 17 (13%), resection: n = 11 (9%) and ablation: n = 1) in a median time of 4.3 months. Absence of access to surgery was due to general contra-indication (n = 10), progression (n = 5), refusal (n = 4) and presence on waiting list (n = 2). Median overall survival of patients with or without downstaging were 50.1 months [8.6–78.8] and 10.2 months [8.1–12.4] (p < 0.001) respectively. Progression free survival (PFS) of patients with or without downstaging were 20.8 months [14.8–26.8] and 5.4 months [4.7–6.1] (p < 0.001) respectively. In patients who achieved downstaging, PFS was higher in patients who had surgery (median not achieved). Two variables were independently associated to downstaging: BCLC score (p = 0.0, 049) and ALBI score (p = 0.042).

**Conclusion:** These results suggest that TARE could be an effective treatment leading to downstaging of 40% patients with unresectable HCC, and allowed curative treatment in 57% of them. Combination of TARE followed by curative treatment is associated with a 2 year survival of 70% vs 0% in patients with no downstaging.

**THU574**

**Preliminary evidence of safety and tolerability of atezolizumab plus bevacizumab in patients with hepatocellular carcinoma and Child-Pugh A and B cirrhosis: a real-world study**

Antonio D’Alessio1,2, Arndt Weinmann3, Peter Galle4, Vincenti Gaillard5, Claudia Angela Maria Fulgenzi1,5, Dominik Bettinger6, Bertram Bengsch6, Arndt Vogel7, Lorenz Balcar4, Bernhard Scheiner8, Suneetha Amara9, Mahvish Muzaffar10, Abdul Rafeh Naqash9,10, Nicola Personeni2,11, Tiziana Pressiani11, Rohini Sharma1, Matthias Pinter4, Alessio Cortellini1, Lorenza Rimassa2,11, David J. Pinato1,12. **Imperial College London, Department of Surgery and Cancer, London, United Kingdom; 2Humanitas University, Department of Biomedical Sciences, Italy; 3Johannes Gutenberg University of Mainz, Mainz, Germany; 4E Hoffmann-La Roche Ltd., Basel, Switzerland; 5Policlinico Universitario Campus Bio-Medico, Division of Medical Oncology, Roma, Italy; 6Department of Medicine II (Gastroenterology, Hepatology, Endocrinology and Infectious Diseases), Freiburg University Medical Center, Faculty of Medicine, University of Freiburg, Freiburg, Germany; 7Harmoner Medical School, Hannover, Germany; 8Division of Gastroenterology and Hepatology, Department of Internal Medicine III, Medical University of Vienna, Vienna, Austria; 9Division of Hematology/Oncology, East Carolina University; 600 Moye Boulevard, Greenville, NC, 27834, USA; 10Medical Oncology/TSET Phase 1 program, Stephenson Cancer Center, University of Oklahoma USA; 11IRCCS Humanitas Research Hospital, Humanitas Cancer Center, Cascina Perseghetto, Italy; 12Division of Oncology, Department of Translational Medicine, University of Piemonte Orientale, Novara, Italy

Email: a.dalesio@imperial.ac.uk

**Background and aims:** Atezolizumab plus bevacizumab (A+B) is a new standard of care for first-line treatment of unresectable hepatocellular carcinoma (HCC). No evidence exists as to its use in routine clinical practice in patients with impaired liver function.

**Method:** This retrospective, multi-centre observational study was conducted across 7 tertiary centres and collected 64 HCC patients consecutively treated with A+B. Safety outcomes included treatment-related adverse events (trAEs) graded according to CTCAE v5.0. We also assessed overall survival (OS), progression-free survival (PFS), overall response (ORR) and disease control rates (DCR) defined by RECIST v1.1 in patients treated according to label.

**Results:** Fifty-four patients had Barcelona Clinic Liver Cancer (BCLC)-C stage HCC (84%), mostly secondary to non-viral aetiology (n = 30; 47%) and Hepatitis C virus (n = 24; 37%). Forty-three patients (67%) suffered from any trAE, of which 11 (17%) were G3 and 1 (2%) G4. Compared to Child-Pugh A (n = 46, 72%), Child-Pugh B patients showed comparable distribution of trAEs, with similar rates of bevacizumab-related bleedings and atezolizumab-related AE. In the 44 patients (69%) with a pre-treatment esophagastroduodenoscopy, presence and grade of varices did not correlate with gastrointestinal bleeding events. Median OS of patients treated in first line was 12.7 months (95% CI, 7.6–12.7), while median PFS was 6.97 months (95% CI, 2.8–11.3). ORR and DCR were respectively 29% and 67%, with no difference between patients with Child-Pugh A and B cirrhosis.

**Conclusion:** This study confirms reproducible efficacy and safety of A + B in routine practice. Child-Pugh B patients had similar tolerability and radiologic response compared to Child-Pugh A patients, warranting prospective evaluation of atezolizumab plus bevacizumab in this treatment-deprived population.
Conclusion: In early-stage iCCA patients, curative treatments are associated with improved survival. Surgical resection and liver transplantation are associated with improved survival compared to ablation.
observational open-label study, and were monitored at least every 12 weeks. Surveillance for HCC was performed by ultrasonography and alpha-fetoprotein (AFP) at each visit. HCC was diagnosed by multiphase dynamic contrast-enhanced MRI. Intention-to-treat analysis was performed with the use of Kaplan-Meier curves and log-rank test. The incidence of HCC was estimated with Cox proportional hazards regression models.

**Results:** Totally 1000 patients who received randomised treatment, 946 (94.6%) patients entered the open-label phase, and 872 (87.2%) completed 84-month follow-up. Overall (during a median follow-up of 89.0 months), 23 (4.6%) in ETV plus BJRG group and 43 (6.5%) patients in ETV plus placebo group developed HCC, cumulative HCC incidence was notably lower for ETV plus BJRG group than ETV plus placebo group (HR 0.52, 95%CI 0.32–0.87, P = 0.001). One (0.2%) patient in the ETV plus BJRG group and 13 (2.6%) patients in the placebo group died. While there was no significant difference in non-HCC events (e.g., colorectal, thyroid or pancreatic cancer, upper gastrointestinal bleeding, ascites, etc.) between the two groups (HR 0.47, 95%CI 0.12–1.99, P = 0.280).

**Conclusion:** Comparing to ETV plus placebo treatment, ETV plus BJRG or ETV plus placebo groups

**THU578**

*In vitro and in vivo preclinical efficacy of PD-L1-targeted liposomal doxorubicin as a combined therapy for the treatment of hepatocellular carcinoma*

Daniela Gabbia1, Antonella Grigoletto2, Luana Cannella1, Ilaria Zanotto1, Veronica Mazzuco1, Gianfranco Pasut1, Sara De Martin1, University of Padova, Dept. of pharmaceutical and pharmacological sciences, Padova, Italy; 2University of Padova, Dept of pharmaceutical and pharmacological sciences, Padova, Italy

**Background and aims:** Hepatocellular carcinoma (HCC), the primary malignancy of the liver and the outcome of chronic liver diseases of different etiologies, remains a global health challenge, due to the lack of effective therapeutic options. The aim of this study is to evaluate a novel liposomal doxorubicin (DXR) formulation targeted with the PD-L1 checkpoint inhibitor atezolizumab, for the selective delivery of DXR to cancer cells, with the double aim of enhancing its activity and decreasing its off-target toxicity.

**Method:** Two liposomal formulations were evaluated, i.e. atezolizumab-targeted liposomal DXR (Stealth Immunoliposomes, SIL_atezolizumab) and untargeted liposomal DXR (Stealth Liposomes, SL). The in vitro cytotoxicity of liposomal doxorubicin was evaluated after 72 h of treatment by means of the ATP assay on the three PD-L1 expressing HCC cell lines Hu7, HepG2 and Hepa1–6 (Figure). In vivo efficacy was evaluated in a syngeneic HCC mouse model, obtained by injecting the murine HCC cells Hepa1–6 in C57BL/6j immunocompetent mice. SIL_atezolizumab and SL were administered e.v. once a week for 4 weeks. Tumor volumes were measured by an electronic caliper and collected and weighed at sacrifice for further analyses.

**Results:** Atezolizumab targeting increased the *in vitro* cytotoxic effect of liposomal DXR in HepG2 and Hepa1–6 cells, showing significant lower IC50 values with respect to SL (p < 0.01 and p < 0.05, respectively). Both SL and SIL_atezolizumab decreased tumor growth in vivo since tumor volumes measured at sacrifice were significantly lower in treated mice compared to controls (p < 0.05). A slight increase of survival was observed in SIL_atezolizumab treated mice.

**Conclusion:** PD-L1-targeted liposomal doxorubicin is effective in limiting HCC cells growth in vitro and in vivo. This approach could open new avenues for HCC therapy, using two already approved two drugs, joined in a novel combined formulation.

**THU579**

*LiMAx facilitates patient selection prior radioembolization for patients with hepatocellular carcinoma in liver cirrhosis*

Catherine Leyh1, Niklas Heucke2, Clemens Schotten1, Matthias Buechter1, Lars Bechmann3, Marc Wichert3, Alexander Dechene4, Ken Hermann5, Antonios Katsounas6, Mustafa Özçürümez7, Dominik Heider8, Svenja Sydor9, Johannes M. Ludwig6, Jens Theysohn6, Robert Damm10, Maciej Powerski10, Maciej Pech10, Ali Canbay7, Jochen Weigt2, Verena Keitel-Anselmino1, Christian Lange1, Jan Best7, Paul Manka2.

1 University of Hospital Essen, Department of Gastroenterology and Hepatology, Essen, Germany; 2 Otto-von-Guericke University Hospital Magdeburg, Department of Gastroenterology, Hepatology and Infectious Diseases, Magdeburg, Germany; 3 University Hospital Knappschaftskrankenhaus Bochum, Department of Internal Medicine, Bochum, Germany; 4 University Hospital Essen, Central Laboratory, Essen, Germany; 5 University Hospital Nürnberg, Nürnberg, Germany; 6 University Hospital Magdeburg, Radiology, Essen, Germany; 7 University Hospital Knappschaftskrankenhaus Bochum, Department of Internal Medicine, Bochum, Germany; 8 University Marburg, Marburg, Germany; 9 University Hospital Knappschaftskrankenhaus Bochum, Department of Internal Medicine, Bochum, Germany; 10 Otto-von-Guericke University Hospital Magdeburg, Radiology, Magdeburg, Germany

**Background and aims:** LiMAx is a non-invasive test for liver function, measuring the maximum metabolic capacity for $^{13}$C-Methacetin by measuring the maximum metabolic capacity for $^{13}$C-Methacetin by
Zumab plus bevacizumab, and cabozantinib) have been approved in Japan for patients with advanced HCC and preserved liver function who are unsuitable for transarterial chemoembolization (TACE) or systemic therapy. However, despite the excellent safety profile of RE, post-therapeutic hepatic decompensation remains a serious complication that is difficult to predict by standard laboratory liver function parameters or imaging modalities. Our study investigates the potential of LiMAx for predicting post-interventional hepatic decompensation.

**Method:** In total, 50 patients with HCC with or without liver cirrhosis and not amenable to conventional locoregional or systemic treatments were included in the study. The study was carried out in a two-step fashion, including a retrospective and a prospective cohort. In both cohorts, LiMAx was carried out one day before RE (baseline). Standard liver function parameters were assessed at baseline, day 28, and day 90 after RE. First, the relationship between baseline LiMAx and pre- and post-interventional liver function parameters was analyzed in the retrospective cohort and subsequently validated in the prospective cohort. Subsequently, the ideal cutoff for LiMAx to predict post-interventional hepatic decompensation has been determined in the prospective part of the study.

**Results:** We observed a significant correlation between baseline LiMAx and Bilirubin, Albumin, ALBI-Grade, and MELD Score, especially at day 28 in the prospective cohort. Patients presenting with Child-Pugh B Score 28 days after RE had a significantly lower baseline LiMAx than those with a Child-Pugh A Score (223.5 μg/kg/h vs. 305 μg/kg/h, p = 0.0263). Using the ROC curve analysis, the potential of LiMAx for predicting hepatic decompensation after RE was determined and compared to MELD Score and ALBI Grade. LiMAx achieved an AUC of 0.817. Patients with LiMAx values <238 μg/kg/h had a significantly higher risk of suffering hepatic decompensation after RE.

**Conclusion:** Patients with low LiMAx values (<238 μg/kg/h) despite Child-Pugh A situation at baseline have a significantly increased risk of hepatic decompensation after RE. Therefore, LiMAx can be used as an additional tool to identify patients at high risk of post-interventional hepatic failure.

**THU580**

The efficacy of molecular targeted therapies after atezolizumab plus bevacizumab in patients with unresectable hepatocellular carcinoma (HCC) in Japan

Koichi Tsujiya1, Yuka Hayakawa2, Yutaka Yasui1, Tatsuya Kakegawa1, Mayu Higuchi2, Kenta Takaura1, Shohi Tanaka1, Chiaki Maeyashiki1, Shun Kaneko1, Nobuharu Tamaki1, Hiroyuki Nakanishi1, Masayuki Kurosaki1, Namiki Izumi1, 1Musashino Red Cross Hospital, Department of Gastroenterology and Hepatology, Japan
Email: tsujiyakamura5@gmail.com

**Background and aims:** In systemic therapy for unresectable HCC, 6 regimens (sorafenib, regorafenib, lenvatinib, ramucirumab, atezolizumab plus bevacizumab, and caboazontinib) have been approved in Japan. Atezolizumab plus bevacizumab (atez+bev) is recommended as 1st-line, and there is no established regimen after atez+bev. We investigated the efficacy of the other 5 regimens after atez+bev.

**Method:** A total of 76 patients who received atez+bev at our institution between Oct 2020 and Sep 2021 were enrolled. Tumor assessments in accordance with RECIST v.1.1 were done using dynamic CT or MRI every 6–12 weeks. Clinical course, including the efficacy of molecular targeted therapies after atez+bev was investigated retrospectively.

**Results:** The median age of the patients was 73 years. The median ALBI score was −2.19, and 58% of the patients were modified ALBI grade 2b. Line of treatment was 1st (n = 41), 2nd (n = 19), 3rd (n = 7), 4th (n = 5), 5th (n = 3), and 6th-line (n = 1). Forty-eight (63%) of the patients were BCLC stage B, and 28 patients were BCLC stage C. Median overall survival (OS) was not reached, and the 6-months survival rate was 83.0%. The median follow-up duration was 6.4 months, and the median time to progression (TTP) was 6.8 months. Overall response rate (ORR) in 1st-line and later-line were 30.5 and 13.5%. Disease control rate (DCR) in 1st-line and later-line were 86.1% and 66.7%. Discontinuation of atez+bev due to disease progression was observed in 33 patients, while discontinuation due to adverse events was reported in 12 patients. In the 12 patients, lenvatinib (n = 4), sorafenib-regorafenib (n = 1), caboazontinib (n = 3), and TACE (n = 3) were performed after atez+bev. Three patients received multiple therapies. Four of 12 (33%) patients received only supportive therapy. In the 33 patients with disease progression, 5 patients (15%) received only supportive therapy, and all 5 patients were pretreatment PS 1 or modified ALBI 2b. Of the 33 patients, 2 were treated with HAIC, and 26 received other molecular targeted therapies after atez+bev. Sorafenib was administered after atez+bev in 5 patients, and 2 patients showed SD. Regorafenib was started in 4 patients, and 2 patients showed SD. Lenvatinib was started in 12 patients, and ORR and DCR were 22% and 67%. Ramucirumab was administered in 3 patients, and 1 patient showed SD. Cabozantinib was started in 14 patients, and ORR and DCR were 14% and 80%. In total, 33 of 45 (73%) patients who discontinued atez+bev received molecular targeted therapy.

**Conclusion:** Discontinuation of atez+bev due to adverse events in real-world practice was similar to the clinical trial, and all patients with pretreatment PS 0 or modified ALBI 1 or 2a could receive post-atez+bev therapies after disease progression. The efficacy of molecular targeted agents after atez+bev would be different from the results of the past clinical trials without immunotherapy.

**THU581**

The LiMAx level before transarterial chemoembolization or radioembolization is a predictor for short-time survival in patients with early-stage HCC

Janett Fischer1, Stella Wellhöner1, Sebastian Ebel2, Bettina Maiwald1,2, Steffen Stroocks2,3, Tim-Ole Petersen2,3, Albrecht Boehlig1, Florian Gerhardt1, Rhea Veelken1, Timm Denecke1, Thomas Berg1, Florian van Bömmel1,1Division of Hepatology, Department of Medicine II, University Hospital Leipzig, Leipzig, Germany; 2Department of Diagnostic and Interventional Radiology, University Hospital Leipzig, Leipzig, Germany; 3Clinic for Diagnostic and Interventional Radiology, St. Elisabeth and St. Barbara Hospital Halle, Halle (Saale), Germany
Email: janett.fischer@medizin.uni-leipzig.de

**Background and aims:** Transarterial chemoembolization (TACE) and transarterial radioembolization (TARE) are standard treatment strategies for patients with hepatocellular carcinoma (HCC). The liver maximum capacity test (LiMAx) is a potential monitoring tool for post-interventional liver failure. The study aimed to investigate the correlation of LiMAx with patients’ response to TACE or TARE treatment and the severity of adverse events after therapy as well as short-term and overall survival.

**Method:** In this study, 69 patients with TACE (n = 57) or TARE (n = 12) treatment were enrolled. Liver function was assessed on the day before as well as at 4 weeks after TACE or TARE using the LiMAx test and the well-established biochemical markers as well as MELD, CHILD Pugh and ALBI scores. Adverse events were each recorded over 4 weeks after the intervention. Survival was followed up until 3 years.

**Results:** A complete response to TACE/TARE and stable disease were observed in 10.3% and 51.5% of patients, respectively, and progressive disease in 38.2%. Mild adverse events developed in 48.5% of patients whereas 14.7% suffered from severe complications such as ascites and hepatic encephalopathy. LiMAx levels did not show a significant association with the occurrence of adverse events, laboratory parameters, liver function-associated scores and tumor response. However, survival analysis showed significant lower 30-day and 60-day survival rates for patients with LiMAx ≤150 μg/kg/h before
Treatment compared to patients with LiMAx >150 μg/kg/h levels (30-day: 86.7% ± 8.8% vs. 100%, p = 0.006; 60-days: 86.7% ± 8.8% vs. 98.1% ± 1.8%, p = 0.048). When the patients were divided into groups according to the BCLC stage (BCLC: A: n = 32, BLCII: n = 29), significant differences in survival rates were detected for early but not for intermediate disease stage. The survival rates of patients with BCLC A stage with LiMAx ≤150 μg/kg/h were significantly lower after 30 days (75.0% ± 15.3% vs. 100%, p = 0.011) and 90 days (62.5% ± 17.7% vs. 95.8% ± 4.1%, p = 0.011) compared to those of patients with higher LiMAx levels. This was even more pronounced after 180 days with 50.0% ± 17.7% vs. 95.8% ± 4.1%, (p = 0.001) survival.

Conclusion: The LiMAx test identifies patients with early stage HCC and reduced short-time survival after transarterial treatment.

THU582
Implementation of a new prognostic scoring system after major hepatectomy in curative intent for perihilar cholangiocarcinoma
Christian Benzing1, Thea-Charlotte Fritsch1, Lena Haiden1, Felix Krenzien1, Alexa Mieg1, Annika Wolfsberger1, Cecilia Atik1, Nora Nevermann1, Uli Fehrenbach2, Wenzel Schöning1, Moritz Schmelzle1, Johann Pratschke1, 1Charité University Medicine Berlin, Department of Surgery | Campus Charité Mitte and Campus Virchow Klinikum, Berlin, Germany; 2Charité University Medicine Berlin, Department of Diagnostic and Interventional Radiology, Berlin, Germany
Email: christian.benzing@charite.de

Background and aims: Major hepatectomy (MH) is the only curative therapy option for patients with perihilar cholangiocarcinoma (PHC). Despite recent advancements in adjuvant treatments and perioperative management, recurrence rates are still high and overall prognosis is poor. Current staging systems such as the American Joint Committee on Cancer (AJCC)/the Union for International Cancer Control (UICC) or the Bismuth staging system fail to adequately depict the patients’ risk profile in terms of tumor recurrence. The present study seeks to establish a reliable scoring system that allows to classify the risk of tumor recurrence for individual patients in order to improve surveillance and adjuvant treatment programs.

Method: In this retrospective study, all patients undergoing MH for PHC at our department between January 2005 and August 2018 were retrospectively reviewed and analyzed. Demographic variables as well as perioperative, histopathological data and information on recurrence and overall survival were collected. After excluding postoperative 90-day mortality (n = 38, 14%), an uni- and multivariate logistic cox regression analysis was performed to identify factors associated with tumor recurrence. Subsequently, a score was assigned to each independent risk factor, which was summed up to a prognostic score ranging from 0 to 3 was created.

Results: We included 232 patients in the analysis. Median age was 64 years (33–86). The majority of patients had Bismuth-Corlette IV tumors (42%, n = 97) and UICC stage IIIb (41%, n = 93). Tumor-free resection margins (R0) were achieved in 160 patients (70%). 131 patients were lymph node negative (N0, 57%). The 1- and 3- and 5-year disease-free survival (DFS) and overall survival (OS) rates were 77%, 36%, and 20% vs. 82%, 45%, and 24%, respectively. Multivariate cox regression showed that R1-status (Hazard Ratio, HR = 1.525, (95% Confidence interval, CI: 1.021–2.277, p = 0.0039), V1 status (HR = 2.187, 95% CI: 1.378–3.470, p = 0.001), and N+ status (HR = 1.856, 95% CI: 1.272–2.709, p = 0.001) were independently associated with tumor recurrence. When calculating the prognostic score, 82 patients (35%) had a score of 0 points, 72 patients (31%) had a score of 1 point, 32 patients (14%) had a score of 2, and 13 patients (6%) had a score of 3 points. Kaplan Meier analysis showed highly significant correlation of disease-free survival (DFS) and overall survival (OS) with the scoring system (p < 0.001).

Conclusion: We proposed a simple scoring system that showed highly significant correlations with the clinical outcome (DFS and OS). This is of particular clinical significance since it allows a better risk stratification when compared to conventional scoring systems such as UICC and Bismuth stages.

THU583
The effect of discordance between preoperative imaging and postoperative pathology on the prognosis of hepatocellular carcinoma
Woo Sun Rou1, Byung Seok Lee2, Hyuk Soo Eun2, Seok Hyun Kim2, Hong Jae Jeon3, In Sun Kwon3, 1Chungnam National University Sejong Hospital, Gastroenterology and Hepatology, Sejong-si, Korea, Rep. of South; 2Chungnam National University Hospital, Gastroenterology and Hepatology, Daejeon city, Korea, Rep. of South; 3Chungnam National University Hospital, Clinical Trial Center, Statistics Office, Biomedical Research Institute, Daejeon city, Korea, Rep. of South
Email: gie001@cnuh.co.kr

Background ans aims: In patients who have undergone surgical resection, the discordance between preoperative imaging and postoperative pathological findings may be found. There was a report that the mismatch of the Milan criteria before and after liver transplantation (LT) was reported to be 22.0–27.2% and had an effect on the survival rate. However, there is no studies about impact of this discordance in patients who have undergone surgical resection. In this study, preoperative imaging and postoperative pathologic findings were compared for tumor size, number, vascular or biliary tract invasion, and lymph node (LN) metastasis. In addition, the survival rate according to the discrepancy for each factor is compared, and according to the number of discrepancies, the impact on HCC prognosis is investigated.

Method: Among the 13, 838 patients with HCC extracted randomly from the 2008–2016 national cohort of the Korean Central Cancer Registry, we selected the 2, 781 patients who had undergone surgical resection or LT. And we evaluated the concordance of tumor maximal diameter, tumor number, bile duct invasion, LN metastasis, and vascular invasion including portal vein (PV), hepatic vein (HV), hepatic artery (HA) by comparing preoperative imaging findings with postoperative pathology findings. In addition, the survival rate was compared by Kaplan-Meier according to the number of discrepancies, and further analyzed by Cox proportional hazards regression analysis.

Results: Vascular invasion including HA, HV and PV invasion had a poorer prognosis than the both negative group when either of the imaging findings or pathological findings were positive (p < 0.001 and p < 0.001, respectively). In particular, PV invasion, when both findings were positive, was significantly worse prognosis (p < 0.001). Bile duct invasion had a poorer prognosis when pathological findings were positive than those that were not (p = 0.001), and there was no difference in survival rate when pathologic findings were negative even if bile duct invasion was suspected on imaging findings (p = 0.911). When analyzing according to the number of mismatched factors among seven factors, as the number of mismatched factors increased, the prognosis of HCC patients was poor (p < 0.001). Multivariate analysis also showed that the number of discrepancies...
This study revealed for the first time that the more factors that did not match the preoperative imaging findings and the postoperative pathological findings is associated with the poorer survival rate in patients undergoing surgical resection as independent predictive factor.

**THU584**

Early Nivolumab addition to Regorafenib in patients with hepatocellular carcinoma progressing under 1st line therapy (GOING trial). Interim analysis and safety profile

Marco Sanduzzi Zamparelli1, Ana M Matilla2, Jose Luis Lledó3, Sergio Muñoz Martinez2, Maria Varela2, Mercedes Iñarraíraegui3, Christie Perelló6, Beatriz Minguez2, Neus Llaw1, Laura Marquez Perez2, Antonio Guerrero2, Gemma Iserte1, Andrés Castano-García4, Laura Carrión4, Jordi Rimola5, María Angeles García-Criado5, Gema Domenech5, Loreto Boix1, Jordi Bruix1, Maria Reig1, Hospital Clinic of Barcelona, IDIBAPS, CIBERehd, University of Barcelona, BCLC group, Liver Unit, Barcelona, Spain; 2Hospital General Universitario Gregorio Marañón, CIBERehd, University of Alcalá, Gastroenterology and Hepatology Department, Madrid, Spain; 3Hospital Universitario Ramón y Cajal, IRYCIS, CIBERehd, University of Alcalá, Gastroenterology and Hepatology Department, Madrid, Spain; 4Hospital Universitario Central de Asturias, UOUP, ISPQ, Universidad de Oviedo, Oviedo, Spain; 5Clínica Universidad de Navarra, IDISNA and CIBEREHD, Liver Unit and HPB Oncology Area, Pamplona, Spain; 6Hospital Universitario Puerta de Hierro, IDIHPMA, CIBERehd, Gastroenterology Department. Hepatology Unit, Madrid, Spain; 7Valld’Hebron Institute of Research (VHIR), Vall d’Hebron Barcelona Hospital Campus.CIBERehd, Universitat Autònoma de Barcelona, Liver Unit, Hospital Universitari Vall d’Hebron, Liver Diseases Research Group, Barcelona, Spain; 8Hospital General Universitario Gregorio Marañón, Gastroenterology Department, Madrid, Spain; 9Hospital Clinic of Barcelona, IDIBAPS, University of Barcelona, BCLC Group, Radiology Department, Barcelona, Spain; 10Medical Statistics Core Facility, IDIBAPS-Hospital Clinic, Barcelona, Spain

Email: mreig1@clinic.cat

**Background and aims:** Regorafenib (Rego) improves survival in patients with hepatocellular carcinoma (HCC) (RESORCE trial) while Nivolumab (Nivo) is also safe and active in terms of radiologic response (15–20% objective response) in second-line. The GOING trial (NCT04170556) is an investigator-initiated phase I/IIa study analyzing the safety of Rego plus Nivo in HCC patients who progress and tolerate sorafenib (Cohort A) or who discontinue atezolizumab plus bevacizumab (Cohort B).

**Method:** Patients from cohort A receive Rego as monotherapy for the first 2 cycles (starting dose 160 mg/day, 3 days on/1 week off) and adjusted for adverse events (AEs) and Nivo is added at day 1 of cycle 3 (the first 10 patients at 3 mg/kg, since they did not present serious AEs (SAE), the final dose is 240 mg every two weeks). Treatment continues until unacceptable AEs, symptomatic tumor progression, patient decision or death. Safety is measured by the rate of AEs, rate of treatment discontinuation and rate of death. Severity of AEs are evaluated according to CTCAE v5.0. A futility analysis using the non-binding Lan and DeMets beta-sampling functions with a boundary of p = 0.814 is mandated when 32.8% of cohort A has data of tumor assessment at least at week 16 by RECIST 1.1.

**Results:** Fifty-one patients have been enrolled in cohort A as of May 15, 2021. The first 30 (BCLC-C 73%) were considered in this safety analysis. All patients developed at least one AE, 29 (96.7%) had Tr-AEs of any grade and 10 (33.3%) had grade 3 (no grades 4 or 5 have been reported). Ten (33.3%) patients had a Rego-related AE, 4 (13.3%) Nivo-related, and 4 (13.3%) Tr-AE grade 3 of special interest. Table 1 describes the profile Tr-AE occurring in >10% of patients. Only 4 (13.3%) patients developed Tr-SAE. 3 (10%) Rego-related and 3 (10%) Nivo-related. Four patients discontinued the study due to physician decision, 2 for progression, and 2 for AEs (one related to study treatment). One patient had surgical resection after treatment discontinuation and a complete necrosis was observed at pathology.

<table>
<thead>
<tr>
<th>Adverse Events</th>
<th>Any Grade</th>
<th>Grade 3</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Patients, n</td>
<td>Patients, %</td>
</tr>
<tr>
<td>Hand-foot-skin reaction</td>
<td>17 (55.4%)</td>
<td>2 (10.0%)</td>
</tr>
<tr>
<td>Asthenia</td>
<td>13 (41.9%)</td>
<td>3 (10.0%)</td>
</tr>
<tr>
<td>Diarrhea</td>
<td>11 (35.4%)</td>
<td>1 (3.3%)</td>
</tr>
<tr>
<td>Decreased Appetite</td>
<td>9 (29.0%)</td>
<td></td>
</tr>
<tr>
<td>Atrial Hypertension</td>
<td>8 (25.8%)</td>
<td>3 (10.0%)</td>
</tr>
<tr>
<td>Hypertransaminasemia</td>
<td>8 (25.8%)</td>
<td>3 (10.0%)</td>
</tr>
<tr>
<td>Hyperbilirubinemia</td>
<td>6 (19.4%)</td>
<td>2 (6.7%)</td>
</tr>
<tr>
<td>Aspartate Aminotransferase Increased</td>
<td>6 (19.4%)</td>
<td>3 (10.0%)</td>
</tr>
<tr>
<td>Abdominal Pain</td>
<td>6 (19.4%)</td>
<td></td>
</tr>
<tr>
<td>Dysphonia</td>
<td>5 (16.1%)</td>
<td></td>
</tr>
<tr>
<td>Alamine Aminotransferase Increased</td>
<td>4 (13.1%)</td>
<td></td>
</tr>
</tbody>
</table>

* None of these Tr-AE was grade 4–5

**Conclusion:** The sequential combination of Reo-Nivo has a manageable safety profile. Less than one third of the patients developed grade 3/4 Tr-AE and there was no treatment-related death. Futility analysis allowed to continue recruitment.

**THU585**

Impact of endobiliary radiofrequency ablation on survival of patients with advanced hepatocellular cholangiocarcinoma under systemic chemotherapy

Christian Möhring1, Maria Angeles Gonzalez-Carmona1, Robert Mahn1, Taotao Zhou1, Alexandra Bartels1, Farsaneh Sadeghlar1, Maximilian Bolch1, Annabelle Vogt1, Dominik Kaczmarek2, Dominik Heling1, Leona Dold1, Jacob Nattermann1, Vittorio Branchi1, Hanno Matthaei2, Steffen Manekeller2, Jörg Kalff2, Christian Strassburg1, Raphael Mohr1, Tobias Weissmüller1, 1University Hospital of Bonn, Germany; Internal Medicine I, Bonn, Germany; 2University Hospital of Bonn, Germany, Department of Surgery, Bonn, Germany

Email: marianelesgc@gmx.net

**Background and aims:** Prognosis of patients with advanced hepatocellular cholangiocarcinoma is still poor. The current standard first-line treatment is systemic chemotherapy with gemcitabine and a platinum derivate. Additionally, endobiliary radiofrequency ablation (eRFA) can be applied to treat biliary obstructions. The aim of this study was to evaluate the additional benefit of scheduled regular eRFA in a real-life patient cohort with advanced hepatocellular cholangiocarcinoma under standard systemic chemotherapy.

**Method:** This is a single center retrospective analysis. All patients with irresectable hepatocellular cholangiocarcinoma treated at University Hospital Bonn between 2010 and 2020 were eligible for inclusion. Patients were stratified according to treatment: standard systemic chemotherapy (n = 26) vs. combination of eRFA with standard chemotherapy (n = 40). Overall survival (OS), progression free survival (PFS), feasibility and toxicity were analyzed using univariate and multivariate approaches.

**Results:** Combined eRFA and chemotherapy resulted in significantly longer median OS (17.3 vs. 8.6 months, p = 0.004) and PFS (12.9 vs. 5.7 months, p = 0.045) compared to the chemotherapy only group. While groups did not differ regarding age, sex, tumor stage and chemotherapy treatment regimen, mean MELD was even higher (10.1 vs. 6.7, p = 0.015) in the eRFA+CT group. The survival benefit of concomitant eRFA was more evident in the subgroup with locally advanced tumors. Severe hematological toxicities (CTCAE grades 3–5) did not
differ significantly between the groups. However, therapy-related cholangitis occurred more often in the combined treatment group (p = 0.031).

Conclusion: Combination of eRFA and systemic chemotherapy was feasible, well-tolerated and could significantly prolong survival compared to standard chemotherapy alone. Thus, eRFA should be considered during therapeutic decision making in advanced extrahepatic cholangiocarcinoma.

THUS586
Interleukin 10 and Interferon Gamma levels are elevated in patients with hepatocellular carcinoma showing response to treatment with atezolizumab and bevacizumab
Sabine Lieb1, Aaron Schindler2, Johannes Niemeyer2, Rhea Veelken2, Janett Fischer2, Rami Al-Sayegh2, Thomas Berg2, Florian van Bömmel2.
1Leipzig University Medical Center, Division of Hepatology, Department of Medicine II, Leipzig, Germany; 2Leipzig University Medical Center, Division of Hepatology, Department of Medicine II, Leipzig, Germany
Email: florian.vanboemmel@medizin.uni-leipzig.de

Background and aims: The combination treatment of the PD-L1 inhibitor atezolizumab plus bevacizumab (atezo/bev) has become standard of care in first line therapy in advanced hepatocellular carcinoma (HCC). However, prediction of treatment response is not well defined. Effector cytokines signalling (e.g. interferon gamma (IFNg) is supposed to drive clinical response to immune checkpoint blockade. We have analysed circulating cytokine pattern in patients treated with atezo/bev.

Method: Thirty-three patients (31 male, mean age of 65.1±11 (range 29–80) years) with advanced HCC (7 BCLC B, 26 BCLC C) treated at the University Cancer Center of Leipzig were retrospectively analysed. Twenty-eight patients had liver cirrhosis (23 Child-Pugh A, 5 Child-Pugh B), two underwent liver transplantation, two showed no hepatic disease and one had fatty liver disease. All together 136 cycles (mean 4.12, range 1–16 cycles) atezo/bev were applied to the patients. Tomography imaging was performed after 3 to 4 cycles of atezo/bev and evaluated according to mRECIST criteria. A cytokine panel including interleukin (IL)-1beta, interferon (IFN) alpha2, IFN-g, TNF alpha, IL-6, IL-8, IL-10, IL-12p70, Monocyte chemotactic protein 1 (MCP-1), IL-17A, IL-18, IL-23 and IL-33 was measured at baseline and correlated with treatment outcomes.

Results: The mean overall survival was 7.53 (range 0–17) months. At the end of observation, 13 Patient showed stable disease (SD), 2 partial response (PR), 1 patient complete response (CR), 2 progressive disease (PD) and 15 patients died. Patients showing either CR, PR or SD at month 3 of treatment had higher mean baseline levels of IFN-g and IL-10 in comparison to patients with PD (IFN-g: 8 ± 5.48 (range 4.18–18.96) vs. 4.6 ± 0.87 (range 4.18–6.79), p < 0.001) and IL-10 (11.19 ± 9.6 (range 4.07–33.64) vs. 5.74 ± 2.05 (range 4.07–11.04), p < 0.001). At month six of treatment, patients with either CR, PR or SD still presented higher mean baseline levels of IFN-g in comparison to patients with PD (8.74 ± 6.01 (range 4.18–18.96) vs. 4.18 ± 0.0, p = 0.026). There was no association of other cytokine levels measured with response to atezo/bev.

Conclusion: Response to atezo/bev in the treatment of HCC may depend on IFN gamma and IL-10 signalling. The value of these cytokines as response predictors needs to be evaluated in a larger cohort.

THUS587
Potential faesability of atezolizumab-bevacizumab therapy in patients with hepatocellular carcinoma: a real-world analysis
Benedetta Stefanini1,2, Laura Bucci1, Valentina Santi1, Nicola Reggiori1, Davide Rampoldi1, Lorenzo Lani1, Franco Trevisani1.
1S. Orsola-Malpighi Polyclinic, Division of Medical Semiotics, Bologna, Italy; 2Bologna, Semiotics Medica, Bologna, Italy
Email: benedetta.stefanini@studio.unibo.it

Background and aims: Option treatments for patients with unresectable hepatocellular carcinoma (HCC) not amenable/ responding to locoregional treatments is represented by systemic therapy, and sorafenib and lenvatinib, two tyrosine-kinase inhibitors (TKIs) are currently the standard of care, providing modest but significant benefit on survival. Recently, the IMBrave-150 trial has demonstrated that the combination of with atezolizumab plus bevacizumab (Atezo-Beva) is the best first-line systemic therapy for HCC patients, showing a clear superiority compared to sorafenib. This study aimed at assessing the real-world potential feasibility of the Atezo-Beva therapy in a large cohort of HCC patients treated with TKIs.

Method: We retrospectively analysed 1448 patients diagnosed with unresectable HCC not amenable/not responding to locoregional treatments, treated with TKIs (sorafenib 98%, lenvatinib 2%) and followed-up from January 2010 to December 2020 by 24 Italian centres. The percentage of patients potentially amenable to Atezo-Beva treatment (according to IMBrave-150 trial criteria) and the overall survival (OS) of eligible/non-eligible patients were assessed.

Results: 423 (29.2%) of patients treated with TKIs were found to be qualified for the Atezo-Beva therapy. Their median OS was 17.3 months (95% CI 19.7–14.9) while that of non-eligible patients was 13.1 months (95% CI 14.5–11.6) (p = 0.038), likely due to better baseline clinical characteristics (Table 1). The main exclusion causes were a Child-Pugh class >A (399 cases) and a performance status >1 (187 cases). The proportion of eligible cases considering, as selection criterion, P<0.0015 0000 (instead of >75000 mmc requested by the IMBrave trial) increased by 43 cases (+2.9%), while including Child-Pugh Class B7 it increased by 85 patients (+5.9%).

<table>
<thead>
<tr>
<th>N (%)</th>
<th>Median (range)</th>
<th>1025 (100%)</th>
<th>96 (21%)</th>
<th>0.198</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age (years)</td>
<td>423 (100%)</td>
<td>69 (33–90)</td>
<td>1025 (100%)</td>
<td>69 (21–92)</td>
</tr>
<tr>
<td>Sex</td>
<td>423 (100%)</td>
<td>344 (81%)</td>
<td>1025 (100%)</td>
<td>182 (18%)</td>
</tr>
<tr>
<td>Child-Pugh Class</td>
<td>423 (100%)</td>
<td>283 (67%)</td>
<td>916 (89%)</td>
<td>17 (6%)</td>
</tr>
<tr>
<td>BCLC</td>
<td>423 (100%)</td>
<td>4 (1%)</td>
<td>966 (94%)</td>
<td>96 (1%)</td>
</tr>
<tr>
<td>MELD Score</td>
<td>423 (100%)</td>
<td>8 (6–23)</td>
<td>900 (88%)</td>
<td>9 (6–31)</td>
</tr>
<tr>
<td>Alpha-fetoprotein</td>
<td>391 (92%)</td>
<td>131 (31%)</td>
<td>838 (81%)</td>
<td>218 (26%)</td>
</tr>
<tr>
<td>ECOG (Performance Status)</td>
<td>423 (100%)</td>
<td>423 (100%)</td>
<td>959 (93.6%)</td>
<td>832 (87%)</td>
</tr>
</tbody>
</table>

1 In Child-Pugh class B 258 (62%) patients showed a score of 7 (B7)
Conclusion: Real world data indicate that no more than one-third of HCC patients treated with TKIs are potentially eligible for Atezo-Beva therapy. These patients have a better OS than non-eligible ones, owing to a better baseline clinical profile. Therefore, TKIs will remain the front-line approach for most of the HCC patients qualified for systemic therapy, due to the stringent selection criteria dictated by immunotherapy trials and the use of TKIs currently extended to Child-Pugh B patients. However, further prospective studies in real life may broaden Atezo-Beva indications.

THU588 Progression patterns and therapeutic sequencing following immune checkpoint inhibition for HCC: an observational study
Thomas Talbot1, Antonio D’Alessio1,2, Matthias Pinter3, Lorenz Balcar1, Bernhard Scheiner1, Thomas Marron4, Tomi Jun5, Sirish Dharmapurui6, Celina Ang7, Anwara Saeed8, Hannah Hildebrand6, Mahvish Muzaffar9, Claudia Angela Maria Fulgenzi1,8, Suneetha Amara7, Abdul Rafeh Naqash7,9, Anuhya Gampa10, Anjana Pillai10, Yinghong Wang11, Uqba Khan12, Pei-Chang Lee13, Yi-Hsiang Huang13,14, Bertram Bengsch13, Dominik Bettinger13, Yehia Abugabal16, Ahmed Kaseb16, Tiziana Pressiani17, Nicola Personeni1,2,17, Lorenzo Rimassa1,17, Naoshi Nishida18, Masatoshi Kudo18, Arndt Weinmann19, Peter Galle19, Ambreen Muhammed1, Alessio Cortellini1, Arndt Vogel19, David J. Pinato1,2,1, Imperial College London, Department of Surgery and Cancer; 2Humanitas University, Department of Biomedical Sciences; 3Medical University of Vienna, Department of Internal Medicine III; 4Tisch Cancer Institute, Mount Sinai Hospital, Department of Medicine, United States; 5Sema4, Stanford, CT, United States; 6Kansas University Cancer Center, Division of Medical Oncology, United States; 7East Carolina University, Division of Hematology/Oncology, United States; 8University Campus Bio-Medico, Department of Medical Oncology, Italy; 9National Cancer Institute, Division of Cancer Treatment and Diagnosis, Bethesda, Maryland, United States; 10The University of Chicago Medicine, Section of Gastroenterology, Hepatology and Nutrition, Chicago, United States; 11The University of Texas MD Anderson Cancer, Department of Gastroenterology, Hepatology and Nutrition, United States; 12Well Cornell Medicine/New York Presbyterian Hospital, Division of Hematology and Oncology, United States; 13Taipei Veterans General Hospital, Division of Gastroenterology and Hepatology, Department of Medicine, Taiwan; 14National Yang Ming Chiao Tung University School of Medicine, Institute of Clinical Medicine, Taiwan; 15Medical Center University of Freiburg, Department of Medicine II, Faculty of Medicine, Germany; 16The University of Texas MD Anderson Cancer Center, Dept of Gastrointestinal Medical Oncology, United States; 17Humanitas Cancer Center, IRCCS Humanitas Research Hospital, Medical Oncology and Hematology Unit, Italy; 18Kindai University Faculty of Medicine, Department of Gastroenterology and Hepatology, Osaka, Japan; 19University Medical Center of the Johannes Gutenberg-University Mainz, 1st Department of Internal Medicine, Gastroenterology and Hepatology, Germany; 20Hannover Medical School, Department of Gastroenterology, Hepatology and Endocrinology, Germany; 21University of Piemonte Orientale “A. Avogadro,” Division of Oncology, Department of Translational Medicine, Italy Email: twt18@ic.ac.uk

Background and aims: Different approaches are available after progression of disease (PD) while on treatment with immune checkpoint inhibitors (ICI) for hepatocellular carcinoma (HCC), including continuation of ICI, switching to tyrosine kinase inhibitors (TKIs) and cessation of therapy. Little is known about progression patterns and their relationship with optimal sequencing and survival outcomes post-ICI.

Method: From an international consortium of 13 tertiary-care referral centres, we screened 604 HCC patients treated with ICIs, including only those who experienced PD by data cut-off. We evaluated post-progression survival (PPS) according to treatment strategy at PD and verified its relationship with radiologic patterns of progression: intrahepatic growth (IHG), new intrahepatic lesion (NIH), extrahepatic growth (EHG), new extrahepatic lesion (NEH) and new vascular invasion (nVI).

Results: 364 (60.3%) patients had PD during observation, mostly following PD-1/PD-L1 monotherapy (80%). Median PPS was 5.3 months (95%CI: 4.4–6.9; 271 events). At data cut-off, 165 patients (45%) received no post-progression anticancer therapy. Both IHI (HR 1.64 [95%CI:1.21–2.22]; p = 0.0013) and nVI (HR 2.15 [95%CI:1.38–3.35]; p = 0.0007) at PD were significantly associated with shorter PPS. Continuation of ICI therapy beyond PD occurred in 64 patients (17.6%). Multivariate models adjusted for progression patterns, treatment line, and ALBI grade and ECOG-PS at PD confirmed receipt of ICI beyond PD with (HR 0.17, 95%CI 0.09–0.32; p < 0.0001), and without subsequent TKI (HR 0.39, 95%CI 0.26–0.58; p < 0.0001) as predictors of prolonged PPS compared to no anticancer therapy.

Conclusion: ICI-TKI sequencing is a consolidated option in advanced HCC, with poorer prognosis predicted by nVI and IHG. Despite lack of recommendation, continuation of ICI beyond progression in HCC is adopted in clinical practice: efforts should be made to identify patients who benefit from this approach.

THU590 GALAD score correlates with therapy response for transarterial and systemic therapies in patients with hepatocellular carcinoma
Anne Olbrich1, Johannes Niemeyer1, Hendrik Seifert1, Olga Gros2, Florian Lordick3, Dirk Forstmeyer3, Daniel Seeboer4, Robert Sucher5, Sebastian Rademacher4, Timm Denecke5, Sebastian Ebel6, Nicolas Linder5, Madlen Matz-Soja1,6, Thomas Berg7, Florian van Bömmel1, Leipzig University Medical Center, Department of Medicine II, Division of Hepatology, Leipzig, Germany; 2HeliOS Clinic Köthen, Department of Anesthesia and Intensive Care, Köthen, Germany; 3Leipzig University Medical Center, University Cancer Center Leipzig (UCCL), Leipzig, Germany; 4Leipzig University Medical Center, Department of Visceral, Vascular, Thoracic and Transplant Surgery, Leipzig, Germany; 5Leipzig University Medical Center, Department of Diagnostic and Interventional Radiology, Leipzig, Germany; 6University of Leipzig, Rudolf-Schönheimer-Institute for Biochemistry, Leipzig, Germany Email: anne.olbrich@medizin.uni-leipzig.de

Background and aims: The GALAD score is a biomarker-based scoring system used for prediction of early hepatocellular carcinoma (HCC) in patients with chronic liver disease. It consists of the two risk factors gender (G) and age (A) and levels of AFP-L3 (L), AFP (A), and DCP (D). So far, a possible association of baseline GALAD score and therapy response was not investigated. For patients with advanced HCC, loco-regional treatment approaches, such as transarterial chemoembolization (TACE) and transarterial radioembolization (TARE), as well as systemic therapies are available, but response to these therapies is highly variable. The study aim is to assess the value of the GALAD model as a response marker to these treatment approaches.

Method: In a retrospective German single-center study, 238 patients with HCC treated with either TARE or TACE or systemic drugs were enrolled. Serum samples at baseline were analyzed to evaluate the prognostic performance of the GALAD score. Treatment efficacy was evaluated by mRECIST criteria based on magnetic resonance imaging (MRI) three months (10–14 weeks) after intervention.

Results: In our patient cohort (n = 238) the mean GALAD score at baseline was 3.96 [range, −5.19–17.89]. Baseline GALAD scores were
patients with HBV-related HCC (HBsAg positive, HBeAg negative) were evaluated in an ongoing pilot, investigator-initiated trial (IIT) conducted to evaluate the safety as well as the antiviral and antitumor activity of SCG101.

Methods: Subjects ST1301 and ST1401 received 5 × 10⁷/kg TCR-T cells, subject ST1204 received 1 × 10⁷/kg. Transduced T cells were detectable in peripheral blood of all three patients up to last visit. Two patients, ST1301 and ST1204, showed a rapid HBsAg reduction of >1.7 log within 28 days after infusion and sustained with continuous decline thereafter. The HBsAg drop was correlated with a transient ALT/AST flare without significant change of other liver function markers including albumin, bilirubin, etc. Tumor response assessment by mRECIST showed that these two patients had stable disease (SD) with target lesion reduction of 14.5% and 6.2%, respectively, and maintained SD up to last visit (96+ and 55+ days). Patient ST1401 had a transient HBsAg drop of ~0.2 log from day 1–4 post treatment and was diagnosed with progressive disease (PD) at day 28. For all patients, no DLT or drug-related serious adverse events (SAEs) have been observed to date. Drug-related adverse events were typical for a T-cell therapy associated cytokine-release syndrome and transient or reversible after treatment.

Conclusion: Systemic SCG101 TCR-T cell therapy was well tolerated and showed promising early signs of clinical efficacy in advanced HBV-related HCC patients who have exhausted available targeted and immunotherapy options. Early and sustained HBsAg reduction demonstrates encouraging antiviral activity with target engagement of SCG101 and might serve as a potential predictive marker of antitumor efficacy. Preliminary data support further systematic clinical evaluation.

THU592

Sven H Loosen¹, Sarah Krieg¹, Tobias E Ring¹, Andreas Krieg², Christoph Roderburg³, Tom Lüdde⁴, ¹University Hospital Düsseldorf, Clinic for Gastroenterology, Hepatology and Infectious Diseases, Düsseldorf, Germany; ²University Hospital Düsseldorf, Department of Surgery (A), Düsseldorf, Germany

Background and aims: Transarterial chemoembolization (TACE) represents a standard of care for intermediate-stage hepatocellular carcinoma (HCC) and is also increasingly performed in patients with cholangiocarcinoma (CCA) or liver metastases. Recently, newer particle-based TACE procedures have been introduced but comprehensive data on clinical trends of TACE as well as its in-hospital mortality in Germany are missing. A systematic evaluation of existing data sets and their careful interpretation can support a rational discussion aiming at further optimizing framework conditions of TACE.

Method: Based on standardized hospital discharge data provided by the German Federal Statistical Office, we systematically evaluate current clinical developments, associated post-interventional complications as well as in-hospital mortality of TACE in Germany between 2010 and 2019.

Results: A total of 49,595 individual cases undergoing TACE were enrolled: subjects ST1301 and ST1401 received 5 × 10⁷/kg TCR-T cells, subject ST1204 received 1 × 10⁷/kg. Transduced T cells were detectable in peripheral blood of all three patients up to last visit. Two patients, ST1301 and ST1204, showed a rapid HBsAg reduction of >1.7 log within 28 days after infusion and sustained with continuous decline thereafter. The HBsAg drop was correlated with a transient ALT/AST flare without significant change of other liver function markers including albumin, bilirubin, etc. Tumor response assessment by mRECIST showed that these two patients had stable disease (SD) with target lesion reduction of 14.5% and 6.2%, respectively, and maintained SD up to last visit (96+ and 55+ days). Patient ST1401 had a transient HBsAg drop of ~0.2 log from day 1–4 post treatment and was diagnosed with progressive disease (PD) at day 28. For all patients, no DLT or drug-related serious adverse events (SAEs) have been observed to date. Drug-related adverse events were typical for a T-cell therapy associated cytokine-release syndrome and transient or reversible after treatment.

Conclusion: Systemic SCG101 TCR-T cell therapy was well tolerated and showed promising early signs of clinical efficacy in advanced HBV-related HCC patients who have exhausted available targeted and immunotherapy options. Early and sustained HBsAg reduction demonstrates encouraging antiviral activity with target engagement of SCG101 and might serve as a potential predictive marker of antitumor efficacy. Preliminary data support further systematic clinical evaluation.

Using ROC analyses the GALAD score for response to transarterial or systemic treatment showed higher AUC (AUC = 0.704; p < 0.001) than the individual biomarkers AFP, AFP-L3, and DCP in the overall cohort (AUC = 0.685, 0.629 and 0.645, respectively).

Conclusion: The GALAD model is a potent predictor of tumor response to transarterial and systemic treatment in HCC at baseline.

THU591
Antiviral and antitumor activity of SCG101, an autologous HBV-specific T cell receptor engineered T cell (TCR-T) therapy in HBV-related advanced hepatocellular carcinoma (HCC) patients after receiving ≥2 prior lines of systemic therapies

Shunda Du¹, Yuhong Zhou², Xiuxuan Qu³, Wei Wu⁴, Ke Zhang⁵, Xueshuai Wan¹, Wei Li², Dongmei Quan³, Karin Wisskirchen⁴, Ulrike Protzer⁶,⁷, Yun Peng Liu², ¹Peking Union Medical College Hospital, Liver Surgery, Beijing, China; ²Zhongshan Hospital, Fudan University, Medical Oncology, Shanghai, China; ³The First Hospital of China Medical University, Medical Oncology, Shenyang, China; ⁴The Sixth People’s Hospital of Shenyang, Hepatobiliary Surgery, Shenyang, China; ⁵SG Cell Therapy, Shanghai, China; ⁶Technical University of Munich, Institute of Virology, Munich, Germany; ⁷Helmholtz Munich, Institute of Virology, Munich, Germany

Email: cmu_trial@163.com

Background and aims: Adoptive cell therapy with TCR-T cells targeting HBV antigens represents an innovative approach for treatment of HBV-related HCC. SCG101 is a first-in-class genetically modified autologous TCR-T with a natural high-avidity TCR directed targeting HBV antigens represents an innovative approach for treatment of HBV-related HCC. SCG101 is a first-in-class genetically modified autologous TCR-T with a natural high-avidity TCR directed targeting HBV antigens.

Methods: Patients with HBV-related HCC (HBsAg positive, HBeAg negative and HBV DNA ≤2 × 10⁷ IU/ml), who are HLA-A*02 positive and have received at least two lines of systemic therapy including small-molecule tyrosine kinase inhibitors and PD-1 checkpoint inhibitors were eligible. Following leukapheresis, SCG101 TCR-T cells were detectable in peripheral blood of all three patients up to last visit. Two patients, ST1301 and ST1204, showed a rapid HBsAg reduction of >1.7 log within 28 days after infusion and sustained with continuous decline thereafter. The HBsAg drop was correlated with a transient ALT/AST flare without significant change of other liver function markers including albumin, bilirubin, etc. Tumor response assessment by mRECIST showed that these two patients had stable disease (SD) with target lesion reduction of 14.5% and 6.2%, respectively, and maintained SD up to last visit (96+ and 55+ days). Patient ST1401 had a transient HBsAg drop of ~0.2 log from day 1–4 post treatment and was diagnosed with progressive disease (PD) at day 28. For all patients, no DLT or drug-related serious adverse events (SAEs) have been observed to date. Drug-related adverse events were typical for a T-cell therapy associated cytokine-release syndrome and transient or reversible after treatment.

Conclusion: Systemic SCG101 TCR-T cell therapy was well tolerated and showed promising early signs of clinical efficacy in advanced HBV-related HCC patients who have exhausted available targeted and immunotherapy options. Early and sustained HBsAg reduction demonstrates encouraging antiviral activity with target engagement of SCG101 and might serve as a potential predictive marker of antitumor efficacy. Preliminary data support further systematic clinical evaluation.
and CCA: 1.40%) as well as between different embolization agents (liquid embolization: 0.80%, loaded microspheres: 0.92%, spherical particles: 1.54% and non-spherical particles: 2.84%), for which we observed large geographic differences in their frequency of use. Finally, in-hospital mortality was significantly increased in centers with a low annual TACE case volume (<15 TACE/year: 2.08% vs. >275 TACE/year: 0.45%).

Conclusion: We identified a variety of factors such as post-interventional complications, the embolization method used as well as the hospitals’ annual case volume, which are associated with an increased in-hospital mortality following TACE. These data might help to further reduce mortality of this routinely performed local-ablative procedure in the future.

THU594

The influence of fasting on tumor-targeted drug delivery

Svea Becker1, Diana Möckel2, Ilaria Biancacci3, Jan-Niklas May2, Qingbi Wang1, Huan Sun1, Marek Weiler2, Iwan Lammers2, Maximilian Hatting1, Christian Trautwein1, Medical Department III, Universitätsklinikum Aachen, Aachen, Germany; 2*Experimentelle Molekulare Bildgebung, RWTH Aachen, Aachen, Germany

Email: svebecker@ukaachen.de

Background and aims: Hepatocellular carcinoma is increasing in industrialized countries. Disease progression is accelerated by a number of risk factors, although it can be reduced to some extent by using intermittent fasting. Tumorous cells are stressed by regular food deprivation because they are constantly proliferating. Fasting has also been established in recent clinical research to be a new therapeutic before tumor therapy leading to maintenance and repair processes such as autophagy. As a result, tumor therapy can be more precise and patients can show a higher survival rate.

Here, we aimed to show how fasting induces changes in the tumor microenvironment facilitating tumor-targeted drug delivery.

Method: We used a well-established syngeneic tumor model with the murine liver hepatoma cell line Hep-55.1C. The tumor was implanted subcutaneously and grew over 3.5 weeks. During tumor growth, the mice were either fasted intermittently every 12 h (IF), once overnight after 20 d for 12 h (STF), or fed ad libitum (a.l.). After 21 d, DSPE-Cy7 labeled liposomes were injected i.v. and the biodistribution of the nanoparticles was observed longitudinally up to 72 h p.i. via hybrid computed- and fluorescence tomography (CT-FLT).

Results: Our analysis demonstrates that mice in the a.l. group have little to no liposome-signal in the tumor but have substantial levels of uptake in reticuloendothelial system organs (RES). The STF group has tumor signals, but the RES-organs still have significant signals. The IF mice had the most signal in the tumor, while the RES-organs had fewer liposome signals detected by the CT-FLT.

In addition, intermittent fasting alters the microenvironment of tumors. Collagen1A1 levels in the IF group were considerably lower. This was accompanied by a considerable rise in the number of vessels that were positive for Lectin. In these tests, there was no difference between STF and a.l. mice.

Conclusion: Our findings show that intermittent fasting prior to tumor therapy improves the likelihood of a more precise and direct delivery method. Fasting softens the tissue and increases blood flow, making it easier to deliver (nano-)therapeutics into the tumor through the bloodstream.

THU595

CXCRI inhibition sensitises NASH-HCC to immunotherapy

Jack Leslie1, John B. G. Mackey2, Thomas Jamieson2, Helen L. Reeves1, Joseph M. Llovet3, Carlin Leo4, Thomas G Bird2, Owen Sansom5, Derek A Mann1, *Newcastle University Medical School, United Kingdom; 2Beaton Institute for Cancer Research, Bearsden, United Kingdom; 3Institut d’Investigacions Biomediques August Pi i Sunyer (IDIBAPS), Barcelona, Spain

Email: jack.leslie@ncl.ac.uk

Background and aims: Non-alcoholic steatohepatitis (NASH) is increasingly a major underlying cause of hepatocellular carcinoma (HCC). Immunotherapy offers great promise for HCC therapy; however, recent published data suggests that NASH is the cause of immune changes that negatively impacts on the efficacy of conventional immune checkpoint inhibition (ICI). Here we aimed to sensitise NASH-HCC to anti-PD1 therapy by targeting neutrophils using a CXCRI2 small molecule inhibitor (AstraZeneca-ADZ5069).

Method: Neutrophil infiltration was characterised in multiple models of murine HCC and in human patient biopsies. Late-stage intervention with anti-PD1 and/or ADZ5069 was performed in two NASH-HCC models (orthotopic and autochthonous). The tumour microenvironment was characterised by a combination of immunohistochemistry, flow cytometry and RNA-seq.
Results: CXCR2⁺ neutrophils were found to be highly represented in both murine and human NASH-HCC. In models of NASH-HCC lacking response to ICI, the combination of AZD5069 with anti-PD1 effectively suppressed tumour burden and extended survival (Fig 1). The combination therapy increased intratumoral CD103⁺XCR1⁺ dendritic cells and CD8⁺ T cells that are associated with anti-tumoral immunity. The therapeutic effect was lost upon genetic impairment of dendritic cells or antibody mediated depletion of CD8⁺ T cells. Combination therapy resulted in an unexpected increase in tumour-associated neutrophils (TANs). These TANs were found to be proliferative and by the use of image mass cytometry to be located within immunological hubs in direct contact antigen presenting cells and CD8⁺ T cells. These immune hubs were enriched for the cytotoxic anti-tumoural protease granzyme B which was found at increased levels in tumours co-treated with CXCR2 antagonist and anti-PD1 compared with monotherapy groups.

TANs in combination-treated tumours displayed a switch from a pro-tumour to anti-tumour progenitor-like neutrophil phenotype, closing resembling a recently characterised acute-inflammatory immature-Ly6G⁻ neutrophil population isolated from lipopolysaccharide- (LPS)-treated mice. Intravenous infusion of these neutrophils into orthotopic tumour bearing mice, sensitised to anti-PD1 therapy, promoting dendritic cell and CD8⁺ T cell recruitment and activation.

Conclusion: CXCR2-inhibition induces multi-cellular reprogramming of the tumour immune microenvironment that promotes ICI treatment of HCC in the context of NASH.
Conclusion: The combination of baseline ALBI grade and SII index can be used as a promising prognostic tool to predict prognosis of uHCC patients receiving sorafenib-regorafenib sequential therapy.

THU597
Induce the endogenous tumor suppressor miR-34a by small molecules to inhibit liver metastasis
Dayana Yaish1, Tomer Frieheim1, Alexander Plotnikov2, Shira Levi1, Hilla Giladi2, Amonn Peled2, Haim Barr2, Eithan Galun1. 1Hadassah University Hospital-Ein Kerem, Goldyne Savad Institute of Gene and Cell Therapy, Jerusalem, Israel; 2Weizmann Institute of Science, The Nancy and Stephen Grand Israel National Center for Personalized Medicine, Rehovot, Israel
Email: dayana.yaish@mail.huji.ac.il

Background and aims: Metastasis originating from different cancers, are commonly spreading to the liver, and as such, are a common cause of death. Recent evidences have indicated the role of microRNAs (miRs) in modulating the metastatic process. There are specific miRs that exhibit tumor-suppressive activity by targeting cancer driver genes. MiR-34a is a well-known tumor suppressor and anti-metastatic miR. We hypothesize that induction of endogenous expression and secretion of miR-34a, could be a new strategy for metastasis therapy.

Method: We performed high throughput screening of synthetic small molecule libraries searching for compounds that induce miR-34a promoter activity and secretion. The compounds were initially tested for their ability to induce EGFP on HepG2 cells carrying a miR-34a-promoter-EGFP reporter. Compounds that induced EGFP levels were tested further for their effect on miR-34a secretion using qRT-PCR analysis performed on RNA extracted from the cell’s media.

Results: We identified 6 compounds which induced miR-34a promoter activity. However, only 2 out of these 6 compounds induced miR-34a secretion. Searching databases for predicted activities of these 2 compounds, revealed that both may repress Cyclin Dependent Kinase 5 (CDK5). We therefore, examined the activity of known CDK5 repressors, Dinaciclib and Flavopiridol. Both molecules induced miR-34a secretion. The compounds were initially tested for their ability to induce EGFP on HepG2 cells carrying a miR-34a-promoter-EGFP reporter. Compounds that induced EGFP levels were tested further for their effect on miR-34a secretion using qRT-PCR analysis performed on RNA extracted from the cell’s media.

Conclusion: Small molecule induction of miR-34a is a therapeutic approach against liver metastasis.

THU598
Prediction of treatment response using contrast-enhanced ultrasonography in patients treated with Atezolizumab and Bevacizumab for unresectable hepatocellular carcinoma
Hitomi Takada1, Shinya Maekawa1, Nobuyuki Enomoto1. 1University of Yamanashi, Gastroenterology and Hepatology, Chuo, Japan
Email: takadahi0107@gmail.com

Background and aims: Atezolizumab plus Bevacizumab therapy (AB) was approved for unresectable hepatocellular carcinoma in 2020. However, the prediction of treatment response that can be easily used in clinical practice is still unknown. In this study, we performed Time-intensity curve (TIC) analyses using the arterial phase of contrast-enhanced ultrasonography (CEUS), and examined its usefulness as a predictive marker of early therapeutic effect after the administration of AB.

Method: Twenty-five patients who received AB for unresectable HCC were included. The initial treatment response after the administration of AB was reported using Response Evaluation Criteria in Solid Tumors (RECIST) after 8–12 weeks. The treatment response was evaluated every 8–12 weeks thereafter. CEUS was performed before administration and early after administration (3–7 days), and TIC analysis was performed using the arterial phase for 2 minutes after injection of the contrast medium. The time to peak (TTP) and the slope of wash-in (Slope) indicators were used for TIC analysis.

Results: The baseline characteristics of 25 patients were 69 (44–81) years old, 20 males, the maximum intrahepatic tumor diameter 64 (21–112) mm, and BCLC stage C 45%. The treatment response was Complete Response 1 case, Partial Response 7 cases, Stable Disease 11 cases, and PD 6 cases. Patients with prolonged TTP and decreased Slope were 36% using CEUS at 3–7 days, and all cases achieved disease control based on the initial CT after 8–12 weeks. There was a significant difference in the median progression-free survivals (PFSs) between patients with and without prolonged TTP and decreased Slope (p = 0.0051). There was a significant difference in the median PFSs between patients with and without decreased α-fetoprotein (AFP) levels (p = 0.019). There was also a significant difference in the median PFSs between patients with and without decreased neutrophil-to-lymphocyte ratio (NLR) (p = 0.038). PFS stratification was possible by the number of positive numbers among the 3 early markers (TTP prolongation and Slope decrease/AFP decrease/NLR decrease) (0/1 vs. 2/3 8.6 vs. 33 weeks, p < 0.001).

Conclusion: Early evaluation using CEUS may be useful in predicting the therapeutic effect in patients treated with Atezolizumab and Bevacizumab for unresectable HCC.

THU599
Efficacy and safety of Atezolizumab plus Bevacizumab-based sequential treatment for unresectable hepatocellular carcinoma: a simulation model
Ciro Celsa1, Giuseppe Cabibbo1, Salvatore Battaglia2, Paolo Giuffrida1, Giacomo Emanuele Maria Rizzo1, Mauro Grova1, Marco Giacchetto1, Gabriele Rancatore1, Caterina Stornello1, Maria Vittoria Grassini1, Giuseppe Badalamenti3, Marco Enea3, Antonio Craxi1, Vito Di Marco1, Calogero Camma1. 1Section of Gastroenterology and Hepatology,

Background and aims: Atezolizumab plus Bevacizumab therapy (AB) was approved for unresectable hepatocellular carcinoma in 2020. However, the prediction of treatment response that can be easily used in clinical practice is still unknown. In this study, we performed Time-intensity curve (TIC) analyses using the arterial phase of contrast-enhanced ultrasonography (CEUS), and examined its usefulness as a predictive marker of early therapeutic effect after the administration of AB.

Method: Twenty-five patients who received AB for unresectable HCC were included. The initial treatment response after the administration of AB was reported using Response Evaluation Criteria in Solid Tumors (RECIST) after 8–12 weeks. The treatment response was evaluated every 8–12 weeks thereafter. CEUS was performed before administration and early after administration (3–7 days), and TIC analysis was performed using the arterial phase for 2 minutes after injection of the contrast medium. The time to peak (TTP) and the slope of wash-in (Slope) indicators were used for TIC analysis.

Results: The baseline characteristics of 25 patients were 69 (44–81) years old, 20 males, the maximum intrahepatic tumor diameter 64 (21–112) mm, and BCLC stage C 45%. The treatment response was Complete Response 1 case, Partial Response 7 cases, Stable Disease 11 cases, and PD 6 cases. Patients with prolonged TTP and decreased Slope were 36% using CEUS at 3–7 days, and all cases achieved disease control based on the initial CT after 8–12 weeks. There was a significant difference in the median progression-free survivals (PFSs) between patients with and without prolonged TTP and decreased Slope (p = 0.0051). There was a significant difference in the median PFSs between patients with and without decreased α-fetoprotein (AFP) levels (p = 0.019). There was also a significant difference in the median PFSs between patients with and without decreased neutrophil-to-lymphocyte ratio (NLR) (p = 0.038). PFS stratification was possible by the number of positive numbers among the 3 early markers (TTP prolongation and Slope decrease/AFP decrease/NLR decrease) (0/1 vs. 2/3 8.6 vs. 33 weeks, p < 0.001).

Conclusion: Early evaluation using CEUS may be useful in predicting the therapeutic effect in patients treated with Atezolizumab and Bevacizumab for unresectable HCC.
Background and aims: Systemic therapies for unresectable hepatocellular carcinoma (HCC) have rapidly increased in numbers over recent years and they should be combined in a rationale sequence to offer the best net health benefit. Atezolizumab plus Bevacizumab now represents the standard of care for first-line treatment, but efficacy and safety of subsequent treatment lines still remain unknown. According to hepatological and oncological guidelines, Sorafenib could be an option for second-line treatment after first-line Atezolizumab plus Bevacizumab and Cabozantinib is the only systemic agent tested as third-line treatment. The aim was to estimate the overall survival (OS) of the sequence of Atezolizumab plus Bevacizumab followed by Cabozantinib (third-line).

Method: A Markov model (Figure 1) was constructed to estimate the OS of the sequence Atezolizumab plus Bevacizumab (first-line) followed by Sorafenib (second-line) followed by Cabozantinib (third-line).

Results: The estimated median OS of the sequential strategy is 28 months (95% Confidence Interval 27–29 months). Rate of SAEs is 67.5%.

Conclusion: This simulation model provides a forecast of the outcomes of the next available sequential systemic treatment of patients with HCC. The sequence including first-line Atezolizumab plus Bevacizumab followed by second-line Sorafenib followed by third-line Cabozantinib leads to a median OS of more than two years, with about two thirds of patients experiencing SAEs. Prospective real-world studies are needed to substantiate the net health benefit of this sequence.
Acute liver failure and drug induced liver injury

FRI001
Obeticholic acid exacerbates the liver fibrosis of bile duct ligation model by inducing the liver expression of osteopontin
Jie Wang1, Yuan Zihang1, Yingying Miao1, Haoran Zhang1, Qipeng Wu1, Xinliang Huang1, Luyong Zhang1,2, Q. W. Yu1, Zhenzhou Jiang1,3,4. China Pharmaceutical University, New Drug Screening Center, Jiangsu Center for Pharmacodynamics Research and Evaluation, Nanjing, China; 2Guangdong Pharmaceutical University, Center for Drug Research and Development, Guangdong, China; 3China Pharmaceutical University, Key Laboratory of Drug Quality Control and Pharmacovigilance, Nanjing, China; 4China Pharmaceutical University, State Key Laboratory of Natural Medicines, Nanjing, China
Email: jiangcpu@163.com

Background and aims: Liver fibrosis is a dynamic process characterized by the deposition of the accumulated extracellular matrix (ECM). To date, there are still no therapeutic medications approved for fibrosis or cirrhosis. Osteopontin (OPN) is a phosphoglycoprotein of ECM, and has been reported to drive ductular reaction (DR) and the formation of periportal scarring. Obeticholic acid (OCA) is approved for Primary Biliary Cholangitis (PBC), and OCA has been shown to improve the fibrosis in NASH patients evaluated in REGENERATE study. But the applications of OCA are limited due to its side effects. The main objective of this study is to investigate the impact of OCA on liver diseases.

Method: The bile duct ligation model was used to evaluate the effect on fibrosis of OCA assessed by assessment of blood markers of liver injury, pathological section, western blotting, RT-PCR, immunohistochemistry and immunofluorescence staining. OPN and Thr-OPN were detected by ELISA. The primary mouse cholangiocytes and human intrahepatic bile epithelium cells were chosen to investigate in vitro.

Results: Compared to control, OCA treatment (40 mg/kg) aggravated BDLD induced liver injury and liver fibrosis in mice, demonstrated by significantly increase in serum ALT, AST, ALP, TGF-β1, hepatic hydroxyproline, Masson Trichrome, H&E, and Sirius red staining as well as immunohistochemistry staining of α-SMA. The serum and liver content of OPN and its another active form, thrombin-cleaved OPN (Thr-OPN), were obviously increased in OCA-treated BDLD mice. Interestingly, there was also a significant increase in the content of Thr-OPN in the liver of OCA-treated sham mice. Next we examined the downstream effects of OPN in liver disease. Immunoblots analysis and immunohistochemistry staining of CK19 revealed that OCA treatment enhanced ductular reaction induced by BDLD and the immunofluorescence staining of CK19 and Ki67 also proved this. Immunoblots analysis of PCNA and immunohistochemistry staining of Ki67 revealed that OCA treatment weakened liver regeneration. RT-PCR analysis of liver nonparenchymal cells revealed that OCA treatment enhanced ductular reaction induced by BDLD, and the expression of integrin αvβ3 receptors in BDLD mice, which is OPN targeted.

Conclusion: OCA aggravated the degree of liver injury and fibrosis in obstructive cholestasis probably associated an apparent increase of OPN in serum and liver. OPN may be a biomarker of liver toxicity caused by OCA.

FRI002
A report on the Australian Drug Induced Liver Injury Network: AusDILIN
Beverly Rodrigues1, Stephen Bloom1,2, Rohit Sawhney1,2, Geoffrey Haar1,2, Maria Bishara1, Ayushi Chauhan1, Paul Gow4, Simone Strasser3, Alan Wigg3, Karl Vaz3, Fadak Mohammadi6, Amanda Nicoll1,2. 1Eastern Health, Gastroenterology, Australia; 2Eastern Health Clinical School, Monash University, Australia; 3Eastern Health, Pharmacy, Australia; 4Austin Health, Gastroenterology, Australia; 5Royal Prince Alfred Hospital, Gastroenterology, Australia; 6Flinders Medical Centre, Gastroenterology, Australia
Email: beverly.rodrigues91@gmail.com

Background and aims: Drug induced liver injury (DILI) may vary in different regions due to population and prescribing differences. Data on DILI in Australia is limited but is necessary to inform local management. We present prospectively collected data from seven Australian liver centres in a new collaboration named AusDILIN.

Method: A prospective multicentre clinical audit was conducted on reported DILI patients between June 2018 to November 2021 inclusive (41 months).

Results: Data on 150 patients was obtained, and showed the commonest causes were: amoxicillin/clavulanic acid (n = 26, 17%), statins (n = 15, 10%) and cephalosporins (n = 12, 8%). Remdesivir was the identified causative agent in 5 (3%) of cases. Sixteen (11%) of patients were icteric on presentation. The median duration to onset and recovery was 3 ± 7.4 weeks, and 8 ± 12.9 weeks, respectively. One hundred and twelve (75%) were managed as inpatients. Forty-seven (31%) received some form of treatment; 11 (7%) were managed with ursodeoxycholic acid and 23 (15%) with corticosteroid monotherapy respectively, although 2 (1%) and 1 (1%) were already on these treatments long-term for chronic conditions. Of the 11 (7%) of patients with unresolved DILI, 4 (3%) were considered for liver transplant. Two (1%) of these were successfully transplanted and 1 (1%) died, with the overall cohort death rate being 4 patients (3%). Fifty patients (33%) were lost to follow up. The DILI persisted beyond 3 and 6 months in 30 (45%) and 10 (7%) of cases, respectively.
**POSTER PRESENTATIONS**

**Table 1: Baseline characteristics of AusDILIN cohort**

<table>
<thead>
<tr>
<th>Category</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Median age (years)</td>
<td>56.37 ± 0.44 [18–94]</td>
</tr>
<tr>
<td>Gender (M: F, n, %)</td>
<td>80 (53%): 70 (47%)</td>
</tr>
<tr>
<td>Ethnicity (n, %)</td>
<td>Caucasian/European: 114 (76%)</td>
</tr>
<tr>
<td></td>
<td>SE Asian/Arabic: 31 (21%)</td>
</tr>
<tr>
<td></td>
<td>African: 2 (1%)</td>
</tr>
<tr>
<td></td>
<td>Unknown: 3 (2%)</td>
</tr>
<tr>
<td>Pattern of liver injury (n, %)</td>
<td>Hepatic: Cholestatic: 54 (36%): 44 (29%)</td>
</tr>
<tr>
<td></td>
<td>Mixed: Unknown: 51 (34%): 1 (1%)</td>
</tr>
<tr>
<td>Treatment offered (n, %)</td>
<td>CS monotherapy: 23 (15%)</td>
</tr>
<tr>
<td></td>
<td>UDCA monotherapy: 11 (7%)</td>
</tr>
<tr>
<td></td>
<td>CS plus UDCA combination therapy: 5 (3%)</td>
</tr>
<tr>
<td></td>
<td>CS plus IM combination therapy: 4 (3%)</td>
</tr>
<tr>
<td></td>
<td>NAC infusion: 2 (1%)</td>
</tr>
<tr>
<td>Clinical outcomes (n, %)</td>
<td>Self-resolved or resolving: 87 (58%)</td>
</tr>
<tr>
<td></td>
<td>Unknown or lost to follow up: 50 (33%)</td>
</tr>
<tr>
<td></td>
<td>Persistent or progressed: 11 (7%)</td>
</tr>
<tr>
<td></td>
<td>Death (DILI ALF): 4 (3%)</td>
</tr>
<tr>
<td>Considered for LTx (n, %)</td>
<td>Transplanted: 4 (3%)</td>
</tr>
<tr>
<td></td>
<td>Resolved: 2 (1%)</td>
</tr>
<tr>
<td></td>
<td>Death: 1 (1%)</td>
</tr>
</tbody>
</table>

HTN = hypertension, Chol = cholesterol, DM = diabetes mellitus, CS = corticosteroids, UDCA = Ursodeoxycholic acid, IM = immunomodulator, NAC = N-acetyl cysteine, LTx = liver transplant, ALF = acute liver failure.

**Conclusion:** DILI is a significant cause of morbidity and mortality in Australia, with a high proportion suffering persistent liver injury, and with the role of treatment remaining undetermined and requiring further study.

**FRI003**

**Incidence, phenotype and prognostic relevance of COVID-19-related liver injury across different age strata**

Lukas Hartl1,2, Katharina Haslinger1,2, Martin Angerer1,2, Mathias Jachs1,2, Benedikt Simbrunner1,2,3, David J. M. Bauer1,2, Bernhard Scheiner1,2, Ernst Eigenbauer4, Robert Strassl5, Monika Breuer5, Oliver Kimberger6, Michael Trauner1, Mattias Mandorfer1,2, Thomas Reiberger1,2,3.

**Medical University of Vienna, Division of Gastroenterology and Hepatology, Department of Medicine III, Vienna, Austria; 2Medical University of Vienna, IT-Systems and Communications, Vienna, Austria; 3Medical University of Vienna, Department of Laboratory Medicine, Division of Clinical Virology, Vienna, Austria; 4Medical University of Vienna, Department of Anaesthesia, Intensive Care Medicine and Pain Medicine, Vienna, Austria**

**Email:** thomas.reiberger@meduniwien.ac.at

**Background and aims:** Severe acute respiratory distress syndrome coronavirus-2 (SARS-CoV-2) caused the pandemic of coronavirus disease of 2019 (COVID-19). Variable abnormalities in liver chemistries have been reported in COVID-19 patients. We assessed the prevalence rates and trajectories of elevated liver enzymes after SARS-CoV-2 infection, as well as their prognostic values across different age strata in a large cohort of COVID-19 patients.

**Method:** Patients with a positive SARS-CoV-2 PCR result between 03/2020–07/2021 at the Vienna General Hospital were included in this study. Patients were stratified for age (i.e. 18–39 vs. 40–69 vs. ≥70 years). Multivariate Cox regression analyses were adjusted for pre-existing liver disease, age, sex, albumin, obesity, diabetes mellitus, cardiovascular disease, lung disease and malignancy.

**Results:** 900 patients (52.4% male) were included with 32.2% aged 18–39 years, 39.7% 40–69 years, and 28.1% ≥70 years age strata, respectively. Frequency of comorbidities, median D-dimer and C-reactive protein increased with age. After SARS-CoV-2 infection, parameters of hepatocellular (aspartate aminotransferase [AST]/alanine aminotransferase [ALT]) and cholestatic liver injury (alkaline phosphatase [ALP]/gamma-glutamyltransferase [GGT]) all significantly increased. AST/ALT and ALP/GGT were elevated in 40.3% (n = 262/650) and 45.0% (n = 287/638) of patients, respectively. The rates of COVID-19-associated liver injury and median levels of liver chemistries were highest in patients aged 40–69 (18–39 years: 8.5% vs. 40–69 years: 16.0% vs. ≥70 years: 4.6%; p < 0.001).

Elevated AST after the first SARS-CoV-2 PCR test was associated with the requirement for hospital admission, ICU admission and intubation throughout all age strata and with a higher frequency of death and liver-related death in patients aged 40–69. Elevated AST and total bilirubin (BIL) at the time of first positive SARS-CoV-2 PCR test independently predicted of mortality in the overall cohort (AST: aHR: 1.47; 95%CI: 1.01–2.14; p = 0.043/BIL: aHR: 2.20; 95%CI: 1.22–3.98; p = 0.009) and in patients aged 40–69 years (AST: aHR: 1.78; 95%CI: 1.04–3.06; p = 0.037/BIL: aHR: 2.18; 95%CI: 1.15–4.13; p = 0.017).

**Conclusion:** A considerable proportion of COVID-19 patients show abnormal liver chemistries. The subgroup of patients aged 40–69 years was at particularly high risk for COVID-19-related liver injury; elevated ALT was predictive of liver-related mortality. AST and BIL at the time of first positive SARS-CoV-2 PCR test were independent predictors of mortality in the overall group, and particularly in patients aged 40–69 years.

**FRI004**

**Two different types of COVID-19 vaccines and serial liver biochemistries**

Grace Lai-Hung Wong1, Vicki Wing-Ki Hui1, Terry Cheuk-Fung Yip1, Yee-Kit Tse2, Vincent Wai-Sun Wong3, Yee-Kit Tse1, Vincent Wai-Sun Wong1.

1The Chinese University of Hong Kong, Medical Data Analytic Centre (MDAC), Hong Kong

**Email:** wonglaihung@cuhk.edu.hk

**Background and aims:** A handful of vaccines against COVID-19 have been approved around the world. These vaccines have excellent safety profiles with few reported side effects. Data concerning the liver safety of COVID-19 vaccines is lacking. We aimed to report the serial liver biochemistries of people before and after receiving COVID-19 vaccines.

**Method:** This was a territory-wide retrospective observational cohort study in Hong Kong. We identified subjects who had received any of the two COVID-19 vaccines approved in Hong Kong-CoronaVac (the inactivated virus technology platform by Sinovac Biotech (Hong Kong) Limited) and Comirnaty (mRNA technology platform by Fosun Pharma in collaboration with the German drug manufacturer BioNTech, the BNT162b2 mRNA vaccine). Serial liver biochemistries at least 3 months before and after the COVID-19 vaccines were reported, in subjects with or without chronic hepatitis B or C.
Pattern – Group:
Circle – HBV/HCV negative
Crosshatch – HBV/HCV positive
Horizontal stripe – Comirnaty
Diagonal stripe – CoronaVac

Figure: Serial liver biochemistries before and after COVID-19 vaccine.
Results: 851 subjects (513 received CoronaVac and 338 received Comirnaty; 56.2% male, median age 52 years old; 6.8% chronic hepatitis B or C) were included. Majority (87%) subjects had normal ALT (1–2 × ULN: 10.8%; >2 × ULN: 2.4%), total bilirubin (1–2 × ULN: 3.3%; >2 × ULN: 0%) and ALP (1–2 × ULN: 5.4%; >2 × ULN: 0.5%) before or at the time of receiving COVID-19 vaccines; these parameters remained stable for up to 3 months after the vaccination. ALT (1–2 × ULN: 11.6%; >2 × ULN: 2.1%), total bilirubin (1–2 × ULN: 3.7%; >2 × ULN: 0%) and ALP (1–2 × ULN: 5.4%; >2 × ULN: 0.8%) at or after the time of receiving COVID-19 vaccines. While patients with chronic viral hepatitis had higher ALT and ALP than those without chronic viral hepatitis at most of the times, these parameters remained normal (ALT: median 24 to 26 U/L vs. 20 to 21 U/L; ALP: median 88 to 90 U/L vs. 80 U/L). Similar serial liver biochemistries were observed in subjects who received CoronaVac and Comirnaty vaccine.

Conclusion: Both types of COVID-19 vaccines have very favourable liver safety profile in people with or without chronic viral hepatitis.

Background and aims: Immune checkpoint inhibitors drug induced-liver injury (ICI-DILI) may be associated with chemotherapy dose reduction and cancer progression. It is unclear whether liver biopsy modifies, or not, the management of ICI-DILI.

The aim of this study was to explore the impact of liver biopsy on the clinical management and the response to corticosteroids according to histological findings.

Method: We conducted a retrospective, single-center study to evaluate the biochemical, histological and clinical data of 28 patients with ICI-DILI who underwent liver biopsy (June 2015 to January 2021) in a teaching hospital in France. The severity of liver injury was graded according to Common Terminology Criteria for Adverse Events version 5.0 guidelines.

Results: Of the 28 patients (median [interquartile range] age 55 [23–80] years, 36% males), 13 patients (46%) had anti PD1 monotherapy, 6 patients (21%) anti PD1/anti CTLA4 combination therapy and 9 patients (32%) other immunotherapy. ICI-DILI occurred later in the other immunotherapy group than in the anti PD1 monotherapy and anti PD1/anti CTLA4 combination therapy groups (18.6 injections [1–60] vs 4 [1–28] and 3 [1–4] respectively, p = 0.047). The type of ICI did not influence the severity of the histological profile of the hepatitis, but patients receiving anti PD1/anti CTLA4 combination therapy had a tendency to more severe hepatitis in comparison to anti PD1 and other immunotherapy (83% of grade 3–4 hepatitis vs 61% and 57% respectively, p = 0.095). We did not observe any severe liver injury in our cohort. Corticosteroids were introduced in 6 (100%) patients of the anti PD1/anti CTLA4 combination therapy group, 7 (54%) patients of the anti PD1 monotherapy group and 4 (44%) patients under other therapy. All patients had a favourable clinical evolution after ICI withdrawal with no significative difference in the ALT normalization interval depending on the introduction of corticosteroids. The response to corticosteroids was similar according to the type of ICI and to the histological findings except for the cholangitic profile which seems to have a poorer response. The interval for ALT normalization was 110 (20–265) days for patients with cholangitic profile without corticosteroids, 120 (18–221) days for patients with cholangitic profile with corticosteroids and 54 (29–79) days for non cholangitic patients (Figure 1).

Conclusion: In ICI-DILI, liver biopsy must not delay patient care but may be useful in identifying patients with a cholangitic profile who have a poorer response to corticosteroids. Corticosteroids could be reserved to patients who do not improve after ICI withdrawal.

Background and aims: Immune checkpoint inhibitors induced liver injury: an observational study

Method: We conduct an observational study in patients with immune-mediated hepatitis due to ICI and submitted to the «ToxImmuno» multidisciplinary meeting in Montpellier between December 2018 and October 2021. Data were collected at diagnosis, week 1, 2 and 4, and once a week until hepatitis recovery. Data regarding cancer, hepatitis treatments, and ICI rechallenge were collected. The hepatitis phenotype is defined by the ratio of serum ALT and ALP [R value = (ALT/ULN)/(ALP/ULN)], and categorized as cholestatic (R ≤ 2), hepatocellular (R ≥ 5), or mixed (2 < R < 5).

Results: Of the 389 patients presented, hepatitis accounted for 14.7% of toxicities due to ICI (n = 57), 52 patients were included. 52.8% were men (n = 28) and the median age was 66 (range 23–87). PD-1 inhibitor was the most prescribed ICI class (n = 48, 92.3%), alone (n = 31, 59.6%), or with CTLA-4 inhibitor (n = 17, 32.7%). Hepatitis
phenotype was cholestatic in 40.4% (n = 21), hepatocellular in 30.8% (n = 16), and mixed in 28.8% (n = 15). Hepatitis were predominantly grade 3, according to the CTCAE system (71.2%, n = 37). No case of severe acute hepatitis has been reported. Liver biopsy was performed in 38.5% (n = 20). Biliary stenosis occurred in 6 patients (28.6%). An extra-hepatic irAE was reported in 46.2% (n = 24). Most patients were treated with corticosteroids (76.9%, n = 40) and ursodeoxycholic acid (UDCA) was in 32.7% (n = 17) patients. ICI was resumed in 46.2% (n = 24), 70.8% received the same ICI (n = 17) and 95.8% received a single ICI (n = 23). The rate of hepatitis recurrence after treatment reintroduction was 37.5% (n = 9). 10 patients died (19.2%), unrelated to ICI.

Conclusion: The frequency of ICI related hepatitis is about 14.7% in our study. This result is consistent with the literature. Future studies should be considered to adapt the treatment to the hepatitis phenotype, particularly in the case of cholestatic pattern, by specifying the place of UDCA.

FRI007
Liver toxicities of immune checkpoints inhibitors for cancer: a multicenter retrospective study
Lucia Parlati1, Mehdi Sakka2, Agnès Bellanger3, Jean François Meritet4, Samir Bouam5, Aurelia Retbi6, Pierre Rufat7, Dominique Bonnefont-Rousselot8, Rui Batista9, Patrick Tilleul10, Dominique Thabut11, Jean-Philippe Spano12, Francois Goldwasser13, Philippe Sogni14, Stanislas Pol12, Vincent Mallet12.

Background and aims: There are uncertainties on the clinical significance of liver toxicities of immune checkpoint inhibitors (ICI). The aim of our study was to compare liver toxicities under ICI and conventional chemotherapy.

Method: We conducted a retrospective, longitudinal cohort study among cancer patients who received systemic chemotherapy with or without ICI between January 1, 2010, and December 31, 2019, in two teaching hospitals of Assistance Publique-Hôpitaux de Paris (France). We measured the incidence of grade 3–4 liver injury after ICI or
Results: The sample comprised 22,206 patients (median [interquartile range] age 63 [52–72] years, 54.4% males), including 953 (4.3%) with ICI. The incidence of grade 3–4 liver injury was 209 (21.9%) and 5,765 (27.1%) for patients treated with and without ICI, respectively (p < 0.001). ICI patients were at risk [aHR 1.46 (1.23–1.75) P < 0.001] for cholestasis without [aHR 0.96 (0.60–1.53) P = 0.860] jaundice. ICI patients were not [aHR 1.12 (0.86–1.45), P = 0.401] at risk for hepatocellular injury. Grade 3–4 liver injury was attributed to ICI-DILI in 26 (2.7%) patients. Grade 4 transaminase and serum bilirubin elevations concerned 6 (0.6%) and 1 (0.1%) ICI-DILI patient, respectively. All patients with ICI DILI had ICI withdrawal, and 11 (42.3%) died thereafter with cancer progression. ICI reintroduction after ICI-DILI was a rare (n = 7; 26.9%) event and was infrequently (n = 1) associated with recurrent liver injury.

Conclusion: Patients treated with ICI were at lower risk of clinically significant liver injury than patients treated with conventional chemotherapy. There may be potential gains from refraining ICI dose reduction in patients with ICI-associated liver injury.

FRI008
Acute severe presentation of autoimmune hepatitis: a 20-year retrospective review of the United States
Thomas Enke1, Daniel Ganger1, Jody Rule2, Richard Stravitz3, Jorge Rakela4, Adrian Reuben5, Norman Sussman6, Anne Larson7, Shannan Tujios2, Nathan Bass8, Sherry Livingston9, Valerie Durkalski-Mauldin9, William M. Lee2. 1Northwestern University Feinberg School of Medicine, Chicago, United States; 2UT Southwestern Medical Center, Dallas, United States; 3Virginia Commonwealth University Medical Center, Richmond, United States; 4Mayo Clinic, Phoenix, United States; 5Medical University of South Carolina, Columbia, United States; 6Baylor College of Medicine, Houston, United States; 7University of Washington Medicine, Seattle, United States; 8University of California San Francisco, San Francisco, United States; 9Medical University of South Carolina, Columbia
Email: thomas.enke@northwestern.edu

Background and aims: Autoimmune hepatitis (AIH) is a common cause of acute liver failure (ALF). Treatment includes steroids in those with acute liver injury (ALI) and liver transplantation (LT) in those who fail to respond or develop ALF. The aim of this study is to better characterize the clinical and laboratory data of patients presenting with ALI or ALF secondary to AIH and to identify a combination of clinical variables that predict 21-day transplant-free survival (TFS).

Method: The study included hospitalized adults presenting with ALI or ALF enrolled in the Acute Liver Failure Study Group Registry between 1998 and 2019 from 32 centers within the United States. A review panel adjudicated the etiology of all cases and those identified as AIH were reviewed. ALI was defined as international normalized ratio (INR) ≥ 2.0 without encephalopathy and ALF as any degree of encephalopathy with INR ≥ 1.5. Laboratory and clinical data were reviewed, and variables significantly associated with 21-day TFS were used to develop a multivariable logistic regression model.

Results: A total of 244 of 3364 cases were identified as AIH and reviewed. 161 patients (66%) were diagnosed with ALF and 83 with ALI (34%). At 21 days, 116 patients (48%) had undergone LT, 69 (28%) had TFS and 59 (24%) had died. Patients presenting with ALI had a higher TFS rate (53%) than patients presenting with ALF (16%). Most presenting with AIH received steroids (73%) and were more likely to have TFS (66%) than those who did not receive steroids...
Table 1: Variables associated with 21-day transplant free survival

<table>
<thead>
<tr>
<th>Predictor</th>
<th>Adjusted odds ratio</th>
<th>95% CI</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bilirubin</td>
<td>0.04</td>
<td>(0.01, 0.15)</td>
</tr>
<tr>
<td>INR b</td>
<td>0.30</td>
<td>(0.16, 0.56)</td>
</tr>
<tr>
<td>Platelet count</td>
<td>1.06</td>
<td>(1.01, 1.10)</td>
</tr>
<tr>
<td>Albumin</td>
<td>3.10</td>
<td>(1.34, 7.16)</td>
</tr>
<tr>
<td>Steroid use with ALF d</td>
<td>31.19</td>
<td>(3.35, 290.05)</td>
</tr>
<tr>
<td>Steroid use with ALF a</td>
<td>1.62</td>
<td>(0.57, 4.58)</td>
</tr>
<tr>
<td>ALF without steroid use</td>
<td>0.78</td>
<td>(0.11, 5.51)</td>
</tr>
<tr>
<td>ALF with steroid use</td>
<td>0.041</td>
<td>(0.01, 0.171)</td>
</tr>
</tbody>
</table>

a = confidence interval. b = international normalized ratio. d = acute liver failure during hospitalization.

Conclusion: Acute severe presentations of AIH are associated with a high mortality. Steroids remain a cornerstone of treatment and nearly half of patients will require LT. Early identification of those needing LT is critical to prevent delays in listing. We developed a model specifically for AIH that may be helpful in predicting 21-day TFS and early identification of patients in need for expedited LT evaluation. Further assessment of model performance and independent model validation are future work.

FRI009
Single-cell metabolic profiling of primary human hepatocytes shows heterogeneous responses to drug metabolism
Eva Sofia Sánchez Quaint1, Maria Richter1, Celia Martínez Jiménez1,2, Maria Colome Tatche1,2,3,4,5, Helmholtz Zentrum Munich, Helmholtz Pioneer Campus, Munich, Germany; 3Technical University Munich, Faculty of Medicine, Munich, Germany; 4Helmholtz Zentrum Munich, Institute of Computational Biology, Munich, Germany; 5Ludwig Maximilian University of Munich, Biomedical Center (BMC), Physiological Chemistry, Munich, Germany; 6Technical University Munich, TUM School of Life Sciences Weihenstephan, Munich, Germany
Email: eva.sanchez@helmholtz-muenchen.de

Background and aims: Drugs are primarily metabolized by hepatocytes in the liver, and primary human hepatocytes (PHHs) are the gold standard model for the assessment of drug efficacy, safety and toxicity in the early phases of drug development. Classic approaches assume that all hepatocytes in culture are homogeneous and share a similar metabolic profile. However, advances in single-cell genomics have shown the relevance of cellular heterogeneity in health and disease conditions. Recently, single-cell RNA sequencing has shown that intrahepatic lipid accumulation in Non-alcoholic fatty liver disease (NASH) affects the transcriptomic profile of parenchymal and non-parenchymal liver cells. The aim of this study is to investigate the metabolic capacity of individual human hepatocytes in vitro, and assess whether the chronic accumulation of lipids enhances cellular heterogeneity.

Method: PHHs isolated from four donors were incubated with a phenotyping 5-probe cocktail (Sanofi-Aventis) using the so-called “cocktail approach.” In order to mimic the hepatic steatosis occurring in NAFLD, hepatocytes were loaded with free fatty acids, resulting in intracellular lipid accumulation. Subsequently, cells were incubated with the five-drug cocktail. After 72 h in culture, hepatocytes were collected and single-cell RNA-sequencing was performed using a droplet-based approach.

Results: Four subgroups of hepatocytes were identified consistently, independently of the treatment condition, and across all four donors.

These subgroups displayed differential gene expression upon cocktail treatment, and xenobiotic metabolism-related specialization. Furthermore, lipid accumulation was found to increase transcriptional variability in two subgroups of hepatocytes, and to differentially affect the expression of genes involved in lipid metabolism. In particular, intracellular fat accumulation was shown to diminish the drug-related metabolic capacity of hepatocytes.

Figure: Graphical abstract summarizing the hypothesis stated.

Conclusion: Our results demonstrate that, upon a metabolic challenge such as exposure to drugs or intracellular fat accumulation, hepatocyte subgroups exhibit heterogeneous transcriptomic responses.

References

FRI010
Management of severe, steroid-resistant and steroid-refractory hepatotoxicity in patients treated with checkpoint inhibitor immunotherapy
Nashla Hamdan1, Marco Lafolla2, Yada Kanjanapan2, Marcus Butler2, Lilian Su2, Philippe Bedard2, Kendra Ross2, Keyur Patel1, Anna Spreatico3, Jordan Feld1, Morven Cunningham1, 2University Health Network, Princess Margaret Cancer Centre, Toronto, Canada; 3University Health Network, Princess Margaret Cancer Centre, Toronto, Canada
Email: morven_c@hotmail.com

Background and aims: Checkpoint inhibitor immunotherapy (ICI) has revolutionized cancer care and is increasingly used in a range of primary malignancies. Treatment is associated with immune-related toxicities which may require ICI discontinuation and immunosuppressive therapies (IST). Management of severe ICI hepatotoxicity is not well defined, especially for patients who respond poorly to initial corticosteroids. We sought to better understand management of severe ICI hepatotoxicity and responses to IST.

Method: Patients receiving ICI in early phase clinical trials at Princess Margaret Cancer Centre, or treated at the Toronto Centre for Liver Disease for ICI hepatotoxicity, were included. Patients with CTCAE Grade (G)3/4 ICI hepatotoxicity (ALT >5 × ULN) were identified and clinical records reviewed for management and outcomes.

Results: From Aug 2012-Oct 2021, 25 patients with G3/4 ICI hepatotoxicity were identified. Most (17; 68%) had metastatic melanoma. Eleven received anti-CTLA-4/PD-1; 9 anti-PD-1, and 5 anti-CTLA-4 monotherapy. All patients initially received corticosteroids for hepatotoxicity (1–2 mg/kg/day prednisone equivalent). Figure 1 shows response to corticosteroids and sequence of additional IST. 13 patients (52%) were steroid-refractory (no response after 48–72 hours) or steroid-resistant (rebound ALT upon steroid...
Ten received steroid dose escalation (up to 2 mg/kg/day) with sustained response in five (50%). Eight (32%) received 2nd line IST with mycophenolate (MMF) for steroid resistant/refractory hepatotoxicity, after median 17.5 days of steroid treatment (IQR 9–21). Four (50%; 16% of total cohort) did not respond to MMF and required 3rd line IST (Tacrolimus; dose targeting trough level of 4–6). Age, sex, liver metastases, prior ICI exposure or peak ALT did not predict need for 2nd or 3rd line IST. ALT normalized in all, after median 14 days (IQR 10–27). Patients on corticosteroid alone had shorter total time on IST than those with additional IST (median 86 days, IQR 41–123) vs 113 days (85–235), p = 0.03). In those given additional IST, rate of ALT improvement tended to be faster with Tacrolimus than MMF (25.5 IU/day (IQR 22–29.5) vs 10.5 IU/day (IQR −3 to 29.5), p = ns in this small cohort). IST-related adverse events occurred in two patients (vertebral fracture; hyperglycaemia). Over median follow up of 30.6 months (range 2.3–81.5), 12 patients died. No patients died of complications of hepatotoxicity.

Conclusion: Up to a third of patients with severe (G3/4) ICI hepatotoxicity may not respond adequately to corticosteroids and require additional IST. MMF is not consistently effective as 2nd line IST. To expedite resolution and minimize IST exposure, Tacrolimus should be considered 2nd line IST alternative. These results will assist development of treatment algorithms for severe ICI hepatotoxicity, for further prospective evaluation.

FRI011
Activation marker CD69 differentiates non-alcoholic steatohepatitis from drug-induced liver injury
Estefanía Caballano-Infantes1, Alberto García García1, Carlos López-Gómez1, A. Cueto2, Mercedes Robles-Díaz3, Aida Ortega-Alonso4, F. Martín-Reyes5, Ismael Alvarez-Alvarez2, Isabel Arranz-Salas6, Francisco Ruiz-Cabello7, Maria Isabel Lucena2,6, Eduardo García-Fuentes4, Raúl J. Andrade1,3, Miren García Cortes1.
1IBIMA, Servicio de Aparato Digestivo, Hospital Universitario Virgen de la Victoria, IBIMA, UMA, Málaga, Spain, Málaga, Spain; 2UMA, Departamento de Farmacología, Málaga, Spain; 3UMA, Departamento de Medicina, Málaga, Spain; 4IBIMA, Servicio de Anatomía Patológica, Málaga, Spain; 5Hospital Universitario Virgen de las Nieves/UGR, Servicio de Análisis Clínicos e Immunología/Departamento de Bioquímica y Biología Molecular II/Immunología, Facultad de Medicina, Granada, Spain; 6IBIMA, Málaga, Spain
Email: edugf1@gmail.com

Background and aims: Activation of the immune system is involved in both non-alcoholic fatty liver disease (NAFLD) and idiosyncratic drug-induced liver injury (DILI). We aimed to identify activation markers in invariant natural killer T (iNKT) and CD4+CD8+ T cells to better understand the pathophysiology of these disorders.

Method: We analyzed the activation profile (CD69, CD25 and HLA-DR) and NKG2D on iNKT cells, and CD4+ and CD8+ T cells by flow cytometry in peripheral blood mononuclear cells from NAFLD, with or without significant liver fibrosis, and DILI patients.

Results: There was an increase in iNKT cells in NAFLD patients compared to DILI or control subjects (p = 0.035 and p = 0.031, respectively). Regarding the cellular activation profile, NAFLD with significant liver fibrosis (F ≥ 2) displayed higher levels of CD69+ iNKT cells compared to NAFLD with none or mild liver fibrosis (F ≤ 1) (p = 0.040) and control patients (p = 0.031). CD69+ iNKT positively correlated with insulin resistance, liver fibrosis indexes FIB4 and APRI, and AST levels. DILI patients showed an increase in CD69+ and HLA-DR+ in both CD4+ and CD8+ T cells, detecting the most relevant difference in the case of CD69+CD8+ T cells.

Conclusion: CD69+ iNKT may be a biomarker to assess liver fibrosis progression in NAFLD. CD69+CD8+ T cells were identified as a potential distinctive biomarker for distinguishing DILI from NAFLD. These results support the involvement of the immune system on NAFLD with significant liver fibrosis and DILI development.

FRI012
Natural antibodies are required for necrotic cell debris clearance and liver repair during necrotic liver injury
Matheus Mattos1, Sofie Vandendriessche1, Sara Schuermans1, Romy Mittenzwei2, Ari Waisman3, Pedro Elias Marques1, Rega Institute Ku Leuven, Leuven, Belgium; 2Institute for Molecular Medicine, University Medical Center of the Johannes Gutenberg-University Mainz, Mainz, Germany
Email: pedro.marques@kuleuven.be

This abstract is under embargo until Thursday 23 June 2022, 13:30 BST. It will be made publicly available on the congress website once the embargo has lifted.
Journalists, industry, investigators and/or study sponsors must abide by the embargo times set by EASL. Violation of the embargo will be taken seriously. Individuals and/or sponsors who violate EASL’s embargo policy may face sanctions relating to current and future abstract submissions, presentations and visibility at EASL Congresses. The EASL Governing Board is at liberty to ban attendance and/or retract data.

Copyright for abstracts (both oral and poster) on the website and as made available during The International Liver Congress™ 2022 resides with the respective authors. No reproduction, re-use or transcription for any commercial purpose or use of the content is permitted without the written permission of the authors. Permission for re-use must be obtained directly from the authors.

FRI014
A new score to predict mortality at baseline in patients not fulfilling KCH criteria for non acetaminophen induced liver failure-The ‘SAFE’ score (Severity of ALF in emergency)
Harshvardhan Tevethia1, Rahul Maival1, Shalini Thapar2, Roshan Koul3, Prashant Mohan Agarwal4, Guresh Kumar2, Ashok Choudhury2, Shiv Kumar Sarin5, 1Institute of Liver and Biliary Sciences, Hepatology, Delhi, India; 2Institute of Liver and Biliary Sciences, Critical Care, Delhi, India; 3Institute of Liver and Biliary Sciences, Radiology, Delhi, India; 4Institute of Liver and Biliary Sciences, Biostatistics, Delhi, India; 5Institute of Liver and Biliary Sciences, Neurology, Delhi, India. Email: harshvardhantevethia@gmail.com

Method: Patients diagnosed to have ALF and not fulfilling KCH criteria at admission were enrolled and electronic data was retrieved from June 2010 to May 2021 from the HIS using a predefined format. All patients underwent CT imaging (Non contrast) of both Brain and abdomen at admission. The Liver volume was calculated (CT) along with predictors of outcome, need for liver transplant, KCH and MELD scores. Cox regression analysis was done at baseline.

Method: We used the Caco-2 human colorectal adenocarcinoma cell line to represent gut and the human hepatic HepaRG line to represent liver. Caco2 cells were incubated with 0, 5, 10 and 20 mM of APAP for 24 hours. Supernatant was transferred onto fresh HepaRG cells for a further 24 hours. Cell cultures were monitored in real time using the ECIS Zθ, an impedance based cellular assay, using multiple frequencies to measure tight junctions, adhesion (4 kHz) and cell membrane integrity (64 kHz). Viability was assessed using PrestoBlue, to monitor cell metabolism, and Promega Celllitter glo for a measure of total ATP. Percentage of APAP metabolized by Caco2 cells was measured using LC-MS/MS. IL-8, IL-1b, IL-6, IL-10, TNF, and IL-12p70 were measured using the CBA Human Inflammatory Cytokines kit flow-cytometry bead assay.

Results: ECIS measurements showed an increase in tight junctions/adhesion in a concentration dependent manner on Caco2 cells. In contrast to previously published work, when using Caco2 preconditioned media, toxicity to HepaRG cells was mitigated with no loss of tight junctions. LC-MS/MS showed that Caco2 cells metabolize 64–68% of total APAP without any adverse effects on their viability. IL-6 and IL-8 produced by HepaRG cells was appropriately reduced suggesting an anti-inflammatory effect of APAP.

Conclusion: We have shown that intestinal cells are capable of removing 2/3 APAP within the intestinal barrier with no compromise of viability or tight junctions mitigating toxicity to hepatic cells. Based on these observations, the intestine is an effective barrier protecting the liver from APAP hepatotoxicity therefore parenteral administration of APAP should be avoided and if no other option intravenous dose should be adjusted accordingly.

Reference

FRI013
Human paracetamol hepatotoxicity is mitigated by the gut-liver axis in vitro
Katie Morgan1, Martin Vandeputte1, Kay Samuel2, Steven Morley1, Natalie Homer3, Martin Waterfall4, Jonathan Fallowfield1,5, Peter Hayes1, John Plevris1, Katie Morgan1, 1University of Edinburgh, Hepatology Dept, Edinburgh, United Kingdom; 2Scottish National Blood Transfusion Service, The Jack Copland Centre 52 Research Avenue North, Edinburgh, United Kingdom; 3University of Edinburgh, Mass spectrometry core, Edinburgh, United Kingdom; 4University of Edinburgh, Flow Cytometry Core Facility, Edinburgh, United Kingdom; 5University of Edinburgh, Centre for Inflammation Research, Edinburgh, United Kingdom Email: katie.morgan@ed.ac.uk

Background and aims: The gut liver axis is a bidirectional system communicating via signals from the microbiome, immune system, dietary and genetic influences. We have previously shown in vitro that APAP disrupts tight junctions in hepatic HepaRG cells in a concentration dependant manner. The aim of this study, was to develop a model of enterohepatic circulation of paracetamol (APAP) in vitro and establish whether intestinal barrier has a hepato-protective effect in the context of APAP toxicity.

Method: We used the Caco-2 human colorectal adenocarcinoma cell line to represent gut and the human hepatic HepaRG line to represent liver. Caco2 cells were incubated with 0, 5, 10 and 20 mM of APAP for 24 hours. Supernatant was transferred onto fresh HepaRG cells for a further 24 hours. Cell cultures were monitored in real time using the ECIS Zθ, an impedance based cellular assay, using multiple frequencies to measure tight junctions, adhesion (4 kHz) and cell membrane integrity (64 kHz). Viability was assessed using PrestoBlue, to monitor cell metabolism, and Promega Celllitter glo for a measure of total ATP. Percentage of APAP metabolized by Caco2 cells was measured using LC-MS/MS. IL-8, IL-1b, IL-6, IL-10, TNF, and IL-12p70 were measured using the CBA Human Inflammatory Cytokines kit flow-cytometry bead assay.

Results: ECIS measurements showed an increase in tight junctions/adhesion in a concentration dependent manner on Caco2 cells. In contrast to previously published work, when using Caco2 preconditioned media, toxicity to HepaRG cells was mitigated with no loss of tight junctions. LC-MS/MS showed that Caco2 cells metabolize 64–68% of total APAP without any adverse effects on their viability. IL-6 and IL-8 produced by HepaRG cells was appropriately reduced suggesting an anti-inflammatory effect of APAP.

Conclusion: We have shown that intestinal cells are capable of removing 2/3 APAP within the intestinal barrier with no compromise of viability or tight junctions mitigating toxicity to hepatic cells. Based on these observations, the intestine is an effective barrier protecting the liver from APAP hepatotoxicity therefore parenteral administration of APAP should be avoided and if no other option intravenous dose should be adjusted accordingly.
males 59.2%. The all-cause mortality in patients not meeting the KCH criteria was 44.8%. The most common etiology was hepatitis E (34.7%) followed by indeterminate etiology (28.6%). On the CT imaging of the brain, cerebral edema was seen in 34% patients; with significantly lower liver volume in the ALF non-survivors than survivors (765 ± 465 cm³ vs. 1265 ± 346 cm³; p < 0.04). On univariate analysis grade >3 Hepatic encephalopathy (HE), ONSD (both right/left eye) >5 mm, jaundice to HE duration >9 days and liver volume <980 cm³ were found to be significant. On multivariate analysis, HE grade 3 (OR = 7.671, 95% CI: 1.943–252.423), jaundice to encephalopathy >9 days (OR = 2.293–268.65) were found to be significant. We developed the “SAFE” score using these variables. A score of 5 gave the AUROC value of 90.9 with p < 0.01 (95% CI: 89.9–91.9) with a sensitivity of 90%, specificity of 71%, positive and negative predictive values of 82% and 73% respectively with Youden index at 50%. On comparison with KCH (50, 95% CI: 33.6–64.4) and MELD score (65.9, 95% CI: 50–81.9) the SAFE score was significantly better at predicting mortality in ALF patients at baseline.

Conclusion: In patients not fulfilling the KCH criteria, the newly developed SAFE score was significantly better in predicting worse outcomes. Its variables indicate the presence of cerebral edema and low liver volume as the main causes of mortality in this subset of patients. Application of the SAFE score should be validated and a routine use of CT brain and liver be practiced for better stratification of ALF patients at baseline.
Ten-year single center experience in hepatotoxicity due to mushroom poisoning

Ozan Sarikaya1, Ilker Turan1, Pulya Günsar1, Ayseunor Arslan2, Nilay Danis3, Perit Celik1, Galip Eroot2, Sezgin Ulukaya4, Murat Zeytunlu5, Omer Ozutemiz2, Ulus Akarca2, Zeki Karasulu1, 1Ege University, Medical Faculty, Gastroenterology, Izmir, Turkey; 2Ege University, Medical Faculty, Internal Medicine, Izmir, Turkey; 3Karabuk University, Gastroenterology, Karabuk, Turkey; 4Ege University, Medical Faculty, Anesthesiology, Izmir, Turkey; 5Ege University, Medical Faculty, General Surgery, Izmir, Turkey

Background and aims: Mushroom poisoning is quite common in Turkey. It can cause acute liver injury and acute liver failure (ALF) requiring liver transplantation. We investigated the outcomes of patients with acute hepatotoxicity due to mushroom poisoning in our cohort.

Method: We retrospectively evaluated the characteristics of patients requiring liver transplantation. We investigated the outcomes of 27 patients presented with nausea and vomiting. In addition, fourteen patients had abdominal pain and sixteen had diarrhea. These patients were admitted to our intensive care unit within an average of 2.5 days (6 hours–8 days) after eating mushrooms from the countryside. In 15 patients (fourteen at admission, one during hospitalization), INR increased >1.5, acute liver failure developed in 4 patients (two patients at admission, hepatic encephalopathy developed in two patients during follow-up). The peak levels of ALT, AST and total bilirubin were 2109 ± 1963 U/L, 1828 ± 1675 U/L, 4.92 (0.1–28.56 mg/dl), respectively. In hospital follow-up, the highest INR levels were found to be an average of 2.29 (±1.56). All patients were treated with N-acetylcysteine (NAC). Seven patients were treated with penicillin G, six patients with silymarin, and two patients with both penicillin G and silymarin. Eight patients underwent plasmapheresis (median 6 times). Two of the four patients with ALF underwent emergency liver transplantation, and one patient died 72 days after transplantation. One patient who developed ALF recovered with medical treatment, while the other patient who could not be transplanted died. In multivariate analysis, INR and chlorine levels at hospital admission were found to be statistically significant factors for death and liver transplantation. (respectively: OR: 17.8 and p: 0.04 and OR: 0.54 and p: 0.04)

Conclusion: In our cohort, the mortality rate of mushroom liver toxicity was 10%. High INR levels and detection of hypochloremia have been associated with serious outcomes such as liver transplantation or mortality, and these parameters may be predictive of urgent liver transplantation.

CC44-induced acute liver injury in C57/BL mice model showed elevated expressions of Na+ taurocholate cotransporting polypeptide on intestinal stellate cells

Johnny Amer1, Reem Shieh1, Ahmed Salhab1, Rifaat Safadi1, 1Hadassah Hebrew University Hospital, Liver Unit, Jerusalem, Israel

Email: johnnymamer@hotmail.com

Background and aims: The Na+ taurocholate cotransporting polypeptide (NTCP/SLC10A1) is believed to be pivotal for hepatic uptake of conjugated bile acids. In the case of acute liver injury (ALI), NTCP is downregulated leading to hepatic and biliary injury, driving inflammatory and fibrotic processes. Several studies linked ALI to cause intestinal mucosa damaged. In this study, we aimed to evaluate whether bile acid (BAs) trafficking interfere with intestinal stellate cells in an ALI of CCl4 mice model.

Method: C57/BL mice were i.p injected (1X) with CCl4 (xxx) to induce ALI. Livers, intestinal stellate cells (ICS) isolated form intestine and serum were obtained from mice and assessed for inflammatory (H&E staining, ALT and pro-inflammatory panel of cytokines), fibrosis (Sirius red staining, a-smooth muscle actin, collagen and fibronectin) and metabolic (BAs, cholesterol, triglyceride, glucose tolerance test (GTT) and fasting blood sugar (FBS) profiles. In addition, ICS were assessed for NTCP and membrane injury of surfactant D (SP-D) and the receptor for advanced glycation end-products (RAGE). BAs trafficking were assessed in ICS and their impact on proliferation and apoptosis were evaluated.

Results: Compared to WT mice, CCl4-induced ALI and was worsened in the histopathology outcome. In addition, serum showed elevated levels of BAs (3-fold; P = 0.002) associated with increased RAGE, TNF-a, MCP-1, INF-γ, IL-1, IL-6 and IL-8 (p < 0.01). Moreover, CCl4-induced ALI showed elevated serum levels in liver enzymes, lipids, glucose and metabolic markers (p < 0.01). ICS showed high expressions of a5MA and were correlated with elevated expressions of NTCP. ICS BAs intracellular concentrations were increased (2-fold) with increased SP-D (1.2-fold) as well as elevation in their apoptotic rate (2.1-fold) in the ALI mice model.

Conclusion: NTCP modulatory expressions on ICS could be an important step in the pathogenesis of ALL. Antagonizing BAs uptake may suggest a therapeutic strategy in improving liver-gut axis.
with COL PMC ‘60–80%’ had the highest cumulative hazard risk for DC (Kaplan-Meier analysis, LogRank = 47.192, p < 0.001).

**Conclusion:** Chronic colchicine use is associated with incident DC in a cohort of new COL users.

**FR018 Inhibition of C-C motif chemokine receptor 2 (CCR2) using a novel in silico designed peptide attenuates macrophage migration in vitro and intrahepatic monocyte recruitment in vivo**

Eline Geervliet1,2, Ralf Weiskirchen2, Ruchi Bansal1,3. 1University of Twente, Medical Cell Biophysics, Enschede, Netherlands; 2RWTH Aachen, Institute of Molecular Pathobiochemistry, Experimental Gene Therapy and Clinical Chemistry, Aachen, Germany; 3University of Twente, Translational Liver Research, Netherlands

**Background and aims:** Acute liver injury is a highly prevalent and a life-threatening disease. Hepatocyte injury induces activation of liver-resident Kupffer cells (KCs) and consequently activation of hepatic stellate cells (HSCs). Hepatocytes, HSCs and KCs secrete C-C motif chemokine ligand 2 (CCL2) and trigger the recruitment of C-C motif chemokine receptor 2 (CCR2) expressing circulating monocytes. This results in chronic liver inflammation that further progresses to liver fibrosis, cirrhosis and/or hepatocellular carcinoma. Blocking the CCR2, using a small molecule CCR2/CCR5 inhibitor cenicriviroc (CVC), has already been proven effective in vitro and in vivo.

**Method:** Receptor binding affinity of the AP2 was characterized using surface plasmon resonance imaging (SPRi) in situ and in vitro. Efficacy of AP2 on CCL2-driven chemotaxis was examined in vitro in mouse RAW 264.7 macrophages and human THP-1 monocytes using transwell assays, and in vivo in an acute carbon tetrachloride induced liver injury mouse model. To assess intrahepatic monocyte infiltration in vivo, liver tissues were mechanically dissociated using Tissue Grinder, and cell population such as CD45+ leukocytes, resident and monocytes-derived macrophages (MoMFs) (CD11b+/++ and F4/80++/+), and T-cells (CD3+) were analyzed using flow cytometry. Furthermore, effects of AP2 on disease progression (inflammatory and fibrosis markers) were assessed using immunohistochemistry. The effects of AP2 were compared with CVC in vitro and in vivo.

**Results:** AP2 (p < 0.01) and CVC (p < 0.05) showed favorable inhibition of CCL2-driven macrophage/monocyte chemotaxis. In vivo, flow cytometric analysis revealed that a decrease in the population of CD45+ cells and CD11b++/F4/80++ MoMFs and (activated) CD11b++/F4/80+++ KCs, while CD3+ T cells in CVC and AP2 treated mice were comparable to that of healthy controls. Immunohistochemical analysis evidenced decreased expression of fibrosis markers (collagen-I and alpha-smooth muscle actin) and an increase in Ki-67 positive hepatocytes in the AP2 treated mouse livers. Our data shows effective amelioration of inflammation and fibrosis by inhibition of CCR2 using CCR2-antagonizing peptide. SPRi and in vitro peptide binding studies are ongoing alongside with more in vivo analysis. The peptide will be evaluated further in a non-alcoholic steatohepatitis (NASH) mouse model.

**Conclusion:** Our CCR2-antagonizing peptide inhibited migration of macrophages/monocytes in vitro and ameliorated inflammation and fibrosis in vivo in an acute liver injury mouse model.
FRI019
Murine intrahepatic regulatory T cells modulate acute liver inflammation by promoting a protective and restorative microenvironment
Ada Kurt1, Karoline Strobl2, Tonika Chester1, Gabriel Osborn1, Paula Ruiz1, Elizabeth H. Gray1, Alberto Sanchez-Fueyo1, Marc Martinez-Llordella1. 1King’s College London, Department of Inflammation Biology, London, United Kingdom; 2Medical University of Vienna, Institute for Cancer Research, Vienna, Austria
Email: ada_sera.kurt@kcl.ac.uk

Background and aims: CD4+CD25+Foxp3+ regulatory T cells (Tregs) exert powerful immunomodulatory effects that are essential to maintain immune homeostasis and prevent the development of immune-mediated diseases. In addition to their immunomodulatory role, recent studies have identified that depending on the tissue compartment they migrate to or reside in, Tregs acquire tissue-specific features and develop cytoprotective and regenerative functions. The liver is an organ known to be deprived in IL-2, a cytokine that is essential for the adequate function and survival of Tregs. The extent to which this affects intra-hepatic Treg phenotype and the capacity of these cells to modulate liver damage has not been adequately investigated. In this study, we aimed to explore the phenotypic and functional diversity of liver resident Tregs during homeostasis. Additionally, we investigated their role in ameliorating liver inflammation and tissue damage by depleting Tregs and increasing their pool by exogenous IL-2 complex (IL-2c) administration in murine models.

Method: Flow cytometry phenotyping and microarray analysis was performed on Foxp3-YFP intrahepatic and splenic Tregs in homeostatic conditions and with the administration of IL-2c for 3 consecutive days. Tregs were depleted in Foxp3-DTR mice by intraperitoneal (i.p) injection of 1μg diphtheria toxin and IL-2c were administered i.p. to wild-type C57Bl/6 mice. The extent of liver damage following a single dose of carbon tetrachloride (CCL4) injury was investigated 24 hours later in both models.

Results: Quantification of Foxp3+CD4+ cells among different tissues showed that the liver exhibited the lowest abundance of Tregs. Analysis in homeostatic conditions revealed that, although intrahepatic Tregs exhibited the core transcriptional Treg signature, they expressed a distinct transcriptional profile. This was characterized by reduced CD25 expression and increased levels of pro-inflammatory Th1 transcripts IL1b and IFNγ. Depletion of Tregs showed that Tregs effectively reduced the magnitude of systemic and intra-hepatic inflammatory responses following CCL4 injury, but they were not directly involved in ameliorating hepatocyte necrosis. In contrast, the administration of IL-2c markedly increased the number of intra-hepatic Tregs and significantly ameliorated liver damage following CCl4 administration. The cytoprotective effect observed in response to IL-2c was associated with the increased expression by Tregs of markers known to regulate their suppressive function.
**Conclusion:** Our results offer insight into the transcriptome and complex immune network of intrahepatic Tregs and how their number and phenotype may affect their ability to modulate liver inflammation. Strategies capable of selectively increasing the pool of intra-hepatic Tregs could constitute effective therapies in inflammatory liver diseases.

**FRIO20**

**Place of steroids and prognosis factors for grade 3 immune-checkpoint inhibitors induced hepatitis: a 6-year prospective study**

Eleonora De Martin1, Alina Lutu 1, Ariane Laparra-Ramakichenin2, Nicolas Golse1, Astrid Laurent Bellue 3, Caroline Robert 2, Lea Duhaut1, Olivier Rosmorduc 1, Catherine Guettier 3, Eleonora De Martin1, Alina Lutu1, Ariane Laparra-Ramakichenin2, Nicolas Golse1, Astrid Laurent Bellue 3, Caroline Robert 2.

**Background and aims:** The management of liver toxicity of immune checkpoint inhibitors (ICI) and the role of steroids is controversial. This study aimed to provide a report of a well-characterized cohort of patients with ICI-induced hepatitis and their management.

**Method:** In this prospective cohort study, patients treated with ICI for metastatic cancer and referred to hepatology unit for grades ≥ 3 hepatitis (06/2015–09/2021) were evaluated and the ones with ICI-induced hepatitis, after exhaustive causal investigations, were included. The decision to introduce steroids and/or ursooexocholic acid (UDCA) was at physician discretion (oncologist/hepatologist).

**Results:** Among 64 included patients, 29 (45%) female, median age 61 years (33–83), the most common cancers were metastatic melanoma (n = 30), renal cancer (n = 12) and epidermoid carcinoma (n = 6). The ICI administered were anti-PD1 (n = 29), anti-PDL1 (n = 9), anti-CTLA-4 (n = 5), anti-PD1+anti-CTLA-4 (n = 21) and ICI+chemotherapy (ex. carboplatin, anti-EGFR) (n = 21). 30% of patients were previously exposed to another ICI. Median time between ICI introduction and first increase of liver tests (LFTs) was 1.80 months (0.82–5.17) months, and between ICI introduction and peak of LFTs was 2.67 months (1.43–5.17) months, median number of doses was 2 (1.75–4). Forty (62%) patients had grade 3 and 24 (38%) grade 4 hepatitis, 33% were symptomatic. At peak median (IQR) LFTs were AST 481 (280–780) IU/L, ALT 320 (164–549) IU/L, total bilirubin 14.5 (10.2–19.2) μmol/L, GGT 366 (150–800) IU/L, ALP 301 (134–513) IU/L, only 2 patients had increased INR. Median IgG were 10.0 (7.8–12.3) g/L. ANA was positive in 49% and ASMA in 3.5% of patients. The diagnosis was histologically confirmed in 91% of patients. Seven patients underwent biliMRI and 3 had cholangitis. No differences were found among patients with grade 3 or 4 hepatitis regarding type of cancer, type of ICI, number of doses, interval between ICI introduction and peak of LFTs. Steroids were introduced in 32 (50%) patients and UDCA was used in 27% of patients. Doses of steroids were 0.5, 1 and 2 mg/kg/day in 8, 21 and 2 patients (not known in 1), respectively. Four patients didn't improve, 1 required increase of steroids, 3 a second immunosuppressive drug, 1 multiple drugs and died of liver failure. Use of steroids was associated with higher AST (p = 0.041), ALT (p = 0.041), total and conjugated bilirubin (p < 0.01 and 0.025) but not with type of ICI, number of doses, interval between ICI introduction and LFTs increase. Among grade 4 patients, 8 (33%) improved without steroids.

**Conclusion:** Grade ≥3 ICI-induced hepatitis was non-severe in the majority of cases. Steroid therapy was introduced in only half of the patients and was associated with higher ALT and bilirubin level. New cut off to indicate the use of steroid therapy is needed.

**FRIO21**

**The role of macrophage ETS Proto-oncogene 2 in acute-on-chronic liver failure**

Lulu He1, Qun Cai3, Xi Liang2, Jiaojiao Xin1, Jing Jiang1, Dongyan Shi1, Keke Ren1, Yun Li1, Jiaxian Chen1, Jinjin Luo1, Jiaqi Li1, Peng Li1, Jun Li1, Lijun2009@zju.edu.cn

**Background and aims:** Acute-on-chronic liver failure (ACLF) is a critical disease caused by acute aggravation of chronic liver disease, with poor prognosis and high mortality. The detailed mechanism of ACLF remains unclear. The purpose of this study was to investigate the value of macrophage ETS Proto-oncogene 2 (ETS2) as a prognostic marker in ACLF, and its role in mouse liver failure model induced by D-GalN/LPS.

**Method:** In this study, peripheral blood monocytes from 50 patients with ACLF, 50 chronic liver disease, and 50 healthy persons were collected for RNA-SEQ sequencing analysis. ACLF patients were divided into ETS2-high and ETS2-low expression group, and the differentially expressed genes between two groups were analysed. A demarcation cut off to indicate the use of steroid therapy is needed.

**Results:** The mRNA expression of ETS2 in peripheral blood of ACLF patients was significantly increased compared with chronic liver disease and healthy persons. The expression of high mobility group box 1 (HMGB1). In vitro, CRISPR-Cas9 was used to knockdown ETS2 in RAW264.7 cells. The changes of inflammatory factors and related signalling pathways were detected with the intervention of HMGB1.

**Conclusion:** Grade ≥3 ICI-induced hepatitis was non-severe in the majority of cases. Steroid therapy was introduced in only half of the patients and was associated with higher ALT and bilirubin level. New cut off to indicate the use of steroid therapy is needed.

**Table: Characteristics of patients treated vs not treated with steroids**

<table>
<thead>
<tr>
<th>Steroids No</th>
<th>Steroids Yes</th>
<th>p</th>
</tr>
</thead>
<tbody>
<tr>
<td>ALT, IU/l</td>
<td>388 [264, 888]</td>
<td>566 [354, 1295]</td>
</tr>
<tr>
<td>AST, IU/l</td>
<td>238 [132, 448]</td>
<td>427 [252, 750]</td>
</tr>
<tr>
<td>Total bilirubin, μmol/l</td>
<td>11.5 [9.10, 18.8]</td>
<td>20.5 [11.8, 49.2]</td>
</tr>
<tr>
<td>Conjugated bilirubin, μmol/l</td>
<td>7.00 [5.00, 10.00]</td>
<td>12.2 [6.00, 38.00]</td>
</tr>
<tr>
<td>GGT, IU/l</td>
<td>390 [155, 659]</td>
<td>315 [184, 981]</td>
</tr>
<tr>
<td>ALP, IU/l</td>
<td>327 [118, 418]</td>
<td>258 [147, 585]</td>
</tr>
<tr>
<td>Interval between first ICI dose and LFTs increase, months</td>
<td>2.07 [0.985, 3.33]</td>
<td>1.38 [0.667, 3.44]</td>
</tr>
<tr>
<td>Interval between first ICI dose and LFTs peak, months</td>
<td>2.53 [1.85, 3.22]</td>
<td>3.42 [3.14, 7.08]</td>
</tr>
<tr>
<td>Number of doses</td>
<td>3.00 [1.50, 4.00]</td>
<td>2.00 [2.00, 4.00]</td>
</tr>
<tr>
<td>Anti-PD1+anti-CTLA4, n(%)</td>
<td>10 [31%]</td>
<td>11 [34%]</td>
</tr>
<tr>
<td>Anti-PD1, n(%)</td>
<td>16 [50%]</td>
<td>13 [41%]</td>
</tr>
<tr>
<td>Anti-PDL1, n(%)</td>
<td>5 [16%]</td>
<td>4 [12%]</td>
</tr>
<tr>
<td>Anti-CTLA4, n(%)</td>
<td>1.0 [3.1%]</td>
<td>4 [12%]</td>
</tr>
</tbody>
</table>
significantly in acute liver failure model. The inflammatory infiltration and necrosis in liver tissue were significantly increased, and the expression of HMGB1 in liver tissue was significantly increased. In vitro results showed that D-GalN could induce HMGB1 release from hepatocytes. Knockout of ETS2 in RAW264.7 significantly increased the expression of HMGB1-induced inflammatory factors, and increased NF-kappa B phosphorylation.

**Conclusion:** ETS2 was a prognostic marker in ACLF and associated with the activation of innate immune. ETS2 alleviates HMGB1 induced macrophage inflammation by decreasing NF-kappa B activity. Knockdown ETS2 in vivo can increase inflammatory response and further aggravate hepatocyte injury.

**FRI022**

**Novel strategies required to further improve outcomes in acute liver failure**

William Bernal1, Mark J. W. McPhail1, Anshuman Singh1, Brian J. Hogan1, Tasneem Pirani1, Sameer Patel1, Robert Loveridge1, Christopher Willars1, Michael Heneghan2, Varuna Aluvihare2, Parthi Srinivasan3, Andreas Prachalias3, Georg Auzinger1, Nigel Heaton3, Julia Wendon1.

1Institute of Liver Studies, King’s College Hospital, Liver Intensive Therapy Unit, London, United Kingdom; 2Institute of Liver Studies, King’s College Hospital, Hepatology, London, United Kingdom; 3Institute of Liver Studies, King’s College Hospital, Liver Transplantation Surgery, London, United Kingdom

**Email:** william.bernal@kcl.ac.uk

**Background and aims:** Care for patients with Acute liver injury (ALI) and Failure (ALF) has advanced significantly in recent years through critical care medical therapy and the targeted use of liver transplantation (LT). Case series have shown changes in the character of illness and its outcomes from the 1970 to early 2000s but the current outcomes are poorly characterised. We examined the changing treatment and outcomes of a large cohort of patients with ALF and ALI admitted to a single specialist ICU.

**Method:** consecutive patients with acute liver disease admitted over the period 1999–2021 were studied, classified in Era 1 (1999–2005), Era 2 (2006–12) and Era 3 (2013–21) and paracetamol (APAP) and non-APAP aetiologies. ALF was assigned in those with hepatic encephalopathy (HE) and ALI in those without. Severity of illness was assessed by presence of HE and laboratory measures. Data is expressed as n (%) or median (IQR). Data underwent univariate and multivariate analysis including logistic regression for the primary outcome of hospital survival.

**Results:** The study cohort comprised 1752 patients (median age 36 (27–48) years, 60% female, 56% APAP), of whom 1177 (68%) had developed ALF. Mortality was 4% in those with ALI and 36% in ALF (p < 0.001). Era 1 comprised 628 patients, Era 2: 577 and Era 3: 547. Over the study period the proportion with HE grade 3 on admission rose from 50% to 61% (p < 0.001), and in both APAP and non-APAP cases measures of liver injury increased: admission INR: APAP 3.3 (2.4–4.9) to 5.6 (3.6–9.1) in Era 3, non-APAP 2.4 (1.6–4.3) to 3.0 (2.1–4.9) both p < 0.001). Survival in ALF rose from 53% in Era 1 to 70% in Era 2 (p < 0.001), plateauing at 71% Era 3. In parallel there was a fall in use of LT from 30% of ALF cases in Era 1 to 22% in Era 3 (p < 0.001). This was seen in both APAP (22% to 13%, p < 0.001) and non-APAP (41% to 31%, p < 0.001) cases. 343 patients underwent LT; post-LT survival increased from 72% in Era 1 to 91% in Era 2 and Era 3 (p < 0.001). Transplant-free survival (TFS) rose from 54% in Era 1 to 70% in Era 3 for APAP and from 29% to 59% in non-APAP cases (both p < 0.001). Non-significant increases in TFS were seen when Eras 2 and 3 were compared (APAP 66% vs. 70% p = 0.47, non-APAP 50% vs 59% p = 0.14).

**Conclusion:** Survival for patients with ALF has markedly improved over the last 20 years, despite an increase in illness severity. Patient survival after LT is high, but its use has fallen, particularly in APAP ALF. TFS has progressively improved but outcomes in non-APAP ALF remain inferior. However, overall survival has now plateaued suggesting a need for new medical therapies and/or a re-evaluation of the use of transplantation.
Background and aims: Hemophilia A is an X-linked bleeding disorder caused by deficiency in factor VIII (FVIII), a cofactor in the intrinsic pathway of the coagulation cascade. Factor VIII is made predominantly in liver sinusoidal endothelial cells but gene therapy efforts using adeno-associated viruses (AAV) have targeted heterologous expression in hepatocytes. Factor VIII gene transfer with a single intravenous infusion of valoctocogene roxaparvovec (AAV5-hFVIII-SQ) has been shown to confer clinical benefit through at least 5 years in people with severe hemophilia A. Molecular mechanisms underlying sustained AAV5-hFVIII-SQ-derived FVIII expression in hepatocytes have not been studied in humans.

Method: In a sub-study of the phase 1/2 clinical trial (NCT02576795), liver biopsy samples were collected from five participants 2.6–4.1 years after AAV5-hFVIII-SQ gene transfer. The objectives of the sub-study were to examine effects on liver histopathology, determine the transduction pattern and percentage of hepatocytes transduced with AAV5-hFVIII-SQ genomes, characterize and quantify episomal forms of vector DNA, and quantify transgene expression (hFVIII-SQ RNA and hFVIII-SQ protein). Separately, we compared patterns and efficiencies of hepatocyte transduction in mice, monkeys, and humans who had all received AAV5-hFVIII-SQ to assess translatability of preclinical findings.

Results: Histopathological examination of human samples revealed no dysplasia, architectural distortion, fibrosis or chronic inflammation. No endoplasmic reticulum stress was detected in hepatocytes expressing hFVIII-SQ protein. Hepatocytes stained positive for vector genomes, and the number of transduced cells increased with AAV5-hFVIII-SQ dose. Molecular analysis demonstrated the presence of stable full-length circular episomal genomes that are associated with long-term expression. Interindividual differences in transgene expression were noted despite the successful administration of identical vector doses. Variability may be related to host-mediated post-transduction mechanisms of vector transcription, hFVIII-SQ protein translation, and secretion. Higher levels of vector genomes were detected in the livers of humans and monkeys than in mice; however, transcription of the vector DNA into RNA occurred more efficiently in mice.

Conclusion: Overall, our results showed that liver histopathology was unremarkable following AAV5-hFVIII-SQ administration and that persistent episomal vector structures were formed. This work elucidates several potential mechanisms that may mediate inter-individual variability in FVIII production and advances our understanding of inter-species translatability.
**Results:** Of 122 ABC patients treated with CKIs, 43 received ribociclib and were included in the analysis, with a median treatment time of 15 months (interquartile range [IQR], 3.5 to 26.5). After a median follow-up time of 21 months (IQR, 15.5 to 30.5), an elevation of liver enzymes of any grade was reported in 13 out of 43 patients (30.2%) and 6 patients (14%) had a DILI, as defined by an ALT $>5 \times$ upper limit of normal (ULN) and/or ALp $>2 \times$ ULN. DILI episodes occurred after a median of 6 months (IQR, 3 to 8) from treatment start and all of them had a hepatocellular pattern. A single case of DILI with autoimmune features was described. Of 6 DILI patients, 1 (17%) underwent temporary and 5 (83%) definitive treatment interruption, achieving liver enzymes normalization within a median of 13 weeks (IQR, 7 to 24). Overall, the occurrence of DILI accounted for over a quarter of the total number of treatment discontinuations. No acute liver failure was reported. Fourteen of 43 patients (33%) died during the study period, none of liver-related cause. Baseline steatosis (RR 13.3, CI 4.5–39.6, $p < 0.01$) and dyslipidemia (RR 3.3, CI 0.8–13.9, $p = 0.05$) were associated with a significant higher risk of DILI. No associations were found when assessing previous exposure to antineoplastic treatments including endocrine agents, concomitant medications, presence of liver metastases, and fibrosis-4 index (FIB-4) at baseline. **Conclusion:** Ribociclib is associated with a significant risk of DILI, turning in a relevant rate of antineoplastic treatment discontinuation in ABC patients. Once confirmed in larger prospective studies, baseline assessment of steatosis and dyslipidemia should be warranted to assist pre-treatment risk stratification.

**FRJ025**

Exogenous fibroblast growth factor 7 improved hepatocyte regeneration and ameliorated CCl4-induced acute liver injury in vivo

Eline Geervliet1,2, Ruchi Bansal1. 1University of Twente, Medical Cell Biophysics, Enschede, Netherlands; 2RWTH Aachen, Institute of Molecular Pathobiochemistry, Experimental Gene Therapy and Clinical Chemistry, Aachen, Germany

Email: eggeervliet@gmail.com

**Background and aims:** During acute and chronic liver injury, hepatocyte damage instigates activation of inflammatory responses and ultimately fibrosis. Fibroblast growth factor-7 (FGF7), that binds specifically to FGFR2b (highly expressed on hepatocytes and liver progenitor cells), plays an important role in cholangiocytes/hepatocytes proliferation and liver regeneration as shown in a mouse model of cholangitis and biliary fibrosis, and partial hepatectomy. Unfortunately, during acute and chronic liver disease this ligand is insufficiently expressed resulting in lack of hepatocyte survival, and progression of liver disease. On the other hand, FGFR2b is upregulated during acute and chronic liver disease making it an excellent therapeutic target. In this research, we aim to target FGFR2b with its natural highly specific ligand FGF7 to improve survival and proliferation of hepatocytes, differentiation of liver progenitor cells, and thereby ameliorating liver disease progression in carbon tetrachloride (CCl4)-induced acute liver injury mouse model.

**Method:** Acute liver injury was induced by a single injection of CCl4. Mice were subsequently treated with vehicle or 1 μg/kg FGF7 twice a day for two days. After treatment, the mice were sacrificed, and the organs were harvested for further analysis. Hepatocyte survival and proliferation, inflammation and fibrosis were evaluated by immunohistochemical staining, and gene and protein expression.

**Results:** Exogenous FGF7 increased liver- and spleen-to-body weight ratio while significantly decreased the liver-to-spleen weight ratio. Immunohistochemical analysis of liver sections showed increased...
proliferation as determined by Ki67 expression. Furthermore, macrophage-inflammation marker, F4/80 and fibrosis marker, collagen-I were significantly decreased upon treatment, see Figure 1. Gene expression analysis of proliferation, inflammation and fibrosis markers followed the similar trend. Extensive protein analysis of hepatocyte survival pathways will be investigated using Western blot.

Conclusion: Our results show that exogenous administration of FGF7 induces hepatocyte survival and leads to amelioration of inflammatory response and fibrosis in acute liver injury. Our study demonstrates that FGF7, FGF7 derivatives or nano-engineered FGF7 may benefit patients with hepatic dysfunction.

FR026
Three COVID-19 medications—remdesivir, molnupiravir and ritonavir-boosted nirmatrelvir—and serial liver biochemistries in 22,456 subjects
Grace Lai-Hung Wong1, Vicki Wing-Ki Hui1, Terry Cheuk-Fung Yip1, Yee-Kit Tse1, Vincent Wai-Sun Wong1. 1The Chinese University of Hong Kong, Medical Data Analytic Centre (MDAC) and Department of Medicine and Therapeutics, Hong Kong
Email: wonglaihung@cuhk.edu.hk

Background and aims: Several medications as treatment for COVID-19 have been approved around the world. These medications have generally good safety profiles, while data regarding the liver safety of these COVID-19 medications and risk of drug-induced liver injury (DILI) are lacking. We aimed to report the serial liver biochemistries of people before and after receiving COVID-19 medications.

Method: This was a territory-wide retrospective observational cohort study in Hong Kong. We identified subjects who had received any of the three COVID-19 medications approved in Hong Kong—remdesivir, molnupiravir and ritonavir-boosted nirmatrelvir. Serial liver biochemistries were observed in subjects who received remdesivir, molnupiravir and ritonavir-boosted nirmatrelvir.

Conclusion: Three registered COVID-19 medications (remdesivir, molnupiravir and ritonavir-boosted nirmatrelvir) vaccines have very favourable liver safety profile in people.

Grant support: This work was supported by the Health and Medical Research Fund (HMRF)-Food and Health Bureau Commissioned Research on COVID-19 (Reference no.: COVID1903002) awarded to Grace Wong.

FR027
Trends in liver transplantation for acute liver failure. A Spanish multicenter study
Isabel Conde1,2, Victoria Aguilera Sancho1,2,3, Sara Martinez4, Tommaso Di Mauro5, Maria Senosiain6,7, Rosa Maria Martin Mateos8,9, Carolina Almohalla7, Maria Luisa Gonzalez Diegez8, Sara Lorente Perez4, Alejandra Otero4, Maria Rodriguez10, Jose Ignacio Herrero11, Isabel Campos-Varela12, Ainhoa Fernandez13, Marina Berenguer1. 1La Fe University and Polytechnic Hospital, Valencia, Spain; 2Instituto de Investigación Sanitaria La Fe de Valencia, Valencia, Spain; 3ISCIII, CIBERehd, Valencia, Spain; 4Hospital Clínico Universitario Lozano Blesa, Zaragoza, Spain; 5Hospital Universitario Cruces, Barakaldo, Spain; 6Hospital Ramón y Cajal, Madrid, Spain; 7Río Hortega University Hospital, Valladolid, Spain; 8Central University Hospital of Asturias, Oviedo, Spain; 9Hospital Universitario da Coruña (CHUAC), A Coruña, Spain; 10General University Hospital of Alicante, Alacant, Spain; 11Clínica Universidad de Navarra, Madrid, Spain; 12La Vall d’Hebron, Barcelona, Spain; 13Gregorio Marañón Hospital, Madrid, Spain
Email: icondemiel@gmail.com

Background and aims: ALF is a critical illness with high morbidity-mortality. LT has improved outcome. Aims: to assess if there have been changes in aetiology, profile and outcomes of patients LT due to ALF in a Spanish multicenter cohort and to identify factors associated with mortality.

Method: Retrospective study of LT due to ALF cohort from 11 hospitals between 2001 and 2020. Baseline features, comorbidities, biochemical data, acute complications, early and late outcomes were recorded.

Results: 218 adults LT due to ALF (2001–2020). The cohort was subdivided in 4 time-groups (G1:2001–2005; G2:2006–2010; G3:2011–2015; G4:2016–2020). The number of ALF LT remained stable (G2: 2.5%, G3:2.2%; G4:2.7%). Mean age: 41 yrs, 62%women, AHT 11.5%, diabetes 3.7%, dyslipidaemia 8.3%, MELD 34 (29.5–38.1), 83.5% caucasic. Main LT indications were viral (26.2%), cryptogenic (26.1%), autoimmune (22.5%), and DILI (17%), 87% meet King’s College criteria. 38% had severe encephalopathy, 22% renal impairment (RI) with haemodialysis, 23% required mechanical ventilation (MV). There was a trend towards an increase of LT for autoimmune (21%, 21%, 31%, 29% in G1–4 respectively, p = 0.88) and DILI (12.5%, 14%, 18%, 21% in G1–4, p = 0.72). Women seem more susceptible to ALF TH over time (58%, 53.5%, 65.6% and 67% in G1–4, p = 0.4). Complications in the early post-LT period were infections (58.7%), RI (25%) and primary dysfunction (24%). Late post-LT complications were AHT (30%), RI (20%) and diabetes (17%), 27% of patients died. Main causes of death were infections (41.5%) and liver-related (20%). Survival was 85%, 81% and 70% at 1, 5 and 10 years. Diabetes, MV, ascites and creatinine were independently associated with poorer survival (HR 4.05, p = 0.054; HR 2.74, p = 0.037; HR 2.48, p = 0.048 and HR 1.47, p = 0.007, respectively).

Conclusion: LT for ALF remained stable in the last years in Spain. Autoimmune and DILI seem to increase over time, being women more susceptible to ALF TH. Patients with diabetes, ascites, high creatinine levels, and MV were associated with poor outcomes after LT.
Figure: (abstract: FR026): Serial liver biochemistries before and after COVID-19 medications.
Thus far, the study comprised 297 patients, 52% men. The etiology whenever clinically pertinent. Isolated liver enzymes elevation (ILEE), and linked them to a possible cause. Table 1: C-HEPBILI frequency in BMT patients*

<table>
<thead>
<tr>
<th>Condition</th>
<th>Population</th>
<th>C-HEPBILI Population</th>
</tr>
</thead>
<tbody>
<tr>
<td>ILEE</td>
<td>120</td>
<td>40.4%</td>
</tr>
<tr>
<td>DILI</td>
<td>55</td>
<td>8.4%</td>
</tr>
<tr>
<td>SOS</td>
<td>15</td>
<td>5.1%</td>
</tr>
<tr>
<td>HH</td>
<td>6</td>
<td>2.0%</td>
</tr>
<tr>
<td>SALI</td>
<td>5</td>
<td>1.7%</td>
</tr>
<tr>
<td>FH</td>
<td>2</td>
<td>0.7%</td>
</tr>
<tr>
<td>GVHD</td>
<td>1</td>
<td>0.3%</td>
</tr>
</tbody>
</table>

*Some patients progressed with more than one C-HEPBILI.

**Conclusion:** C-HEPBILI is frequent after BMT, is more common in women, and is associated with considerable morbidity, as well as an increase in the hospital stay. DILI was a relevant complication. Allogeneic haploidentical BMT was the most associated with C-HEPBILI.

**Background and aims:** Post-bone marrow transplantation (BMT) hepatobiliary complications (C-HEPBILI) may occur in up to 80% of the cases. We evaluated the frequency and clinical characteristics of C-HEPBILI in patients undergoing BMT at a referral center.

**Method:** This is a cross-sectional study that analyzed patient data from 2017 to 2021, including demographics, the period between BMT and C-HEPBILI diagnosis, outcome, and length of hospital stay. Drug-induced liver disease (DILI), sepsis-associated liver injury (SALI), sinusoidal obstruction syndrome (SOS), graft versus host disease (GVHD), hypoxic hepatitis (HH), and fulminant hepatitis (FH), among others, were evaluated. We diagnosed DILI according to MAGIC guidelines. For SALI, we considered the infectious context and a total bilirubin ≥2 mg/dL and ALP or ALT ≥2 × ULN. We used the EBMT, Atlanta, and Baltimore criteria to diagnose SOS and considered hepatic GVHD when patients had skin and or intestinal GVHD and increased liver enzymes that improved after treatment. For alterations that did not meet the previous criteria, we defined liver enzymes elevation as an increase ≥1.5 ULN, named this condition isolated liver enzymes elevation (ILEE), and linked them to a possible etiology whenever clinically pertinent.

**Results:** Thus far, the study comprised 297 patients, 52% men. The mean age of the total population and the C-HEPBILI patients was 49.6 (±14.1) and 48.7 (±13.6) years, respectively; 164 of 297 patients (55%) had C-HEPBILI; 91 of them (55%) were women. Table 1 describes all the cases. We evaluated the frequency and clinical characteristics of C-HEPBILI in patients undergoing BMT at a referral center.

**Background and aims:** Multidrug resistance protein 2 (MRP2) is a bottleneck in bilirubin excretion. Its loss is sufficient to induce hyperbilirubinemia, a prevailing characteristic of acute liver failure (ALF), that is closely associated with clinical outcome. This study scrutinizes the transcriptional regulation of MRP2 under different pathophysiological conditions.

**Method:** Thirty-six patients, 14 with quiescent liver cirrhosis and 22 with ALF, were enrolled. Hepatic MRP2, FXR, and FOXA2 expression were examined by immunohistochemistry. Clinicopathologic association was analysed. MRP2 regulatory mechanisms were investigated in primary hepatocytes, Fxr−/− mice and LPS-treated mouse model.

**Results:** In normal hepatocytes, homeostatic MRP2 transcription is mediated by the nuclear receptor Fxr/RXR complex. Fxr−/− mice lack apical MRP2 expression and rapidly progress into hyperbilirubinemia. In ALF patients, hepatic FXR expression is undetectable, however, the patients without infection maintain apical MRP2 expression and do not suffer from hyperbilirubinemia. These patients express robust FOXA2 in hepatocytes. FOXA2 upregulates MRP2 transcription through binding to its promoter. Physiologically, nuclear FOXA2 translocation is inhibited by insulin. In ALF, high levels of glucagon and TNF-α induce FOXA2 expression and nuclear translocation in hepatocytes. Impressively, ALF patients with sepsis express few FOXA2, lose MRP2 expression, and show severe hyperbilirubinemia. In this case, LPS inhibits FXR expression, induces FOXA2 nuclear exclusion, and thus destroys the compensatory MRP2 upregulation. In both Fxr−/− and LPS-treated mice, ectopic FOXA2 expression restored apical MRP2 expression and serum bilirubin levels.

**Conclusion:** Upregulation of FOXA2 to maintain MRP2 is an efficient strategy to prevent hyperbilirubinemia.
NAFLD: Diagnostics and non-invasive assessment

FRI030
Machine learning encoding of liver biopsy images enables prediction of molecular measurements in a NASH F3/F4 fibrosis clinical cohort

Michael D. Bereket1, Francesco Paolo Casale1, Rohit Loomba2, Arun Sanyal2, Stephen Harrison2, Zobair Younossi3, Catherine Jia4, David Lopez4, Li Li4, Robert Myers4, David Breckinridge6, Andrew Billin6, Eilon Sharon1, Matthew Albert1, Theofanis Karaletsos1, Daphne Koller1. 1Insitro, South San Francisco, United States; 2University of California San Diego, La Jolla, United States; 3Virginia Commonwealth University, Richmond, United States; 4University of Oxford, Radcliffe Department of Medicine, United Kingdom; 5Inova Fairfax Medical Campus, Falls Church, United States; 6Gilead Sciences, Inc., Foster City, United States
Email: research_operations@insitro.com

Background and aims: Machine learning (ML) models of biopsy images have the potential to improve the characterization of liver state by identifying biologically relevant phenotypes that are not captured by standard histological endpoints. To explore this possibility, we develop and compare ML models that predict transcriptomic and genetic endpoints based on standard histology readouts or ML derived histological features. We focus our genetic analysis on the PNPLA3 I148M genotype, which has been robustly linked to NAFLD/NASH risk through GWAS studies (Romeo et al, 2008; Anstee et al, 2020).

Method: Pathologist scores (NASH CRN and Ishak fibrosis scores), quantitative microscopy measurements (alpha-SMA, collagen, and fat content), H&E-stained biopsy images, liver bulk RNA-seq, and PNPLA3 I148M genotypes are curated from the STELLAR3, STELLAR4, and ATLAS clinical trial F3/F4 fibrosis cohorts. We use self-supervised ML methods (trained with no clinician annotations) to generate quantitative embeddings that represent histological phenotypes. We fit generalized linear models to predict the molecular endpoints from the standard and ML-derived biopsy features, training on a random split of half the data and predicting on held-out samples. All genetic association testing focuses on subjects of European ancestry due to population stratification concerns and considers 10 genotype principal components, age, and sex as covariates.

Results: Predictions of gene expression are improved with the ML biopsy embeddings relative to the standard histological endpoints (A). While the I148M variant is enriched in this cohort relative to the general population (allele frequency G = 0.46 vs G = 0.22 in gnomAD EUR samples), we do not observe any association between pathologist or quantitative microscopy measurement and I148M genotype (p > 0.05). Similarly, genotype predictions from these measurements are not significantly associated with the I148M genotype. However, genotype predictions using the self-supervised ML biopsy embeddings are significantly associated with I148M genotype in the held out samples (p = 4E-9, n = 378; B). Tiles that influence these genotype predictions are visualized in C.

Conclusion: ML models of H&E biopsy images identify histological features that improve predictions of molecular endpoints relative to standard histological readouts. Notably, we identify a histological phenotype associated with PNPLA3 I148M genotype in F3/F4 fibrosis NASH patients that is not captured by standard histological endpoints. This result supports the potential for ML models to provide orthogonal characterizations of histological state, enabling novel insights on the interplay of clinical phenotypes, transcriptomic state, and genetic backgrounds in NASH patients.

FRI031
Validation of AI-assisted method of liver fat measurement in adults with type 2 diabetes

Athena Dworakowski1, Wenjie Pang1, Sherif Boulos1, Sofie De Meyer1, Jian Yeo2, Gaurav Gulsin2, Abhishek Dattani2, Emer Brady2, Joanna Bilak2, Sarah Ayton2, Alastair Moss2, Michael House3, Tim St Pierre3, Gerry McCann3, 1Resonance Health, Burswood, Australia; 2University of Leicester, Department of Cardiovascular Sciences, United Kingdom; 3The University of Western Australia, School of Physics, Crawley, Australia
Email: sofied@resonancehealth.com

Background and aims: Type 2 diabetes (T2D) is strongly associated with the development of non-alcoholic fatty liver disease (NAFLD), which is an emerging independent risk factor for cardiovascular...
dysfunction. HepaFat-AI® is a software device developed using artificial neural networks (ANN) and provides rapid (less than one minute) automated liver fat quantification from magnetic resonance images without the need for labour-intensive manual image analysis. The aims of this study were to compare HepaFat-AI against the histologically validated HepaFat-Scan® technique as a reference standard in a cohort of asymptomatic adults with T2D.

**Method:** One hundred and thirty-three adults (97% T2D, mean age 62.6 ± 7.6 years, 60% male) underwent magnetic resonance imaging (MRI) of the liver and heart. Nineteen were excluded due to incorrect imaging parameters or breathing artifacts, leaving a sample of 114 subjects. Volumetric liver fat fraction (VLFF) was analysed twice, first manually with HepaFat-Scan based on the 3-point Dixon principle and then automatically processed using HepaFat-AI. HepaFat-AI was previously trained on 889 individual HepaFat-Scan datasets from both 1.5 T and 3 T scanners and generates a report comprising VLFF measurements, proton density fat fraction (PDFF), and steatosis grade. Bland-Altman analysis was performed to determine the 95% limits of agreement between the two methods of measuring VLFF. The diagnostic performance of HepaFat-AI for predicting HepaFat-Scan steatosis grade 1 or above was also analysed in terms of sensitivity, specificity, and accuracy.

**Results:** Bland-Altman analysis showed that on average HepaFat-AI yields slightly higher VLFF results with a bias of +0.42 (95%CI 0.10–0.74)%VLFF against HepaFat-Scan. The 95% limits of agreement between the two methods were -3.02 and +3.85%VLFF. The sensitivity and specificity of HepaFat-AI for predicting HepaFat-Scan determined steatosis grade of 1 or above were 0.97 (95% CI 0.84–0.99) and 0.88 (95% CI 0.64–0.99) respectively. With HepaFat-Scan as the reference standard, HepaFat-AI had an accuracy of 0.90 (95% CI 0.84–0.95) for grading steatosis above or below the grade 0/1 boundary.

**Conclusion:** HepaFat-AI provides a rapid and automated liver fat quantification analysis of MR images which has important implications for cost and may provide a fast alternative point-of-care testing for T2D adults with liver disease.

**FRJ032**
Identifying advanced liver disease in asymptomatic patients in primary care: an evaluation of patient outcomes 24 months after implementing a primary care liver pathway and community liver service
Tina Reinson1, Chris Byrne2, Mead Mathews3, Janisha Patel4.
1University of Southampton, Primary Care, Population Sciences and Medical Education, Southampton, United Kingdom; 2University of Southampton, Human Development and Health, Southampton; 3St Mary’s Surgery, Southampton, United Kingdom; 4University Hospital Southampton, Hepatology, Southampton
Email: t.reinson@soton.ac.uk

**Background and aims:** In 2019, Southampton Clinical Commissioning Group implemented a liver guidance pathway and community liver service to help early detection and reduce the number of deaths from liver disease. The liver guidance pathway supports primary care clinicians identify patients at risk of liver disease to access early intervention before developing to advanced liver disease. The community liver service provides vibration controlled transient elastography (VCTE) assessment to patients who, after following the liver guidance pathway, have been identified as having severe liver fibrosis. This study aims to evaluate the patient outcomes 24 months after implementing the liver pathway and VCTE service.

**Method:** All patients referred to the Southampton community liver service between January 2019 and December 2020. Demographics recorded included: Age, sex, body mass index (BMI), alcohol consumption (high or low), VCTE reading (kPa), diagnosis (alcohol related liver disease, non-alcoholic fatty liver disease or both) and patient outcomes (stay in primary care or refer to secondary care for clinical management).

**Results:** 527/632 patients referred to the community liver service received a VCTE assessment.16.6% (n=105) did not attend their appointment and for 0.9% (n=5), no valid VCTE reading was obtained. The median (IQR) age of patients was 58 (46–65) years, 58.6% were male; median (IQR) BMI was 30.5 (27.1–35.1) kg/m² and alcohol...
consumption in 23.9% (n = 126) was graded as high (defined as drinking more than the UK recommended alcohol guidelines). Mean (SD) VCTE was 9.5 (9.2) kPa, of whom 8% (n = 42) had a reading of >20.0 kPa. 77.4% (n = 408) were diagnosed with non-alcoholic fatty liver disease (NAFLD); 15.7% (n = 83) with alcohol related liver disease (ARLD) and 6.8% (n = 36) with both NAFLD and ARLD. 27.9% (n = 147) of patients were found to have a liver fibrosis stage of F3/F4 (9.7 kPa–13.5 kPa) and were referred to secondary care. 71.0% (n = 374) had a liver fibrosis stage of F0–F2 (between 3.0 kPa and 9.6 kPa) and were referred back to primary care for repeat VCTE assessment in 3 years time.

Figure: Summary of patient pathway through the community-based liver scanning service.

**Conclusion:** 8% asymptomatic patients identified as having advanced liver disease/cirrhosis and ~20% identified as being at risk of developing progressive liver fibrosis, are now being monitored by secondary care. The remaining patients (71%) are being monitored in primary care and will be referred for repeat VCTE assessment in 3 years time.

Acknowledgements: Lucie Llesi, NHS Southampton Clinical Commissioning Group.
Online education significantly improved gastroenterologists’ knowledge of the diagnostic and monitoring techniques used in liver fibrosis

James White, Elaine Bell, Briana Betz, Jörn Schattenberg
1Medscape Global Education, London, United Kingdom; 2Medscape LLC, New York, United States; 3University Medical Center Mainz, I. Department of Medicine, Mainz, Germany
Email: jrwhite@webmd.net

Background and aims: Non-alcoholic steatohepatitis is a leading cause of liver fibrosis. Progression of liver fibrosis to advanced stages is linked to severe outcomes and increased healthcare costs. Non-invasive techniques, including biomarkers and elastography, improve the diagnosis and monitoring of liver fibrosis. Unmet educational needs are one barrier in the use of non-invasive techniques. We assessed whether online continuing medical education (CME) could improve physicians’ knowledge and confidence of appropriate diagnostic and monitoring techniques in liver fibrosis.

Method: Gastroenterologists (n = 220) participated in a chapterised video activity entitled “Evolution of Diagnosis and Monitoring for Liver Fibrosis” which covered guideline recommendations, identification of patients at risk of progression, and non-invasive pathways for identifying advanced fibrosis. Educational effect was assessed using a repeated-pair design with pre-/post-assessment. 3 multiple choice questions assessed knowledge and 1 question, rated on a Likert-type scale, assessed confidence. A paired samples t-test was conducted for significance testing on overall average number of correct responses and for confidence rating, and a McNemar’s test was conducted at the question level (5% significance level, p < 0.05).

Results: Results showed significant overall improvement in average percentage of correct responses (45% pre- to 63% post-education, p < 0.001, Cohen’s d = 0.56). The percentage of gastroenterologists that answered all questions correctly improved from 9% pre- to 30% post-education. Whilst 23% improved and 27% reinforced their knowledge regarding which set of markers is included in the Enhanced Liver Fibrosis (ELF) score, 50% of gastroenterologists still lack this information after education (p < 0.001). Post-activity, 41% of gastroenterologists had a measurable increase in confidence in using non-invasive techniques in clinical practice to identify patients with advanced fibrosis (p < 0.001), with an average confidence shift of 58%.

Conclusion: Participation in an online chapterised video activity significantly improved physicians’ knowledge and confidence of appropriate diagnostic and monitoring techniques in liver fibrosis. Despite this, further education regarding the markers included in the ELF score is needed for gastroenterologists.

Figure: (abstract: FRI033)
**FRI035**

**Health outcomes and risk assessment in chronic liver disease (HERALD): a large Swedish research platform**

Emilie Toresson Grip1,2, Oskar Ström1,2, Hannes Hagström1,3,4
1Karolinska Institutet, Department of Medicine Huddinge, Sweden; 2Quantify Research AB, Stockholm, Sweden; 3Karolinska University Hospital, Division of Hepatology, Department of Upper GI Diseases, Stockholm, Sweden; 4Karolinska Institutet, Clinical Epidemiology Division, Department of Medicine Solna, Stockholm, Sweden

Email: emilie.toresson.grip@ki.se

**Background and aims:** The ’HEalth outcomes and Risk Assessment in chronic Liver Disease’ (HERALD) study is a multi-stakeholder Swedish research-platform linking national and regional registries to investigate the epidemiology and risk factors of liver outcomes, resource-use and costs, in patients with chronic liver diagnoses (CLD) or liver-related laboratory tests. HERALD is also planned to include data from the National Diabetes Register and other countries during 2022, and is open to international collaboration.

**Method:** A CLD cohort will consist of all patients ≥18 years with ≥1 CLD diagnosis (ICD-10) in the Swedish Patient Register, or primary care from the Stockholm region. A Fib-4 cohort will consist of patients with laboratory tests (AST, ALT and platelets), required for estimating the performance of several indices for detecting fatty liver disease (FLD).

**Results:** A feasibility study was completed in 2020 and ethical approval for HERALD was granted in August, 2020. During 2001–2019, the number of patients with NAFLD was 16,285, with at least 270,000 patients expected in the Fib-4 cohort.

**Conclusion:** This study is the result of a research collaboration between academia and analytical and pharmaceutical industry. HERALD will be the largest data collection to date to estimate a contemporary prevalence of liver disease and advanced fibrosis in a broad, unselected population of healthcare-seeking individuals in Sweden. Furthermore, HERALD will utilize clinical and non-clinical information to characterize patients with different risk profiles and to estimate long-term societal burden associated with severe liver outcomes in clinical practice over a 20-year period.

**FRI036**

**Impact of alcohol use on the diagnostic performance of serum-based indices for fatty liver disease**

Oscar Danielsson1, Markku Nissinen2, Katja Pahkala2,3,4, Terho Lehtimäki5,6, Olli Raitakari2,3,7, Fredrik Åberg8, 1Clinic of Gastroenterology, Helsinki University Central Hospital and University of Helsinki, Helsinki, Finland, Finland; 2Centre for Population Health Research, University of Turku and Turku University Hospital, Turku, Finland, Finland; 3Research Centre of Applied and Preventive Cardiovascular Medicine, University of Turku, Turku, Finland, Finland; 4Paavo Nurmi Centre, Unit of Health and Physical Activity, University of Turku, Turku, Finland, Finland; 5Department of Clinical Chemistry, Fimlab Ltd., Finland, Finland; 6Faculty of Medicine and Health Technology, Finnish Cardiovascular Research Center-Tampere, Tampere University Tampere, Finland, Finland; 7Department of Clinical Physiology and Nuclear Medicine, Turku University Hospital, Turku, Finland, Finland; 8Transplantation and Liver Surgery, Helsinki University Central Hospital and University of Helsinki, Finland

Email: oscar.danielsson@hhus.fi

**Background and aims:** Non-alcoholic fatty liver disease (NAFLD) and alcohol-related liver disease (ARLD) frequently co-exist, and recently proposed diagnostic criteria for metabolic-dysfunction associated fatty liver disease (MAFLD) have removed strict cut offs for alcohol use. While several indices exist for detection of NAFLD, there is paucity of study on how alcohol use possibly impact their diagnostic performance. We analysed the effect of various level of alcohol use on the performance of several indices for detecting fatty liver disease (FLD).

**Method:** From the Cardiovascular Risk in Young Finns study, we included participants who underwent abdominal ultrasound (US) in 2010–2012 for detection of FLD and had serum analyses available from the same time for calculation of the Fatty Liver Index (FLI), Hepatic Steatosis Index (HSI) and Lipid Accumulation Product (LAP). Alcohol use was assessed by questionnaires. Predictive performance for FLD was assessed by AUROC, logistic regression, sensitivity, specificity, and positive and negative predictive values (PPV and NPV) according to alcohol consumption.

**Results:** Study comprised 1426 individuals (mean age 42.1 years, 42.6% males, mean BMI 26.3 kg/m², mean alcohol use 9.4 g/day), of which 234 (16%) had FLD by US. High risk index-scores were observed in 27.2%, 24.7% and 54.8% (FLI, HSI and LAP, respectively) of the study population. When daily alcohol consumption was <50 grams, all indices discriminated FLD with AUROCs of 0.82–0.88. Among heavy drinkers (>50 g/day), AUROCs were 0.61–0.66. Alcohol use correlated weakly with both FLI (r = 0.09) and LAP scores (r = 0.16, both p-values <0.001), no significant correlation for HSI.
Conclusion: With alcohol consumption below 50 g/day, FLI, HSI and LAP perform well for detection of FLD, all with comparable performance. With higher alcohol consumption, their diagnostic performance is reduced substantially.

FRI037
Liver stiffness on magnetic resonance elastography and liver-related outcomes in nonalcoholic fatty liver disease: a systematic review and meta-analysis of individual participants
Veeral Ajmera1, Kun Yang1, Beom Kyung Kim1, Abdul Majzoub2, Nobahar Tamaki3, Atsushi Nakajima4, Ramazan Idilman5, Mesut Gumussoy5, Digdem Kuru Öz5, Ayse Erden5, Natalie Quach6, Xin Tu6, Xinlian Zhang6, Mazen Noureddin7, Alina Allen8, Rohit Loomba6, 2Conemaugh Memorial Medical Center; 3Musashino Red Cross Hospital, Japan; 4Yokohama City University Medical Center; 5Ankara University, Turkey; 6University of California San Diego, United States; 7Cedars Sinai Medical Center, United States; 8Mayo Clinic, United States
Email: v1ajmera@ucsd.edu

Background and aims: Magnetic resonance elastography (MRE) is a reproducible, accurate, continuous biomarker of liver fibrosis, however, limited data characterize its association with outcomes. We conducted a systematic review and pooled analysis of individual participant data from published studies and additional identified cohorts to evaluate the association between liver stiffness on MRE and liver-related outcomes.

Method: A systematic search identified 6 cohorts of adults at risk for NAFLD who underwent MRE and were assessed for liver-related outcomes. In a pooled analysis, logistic regression and Cox proportional hazards models were used to assess the association between liver stiffness on MRE and liver-related outcomes including a composite primary outcome defined as varices needing treatment, ascites and hepatic encephalopathy. Secondary outcomes included hepatocellular carcinoma (HCC) and death. Cumulative incidence curves evaluated time to first event for the primary outcome.

Results: Our pooled analysis included 2275 patients (54% women) with a mean age 57.5 (±15) years and mean MRE at baseline of 4.01 (±2.17) kPa. A total of 948 events occurred in 458 participants. Each 1 kPa increase in liver stiffness was associated with OR = 1.22 (95% CI:1.16–1.29, p < 0.001) increased odds of the primary outcomes at baseline. Among 1983 patients with a median (IQR) of 3 (4.14) years of follow up time the 1- and 3-year risk of the primary outcome was 0.6% and 1.5% for MRE ≤5 kPa, 7.2% and 16.6% for 5–8 kPa and 8.5% and 18.8% for MRE >8 kPa respectively (Figure). The hazard ratio (HR) for the primary outcome, HCC and death for MRE >8 kPa were HR = 17.3 (95% CI:10.1–29.7, p < 0.001), HR = 23.3 (95% CI:7.94–68.2, p < 0.001) and HR = 4.84 (95% CI:3.22–7.27, p < 0.001) respectively, compared to <5 kPa. The MEFIB index defined as positive when MRE ≥3.3 kPa and FIB-4 ≥1.6 had a strong association with the primary outcome HR = 21.8 (95% CI:11.0–43.2, p < 0.001) and excellent negative predictive value for hepatic decompensation (Figure).

Conclusion: Liver stiffness assessed by MRE is associated with liver-related outcomes and death and the combination of MRE and FIB-4 has excellent negative predictive value for hepatic decompensation.
FRI038
Utilising features of metabolic syndrome to cost-effectively improve metabolic dysfunction-associated fatty liver disease diagnosis rates
Cassandra Baiano1, Jennifer Nobes1, Iain Macpherson1, Callum Livingstone1, Madeleine Caven1, Paul Brennan1, Ellie Dow2, John Dillon1. 1School of Medicine-University of Dundee, United Kingdom; 2NHS Tayside, United Kingdom
Email: cbaiano@dundee.ac.uk

Background and aims: The international consensus currently defines Metabolic Dysfunction-associated Fatty Liver Disease (MAFLD) as obesity, multiple metabolic risk factors, or type 2 diabetes mellitus plus hepatic steatosis on imaging. To facilitate the diagnosis of liver diseases, like MAFLD, in the community, an algorithm-based diagnostic tool (intelligent liver function testing, iLFT) that uses biochemical tests and clinical information has been developed. 22% of iLFT results are initially descriptive (i.e. isolated raised ALT) with no definitive aetiology but are identified as MAFLD after costly, prolonged investigations. This study aimed to identify whether features of the metabolic syndrome could be used to cost-effectively increase MAFLD diagnosis in the community while decreasing the need for imaging or liver clinic attendance.

Method: A retrospective analysis of iLFT patients from 2018 to 2020 was conducted. Medical records were used to identify BMI, features of metabolic syndrome, and steatosis on ultrasound scan (USS). Logistic regression analyses assessed which features of metabolic syndrome could predict USS steatosis. New MAFLD diagnostic pathways within iLFT were modelled with a cost-benefit analysis.

Results: 2720/6791 patients had no cause for deranged liver function tests identified by iLFT or had suspected MAFLD, of which 646 had sufficient health data for analysis.

While glucose impairment is the only statistically significant feature to predict USS steatosis across BMIs (p < 0.000, Sen = 41%, PPV = 88%), prediction can be optimised by stratifying patients into three BMI categories (≤26, 27–34, ≥35). In patients with BMI ≥35 (n = 114), any one feature of metabolic syndrome is a strong enough predictor of USS steatosis that MAFLD can be diagnosed and managed in the community and USS and liver clinic can be avoided (p < 0.003, Sen = 85%, PPV = 91%). In BMI 27–34 (n = 275), glucose impairment is a strong enough predictor of USS steatosis that MAFLD can be diagnosed and managed in the community, and USS and liver clinic can be avoided (p < 0.007, Sen = 35%, PPV = 89%). In patients with a high NAFLD fibrosis score or BMI ≤26 (n = 257), both ultrasound and liver clinic are still required for assessment.

Conclusion: New MAFLD diagnostic pathways that stratify patients by BMI and include features of metabolic syndrome to predict fatty infiltration on USS could cost-effectively increase MAFLD diagnosis in the community and reduce referral to USS by 26% while reducing referral to liver clinic by 24% (Sen = 100%, PPV = 98%).

FRI039
Non-invasive assessment of type VII collagen degradation is related to NAFLD activity but not fibrosis stage
Mette Juul Nielsen1, Peder Frederiksen1, Morten Karsdal1, Diana Leeming1, Jörn Schattenberg2. 1Nordic Bioscience A/S, Herlev, Denmark; 2University Medical Centre of the Johannes Gutenberg-University Mainz, Mainz, Germany
Email: mjn@nordicbio.com

Background and aims: Type VII collagen is an anchoring fibril collagen crucial for the function and stability of the extracellular matrix (ECM) by linking basement membrane and interstitial matrix collagens together. Remodeling of the basement membrane is observed in early stage pericellular fibrosis, whereas accumulation
of interstitial matrix collagens is observed during advanced fibrosis. The role of type VII collagen in liver fibrosis is unknown. The aim of this study was to investigate the role of type VII collagen using a collagen neoepitope technology in relation to fibrosis development in NAFLD patients.

Method: Degradation of type VII collagen was assessed by the novel neoepitope marker, C7M, developed by Nordic Bioscience A/S, in serum samples from 140 NAFLD patients with biopsy confirmed liver fibrosis F0–F4 and NAS 0–7 in a cross-sectional study design. Histopathological staging of fibrosis, steatosis, hepatocyte ballooning and lobular inflammation was scored according to the Kleiner scoring system.

Results: Patients had median age of 53.5 (IQR 43–60) years and median BMI of 32.2 kg/m² (IQR 29.0–36.1) of which 74 (53%) were male (p = 0.499). Serum C7M significantly correlated with the NAS (r = 0.235; p < 0.003), the grade of hepatocyte ballooning (r = 0.278; p = 0.001), and steatosis (r = 0.285; p < 0.001) but not the degree of lobular inflammation (r = 0.161; p = 0.065) or the histological fibrosis stage (r = –0.005; p = 0.962). C7M was significantly elevated in patients with NAS ≥ 3 compared to NAS < 2 (p < 0.001). A 30% and 18% increase in C7M was observed from hepatocyte ballooning grade 0 to 1–2 (p = 0.001) and from steatosis grade 0–1 to 2–3 (p = 0.004), respectively. In the same cohort, the levels of the fibrogenic collagen marker, PRO-C3, was increased in the population with advanced vs early fibrosis (p < 0.0001), as well as in patients with steatosis (p = 0.0001), hepatocyte ballooning (p = 0.0001), and lobular inflammation (p < 0.0001).

Conclusion: Degradation of type VII collagen may be an early indicator of increased protease activity, related to linkage disruption of the ECM structure between basement membrane and interstitial matrix collagens in liver fibrosis development in patients with NAFLD.

FRI040
Reliability of histologic disease activity measures in non-alcoholic fatty liver disease (NAFLD) and development of an expanded NAFLD activity score
Rish Pai1, Vipul Jairath2,3,4, Malcolm Hogan3, Guanyong Zou3,4,5, Oyedeye Adeyi2, Quentin Anstee6,7, Bashar Agel8, Cynthia Behling9,10,11, Elizabeth Carey3, Andrew Clouston12, Kathleen Corey13,14, Brian Feagan2,3,4, David E. Kleiner15, Christopher Ma16,17, Stefanie McFarlane4, Mazen Noureddin18, Vlad Ratziu19

Background and aims: In clinical trials of non-alcoholic steatohepatitis (NASH), the Non-alcoholic Steatohepatitis Clinical Research Network (NASH CRN) histologic scoring system is the current gold standard histology assessment but has demonstrated intra- and inter-observer variability. An expert panel determined in a prior Research and Development/University of California Los Angeles (RAND/UCLA) process that existing histologic scoring systems do not fully capture NASH disease activity and fibrosis. We evaluated the intra- and inter-rater reliability of histologic disease activity measures and correlated these measures with a disease activity visual analogue scale (VAS) to propose an exploratory expanded non-alcoholic fatty liver disease (NAFLD) activity score (NAS) index comprising optimized items.

Method: Four liver pathologists assessed 40 liver biopsies representing the full spectrum of NAFLD. These central readers were blinded to clinical information, completed standardized training, and scored each histologic measure twice, with ≥2 weeks between each assessment. Scored measures included existing histologic indices, the component items of these indices, and additional items identified in the prior RAND/UCLA study. Reliability was assessed using intra-class correlation coefficients (ICCs).

Results: The ICCs for existing NAFLD activity indices demonstrated substantial to almost perfect intra-rater reliability (ICC, 0.80–0.85) and moderate to substantial inter-rater reliability (ICC, 0.60–0.72). Ballooning degeneration items (ICC, 0.68–0.79), including those that extended scores from 0 to 2 to 0–4, and steatosis items (ICC, 0.72–0.80) had substantial inter-rater reliability. Fibrosis measures demonstrated substantial to almost perfect inter-rater agreement (ICC, 0.70–0.87). Items for ballooning degeneration and Mallory-Denk bodies (MDBs) had large correlations with the disease activity VAS (r = 0.66–0.96) and were used to develop an expanded NAS (intra-rater ICC, 0.90; inter-rater ICC, 0.80). Steatosis items were poorly correlated with the disease activity VAS (r = –0.02 to 0.12).

Conclusion: Histologic indices, including the expanded NAS, had almost perfect intra-rater reliability and moderate to substantial inter-rater reliability, Ballooning degeneration and MDBs were used for the expanded NAS based on their strong correlations with disease activity. Future evaluation of the responsiveness of these measures is needed.

FRI041
Evaluating future risk of NAFLD fibrosis in adolescents: prediction and decision curve analysis
Kushala Abeysekera12, Julian Hamilton-Shield1, James Orr2, Fiona Gordon1, Laura Howe1, Jon Heron1, Matthew Hickman1

Background and aims: Elevated body mass index (BMI) is the major risk factor for nonalcoholic fatty liver disease (NAFLD) development. Using data from the Avon Longitudinal Study of Parents and Children (ALSPAC), we sought to investigate whether other variables from adolescence could improve prediction of future NAFLD fibrosis risk at 24 years, above BMI.
Method: Aged 24 years, 4018 ALSPAC participants had transient elastography (TE) using Echosens 502 Touch. 513 participants with harmful alcohol consumption were excluded. 2.7% had ≥F2 equivalent fibrosis. Logistic regression models examined which factors that were measured at age 17 were predictive of NAFLD fibrosis in young adults. Predictors included sex, BMI, central adiposity, lipid profile, blood pressure, liver function tests, homeostatic model assessment for insulin resistance (HOMA-IR), and steatosis at 17 years (based on ultrasound). A model including all these variables reflected “standard of care” (SoC). Models were compared using area under the receiver operator curve (AUROC) and Bayesian Information Criterion (BIC), analysis, which penalises model complexity. Models were tested in participants with overweight and obese standardised BMIs (BMI SDS) centiles at the 17-year time point. A decision curve analysis (DCA) was performed to evaluate the clinical utility of models at 17-years predicting NAFLD fibrosis at a threshold probability of 0.1. Datasets were imputed up to the number of available TE outcomes.

Results: In adolescents with overweight/obese BMI SDS centiles, the SoC model had the highest AUROC (AUROC 0.84 [SD 0.03]). However following BIC analysis, BMI SDS at 17 years was the best predictor of NAFLD fibrosis at 24 years. A DCA examining overweight/obese adolescent participants demonstrated the model that had greatest net benefit, above a treat all assumption, was the SoC model although the net benefit was marginal (0.0054 [IQR 0.0034–0.0075]). This was equivalent to 5 more NAFLD fibrosis cases being detected per 1000 patients.

Conclusion: SoC measurements are not superior to BMI SDS in adolescence at predicting NAFLD fibrosis development in young adulthood. Additional SoC measurements provide incremental but small benefit in detecting true positive fibrosis cases. Thus, with the agenda of reducing long-term morbidity and mortality associated with fibrosis, providing targeted interventions to overweight and obese adolescents is important to prevent progression to fibrosis.

Background and aims: Non-alcoholic fatty liver disease (NAFLD) is becoming a major health problem, resulting in hepatic, metabolic and cardio-vascular morbidity. Our study aims at evaluating new ultrasonographic tools to detect and measure hepatic steatosis.

Method: After local approval and patient consent, we included 73 patients addressed to a hepatology consultation for NAFLD suspicion or follow-up. They underwent ultrasonographic measurement of liver sound speed estimation (SSE) and attenuation coefficient (AC) using Aixplorer MACH 30 (Supersonic Imagine, France), and continuous Controlled Attenuation Parameter (cCAP) using Fibroscan (Echosens, France). Hepatic steatosis was then classified according to MRI proton density fat fraction (PDFF). Receiver operating curve (ROC) analysis was performed to evaluate the diagnostic performance in the diagnosis of steatosis.

Results: Our 73 patients (35 males and 38 females) had high mean age, BMI, weight, and waist circumference, respectively 60 years, 29.4 kg/m², 85 kg and 104 cm. 67% had a metabolic syndrome and 15% significant liver fibrosis. According to PDFF, 18 (24.7%) patients had no steatosis (PDFF <6.5%, S0), 30 (41.1%) suffered from mild steatosis (6.5 <PDFF <16.5%, S1), 8 (10.9%) from moderate steatosis (16.5 <PDFF <22%, S2), and 17 (23.3%) from severe steatosis (PDFF >22%, S3). SSE, AC and cCAP correlate with PDFF, with respective Spearman correlation coefficient of −0.50, 0.51 and 0.65 (p < 0.01).
Mean SSE, AC and cCAP values significantly differ between non-steatotic and steatotic patients (S1–S3). SSE values also differs between S1 and S2–S3 steatosis (p = 0.04). An SSE threshold of 1524 m/s had a sensitivity of 69% and a specificity of 74% for the diagnosis of steatosis (S1–S3). The corresponding area under the ROC curve (AUC) was 0.77 (95% CI 0.66–0.88, p < 0.01). An AC threshold of 0.41 dB/cm/MHz had a sensitivity of 91% and a specificity of 79% for the diagnosis of steatosis (S1–S3). The corresponding AUC was 0.91 (95% CI 0.84–0.98, p < 0.01). An cCAP threshold of 263 dB/m had a sensitivity of 82% and a specificity of 78% for the diagnosis of steatosis (S1–S3). The EASL-suggested threshold of 275 dB/m has a sensitivity of 75% and a specificity of 94%.

Conclusion: SSE and AC, simultaneously measured using Aixplorer MACH 30 system, demonstrate their reliability to detect liver steatosis. AC has high sensitivity for all-grade steatosis detection, with AUC >0.90, despite having more than 40% of our patients suffering from mild steatosis (S1).

To be noted that mean SSE values significantly differ between S1 and S2–S3 patients, maybe allowing for future ultrasonographic steatosis grading.

cCAP has good overall performances, but optimal thresholds are yet to be determined, and is not able to distinguish between different grades of steatosis.

FRI043
Community NAFLD screening programme in patients with type 2 diabetes mellitus indicates high burden of undiagnosed liver disease
Emma McCormick1, Noelle Cullen1, Suzanne Norris1, Oonagh O’Hagan2, a St James’ s Hospital, Hepatology, Dublin, Ireland; 2 Meighers Pharmacy Group, Dublin, Ireland
Email: emmamccormick@rcsi.ie

Background and aims: NAFLD is the most common liver disease in Western countries, affecting 1 in 4 adults, with prevalence mirroring that of obesity and T2DM. The presence of hepatic fibrosis is an important predictor of premature mortality and liver-related morbidity and mortality. Vibration-controlled transient elastography (VCTE) is a validated non-invasive test with NPV >90% for detection of advanced fibrosis/cirrhosis, but is largely confined to specialist centres. The lack of optimised public health screening strategies to detect liver fibrosis in adults remains a healthcare challenge. The aim of this study was to assess the feasibility of VCTE as a screening method to detect hepatic fibrosis in patients with identified risk factors for NAFLD in a community healthcare setting.

Method: 206 patients (94 male, 112 female.) with risk factors for NAFLD were identified via dispensing records in community pharmacies and invited to register for VCTE appointment. VCTE assessments were performed in 4 community pharmacies over 14 dates between June and July 2021 and results sent to patients’ GPs. Patients with liver stiffness measurements (LSM) >8.2 kPa were referred to a specialist Hepatology clinic for follow up.

Results: The median age was 63 years (range 27–84). 88% of patients had T2DM and 53% had a BMI >30. The median CAP score was 291 dB/m (range 160–400), and 45% of patients had a CAP score ≥300 dB/m. The median LSM was 5.8 kPa. 31% of patients had LSM ≥7.1 kPa, 15% had LSM ≥9.1 kPa and 6.7% had LSM ≥12.5 kPa. Only 19% of patients had both a normal CAP and LSM.

Conclusion: This is the first study to assess VCTE screening for hepatic fibrosis beyond traditional healthcare settings, and demonstrates that community-based risk-stratified screening leads to earlier identification of patients with liver fibrosis. Community pharmacy is a readily accessible healthcare setting in which access to non-invasive assessments of liver fibrosis outside of the hospital setting could be offered with potential significant cost savings to the healthcare system.
Conclusion: ALAT elevations are more frequent in Greenlanders than in Danes with T2DM, and ALAT increases with 8.0% for each metabolic syndrome criteria fulfilled. Accordingly, ALAT may be a useful and easily accessible tool to monitor NAFLD in patients with T2DM in Greenland. The median FIB-4 score is lower in Greenlanders compared with Danes, suggesting a lower degree of liver fibrosis. These findings need further evaluations preferably including comparisons with histopathology.

# FRI045
A baseline signature of metabolites involving the gut-liver axis predicts MRI-PDFF response to FASN inhibitor TVB-2640: results from the FASCINATE-1 study
Rohit Loomba1, Marie O’Farrell2, Eduardo Martins2, Katharine Grimmer2, Alithrea Zetter2, Cristina Alonso1, Ibon Martinez-Arranz2, George Kemble3, Stephen Harrison4, UC San Diego School of Medicine, Dept of Gastroenterology, La Jolla; 2Sagmet Biosciences, San Mateo, United States; 3OWI Metabolomics, Derto, Spain; 4Pinnacle Clinical Research, San Antonio, United States
Email: roloomba@ucsd.edu

Background and aims: TVB-2640 is a potent FASN inhibitor in Ph2b development for NASH. FASN is an attractive target because de novo lipogenesis drives steatosis, causes lipotoxicity, and is necessary for fibrogenesis. A 12 wk Ph2a study FASCINATE-1 was completed and met its primary endpoint. TVB-2640 reduced liver fat by 28.1% (p = 0.001) at 50 mg with a 61% MRI-PDFF response rate (decrease ≥30%). p = 0.001, and decreased biomarkers including ALT, PRO-C3, PIIINP, CK-18 and lipotoxins. NASH clinical studies are often confounded by high pbo but relatively low drug response rates. The objective of this work was to identify predictive biomarkers of MRI-PDFF response using metabolomic and SNP profiling of baseline blood samples from patients in FASCINATE-1.

Method: Metabolomic plasma profiling of ~460 species was performed on the OWL platform for pbo, 25 mg, 50 mg. Two machine learning approaches, Random Forest (RF) and Support Vector Machine were applied to baseline data. Using% change in MRI-PDFF as a continuous variable, a signature was developed using 50% of samples and tested using the other 50% with extensive cross-validation for sample size. Genotyping of SNPs relevant to NAFLD was completed for 19 patients to date (6 pbo, 13 on 50 mg, 79% Hispanic). Correlative analysis included metabolomics, genomics and other NASH biomarkers.

Results: A 6-metabolite signature was identified that enriches for MRI-PDFF response to TVB-2640. This showed 79% accuracy, 88% positive predictive value and 63% negative predictive value by the RF method. The components are ursooxycholic acid, glycocholic acid, DL-2-Aminobutyric acid, Sarcosine, D (-)-2-Aminobutyric acid and phosphatidyl choline (O-18:0/22:4). The composition of several bile acid derivatives suggests a role for the gut liver axis in TVB-2640 response. Overall, secondary bile acids were tested although not statistically significant. Analysis of pbo and independent validation is ongoing to refine this signature. SNP analysis showed allele variants in PNPLA3 rs738409, TMF6SF2 rs58542926 and MBOAT7 rs641738 in 68%, 16% and 53% of patients respectively, consistent with literature. MRI-PDFF responders included patients with wild type, hetero- or homozygous PNPLA3 rs738409. The effect of PNPLA3 genotype on baseline metabolomic profile will be assessed. Additional predictive signatures are under development using a combination of metabolomics and genomic profiling.

Conclusion: TVB-2640 decreased liver fat and markers of inflammation, lipotoxicity and fibrosis. Plasma metabolomics identified a baseline predictive signature of MRI-PDFF response to FASN inhibition, which indicates a role for the gut-liver axis. The Ph2b FASCINATE-2 study will incorporate microbiome analysis and the signature will be retrospectively tested and extended to histology analysis.

# FRI046
Enchanced Liver Fibrosis test in predicting severe liver-related outcomes in the general population
Kustaa Saarinen1,2, Martti Färkkilä1,2, Antti Jula3, Iris Erlund4, Terhi Vihervaara2, Annamari Lundqvist1, Fredrik Aberg1, 1Helsinki University Hospital, Abdominal Center, Helsinki, Finland; 2University of Helsinki, Helsinki, Finland; 3Finnish Institute for Health and Welfare, Helsinki, Finland; 4Helsinki University Hospital, Transplantation and Liver Surgery Clinic, Finland
Email: kustasaarinen@gmail.com

Background and aims: Liver fibrosis is the most important prognostic factor for liver-related morbidity and mortality in liver diseases in population including non-alcoholic fatty liver disease and alcohol-related liver disease. Existing methods for liver fibrosis assessment are either not suitable or show suboptimal performance for fibrosis screening in unslected populations. The Enhanced Liver Fibrosis (ELF) test, a composite score based on three serum-based markers of matrix turnover tissue inhibitor metalloproteinase 1 (TIMP-1), human procollagen type III amino terminal propeptide (PIIINP) and hyaluronic acid (HA) can detect advanced fibrosis and predict liver-related outcomes in various types of chronic liver diseases, but studies in large general population cohorts are lacking. We evaluated the performance of the ELF test in predicting liver related outcomes at the population level.

Method: ELF was measured at baseline from frozen serum samples of adult (age ≥30 years) participants of the Finnish Health 2000 study, a population-based epidemiological survey conducted in year 2000–2001. Subjects with baseline liver disease were excluded. Data were linked with national healthcare registers for hospitalization, cancer and death related to severe liver disease.

Results: The cohort comprised 6040 individuals (46% men, mean age 52.7 ± 15 years, BMI 26.9 kg/m², median alcohol use 74.9 g/week, 10% with diabetes). ELF was <9.8 in 5243 (87%), 9.8–11.3 in 741 (12%), and ≥11.3 in 56 (0.9%). During a median follow-up of 13.1 years, 67 severe liver-related outcomes occurred. By age- and sex-adjusted Cox regression, hazards ratios (HRs) for liver outcomes were 6.44 (95%CI 3.37–12.29) with ELF 9.8–11.3, and 24.37 (95% CI 8.55–69.50) with ELF ≥11.3, compared to ELF <9.8. Corresponding cumulative Aalen-Johansen incidences are shown in the figure. The C-statistic of ELF for predicting liver outcomes was 0.82 (95% CI 0.72–0.91) at 5 years and 0.73 (0.65–0.81) at 10 years.
Conclusion: The ELF test predicts severe liver-related outcomes in the general population. The ELF test could thus be used for initial stratification of the population regarding risk for future liver disease.

FRI047
Radiowater perfusion PET of the liver, and its value as a biomarker to discriminate between NAFLD and NASH, and activity and fibrosis grade
Olof Eriksson1, Kerstin Heurling1, Paul Hockings1, Edwin Johansson1, Alkwin Wanders1, Håkan Ahlström1, Lars Johansson1, Johan Vessby1, Fredrik Rorsman2, Mark Lubberink4, Antanase Medical AB, Sweden; 2Aalborg University Hospital, Aalborg, Denmark; 3Uppsala University Hospital, Sweden; 4Uppsala University Hospital, Uppsala, Sweden
Email: olof.eriksson@ilk.uu.se

Background and aims: The lack of non-invasive, biopsy free and repeatable assessments for fibrosis and activity stage in NAFL and NASH is a significant hurdle in respect to clinical diagnosis and evaluation of novel interventions. Radiowater PET has been shown to be a sensitive technique to quantify blood flow and identify perfusion defects in e.g. cardiology and neurology. We hypothesized that pathological changes in liver perfusion and arterial and portal blood flow could be detected by radiowater PET. The aim of this clinical study was to assess the value of radiowater PET for distinguishing between NAFL and NASH, as well as predicting activity and fibrosis grade in direct comparison with established biomarkers.

Method: A subset of patients with suspected NAFL/NASH (N = 30) recruited within the NASH AM-02 study was examined by radiowater PET/MRI, as well as transient elastography (FibroScan), in addition to sampling for established biomarkers of liver fibrosis. NAFL/NASH diagnosis as well as activity and fibrosis grade were verified by hepatic biopsy. Dynamic radiowater PET data of the liver was used to assess total hepatic blood flow, portal vein flow, hepatic arterial flow and portal flow fraction. The ROC AUC, the Youden cut-off and sensitivity/specificity were calculated for discrimination between (a) NAFL vs NASH, (b) activity grade 0–1 vs 2–4 and (c) fibrosis grade 0–1 vs 2–4. The correlation between parameters and activity grade 0–4 and fibrosis grade 0–4 was estimated by Spearman's correlation coefficient.

Results: In total 30 patients were examined in this sub-study and diagnosed with NAFL (n = 11) or NASH (n = 19), fibrosis grade 0–1 (n = 17) or 2–4 (n = 13) and activity grade 0–1 (n = 11) or 2–4 (n = 19). The ROC UAS as well as the Spearman's correlation coefficient for each parameter is reported in Table 1.

Conclusion: Radiowater PET has similar value as biomarker for distinguishing between NAFL/NASH and identifying activity grade, but not fibrosis grade, as transient elastography and established plasma markers.

Table 1: (abstract: FRI047).

<table>
<thead>
<tr>
<th>Parameter</th>
<th>ROC AUC (Youden cut-off), p-value1</th>
<th>Liver stiffness</th>
<th>CK18 M30</th>
<th>ALT</th>
<th>AST</th>
</tr>
</thead>
<tbody>
<tr>
<td>PET Total blood flow [mlg/min]</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>PET Portal vein blood flow [mlg/min]</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>PET Portal vein flow fraction [1/1]</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Fibroscan</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

1 p-value for testing if variable is able to predict group, i.e. p-value for testing OR differ from 1. *p < 0.1, **p < 0.05, ***p < 0.0001.

FRI048
The combination of the ELF and FIB-4 scores have high predictive performance for significant fibrosis in patients with NAFLD
Zobair Younossi1,2, Sean Felix2, Thomas Jeffers2, Elena Younossi2, Fatema Nader2, Andrei Racila1,2, Brian Lam2, Maria Stepanova1, Inova Health System, Medicine Service Line, Falls Church, United States; 2Betty and Guy Beatty Center for Integrated Research, IHS, Falls Church, United States; 3Center for Outcomes Research in Liver Disease, Washington DC, United States
Email: zobair.younossi@inova.org

Background and aims: Patients with nonalcoholic fatty liver disease (NAFLD) and fibrosis of stage 2 or greater (clinically significant fibrosis) are at risk for adverse outcomes, and are commonly considered to be candidates for clinical trials. Although non-invasive tests (NITs) for fibrosis have good negative predictive value (NPV), they tend to have suboptimal positive predictive value (PPV) for determining significant fibrosis. Our aim was to use a combination of two NITs to rule in and to rule out significant fibrosis among patients with NAFLD.

Method: Data were collected from patients with confirmed NAFLD diagnosis. Serum and liver biopsies were obtained for all patients. The Enhanced Liver Fibrosis (ELF) and FIB-4 NITs were calculated. Liver biopsies were read by a single hepatopathologist and scored according to the NASH CRN criteria, from stage 0 (no fibrosis) to 4 (cirrhosis). Significant fibrosis stage was defined as stage F2–F4.

Results: There were 463 NAFLD patients included: 48 ± 13 years old, 31% male, 35% type 2 diabetes. Of included patients, 39% had significant fibrosis; mean ELF score was 9.0 ± 2.9, mean FIB-4 score was 1.22 ± 1.05. Patients with significant fibrosis were older, more commonly male, had lower BMI but more components of metabolic syndrome (type 2 diabetes, hypertension, hyperlipidemia), higher ELF and FIB-4 scores (p < 0.0001). The performance of the two NITs in identifying NAFLD patients with significant fibrosis was as follows: AUC (95% CI) = 0.78 (0.74–0.82) for ELF, 0.79 (0.75–0.83) for FIB-4. A combination of ELF score ≥9.8 and FIB-4 ≥1.96 returned PPV of 95% which can reliably rule in significant fibrosis (sensitivity 22%, specificity >99%), while an ELF score ≥7.7 and FIB-4 ≥0.30 had NPV of 95% which can be used to rule out significant fibrosis (sensitivity 98%, specificity 22%); based on the latter, a rule to rule out significant fibrosis could be rewritten as follows: ELF <7.7 or FIB-4 <0.30.

Conclusion: The combination of ELF and FIB-4 can provide an easy algorithm with both high NPV and high PPV to rule out or rule in significant fibrosis in NAFLD. These data can be used to risk-stratify NAFLD patients in clinical practice as well as identify those who could be candidates for clinical trials.
Background and aims: Changes in the metabolic phenotype occur with age in patients with non-alcoholic fatty liver disease (NAFLD), however, the time of their occurrence and the connection with the processes and markers of aging remain not fully understood. Our aim was to establish the relationship between biological age (BA) and the global methylation level (GML) with metabolic parameters in patients with NAFLD.

Method: Our study included 106 patients with NAFLD with a mean age of 51.4 ± 8.9 years (62.3% women). All patients were divided into groups according to age: group 1-young patients (<45 years), group 2-middle-aged (45–59 years), group 3-the elderly (≥60 years). The diagnosis of NAFLD was based on the fatty liver index and fibrosis-4 index. Anthropometric and biochemical parameters were determined in all patients. The GML is the content of 5-methylcytosine in the DNA of mononuclear blood cells was detected with ELISA as a marker of aging. BA was calculated according to the method of A.G. Gorelikin, B. B. Pinkhasov.

Results: Analysis of anthropometric, lipid profile and liver parameters in patients with NAFLD depending on age revealed significant differences in the level of triglycerides (TG) (p = 0.043), BA (p = 0.002) between groups 1 and 2, and in BA (p = 0.002) between groups 1 and 3. There was a significantly higher proportion of young patients with an increased percentage of body fat (FAT) ($\chi^2 = 4.011; p = 0.045$) compared to middle-aged patients. Correlation analysis in group 1 showed a positive association between calendar age (CA) and visceral fat (VIS) (p = 0.023) and a negative one between CA and alkaline phosphatase (AP) (p = 0.017), BA was associated with VIS (p = 0.016), and the GML with ALT (p = 0.036). In group 2 there was no relationship between CA and the observed parameters, while BA was positively associated with FAT (p = 0.012), VIS (p = 0.002), and alkaline phosphatase (AP) (p = 0.017), TG (p = 0.019), very low-density lipoprotein cholesterol (VLDL-C) (p = 0.019) and had a negative relationship with the percentage of skeletal muscle (MUS) (p = 0.021) and AP (p = 0.042). The GML in this group was associated with body mass index (BMI) (p = 0.040), TG (p = 0.002), VLDL-C (p = 0.003). In group 3, CA had a direct association with VIS (p = 0.021) and a reverse one with total cholesterol (TC) (p = 0.005), BA was not associated with indicators that were not used for calculation, the GML was directly related to hip circumference (HC) (p = 0.035) and AP level (p = 0.011).

Conclusion: BA has been associated with anthropometric, lipid and liver parameters in middle-aged patients with NAFLD. The GML has been related to the levels of HC, BMI, TG, VLDL-C, ALT, AP; mainly in middle-aged patients with NAFLD, which may be associated with more pronounced changes in the metabolic profiles of this age group. The data obtained can be useful for the prevention of accelerated aging rates in patients with NAFLD.
Background and aims: Nonalcoholic fatty liver disease (NAFLD) patients with ≥stage 2 fibrosis are at an increased risk for developing liver-related morbidity and mortality. We performed a head-to-head comparison to evaluate the diagnostic test accuracy and predictive performance of MAST (magnetic resonance imaging-aspartate aminotransferase) versus MEFIB (the combination of magnetic resonance elastography [MRE] and FIB-4).

Method: NAFLD patients with a liver biopsy and MRE were analyzed from two prospective cohorts, the University of California San Diego (n = 414) and Yokohama City University (n = 314). Diagnostic performances for significant fibrosis (stage ≥2) were assessed using area under receiver operating characteristic curves (AUROCs).

Results: The mean age was 55.3 years and 48.1% were male. Significant fibrosis was observed in 46.4%. MEFIB was superior than MAST with AUROCs of categorized MEFIB (rule-in, intermediate, and rule-out) and MAST (>0.242, 0.165–0.242, and <0.165) being 0.889 (95% confidence interval [CI] 0.864–0.914) and 0.769 (95% CI 0.733–0.805), respectively (p < 0.001). Positive predictive value for significant fibrosis of MEFIB rule-in criteria was significantly higher, compared to MAST >0.242 (94.2% versus 88.2%, respectively; p = 0.031). Negative predictive value for significant fibrosis of MEFIB rule-out criteria was also significantly higher, compared to MAST <0.165 (89.8% versus 73.3%, respectively; p < 0.001). When MAST was analyzed as a continuous variable, its AUROC improved to 0.890 (95% CI 0.866–0.914).

Conclusion: For the identification of high-risk patients with NAFLD, MEFIB is significantly superior to categorized MAST. As continuous MAST score had high AUROC, the optimal cutoffs should be modified. Conversely, MEFIB, as a simple and easy algorithm, has practical advantages with a more reliable diagnostic performance as well as a better rule-in/-out ability.
Conclusion: Investigating suspected advanced fibrosis using positive NIT results, with combined TE and MRI assessment of cT1 increased the diagnostic accuracy of high-risk NASH by 21% and reduced liver biopsy by 28%. Screening tests based on NITs for fibrosis alone are inadequate for risk stratification and diagnosis of NASH. Inclusion of MRI-assessed cT1 in NAFLD/NASH clinical diagnostic pathways improves diagnostic accuracy and reduces the need for biopsy and for specialist referral, which would result in downstream cost savings.

FRI053
The PNPLA3 (rs738409) G/G-genotype is associated with presence of NASH and increased long-term risk of cirrhosis in NAFLD
Magnus Holmer1, Robin Zenlander1, Axel Wester1, Mattias Ekstedt2, Patrik Nasr2, Stergios Kechagias2, Stefano Romeo3, Per Stal1, Hannes Hagström1, 1Karolinska Institutet, Department of Medicine, Huddinge, Stockholm, Sweden; 2Linköping University, Division of Diagnostics and Specialist Medicine, Department of Health, Medicine and Caring Sciences, Linköping, Sweden; 3University of Gothenburg, Department of Clinical and Molecular Medicine, Gothenburg, Sweden
Email: magnus.holmer@ki.se

Background and aims: Mutations in several genes are linked to a worse histopathological profile in patients with nonalcoholic fatty liver disease (NAFLD). It is unclear if these genotypes impact long-term outcomes. Here, we investigated the prognostic importance of PNPLA3, TM6SF2, MBOAT7 and GCKR genotypes on the development of cirrhosis, liver related events (LRE) and all-cause mortality in a well-defined cohort of patients with NAFLD.

Method: DNA samples were collected from 546 patients with NAFLD. Presence of advanced fibrosis was established through liver biopsy (stage 3–4) or elastography (≥15 kPa), while presence of nonalcoholic steatohepatitis (NASH) was defined only by histology. A total of 5396 outcomes. Cox regression models were used to estimate adjusted hazard ratios (aHR) for these outcomes.

Results: In patients with NAFLD, the G/G genotype of PNPLA3 (rs738409) was associated with a higher prevalence of NASH at the time of biopsy (OR 3.67 [95% CI = 1.66–8.08]), but not with advanced fibrosis (OR 1.81 [95% CI = 0.79–4.14]). In NAFLD subjects without advanced fibrosis at baseline, the G/G genotype was associated with a higher risk of developing cirrhosis and LRE (aHR 3.43 [95% CI = 1.02–11.25]), Figure 1) after adjustments for age, sex, body mass index and type 2 diabetes during a median follow-up of 18.1 years. However, no increased risk was found for patients with advanced fibrosis at baseline (aHR 0.67, [95% CI = 0.13–3.43]). Compared to controls, NAFLD cases had a higher rate of developing cirrhosis and the increased risk correlated to PNPLA3 and GCKR genotypes. Mortality was not affected by any genetic variant.

Figure 1: Kaplan-Meier estimate of cirrhosis and LRE-free time in patients with NAFLD without advanced fibrosis at baseline. LRE = Liver related events.

Conclusion: The G/G genotype in PNPLA3 is associated with an increased risk of progression to cirrhosis in NAFLD. This was confined to patients without advanced fibrosis at baseline. Our results suggest that assessment of PNPLA3 genotype can be of clinical relevance in non-cirrhotic patients with NAFLD to individualize monitoring and therapeutic strategies.

FRI054
Hepatic expression of secreted calcium-binding protein 2 by hepatic stellate cells is associated with human non-alcoholic fatty liver disease progression
Frederik Larsen1, Mike Terkelsen1, Sofie Bendixen1, Daniel Hansen1, Charlotte Wernberg2, Mette Lauridsen2, Tina Di Caterino3, Fabio Avolio1, Majken Siersbaek1, Vineesh Indira Chandran1, Jonas Graversen1, Aleksander Krag1, Lars Groentved1, Kim Ravnskjaer1, 1University of Southern Denmark, Odense, Denmark; 2Sydvestjysk Sygehus, Esbjerg, Denmark; 3Odense University Hospital, Odense, Denmark

Email: tibert@bmb.sdu.dk

Background and aims: Non-alcoholic fatty liver disease (NAFLD) and its progressive form, non-alcoholic steatohepatitis (NASH), is the hepatic manifestation of obesity-induced metabolic syndrome. Activated Hepatic stellate cells (aHSCs) play a pivotal role in hepatic fibrosis, a defining process of NAFLD pathogenesis. Thus, secreted aHSC-specific proteins may hold promise as non-invasive biomarkers for diagnosis of NASH. Histological assessment of liver biopsies is the golden standard in diagnosis of NASH. Liver biopsy, however, is associated with risk for the patient and does not fully capture the tissue heterogeneity of the fibrotic liver.

Method: RNA sequencing was performed on liver needle biopsies from a histopathologically characterized severely obese (BMI >35) discovery cohort (n = 30). Bioinformatical analysis was used to identify potential biomarkers and their hepatocellular origin. Detection of mRNA in liver tissue and protein levels in plasma was performed using single molecule fluorescence in situ hybridization (smFISH) and ELISA, respectively.

Results: Hepatic expression of secreted modular calcium-binding protein 2 (SMOC2) was upregulated in NASH patients compared to healthy obese patients (padj <0.001). Single-cell RNA sequencing data indicated hepatic SMOC2 expression by quiescent and aHSCs exclusively, which was validated using smFISH. Moreover, plasma [SMOC2] was elevated in NASH patients compared to healthy obese patients (p <0.001) with a predictive accuracy of AUROC 0.88 (steatosis activity score >2).

Conclusion: Plasma [SMOC2] shows promise as a non-invasive biomarker for diagnosis of NASH. Linkage of plasma [SMOC2] to aHSCs, moreover, may directly reflect key cellular changes associated with NASH progression.
Background and aims: Multiple non-invasive tests (NITs) have been developed to evaluate NAFLD patients. However, the availability of NITs varies from country to country, and little is known about their implementation and adoption in clinical practice. This study aimed to explore clinicians’ perspectives on barriers and facilitators that influence the adoption of NITs.

Method: This cross-sectional study was performed using an exploratory mixed-methods approach. Twenty-seven clinicians from different countries, with a wide age range (from 30 to 63), specialties, and years of experience, were purposefully sampled. All participants filled in a questionnaire; 16 of those participated in a follow-up semi-structured interviews. Qualitative and quantitative data were collected and summarized using the recently published Non-adoption, Abandonment, Scale-up, Spread, and Sustainability (NASSS) framework for new medical technologies in healthcare organizations on seven domains: 1) the condition, 2) the technology, 3) the value proposition, 4) the adopters, 5) the organization, 6) the wider system, and 7) embedding and adaptation over time (see Figure 1).

Results: Several influencing factors were reported in different domains of the NASSS framework (see Figure 1). Among those, insufficient knowledge and limited awareness, impractical practice guidelines not yet built upon robust evidence for specific patient populations and care settings, need for extra training to perform the tests, difficult interpretation, and absence of sufficient reimbursement systems were perceived as the most important barriers. Other factors were indicated as important facilitating factors: ease of use and quick measurement process, evidence showing better performance compared to other available tests, local champions (clinicians with special interest in and knowledge about the new test), proper functional payment system and existence of resources in academic hospitals.

Conclusion: Adoption of new diagnostic NAFLD tests is a complex process and can be promoted or restricted by several factors, such as robust evidence, practical guidelines, a proper payment system, and local champions. As this study was restricted to clinicians, future studies could explore other stakeholders’ perspectives necessary to improve the adoption of new biomarker-based NITs into clinical practice.

**FR055**

Clinicians’ perspectives on barriers and facilitators for the adoption of non-invasive liver tests: a mixed-method study

Yasaman Vali1, Roel Eijk2, Timothy Hicks3, Will Jones3, Jana Suklan3, Vlad Katzin2, Adriaan G. Holleboom3, Miranda Langendam1, Quentin Anstee4, Patrick Bossuyt1, 1Amsterdam UMC, University of Amsterdam, Department of Epidemiology and Data Science, Amsterdam, Netherlands; 2Athena Institute, VU University Amsterdam, Faculty of Science, Amsterdam, Netherlands; 3NIHR Newcastle In Vitro Diagnostics Co-Operative, Newcastle University, Newcastle upon Tyne, United Kingdom; 4University Paris-Diderot, Assistance Publique-Hôpitaux de Paris, hôpital Beaujon, Paris, France; 5Amsterdam University Medical Centers, Department of Internal and Vascular Medicine, Amsterdam, Netherlands; 6Newcastle University, The Newcastle Liver Research Group, Translational & Clinical Research Institute, Faculty of Medical Sciences, Newcastle upon Tyne, United Kingdom

Email: y.vali@amc.uva.nl

Background and aims: Multiple non-invasive tests (NITs) have been developed to evaluate NAFLD patients. However, the availability of NITs varies from country to country, and little is known about their implementation and adoption in clinical practice. This study aimed to explore clinicians’ perspectives on barriers and facilitators that influence the adoption of NITs.

Method: This cross-sectional study was performed using an exploratory mixed-methods approach. Twenty-seven clinicians from different countries, with a wide age range (from 30 to 63), specialties, and years of experience, were purposefully sampled. All participants filled in a questionnaire; 16 of those participated in a follow-up semi-structured interviews. Qualitative and quantitative data were collected and summarized using the recently published Non-adoption, Abandonment, Scale-up, Spread, and Sustainability (NASSS) framework for new medical technologies in healthcare organizations on seven domains: 1) the condition, 2) the technology, 3) the value proposition, 4) the adopters, 5) the organization, 6) the wider system, and 7) embedding and adaptation over time (see Figure 1).

Results: Several influencing factors were reported in different domains of the NASSS framework (see Figure 1). Among those, insufficient knowledge and limited awareness, impractical practice guidelines not yet built upon robust evidence for specific patient populations and care settings, need for extra training to perform the tests, difficult interpretation, and absence of sufficient reimbursement systems were perceived as the most important barriers. Other factors were indicated as important facilitating factors: ease of use and quick measurement process, evidence showing better performance compared to other available tests, local champions (clinicians with special interest in and knowledge about the new test), proper functional payment system and existence of resources in academic hospitals.

Conclusion: Adoption of new diagnostic NAFLD tests is a complex process and can be promoted or restricted by several factors, such as robust evidence, practical guidelines, a proper payment system, and local champions. As this study was restricted to clinicians, future studies could explore other stakeholders’ perspectives necessary to improve the adoption of new biomarker-based NITs into clinical practice.

**FR056**

Ectopic fat deposition in the liver and pancreas and the presence of excess visceral adipose tissue significantly increase hospitalisation risk following COVID-19

Tom Waddell1,2, Adriana Roca-Fernandez2, John McGonigle2, Arun Jandor2, Valentina Carapella2, Helena Thomaides-Brears2, Andrea Dennis2, John Michael Brady2, Rajarshi Banerjee2, 1The University of Oxford, Department of Engineering Science, Oxford, United Kingdom; 2Perspectum Ltd, Oxford, United Kingdom

Email: tom.waddell@perspectum.com

Background and aims: In patients with COVID-19, obesity may increase risk of hospitalisation, use of mechanical ventilation and patient mortality. High liver fat, body mass index (BMI) and male sex are significant predictors of hospitalisation risk following COVID-19. However, BMI is a poor indicator of body fat distribution. Here, we studied ectopic fat accumulation within the liver and pancreas and body composition through multiparametric magnetic resonance (mpMR) and compared participants with and without hospitalisation for COVID-19.

Method: Participants with laboratory-confirmed or clinically suspected SARS-CoV-2 infection were recruited to the COVERScan study (NCT04369807; median time from initial symptoms = 177 days) and underwent a multi-organ mpMR scan (CoverScan, Perspectum Ltd). Measures of liver and pancreatic fat (PDF7), liver fibroinflammation (cT1) and body composition [visceral adipose tissue (VAT), subcutaneous adipose tissue (SAT), skeletal muscle index (SMI)] were analysed. Differences between participants hospitalised (n = 59) and not hospitalised (n = 348) for COVID-19 were assessed using Wilcoxon signed-rank tests. Univariate and multivariate analyses were performed on all biomarkers to assess the hospitalisation risk. Data presented are median values.

Results: Approximately 6 months after initial symptoms, participants hospitalised following COVID-19 had significantly elevated pancreatic fat (3.8% vs 2.8%, p < 0.012) and liver fat (3.8% vs 2.4%, p < 0.01) and liver cT1 (735 ms vs 706 ms, p < 0.01) compared to those who convalesced at home. Though hospitalised participants had a significantly elevated BMI (27 kg/m² vs 25 kg/m², p = 0.014), it was VAT, but not SAT, that was significantly elevated (132 cm² vs 86 cm², p < 0.01). Univariate analysis revealed that male sex, advanced age and elevated BMI, VAT, pancreatic fat, liver fat, and liver cT1 were all significantly predictive of hospitalisation following COVID-19. In multivariate analysis, only age remained significantly predictive of hospitalisation. In hospitalised people with obesity (>30 kg/m²), VAT, liver cT1 and liver fat, but not BMI nor pancreatic fat, remained significantly elevated [VAT: 220 cm² vs 152 cm², p = 0.01 (Figure 1); liver fat: 9.9% vs 4.2%, p = 0.003; liver cT1: 782 ms vs 742 ms, p = 0.012].
Conclusion: mpMR revealed significantly elevated visceral and ectopic fat deposition within the liver and pancreas in hospitalised participants following COVID-19. In obese participants, BMI was not significantly different in hospitalised, and non-hospitalised patients, whereas visceral fat, liver fibroinflammation and liver fat were significantly elevated. Our work highlights body fat distribution an important consideration for COVID-19 risk profiling, which cannot be sufficiently evaluated based on BMI alone.

FRI057
Genomic and metabolomic profiles and their correlations with preclinical signs of endothelial dysfunction measured by peripheral arterial tonometry in non-alcoholic fatty liver disease

Mario Masarone1, Jacopo Troisi2,3, Benedetta Maria Motta1, Martina Lombardi2,3, Pietro Torre1, Roberta Sciorio1, Marco Aquino1, Marcello Persico1,1University of Salerno, Internal Medicine and Hepatology Unit, Department of Medicine, Surgery and Odontostomatology “Scuola Medica Salernitana”, Baronissi (Salerno), Italy; 2Theoreo srl, Montecorvino Pugliano (Salerno), Italy; 3University of Salerno, Department of Chemistry and Biology, “A. Zambelli”, Fisciano (Salerno), Italy
Email: mario.masarone@gmail.com

Background and aims: NAFLD is associated with insulin resistance, metabolic syndrome (MS) and diabetes and it is an independent CVD risk factor. Endothelial Dysfunction (ED) plays a central role in the pathogenesis of CVD. Preclinical ED can be detected by vascular reactivity studies, such as Peripheral Arterial Tonometry (PAT). Genome Wide Studies (GWAS) identified Single Nucleotide Polymorphisms (SNPs) associated to NAFLD progression. Some of them (ie TM6SF2) have been postulated to influence CVD risk. The use of specific biomarkers related to ED presence in NAFLD may allow an early identification of CVD risk and provide crucial insights into its pathophysiology. This could be addressed through untargeted metabolomics and genomic approaches. Aims: to identify metabolomics signatures able to discriminate the presence of ED by combining data provided by metabolomics analyses with those from PAT, and to correlate them with anthropometric, laboratory and genomic profiles of NAFLD subjects.

Method: Serum was collected from 107 subjects with biopsy-proven NAFLD (55.9% NAFL; 26.6% NASH; 17.5% NASH-Cirrhosis) without clinically evident CVD. Metabolomics analysis was performed by mass spectrometry. The resulting profiles were correlated with PAT scores, revealed by an EndoPAT-2000 device, and with genomic profiles of 4 SNPs of NAFLD (PNAPL3; TM6SF2; GKR; MBOAT).

Results: Class separation in metabolomics profiles between patients with and without ED (EndoPAT cut-off = 0.51) was obtained through a “Partial Least Square Discriminant Analysis” (PLS-DA), which was also used to identify the discriminating metabolites. According to the PLS-DA score plot, two metabolomics profiles were identified, significantly different, in the two groups (R2 = 0.58, p = 0.001). The metabolites profiles are presented in figure 1. By comparing PAT scores of patients with simple steatosis (NAFL) (n=61, 19 with ED), NASH (n=28, 12 with ED), and NASH-cirrhosis (n=17, 9 with ED) no significant difference was observed (p = 0.34), suggesting that CVD risk is not associated with the degree of liver disease. Moreover, the clinical and genetic parameters associated to ED were type 2 diabetes, MS and BMI (directly) and TM6SF2 dominant model (CC+CT) (inversely) at the univariate and only MS at a multivariate analysis.

Conclusion: NAFLD patients with and without ED exhibit significant differences in their metabolomics profiles, demonstrating that they could be a useful early diagnostic tool for assessing CVD risk and providing an in-depth understanding of its underlying mechanisms. Among the NAFLD associated SNPs, only TM6SF2 mutation was correlated to a reduced prevalence of ED, but the only independent factor for ED was MS presence.

FRI058
Determinants of liver stiffness measurements in patients with NAFLD: an individual patient data meta-analysis

Ferenc Mozés1, Emmanuel Selvaraj2-3, Arjun Jayaswal3, Jerome Boursier4, Céline Fournier4, Elisabetta Bugianesi6, Ramy Younes7, Salvatore Petta8, Sanjiv Mahadeva9, Wah-Kheong Chan9, Peter Eddowes10, Philip N. Newsome11, Gideon Hirschfield12, Vincent Wai-Sun Wong13, Victor de Lédinghen14, Jeremy Cobbold2, Won Kim15, Myoung Seok Lee16, Cristophe Cassignotto17, Geraldine Ooi18, Atsushi Nakajima19, Masato Yoneda19, Ming-Hua Zheng20, Andreas Geier21, Theresa Tuthill22, M. Julia Brosnan22, Quentin Anstee23, Stephen Harrison1, Patrick Bossuyt24, Michael Pavlides2-3, 1University of Oxford, Oxford Centre for Magnetic Resonance (OCMR), Oxford, United Kingdom; 2University of Oxford, Translational Gastroenterology Unit, Oxford, United Kingdom; 3University of Oxford, Oxford Centre for Magnetic Resonance (OCMR), Oxford, United Kingdom; 4Université d’Angers, Laboratoire HIFIH, Angers, France; 5Echosens, Paris, France; 6University of Turin, Department of Medical Sciences, Turin, Italy; 7Boehringer Ingelheim, Ingelheim am Rhein, Germany; 8University of Palermo, Section of Gastroenterology and Hepatology, PROMISE, Palermo, Italy; 9University of Malaya, Gastroenterology and Hepatology Unit, Department of Medicine, Faculty of Medicine, Malaysia; 10Nottingham University Hospitals NHS Trust and University of Nottingham, National Institute for Health Research Nottingham Biomedical Research Centre, Nottingham, United Kingdom; 11University Hospitals Birmingham NHS Foundation
Background and aims: Liver stiffness measurements (LSM) performed with FibroScan are used in the clinical assessment of patients with non-alcoholic fatty liver disease (NAFLD). Fibrosis is the main determinant of LSM, but the contribution from other determinants and how they vary in patient subgroups is less well studied. Our aim was to describe the dependence of LSM on histological, demographic and laboratory parameters. 

Method: Data sets including LSM, demographics, histology- and lab parameters were reported in 2768 patients. Parameters with correlation $r > 0.15$ with LSM were selected as possible determinants of LSM in the entire patient group. Linear regression models were built by adding one predictor at a time to a base model including the log-transformed LSM and fibrosis stages as indicator variables. Partial $R^2$ values were compared to evaluate the contribution of each variable in explaining the variability of log-transformed LSM. A separate analysis evaluated the interaction between age and fibrosis stage.

Results: NASH CRN fibrosis stage, lobular inflammation and ballooning grades, age, aspartate aminotransferase (AST), platelet count (Plt), gamma-glutamyltransferase (GGT), BMI and presence of T2DM correlated with LSM with $r > 0.15$. Mean age was 51 years, mean BMI was 30 kg/m², 41% of patients had T2DM. Fibrosis stage explained most of the variance ($R^2 = 0.411$) in log-transformed LSM, followed by BMI ($partial R^2 = 0.051$), GGT ($partial R^2 = 0.023$), and AST ($partial R^2 = 0.022$) (see Table). Furthermore, including an interaction term between fibrosis stage and age explained log-transformed LSM better than only considering the main effect of fibrosis stage ($F$-statistic $= 3.171, p = 0.007$).

<table>
<thead>
<tr>
<th>Model predictors</th>
<th>Partial R²</th>
<th>$R^2$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age</td>
<td>0.0018</td>
<td>0.0018</td>
</tr>
<tr>
<td>BMI</td>
<td>0.0514</td>
<td>0.0514</td>
</tr>
<tr>
<td>Plt</td>
<td>0.0068</td>
<td>0.0068</td>
</tr>
<tr>
<td>AST</td>
<td>0.0221</td>
<td>0.0221</td>
</tr>
<tr>
<td>GGT</td>
<td>0.0232</td>
<td>0.0232</td>
</tr>
<tr>
<td>T2DM</td>
<td>0.0183</td>
<td>0.0183</td>
</tr>
<tr>
<td>Ballooning grade</td>
<td>0.0119</td>
<td>0.0119</td>
</tr>
<tr>
<td>Lobular inflammation grade</td>
<td>0.0132</td>
<td>0.0132</td>
</tr>
</tbody>
</table>

Conclusion: Our data confirm that fibrosis is the main determinant of LSM in patients with NAFLD, with BMI, GGT and AST explaining most of the remaining variance. However, LSM was less dependent on fibrosis stage in younger patients—a result that deserves further exploration. Our findings should be taken into account when interpreting LSM results from these patients.

FRI059 Knowledge of liver fibrosis stage among adults with non-alcoholic fatty liver disease/non-alcoholic steatohepatitis improves adherence to life style changes

Carriera, Patrizia1, Abbasmourad1, Fabienne Marcellin2, José Luis Calleja Panero3, Camelia Protopopescu1, Jeffrey Lazarus4,5.

1 Aix Marseille Univ, Inserm, IRD, SESSTIM, Sciences Economiques & Sociales de la Santé & Traitement de l’Information Médicale, ISSPAM, Marseille, France; 2 Aix Marseille Univ, Inserm, IRD, SESSTIM, Sciences Economiques & Sociales de la Santé & Traitement de l’Information Médicale, ISSPAM, Marseille, France; 3 Department of Gastroenterology and Hepatology, Hospital Universitario Puerta de Hierro de Majadahonda, Madrid, Spain; 4 Barcelona Institute for Global Health (ISGlobal), Hospital Clinic, University of Barcelona, Barcelona, Spain; 5 University of Barcelona, Faculty of Medicine, Barcelona, Spain

Email: abbas.mourad@inserm.fr

Background and aims: Non-alcoholic fatty liver disease (NAFLD) continues to rise in many countries, paralleling the epidemic of obesity worldwide. NAFLD can evolve into non-alcoholic steatohepatitis (NASH) depending on age, lifestyle, and metabolic risk factors. Both diseases are managed with lifestyle interventions, but unawareness of liver disease severity may compromise adherence. An international survey of people living with NAFLD/NASH was conducted for the first time to identify correlates of a lack of knowledge about fibrosis status, and to assess whether this unawareness was associated with poor adherence to lifestyle changes.

Method: We recruited 1411 adults living with NAFLD/NASH in Canada, France, Germany, Italy, Spain, and the United Kingdom who were registered on the online patient community platform Carenity. Weighted binary and multinomial logistic regressions were performed to estimate the effect of explanatory variables on unawareness of fibrosis stage and poor adherence to lifestyle changes, respectively, in univariable and multivariable analyses.

Results: In the study group, men accounted for 54.1%, 15.5% of the participants had obesity, and 75.3% of NAFLD patients reported being in an early fibrosis stage. Of the total, 59.2% were unaware of their fibrosis stage, and 34.4% reported non-adherence to lifestyle changes. After multiple adjustments (Figure 1), older people were found to be at more risk of not knowing their fibrosis stage. Individuals who were aware of their fibrosis stage were more likely to have discussed their liver tests with their physicians throughout the previous year ($AOR = 0.24; 95%CI: 0.16–0.36$), and to have been diagnosed throughout the 5 years preceding the survey ($AOR = 0.59; 95%CI: 0.38–0.91$). Individuals with a body mass index (BMI) $≥ 35$ were over twice as likely to not know their fibrosis stage ($AOR = 2.26; 95%CI: 1.37–3.40$). Unawareness about fibrosis stage was significantly associated with poor adherence to lifestyle changes ($AOR = 1.70; 95%CI: 1.14–2.41$). Individuals with obesity (BMI $≥ 30$) had a threefold higher risk of having poor adherence to lifestyle changes ($AOR = 3.12; 95%CI: 1.74–5.60$). People reporting having received support from nurses and other health staff were more likely to be adherent to lifestyle changes ($AOR = 0.37; 95%CI: 0.25–0.54$).
Conclusion: As fibrosis stage is becoming the main predictor of NAFLD progression, patient's knowledge of their fibrosis stage should become a priority to improve liver health. Given the seriousness of NASH-related morbidity and mortality, improving patient-provider communication, especially for people with obesity, about liver fibrosis stage, its associated risks, and how to mitigate them, is essential. Training healthcare professionals and promoting patient educational programs to support behavior changes should also be included in the educational agenda.

FRI060
The MRI and AST (MAST) score is correlated with noninvasive and histologic markers of fibrosis in patients with advanced fibrosis due to NASH
Mazen Noureddin1, Kris V. Kowdley2, Anita Kohli3, Aasim Sheikh4, Guy Neff3, Bal Raj Bhandari5, Nadege Gunn6, Stephen Caldwell8, Zachary Goodman4, Dora Ding9, Lily Ma10, Jay Chuang10, Ryan Huss10, Chuhan Chung10, Robert Myers10, Keyur Patel11, Brian Borg12, Reem Ghalib13, John Poulos14, Ziad H. Younes15, Magdy Elkhashab16, Tarek Hassanein17, Rajalakshmi Iyer18, Peter Ruane19, Mitchell Shiffman20, Simone Strasser21, Guy Neff5, Bal Raj Bhandari6, Nadege Gunn7, Stephen Caldwell8, Zachary Goodman9, Dora Ding10, Lily Ma10, Jay Chuang10, Ryan Huss10, Chuhan Chung10, Robert Myers10, Keyur Patel11, Brian Borg12, Reem Ghalib13, John Poulos14, Ziad H. Younes15, Magdy Elkhashab16, Tarek Hassanein17, Rajalakshmi Iyer18, Peter Ruane19, Mitchell Shiffman20, Simone Strasser21, Vincent Wai-Sun Wong22, Rohit Loomba23, Naim Alkhouri2, Fatty Liver Program, Cedars-Sinai Medical Center, Los Angeles, CA, United States; 2Liver Institute Northwest, Seattle, WA, United States; 3Arizona Liver Health, Chandler, AZ, United States; 4GI Specialists of Georgia, Marietta, GA, United States; 5Covenant Research, LLC, Sarasota, FL, United States; 6Delta Research Partners, LLC, Bastrop, LA, United States; 7Pinnacle Clinical Research, Austin, TX, United States; 8University of Virginia, Charlottesville, VA, United States; 9Gilead Sciences Inc., Foster City, CA, United States; 10University of Toronto, Toronto, ON, Canada, Canada; 11Southern Therapy and Advanced Research, Jackson, MS, United States; 12Texas Clinical Research Institute, Arlington, TX, United States; 13Cumberland Research Associates, Fayetteville, NC, United States; 14Gastro One, Germantown, TN, United States; 15Toronto Liver Centre, Toronto, ON, Canada, Canada; 16Southern California Research Center, Coronado, CA, United States; 17Iowa Digestive Disease Center, Clive, IA, United States; 18Iowa Health Sciences Center, Iowa City, IA, United States; 19Ruane Medical and Liver Health Institute, Los Angeles, CA, United States; 20Bonn Secours Mercy Health, Richmond, VA, United States; 21Royal Prince Alfred Hospital and The University of Sydney, New South Wales, Australia, Australia; 22Department of Medicine and Therapeutics, The Chinese University of Hong Kong, Hong Kong, Hong Kong; 23NAFLD Research Center, University of California at San Diego, La Jolla, CA, United States

Email: mazen.noureddin@chs.org

Background and aims: The MAST Risk score is a noninvasive tool that includes AST and MRI-based assessments of liver stiffness (LS) by elastography (MRE) and steatosis by proton density fat fraction (MRI-PDFF), for the identification of patients at risk of progressive NASH. Our aims were to evaluate the effects of cilofexor (CILO) and firsocostat (FIR) on MAST, and associations between treatment-induced changes in MAST with histologic and noninvasive test (NIT) responses in patients with advanced fibrosis due to NASH.

Method: NASH patients with histologically-confirmed, advanced fibrosis (NASH CRN F3–F4) in the phase 2b ATLAST trial were treated with regimens including CILO 30 mg (n = 40), FIR 20 mg (n = 40), CILO + FIR (n = 78), or placebo (n = 39), once daily for 48 weeks (W48). Liver histology was evaluated by a central reader and a machine learning (ML) approach (PathAI; Boston, MA). Endpoints included a ≥1-stage improvement in fibrosis without worsening of NASH (primary endpoint [PE]), ≥2-pt reduction in NAFLD Activity Score (NAS response [NAS-R]), and LS by vibration-controlled transient elastography (VCTE) and ELF responses (ELF-R), defined as ≥25% and ≥0.5-unit reductions from baseline (BL) to W48, respectively. Changes in MAST were evaluated using Wilcoxon rank sum and Fisher's exact tests.

Results: At BL, 56% of patients had cirrhosis (F4); median MAST Risk score was higher in those with F4 vs F3 fibrosis (0.36 vs 0.24; p = 0.003). Across study groups, BL MAST was significantly correlated with ELF score (ρ = 0.53), LS by VCTE (ρ = 0.48), hepatic collagen content (ρ = 0.37) and α-SMA expression by morphometry (ρ = 0.26), serum bile acids (ρ = 0.44), ML NASH CRN fibrosis score (ρ = 0.39), and proportionate areas of NASH CRN F4 (ρ = 0.38), portal inflammation (ρ = 0.36), and hepatocellular ballooning (ρ = 0.27; all p < 0.05), but not proportionate areas of steatosis or lobular inflammation. Compared with placebo (median change in MAST from BL to W48: −0.04), greater improvements in MAST at W48 were observed with FIR (−0.23; p = 0.03); differences with CILO (−0.06, p = 0.46) and CILO + FIR (−0.05; p = 0.68) were not statistically significant. Compared to non-responders, greater improvements in MAST from BL to W48 were observed in patients with NAS-R and LS by VCTE-response, but not ELF or PE response (Figure).

Conclusion: In patients with advanced fibrosis due to NASH, the MAST Risk score is correlated with noninvasive and histologic measures of fibrosis and may be a useful marker of treatment response beyond conventional histologic methods.
**FR1061**

**Independent determinants of CAP values in healthy individuals with dysmetabolism**

Cristiana Bianco¹, Serena Pelusi², Eleonora Giacopuzzi Grigelli², Luigi Santoro³, Francesco Malvestiti¹,³, Melissa Tomasì³, Ilaria Marini¹, Sara Margarita¹, Rossana Carpani¹, Danièle Prati¹, Luca Valenti¹,³.

¹Precision Medicine, Department of Transfusion Medicine and Hematology-Fondazione IRCCS Ca’ Granda Ospedale Maggiore Policlinico; ²Università degli Studi di Milano; ³Università degli Studi di Milano, Department of Pathophysiology and Transplantation

**Background and aims:** Controlled attenuation parameter (CAP) values determined during vibration controlled transient elastography correlate with hepatic fat content and can non-invasively assess the presence of fatty liver with moderate accuracy. Aim of the study was to examine the clinical and metabolic determinants of CAP in a cohort of apparently healthy individuals with dysmetabolism.

**Method:** We assessed CAP in 953 consecutive blood donors with dysmetabolism features (hypertension, hyperglycemia, overweight/obesity, low HDL/high tryglicerides), who participated in a primary prevention program (LIVER-BIBLE cohort up to July 2021). CAP values determined during vibration controlled transient elastography were most strongly associated with the severity of hyperinsulinemia (p < 10⁻⁵), insulin (p = 0.0003), HDL, HbA1c, BMI and alcohol consumption (p < 0.05 for all). Fatty liver index predicted CAP ≥ 275 dB/m with low-moderate accuracy (AUROC = 0.70), whereas ALT with low accuracy (AUROC = 0.60). In univariable analyses, APRI was associated with overall mortality (hazard ratio [HR]: 5.01 [95% confidence interval (CI): 1.27–19.78]; p = 0.021), as was FIB-4 (HR: 1.53 [95%CI: 1.18–1.99]; p < 0.002), the MetS (HR: 1.28 [95%CI: 1.11–1.49]; p < 0.001), the Forns (HR: 1.24 [95%CI: 1.08–1.42]; p = 0.002), and the FLI (HR: 1.03 [95%CI: 1.01–1.04]; p = 0.002), but not the BARD-score (HR: 1.16 [95%CI: 0.97–1.38]; p = 0.097). The FLI-score (HR: 1.02 [95%CI: 1.01–1.03]; p = 0.006) and the MetS (HR: 1.17 [95%CI: 1.07–1.28]; p = 0.001) were univariably associated with malignant events. For major adverse CV events, results were similar (FLI-score: HR: 1.03 [95%CI: 1.02–1.05]; p < 0.001; MetS: HR: 1.30 [95%CI: 1.31–1.73]; p < 0.001). Furthermore, the Forns (HR: 1.13 [95%CI: 1.04–1.23]; p = 0.005), as well as the FLI-score (HR: 1.03 [95%CI: 1.02–1.04]; p < 0.001) and the MetS (HR: 1.32 [1.21–1.43]; p < 0.001) were associated with a combined CV endpoint. In multivariable analyses including age, BMI, mean arterial pressure, FRS, and respective scores significantly associated in univariable analyses, none of the scores remained independently associated with overall mortality and malignant outcomes. Interestingly, the MetS remained independently associated with major adverse CV events (aHR: 1.36 [95%CI: 1.11–1.65]; p = 0.003) and the FLI-score for combined CV endpoints (aHR: 1.02 [1.01–1.04]; p = 0.010).

**Conclusion:** While specific liver-related scores (i.e., FIB-4, APRI) are strongly associated with outcomes in liver diseased patients, their prognostic value is limited in the general population. Most of the scores of interest were univariably associated with overall mortality; however, these associations vanished when adjusting for other variables. Importantly, the MetS as well as the FLI-score showed independent associations with CV events, suggesting a strong correlation of fatty liver disease and rate of CV outcomes in the general population.

---

**FR1062**

**Performance of liver-related clinical scores in the SAPHIR study**

Lorenz Balcar¹,², Georg Semmler¹,²,³, Stephan Zandanell¹, David Niederseer⁴, Sophie Geneslucker⁴, Alexandra Feldman⁴, Christian Datz⁵, Bernhard Paulweber⁵, Elmar Aigner¹.

¹Pancreas Medical University of Salzburg, First Department of Medicine, Salzburg, Austria; ²Medical University of Vienna, Division of Gastroenterology and Hepatology, Department of Internal Medicine III, Vienna, Austria; ³General Hospital Oberndorf, Department of Internal Medicine, Oberndorf bei Salzburg, Austria; ⁴University Hospital Zurich, Department of Cardiology, Zurich, Switzerland

**Background and aims:** There are several established clinical scores for patients with chronic liver diseases; however, the prognostic value of these scores in the general population is unclear. Therefore, our study aimed to evaluate the value of liver-related risk-scores in a population-based cohort with a 20-year follow-up.

**Method:** We included participants from the SAPHIR study from the city of Salzburg, Austria. We calculated Cox regression models for (i) overall mortality, (ii) malignancy-related-, (iii) major adverse cardiovascular (CV)-, and (iv) composite CV events (minor/major adverse CV events).

**Results:** Overall, 1646 patients were included (mean age 52 ± 6 years; 63% male). Mean BMI was 27 ± 4 kg·m⁻² and 15% of patients had metabolic syndrome (MetS) at baseline. Mean Framingham risk score (FRS) was 12 ± 4 points, indicating an intermediate risk for developing CV diseases within 10 years. Median follow-up was 18.7 years (IQR: 15.4–20.5). In univariable analyses, APRI was associated with overall mortality (hazard ratio [HR]: 5.01 [95% confidence interval (CI): 1.27–19.78]; p = 0.021), as was FIB-4 (HR: 1.53 [95%CI: 1.18–1.99]; p < 0.002), the MetS (HR: 1.28 [95%CI: 1.11–1.49]; p < 0.001), the Forns (HR: 1.24 [95%CI: 1.08–1.42]; p = 0.002), and the FLI (HR: 1.03 [95%CI: 1.01–1.04]; p = 0.002), but not the BARD-score (HR: 1.16 [95%CI: 0.97–1.38]; p = 0.097). The FLI-score (HR: 1.02 [95%CI: 1.01–1.03]; p = 0.006) and the MetS (HR: 1.17 [95%CI: 1.07–1.28]; p = 0.001) were univariably associated with malignant events. For major adverse CV events, results were similar (FLI-score: HR: 1.03 [95%CI: 1.02–1.05]; p < 0.001; MetS: HR: 1.30 [95%CI: 1.31–1.73]; p < 0.001). Furthermore, the Forns (HR: 1.13 [95%CI: 1.04–1.23]; p = 0.005), as well as the FLI-score (HR: 1.03 [95%CI: 1.02–1.04]; p < 0.001) and the MetS (HR: 1.32 [1.21–1.43]; p < 0.001) were associated with a combined CV endpoint. In multivariable analyses including age, BMI, mean arterial pressure, FRS, and respective scores significantly associated in univariable analyses, none of the scores remained independently associated with overall mortality and malignant outcomes. Interestingly, the MetS remained independently associated with major adverse CV events (aHR: 1.36 [95%CI: 1.11–1.65]; p = 0.003) and the FLI-score for combined CV endpoints (aHR: 1.02 [1.01–1.04]; p = 0.010).

**Conclusion:** While specific liver-related scores (i.e., FIB-4, APRI) are strongly associated with outcomes in liver diseased patients, their prognostic value is limited in the general population. Most of the scores of interest were univariably associated with overall mortality; however, these associations vanished when adjusting for other variables. Importantly, the MetS as well as the FLI-score showed independent associations with CV events, suggesting a strong correlation of fatty liver disease and rate of CV outcomes in the general population.
FRIO63
Correlations of 2D-Shear wave and transient elastography liver stiffness measurements in patients with non-alcoholic fatty liver disease
Dimitrios Karagiannakis1, Georgios Markakis1, Dimitra Lakiotaki1, Elisavet Michailidou2, Paraskevi Fytili1, Evangelos Cholongitas1, Ioannis Vlahogiannakos1, George Papatheodoridis1, 1Laiko General Hospital, Medical School, National and Kapodistrian University of Athens, Greece
Email: d.karagiannakis@hotmail.com

Background and aim: The performance of transient elastography (TE) has been widely assessed, while 2D-Shear wave elastography (2D-SWE) is a newer elastographic technique. The aim of the study was to investigate if liver stiffness measurements (LSM) of 2D-SWE are correlated with LSM of TE for the evaluation of liver fibrosis in patients with non-alcoholic fatty liver disease (NAFLD).

Methods: In total, 552 consecutive patients with NAFLD were included [median age: 55 (range:19–87) years, Males: 288 (52.5%)]. Mean waist circumference was 105 ± 13 cm and median BMI 28.7 (17.3–79.7) kg/m² [Normal BMI (<25): 94 (17%); Overweight (BMI = 25–30): 94 (17%); Obese (BMI >30): 192 (34.8%)]. Liver fibrosis was assessed by TE (M/XL probe) and 2D-SWE at the same time. CAP was performed for the estimation of the degree of liver steatosis.

Results: Median LSM of TE was 5.5 (2.8–75) kPa and of 2D-SWE 62 (3.7–46.2) kPa. TE (and CAP) and 2D-SWE were not feasible in 18 (3.5%) and 26 (4.7%) patients respectively. Mean CAP value was 290 ± 54 dB/m. One hundred and twenty eight patients (23.2%) had mild steatosis (CAP <250 dB/m) and 406 (73.6%) had moderate/severe steatosis (CAP≥250 dB/m). LSMs by TE and 2D-SWE were correlated in normal BMI (r: 0.774; p < 0.001), overweight (r:0.774; p < 0.001) and obese (r: 0.75; p < 0.001) patients, as well as in patients with CAP ≤250 dB/m (r = 0.63; p < 0.001) and CAP >250 dB/m (r = 0.743; p < 0.001). According to TE measurements, patients were sub-classified to those without moderate fibrosis (F0–F1; LSM by TE <7 kPa; n = 388 or 70.3%), moderate/severe fibrosis (F2/F3; LSM:7–13 kPa; n = 117/19.3%) and cirrhosis (F4; LSM:13 kPa; n = 57/10.3%). A significant correlation between TE and 2D-SWE was found in all these subgroups (r:0.458; r:0.624; r:0.696, respectively; all p < 0.001). The accuracy of 2D-SWE for detecting patients with moderate/severe fibrosis diagnosed by TE was 89.7% (LSM cut-off 6.87 kPa: 87% sensitivity, 81.2% specificity for discrimination between moderate/severe (F2/F3) and no moderate fibrosis (F0–F1). The accuracy of 2D-SWE for diagnosing patients with cirrhosis diagnosed by TE was 99.1% (LSM cut-off 12.16 kPa: 90.4% sensitivity, 95.9% specificity).

Conclusion: LSMs by 2D-SWE correlate with those of TE and therefore 2D-SWE can reliably substitute TE in the evaluation of liver fibrosis in patients with NAFLD. Similar LSM cut-off values of TE and 2D-SWE can be applied in order to classify NAFLD patients into fibrosis stages.

FRIO64
Performance of the Enhanced Liver Fibrosis (ELF) test in real world practice versus clinical trials of non-alcoholic steatohepatitis
Maria Stepanova1,2,3,4, Sean Felix2,3, Thomas Jeffers2,3, Elena Younossi2,4, Brian Lam2,3, Linda Henry1,2,3,4, Zobair Younossi1,2,3,4, Inova Health System, Medicine Service Line, 2Betty and Guy Beatty Center for Integrated Research, IHS; 3Inova Health System, Center for Liver Disease, Department of Medicine; 4Center for Outcomes Research in Liver Disease
Email: zobair.younossi@inova.org

Background and aims: The ELF score is calculated using three direct markers of fibrosis [hyaluronic acid (HA), amino-terminal propeptide of type III collagen (PIIINP), tissue inhibitor of matrix metalloprotei-

patients with NAFLD enrolled in clinical trials and in patients seen in a real-life hepatology clinic.

Method: Data collected from two non-overlapping samples of NAFLD patients were used in this study (Group 1: real world hepatology practice, Group 2: enrollees from NASH Clinical trials). Both groups were matched according to presence of advanced fibrosis. Clinical data, liver biopsy, and serum were collected for each included patient. ELF scores were calculated using an ADVIA Centaur XP analyzer. Liver biopsies were scored by a single hepatopathologist 0–4 using CRN criteria; advanced fibrosis was defined as stage 3 (bridging fibrosis) or 4 (compensated cirrhosis). Performance of ELF for predicting advanced fibrosis was assessed in both groups.

Results: A total of 1, 379 subjects were available [Group 1: N = 467, age 48 ± 13 years old, 31% male, 35% type 2 diabetes, 24.6% advanced fibrosis, mean (SD) ELF score was 9.0 ± 1.2, based on published cutoffs, 78% had ELF <9.8 (low-risk), 17% 9.8 ELF <11.3 (moderate risk), and 5% ELF ≥11.3 (high-risk); Group 2: N = 912, age 54 ± 11 years old, 43% male, 55% type 2 diabetes, 26% advanced fibrosis; mean (SD) ELF 9.6 ± 1.1 including 61% with low-risk, 33% moderate risk, 6% high-risk ELF scores]. Area under the ROC curve (AUC) (95%) for predicting advanced fibrosis by ELF was 0.81 (0.77–0.85) in Group 1. The cutoff of ELF ≥9.8 returned sensitivity 57% (47%–66%), specificity 89% (86%–92%), positive predictive value (PPV) 63% (54%–70%), negative predictive value (NPV) 86% (83%–89%); in addition, the cut-off of ELF ≥11.3 returned specificity 99% (98%–100%), sensitivity 19% (12%–28%), PPV 88% (69%–96%), NPV 79% (77%–80%). In Group 2, ELF had AUC (95% CI) = 0.80 (0.77–0.82) for predicting advanced fibrosis which was identical to that seen in Group 1. The cutoff of ELF ≥9.8 returned sensitivity 74% (68%–79%), specificity 74% (70%–77%), positive predictive value (PPV) 50% (45%–55%), negative predictive value (NPV) 85% (86%–91%); in addition, the cut-off of ELF ≥11.3 returned specificity 98% (97%–99%), sensitivity 17% (12%–22%), PPV 77% (66%–89%), NPV 77% (74%–80%).

Conclusion: The non-invasive serum-based ELF test performs well in identifying high risk NAFLD patients in both real-life and clinical trial settings.
Results: 389 NAFLD patients were included with F3–4 prevalence 48.6%, 54.5% male, mean age 48.5±13.2 years, diabetes in 30.1%, and BMI 32.4 ± 7.0 kg/m². Overall, 51 (13.1%) patients had an adverse liver-related outcome over median 3.14 years, and included hepatic decompensation in 9.5%, HCC 4.1%, liver transplant 5.4%, mortality 2.6% and liver-related mortality 2.1%. AUC measures for the ML predictive models were: hepatic decompensation 0.958, HCC 0.770, liver transplant 0.931, all-cause mortality 0.831, and liver-related mortality 0.859. ML feature importance for predictive variables was determined for each outcome. FIB-4, AST:ALT ratio, and age had the greatest feature importance for NIT and clinical variables respectively. US-based parameters did not have significant feature importance for liver-related outcomes compared to clinical or biochemical features.

Conclusion: ML models based on readily available clinical, biochemical, and US-based variables were able to accurately predict adverse liver-related outcomes in a tertiary cohort of biopsy-proven NAFLD patients. Age, AST:ALT ratio, and FIB-4, but not US-based parameters, contributed significantly to ML predictive models for clinical outcomes.

FR066
Incorporating a two-tiered liver fibrosis assessment into annual diabetes review in primary care-3 year follow up study
Rajan Bhandari1, Dina Mansour1, 1Q E hospital Gateshead, United Kingdom
Email: dmansour299@yahoo.co.uk

Background and aims: We previously presented the outcome of a pathway incorporating 2-tiered fibrosis assessment into annual diabetic reviews in primary care. This 3 year follow up study looks at Outcomes in patients referred into secondary care with moderate-advanced fibrosis

Method: All patients aged >35 years with T2DM attending annual review at two primary care practices in North East England between April 2018 and September 2019 (n = 467) had a Fib-4 requested, followed by transient elastography (TE) if the Fib-4 was above the high sensitivity threshold. Those with a liver stiffness >8 kPa were reviewed in secondary care. This pathway was continued in both practices after the end of the initial study period. We reviewed the outcomes of all patients referred to secondary care; the number of patients referred in the subsequent years with ongoing case-finding; and any patients missed from initial screening presenting with decompensated/symptomatic disease.

Results: Of 467 patients in the initial study, 58 were referred for TE. 25 had a LSM-8 kPa and 20 had advanced disease (on imaging/biopsy/endoscopy). 6/20 (30%) patients with advanced disease have died- 2/20 liver related deaths (hepatocellular carcinoma (HCC) and decompensated cirrhosis); 1 patient diagnosed with HCC was treated with curative transarterial chemoembolisation; 3 patients had varices on OGD (2 started on carvedilol for primary prophylaxis); 12 remain under follow up. In all patients with LSM >8 kPa (n = 25): 8/ 25 (32%) died (3/8 from COVID-19); 24% (6) LSM improved, 8% (2) LSM deteriorated; 32% (8/25) lost weight. No patients missed by the pathway presented with decompensated disease. Serial Fib-4 at annual screening 2019–2021: 4 patients new raised Fib-4 scores-1 DNA, 1 TE is awaited, 1 LSM <8 kPa (discharged), 1 advanced disease (LSM 17.1 kPa).

Conclusion: Incorporation of a two-tiered liver fibrosis assessment into primary care annual diabetic screening significantly improves identification of advanced liver disease and no patients have presented with advanced disease out-with the pathway. It allows for early detection and interventions against the complications associated with advanced liver disease. Mortality in patients with advanced liver disease remains high. Referrals for TE and into secondary care dramatically reduce after the initial year of case finding.
the rule-in criteria, the positive predictive value (PPV) was 71.6% for FAST, 74.2% for MRAST, 82.6% for F-CAST, and 78.1% for M-PAST in combined cohort. When used as the rule-out criteria, negative predictive value (NPV) was 85.2% for FAST, 88.8% for MRAST, 85.3% for F-CAST, and 87.3% for M-PAST. Indeterminate patients by the FAST, MRAST, F-CAST and M-PAST were 48.5%, 49.9%, 32.5% and 28.1%, respectively.

Conclusion: MRAST has equal diagnostic accuracy with FAST for NASH with NAS≥4 and F≥2. In addition, our results supported the higher utility of a two-step strategy using F-CAST and M-PAST over one-step method (FAST and MRAST) for detecting NASH with NAS≥4 + F≥2.

FRI068
Impact of artificial intelligence assistive tool on the histopathologic review of fibrosis in non-alcoholic steatohepatitis patients
Aileen Wee1, Wei Qiang Leow2, Gwyneth Soon3, Elaine Chng4, Dean Tai5, Yayun Ren6, Jia Ling Chong2, Yee Chen Ng5, Feng Liu5, Lai Wei6, Arun Sanyal1. 1Department of Pathology, Yong Loo Lin School of Medicine, National University of Singapore, Singapore; 2Department of Anatomical Pathology, Singapore General Hospital, Singapore and Duke-NUS Medical School, Singapore; 3Department of Pathology, National University Hospital, Singapore; 4HistolIndex Pte. Ltd., Singapore; 5Peking University People’s Hospital, Peking University Health Science Center, Beijing Key Laboratory of Hepatitis C and Immunotherapy for Liver Diseases, Beijing, China; 6Hepatopancreatobiliary Center, Beijing Tsinghua Changgung Hospital, Tsinghua University, Beijing, China; 7Virginia Commonwealth University, Richmond, Virginia, USA
Email: patweea@nus.edu.sg

Background and aims: Inter-observer variability for categorical scores of liver fibrosis among pathologists ranges from fair to moderate weighted kappa. Artificial intelligence (AI) and advances in digitised whole-slide images (WSI) facilitated the use of an AI-assistive tool in pathology to improve histopathologic interpretation. Second harmonic generation/two-photon excitation fluorescence microscopy with qFibrosis stage and continuous values (SHG/TPEF) microscopy with AI can provide standardised evaluation. This pilot study aims to explore the impact of AI tools on the overall agreement on fibrosis assessment between pathologists.

Method: Unstained sections of liver biopsies from 50 non-treated patients with NASH (F0–F4) were taken from Peking University People’s Hospital and fibrosis was quantitated using SHG/TPEF microscopy (qFibrosis). To evaluate performance metrics for assisted and unassisted reads, pathologists interpreted images in both modalities in 2 sessions separated by a wash-out period of at least 3 weeks. H&E and MT-stained images were digitised and uploaded onto a WSI platform, and the assisted reads included an additional SHG image with qFibrosis stage and continuous values. 3 pathologists participated in this study, with experiences ranging from 5 to 40 years.

Results: The qFibrosis AI tool has been validated in studies, showing >95% agreement. When assisted by the qFibrosis AI tool, the concordance rate between pathologists improved to near perfect agreement, with 0.82 linear weighted kappa, as compared to 0.72 for the unassisted review. Mean overall percentage agreement between pathologists improved from 89.38% to 92.93% (p = 0.032). Mean linear weighted kappa for intra-observer agreement is also higher, achieving 0.91 kappa compared to 0.79 for unassisted reads. The effect of AI assistance on fibrosis assessment consistency was examined by reviewing the percentage of patients who remained staged between F1–F3 after the initial reads. Using qfibrosis, 95.3% of the patients were retained versus 82% for the unassisted review.

Table: Mean percentage agreement and weighted kappa (linear) for assisted and unassisted reads.

<table>
<thead>
<tr>
<th></th>
<th>Unassisted</th>
<th>Assisted</th>
</tr>
</thead>
<tbody>
<tr>
<td>Inter-observer</td>
<td>Mean Percentage Agreement</td>
<td>89.38%</td>
</tr>
<tr>
<td></td>
<td>Mean Weighted Kappa (Linear)</td>
<td>0.7157</td>
</tr>
<tr>
<td>Intra-observer</td>
<td>Mean Percentage Agreement</td>
<td>92.08%</td>
</tr>
<tr>
<td></td>
<td>Mean Weighted Kappa (Linear)</td>
<td>0.7861</td>
</tr>
</tbody>
</table>

Conclusion: qFibrosis as an AI assistive tool can improve inter-pathologist weighted kappa to near perfect agreement with 93% agreement and 95% retention rate. qFibrosis has been well validated and enable pathologists with varying experience to establish similar performance in fibrosis evaluation. This has important implications in the development of drugs for NASH treatment.

FRI069
PRO-C3 based sequential algorithm can screen high-risk NASH and severe fibrosis in asian NAFLD population
Liang-Jie Tang1, Gang Li1, Mohammed Elslam2, Pei-Wu Zhu3, Sun-Dan Chen4, Howard Ho-Wai Leung5, Ou-Yang Huang1, Grace Lai-Hung Wong6,7, Yu-Jie Zhou8, Morten Karsdal9, Diana Leeming9, Chris Byrne10, Giovanni Targher11, Jacob George2, Vincent Wai-Sun Wong6,7, Ming-Hua Zheng12,13. 1The First Affiliated Hospital of Wenzhou Medical University, NAFLD Research Center, Department of Hepatology, Wenzhou, China; 2Westmead Hospital, Westmead, and University of Sydney, Storr Liver Centre, Westmead Institute for Medical Research, Sydney, Australia; 3The First Affiliated Hospital of Wenzhou Medical University, Department of Laboratory Medicine, Wenzhou, China; 4The First Affiliated Hospital of Wenzhou Medical University, Department of Pathology, Wenzhou, China; 5The Chinese University of Hong Kong, Department of Anatomical and Cellular Pathology, Hong Kong, China; 6The Chinese University of Hong Kong, Department of Medicine and Therapeutics, Hong Kong, China; 7The Chinese University of Hong Kong, State Key Laboratory of Digestive Disease, Hong Kong, China; 8Shanghai Jiao Tong University, Division of Gastroenterology and Hepatology, Key Laboratory of Gastroenterology and Hepatology, Shanghai, China; 9Nordic Bioscience Biomarkers and Research A/S, Herlev, Denmark; 10University Hospital Southampton, Southampton General Hospital, Southampton National Institute for Health Research Biomedical Research Centre, Southampton, United Kingdom; 11University and Azienda Ospedaliera Universitaria Integrata of Verona, Section of Endocrinology, Diabetes and Metabolism, Department of Medicine, Verona, Italy; 12Wenzhou Medical University, Institute of Hepatology, Wenzhou, China; 13Key Laboratory of Diagnosis and Treatment for the Development of Chronic Liver Disease in Zhejiang Province, Wenzhou, China
Email: zhengmh@wmu.edu.cn

Background and aims: With non-alcoholic fatty liver disease (NAFLD) incidence and prevalence increasing, there is an urgent
need for non-invasive diagnostic tests to accurately screen high-risk patients for liver inflammation and fibrosis. We evaluated the diagnostic performance of a new sequential algorithm for assessing liver inflammation and fibrosis in NAFLD.

**Method:** Data from two prospective Asian cohorts (327 biopsy-confirmed patients with NAFLD [262 from Wenzhou, 65 from Hong Kong]) were studied. The area under the receiver operating characteristic curve (AUROC) was used to test the diagnostic performances of FAST, ADAPT, Agile 3+ and Agile 4, and for comparison with other widely used non-invasive fibrosis scores.

**Results:** For progressive non-alcoholic steatohepatitis (NASH) patients (NASH + NAFLD activity score (NAS) ≥4 + F ≥2), the AUROC of FAST score was 0.801 (95% confidence interval (CI): 0.739–0.863), and the negative predictive value (NPV) was 0.951. For advanced fibrosis (F3) and cirrhosis (F4), the AUROC of ADAPT, Agile 3+ and Agile 4 were 0.879 (95% CI: 0.825–0.933), 0.805 (95% CI: 0.725–0.886) and 0.943 (95% CI: 0.892–0.994), and the NPV was 0.972 and 0.992, respectively. A new sequential algorithm of ADAPT + Agile 4 combination was better than other combinations (AUROC = 0.88, 95% CI: 0.824–0.935). This new combination algorithm approach can more accurately screen out high-risk patients (i.e. the number of true positive (TP) groups has increased from 21%, 26%, and 31% to 32%), while reducing the number of patients requiring liver biopsy (including false positive (FP)), false negative (FN) and indeterminate groups from 29% and 26% to 20% (Figure). At the same time, in all subgroup analyses (stratifying by sex, age, diabetes, NAS, BMI and ALT), ADAPT + Agile 4 had good diagnostic performance.

**Conclusion:** The new sequential algorithm reliably assesses inflammation and fibrosis in NAFLD patients, making it easier to exclude low-risk patients and recommending high-risk patients for referral treatment, while reducing the need for liver biopsy.
Background and aims: Non-alcoholic fatty liver disease (NAFLD) covers a spectrum of diseases from simple steatosis (SS) to non-alcoholic steatohepatitis (NASH), with a significant risk of progressing to fibrosis. Fibrosis is considered as the most important predictive factor in the prognosis and mortality of NAFLD patients. Liver biopsy is widely accepted as the gold standard for its diagnosis and reliable non-invasive methods are unavailable. We investigated the diagnostic performance of plasma Ficelin-2 (FCN-2) (FCN-2)-2, identified by an in silico approach for the diagnosis of fibrosis in NAFLD. Method: For the in silico analysis, a biological network was built to identify proteins related to fibrogenesis using molecular databases and bioinformatic tools. Of the several markers identified, FCN-2 met the criteria as one of the most interesting candidates that follows the fibrotic process aside from being secreted in the plasma. For the validation phase, 76 morbidly obese (MO) subjects with biopsy-proven NAFLD were stratified according to fibrosis stage (minimal F0–F1, n = 43; moderate–advanced F2–F4, n = 33). Plasma FCN-2 levels were determined by enzyme-linked immunosorbent assay and the diagnostic performance was assessed. Results: Although FCN-2 did not differentiate the steatosis stage of NAFLD, plasma FCN-2 levels significantly decreased when liver damage progresses from minimal to moderate/advanced fibrosis (p < 0.0001). Interestingly, FCN-2 levels correlated inversely with lobular inflammation (p = 0.0002) and portal inflammation (p = 0.0007) histological features of NAFLD. When stratified according to sex, the FCN-2 plasma levels are similar between males and females. The diagnostic performance of plasma FCN-2 in detecting F2 fibrosis was higher than those of other current fibrosis’ indices (FORNS, FIB-4) (AUROC 0.76, 0.72, and 0.67, respectively). Furthermore, when combined with other tests (GGT and APRI), the score index yield an excellent discrimination power with AUC of 0.80 in identifying advanced fibrosis. Conclusion: Plasma FCN-2 can be used as potential biomarker for discriminating moderate/advanced from minimal fibrosis in the context of NAFLD. Validation in larger cohorts will be required for its clinical utility. The use of FCN-2 alone or in combination with other tests may provide an alternative to minimize the need for biopsies to detect fibrosis in NAFLD patients.

Background and aims: Patients with ≥F3 fibrosis are grouped as compensated advanced chronic liver disease (cACLD). Baveno six consensus recommended the rule in and out liver stiffness measurement (LSM) cut-offs for diagnosing compensated advanced chronic liver disease (cACLD) as 10 kPa and 15 kPa. Baveno seven suggested lowering the cACLD cut-off for NAFLD, though it is supported by scanty data. We aimed to identify the LS cut-off for cACLD in people with non-alcoholic fatty liver disease (NAFLD).

Method: Included 330 patients with biopsy proved NAFLD (male 173 [52.4%]; age, median [interquartile range] 39 [33–47] years; body mass index 32.6 (25.6–44.4) kg/m2; diabetes 102 (30.9%). All the LS measurements were done by a single operator, after overnight fasting using a standard measurement technique. All the LS measurements were done within four weeks of liver biopsy.

Results: Liver biopsy revealed ≥F3 fibrosis, i.e., cACLD, in 70 (21.2%). Measured LS were <10, 10 to <15 and ≥15 kPa in 230 (69.7%), 46 (13.9%) and 54 (16.4%), respectively. Baveno six criteria achieved a sensitivity (rule out) and specificity (rule-in) of 72.9% and 93% for cACLD. The area under receiver operator characteristic (AUROC) curve of LSM for predicting cACLD was 0.862 (0.810–0.914). The LS <8 to 13, and >13 kPa were present in 182 (55.2%), 82 (24.8%) and 66 (20%), respectively. A new cut-off at 8 kPa and 13 kPa showed sensitivity and specificity of 90% each. Univariate analysis identified age, diabetes, and LS as independent predictors of cACLD, but platelet count and albumin were not statistically significant. On multivariate analysis, only LS (OR, 1.201, 95% CI, 1.139–1.267) and diabetes (OR, 2.592, 95% CI, 1.298–5.179) were independent predictors of cACLD. The AUROC for the model with LSM and diabetes was 0.863 compared with 0.862 for LSM alone (Delong test, P = 0.934). The AUROC for predicting cACLD with BMI <25 kg/m2 and ≥25 kg/m2 was 0.945 (0.886–1.000) and 0.844 (0.784–0.904), respectively.

Conclusion: LS cut-offs set at <8 and >13 kPa perform better to diagnose cACLD than the Baveno 6 criteria. The presence of diabetes and body mass index needs to be accounted for while interpreting the cut-offs.
healthy volunteers [44 yr (32–53); 66% male; BMI 23 kg/m² (21–25)] and published literature, and the prevalence of abnormalities for each organ was assessed using Fisher’s exact tests. Statistical significance of co-prevalence was assessed by simulation assuming that values were independently binomially distributed.

**Results:** In this cohort of established T2D patients, characterised by abnormal body composition (high SAT and VAT, low SMI), there was a high prevalence of multi-organ abnormality (86% with at least 2 organs affected). There was evidence of fatty infiltration and/or fibroinflammatory changes in the liver (72% of patients), co-occurring with abnormality in pancreas (38%), spleen (44%), kidney (64%), and aorta (71%). High-risk non-alcoholic steatohepatitis (NASH) was significantly more prevalent in the obese (p < 0.005). Prevalence of low SMI and elevated pancreatic fat were associated with duration of T2D (p < 0.05). Aortic stiffness was significantly associated with organ steatosis (p < 0.05, Figure).

![Figure: Co-prevalence of organ abnormality in T2D patients with liver abnormality.](image)

**Conclusion:** Elevated levels of fat and fibroinflammation were highly prevalent in the liver, pancreas, spleen, and kidney with evidence of atherosclerosis and sarcopenia in most patients with T2D. The use of glucose-lowering therapies associated with weight loss, such as GLP-1 receptor agonists and SGLT2 inhibitors, are likely to have a beneficial effect on mobilising ectopic fat.

**FR1074**

**Plasma TREM2, a novel non-invasive biomarker for diagnosis of NASH in NAFLD patients with elevated liver stiffness**

Charlotte Wernberg1,2, Vinees Indira Chandran3, Mette Lauridsen2, Frederik Larsen5, Maria Kjølgaard Skytte3, Camilla Dalby Hansen4, Majken Siersbæk4, Tina De Caterino5, Sønke Detlefsen3, Yaseelan Palarasah3, Kim Ravnskjaer4, Lars Groentved4, Søren Kragh Moestrup6, Maja Thiele1, Jonas Graversen5, Aleksander Krag1.

1Odense University Hospital, Centre for Liver Research, Department of Gastroenterology and Hepatology, Odense, Denmark; 2University Hospital of South Denmark, Department of Gastroenterology and Hepatology, Esbjerg, Denmark; 3Department of Molecular Medicine, Odense C; 4University of Southern Denmark, Department of Biochemistry and Molecular Biology, Odense, Denmark; 5Odense University Hospital, Department of Clinical Pathology, Odense, Denmark;

Email: charlotte.wilhelmina.wernberg@rsyd.dk

**Background and aims:** Non-invasive markers of non-alcoholic steatohepatitis (NASH) is still an unmet clinical need, but also represent a key barrier in NASH clinical trials. Here we investigate the diagnostic accuracy of soluble plasma Triggering Receptor Expressed on Myeloid cells 2 (plasma TREM2) as a circulating biomarker for NASH in patients with NAFLD and elevated liver stiffness.

**Method:** A cross-sectional design with a derivation (n = 48) and a validation cohort (n = 170) among patient with suspected NAFLD, a valid liver biopsy and liver stiffness measure (LSM) >7.9 kPa, was applied. Soluble TREM2 in plasma was measured by quantitative immunoassay. Since patients with low fibrosis score are not eligible for clinical trials, we excluded patients with LSM <8.0. At risk NASH was defined as patients with non-alcoholic fatty liver disease (NAFLD) activity score (NAS) ≥4.

**Results:** Plasma TREM2 levels were significantly elevated in the derivation cohort in at-risk NASH patients with NAS≥4 as compared with NAS<4 subjects, with an area under the receiver operating characteristics curve (AUROC) 0.92 (95% CI: 0.84–0.99). Plasma TREM2 level was 2.1-fold increased in at-risk NASH patients and a strong diagnostic accuracy was confirmed in the validation cohort with an AUROC 0.83 (95% CI: 0.77–0.89, p < 0.0001). TREM2 level was associated with histologic features i.e., steatosis, lobular inflammation, and ballooning (p < 0.0001) but not fibrosis. Clinical cut-offs for rule-in and rule-out (90% sensitivity and 90% specificity) were settled and TREM2 values <38 ng/ml was found to be the optimal rule-out cut-off (sensitivity 90%, specificity 51%) whereas TREM2 level >65 ng/ml was the optimal rule-in cut off for at-risk NASH (sensitivity 89.9% and specificity 52%).

**Conclusion:** Plasma TREM2 is a promising novel blood-based single biomarker that can rule out or rule in presence of NASH with high accuracy.

**FR1075**

**Unbiased clustering of exhaled breath profiles in metabolic dysfunction-associated fatty liver disease identifies a patient phenotype at higher risk of disease progression**

Rohit Sinha1, Paul Brinkman2, Khalida Ann Lockman1, Alan Jaap1, Peter Hayes1, John Plevris1. 1Hepatology Laboratory and Centre of Liver and Digestive Diseases, The University of Edinburgh, Edinburgh, United Kingdom; 2UMC Amsterdam, The Department of Respiratory Medicine, Amsterdam, Netherlands; 3Edinburgh Centre for Endocrinology & Diabetes, Royal Infirmary of Edinburgh, Edinburgh, United Kingdom

Email: rohit.sinha@nhs.net

**Background and aims:** Human breath contains numerous volatile compounds which reflect the metabolic activity. Electronic nose (eNose) technology can distinguish metabolic dysfunction-associated fatty liver disease (MAFLD) from healthy with reasonable confidence [1, 2]. We hypothesised breath prints obtained from eNose could identify patient subgroups at higher risk for progression within the MAFLD spectrum.

**Method:** The study was a prospective single-centre cohort study (ClinicalTrials.gov: NCT02950610). eNose is a custom-made device made up of five-sensor arrays, each containing four sensors, previously validated in respiratory and liver disease [1, 3]. eNose on the exhaled breath was performed on well characterised MAFLD patients (n = 60)-Child’s A MAFLD cirrhotics (n = 30) and non-
cirrhotic MAFLD (n = 30), previously described [1]. Data were analysed using R studio (v 2.3.2) and SPSS 21. An unbiased machine learning clustering technique was applied. First hierarchical ward clustering, combined with similarity profile analysis, was used to assess the number of significant cluster groups. Between-cluster comparisons and Games-Howell post hoc analyses of clinical variables at baseline were performed using the Kruskal-Wallis test for continuous data and the chi-square test for categorical data.

**Results:** Data reduction to 3 principal components (PCs) explained 97.8% of the total variance. Three groups of patients with MAFLD disease were delineated solely based on their exhaled breath profiles. Three clusters were identified; cluster 1 consists of 23 patients, cluster 2 consists of 24 patients, and cluster 3 consists of 13 patients. The clusters were comparable in clinical phenotyping. Cluster 2 was identified as a higher risk group with significant differences in serum hyaluronic acid levels (p = 0.001), endoscopic evidence for portal hypertension (p = 0.003) and exhaled breath concentration of dimethyl sulphide (p = 0.041) and D-limonene (p = 0.015).

**Conclusion:** This study shows that unbiased clustering of exhaled breath profiles captured using eNose technology identifies three phenotypes within the MAFLD spectrum. One of the three clusters included most patients with more advanced liver disease. These results warrant prospective studies on the potential of exhaled breath fingerprinting using eNose technology as point-of-care diagnostics in the surveillance of patients with established metabolic dysfunction-associated fatty liver disease.

**FRI076**

The pericellular basement of the hepatocytes is highly affected by bariatric surgery in obese patients with non-alcoholic fatty liver disease

Ida Lønsmann Lønsmann1,2, Pierre Bel Lassen3-4, Diana Leeming2, Morten Karsdal2, Mette Juul Nielsen2, Karine Clément3,4, 1University of Southern Denmark, Faculty of Health Research, Odense, Denmark; 2Nordic Bioscience A/S, Biomarkers and Research, Herlev, Denmark; 3Sorbonne Université, INSERM, Paris, France; 4Assistance Publique Hôpitaux de Paris, Nutrition Department, Paris, France

**Background and aims:** Bariatric surgery decreases the severity of non-alcoholic fatty liver disease (NAFLD) in patients with severe obesity by improving liver histology and liver function tests. Nevertheless, there is a need for non-invasive biomarkers for monitoring treatment efficacy in NAFLD. The extracellular matrix (ECM) of the liver is subject to major changes during disease progression. The ECM basement membrane (BM) consists of mainly type IV collagen produced by hepatocytes. Changes in BM have been associated with early liver injury, repair mechanisms and pericellular fibrosis. The aim of this study was to investigate changes in biomarkers targeting two distinct epitopes reflecting BM remodeling of type IV collagen (PRO-C4 and C4M) after bariatric surgery (BS) as well as in relation to baseline liver histology.

**Method:** 60 weight stable patients with severe obesity (BMI >35 kg/m²) were examined at baseline and 12 months after BS-induced weight loss. Liver biopsies were performed during BS. Serological levels of PRO-C4 and C4M were measured using competitive ELISAs and change from baseline to 12-months follow-up were evaluated using a linear mixed effect model adjusted for outcome, sex, BMI and type 2 diabetes were used to evaluate the association of PRO-C4 and C4M with hepatocyte ballooning, steatosis, lobular inflammation and fibrosis at baseline.

**Results:** The cohort consisted of 56.7% females with a mean age of 46 and BMI of 49.0 kg/m². 66.7% of the patients were F2. Interestingly, baseline levels of both PRO-C4 and C4M decreased with increasing hepatocyte ballooning (p < 0.0001) and PRO-C4 decreased with increasing lobular inflammation (p = 0.022), while this association was borderline significant for C4M (p = 0.055). No significant associations were observed for collagen type IV remodeling with liver steatosis or fibrosis at baseline. Furthermore, median PRO-C4 and C4M levels decreased significantly from baseline to 12-months post BS by 21% (p = 0.01) and 14% (p < 0.001), respectively.

**Conclusion:** Hepatocytes are embedded in the BM, and changes in hepatocyte health is reflected by remodeling of the adjacent ECM. This study shows that BM remodeling is associated with liver histopathology. Consequently, serological biomarkers of type IV collagen remodeling could be used as markers of treatment efficacy in NAFLD patients.

**FRI007**

A re-appraisal of the diagnostic performance of ultrasonography for fatty liver disease

Chul-min Lee1, Eileen Yoon2, Jonghyun Lee3, Mi Mi Kim1, Bo-Kyeong Kang1, Dae Won Jun2, Hyunwoo Oh4, Hye Young Lee4, Sang Bong Ahn1, Joo Hyun Sohn5, Huiyul Park1, 1Hanyang University College of Medicine, Department of Radiology, Seoul, Korea, Rep. of South; 2Hanyang University College of Medicine, Department of Internal Medicine, Seoul, Korea, Rep. of South; 3Hanyang University College of Medicine, Department of Medical and Digital Engineering, Seoul, Korea, Rep. of South; 4Uljeongbu Eulji Medical Center, Department of Medicine, Gyeonggi-do, Korea, Rep. of South; 5Nowon Eulji Medical Center, Eulji University School of Medicine, Department of Internal Medicine, Seoul, Korea, Rep. of South; 6Hanyang University Guri Hospital, Department of Medicine, Gyeonggi-do, Korea, Rep. of South; 7Uljeongbu Eulji Medical Center, Department of Family Medicine, Gyeonggi-do, Korea, Rep. of South

**Background and aims:** Previous studies showed that ultrasonography (USG) has high specificity but low sensitivity for diagnosing fatty liver. Especially, the diagnostic performance of USG for mild fatty is low. We tried to re-appraisal the diagnostic performance of USG for fatty liver disease at this point.

**Method:** We performed a retrospective, multi-nation, multi-center, cross-sectional, and observational study. We included subjects who underwent both the USG and magnetic resonance proton density fat fraction (MR PDFF) within the six-month interval. The diagnostic performance of USG for fatty liver disease was evaluated as MR PDFF reference standard using sensitivity, specificity, positive and negative predictive value (PPV and NPV), diagnostic accuracy, and area under the receiver operating characteristics curve (AUC).

**Results:** We included a total of 5056 subjects in this study. The USG showed a sensitivity of 89.1%, specificity of 81.0%, and AUC of 0.850 for diagnosing any fatty liver (MR PDFF ≥6.5%). Furthermore, the sensitivity, specificity, and AUC of USG for diagnosing mild fatty liver (6.5% ≤ MR PDFF ≤ 14%) were 83.4%, 81.0%, and 0.822,
Background and aims: The American Association for the Study of Liver Disease does not recommend screening for non-steatohepatitis (NASH) among patients with type 2 diabetes (T2DM) while the European Association of the liver (EASL) recommends screenings. Both organizations have called for cost effective analysis (CEA) which has been recently published from the US population. Our aim was to assess the value of screening for NASH with significant fibrosis (fibrotic NASH) in five separate European populations.

Method: We performed cost-utility analyses of four separate fibrotic-NASH screening strategies using third-party, public sector payer perspectives for five European countries, each for two separate hypothetical populations initially aged 55 years with either T2DM and fibrotic-NASH, or fibrotic-NASH and no T2DM, and compared it to the strategy of not screening these populations for fibrotic-NASH. Screening methods involved combinations of Fibrosis-4 (FIB-4) followed by Fibroscan® or liver biopsy for detecting fibrotic NASH indicated per recent EASL guidelines. An incremental cost-effectiveness ratio (ICER) of ≤50,000 local currency units per incremental quality-adjusted life year was considered cost-effective.

Results: When screening T2DM+ fibrotic-NASH patients aged 55 years first with FIB-4 followed by Fibroscan®, and then treating detected fibrotic NASH patients with an intensive lifestyle intervention, this is shown to be a cost-effective strategy in all of the country-specific analyses when compared to not screening these patients (Figure 1). These outcomes hold steady both in the base case assessment and in the sensitivity analyses of the model. Screening approaches involving liver biopsy were found non-cost-effective in all studied countries. The results have not changed when we assessed the analysis starting screening at age 40.

Conclusion: Screening for fibrotic-NASH in T2D persons over the age of 55 as well as younger patients (over 40 years) is cost effective in European countries. Given the increasing burden of NAFLD/NASH and the expected approved medications, we recommend screening patients with T2D for fibrotic-NASH in Europe.

FRI079
Free Light Chains as a potential biomarker of inflammation and fibrosis in non-alcoholic steatohepatitis
Antonio Liguori1,2, Umberto Basile2,3, Cecilia Napodano2,3, Lidia Tomasello1,2, Fabrizio Mancuso1,2, Luca Di Galleone1,2, Giuseppe Marrone1,2, Marco Biolato1,2, Antonio Gasbarrini1,2, Gian Ludovico Rapaccini1,2, Antonio Grieco1,2, Luca Miele1,2.
1 Fondazione Policlinico Universitario A. Gemelli, IRCCS, Dipartimento Scienze Mediche e Chirurgiche, Roma, Italy; 2 Università Cattolica del Sacro Cuore, Roma, Italy; 3 Fondazione Policlinico Universitario A Gemelli, IRCCS, Dipartimento Scienze di laboratorio e infettivologiche, Roma, Italy
Email: lig.antonio91@gmail.com

Background and aims: Non-alcoholic fatty liver disease (NAFLD) is the most common chronic liver disease worldwide. Almost 20–30% of NAFLD patient develop steatohepatitis (NASH) characterized by hepatocyte ballooning, lobular inflammation and progressive fibrosis. Inflammation process in NASH is known to be associated with overexpression of pro-inflammatory biomarkers (IL1-beta, IL6, TNF-alfa). Polyclonal free light chains (FLC) reflect B cell activation and could give insight into the activity of the adaptive immune system in a variety of inflammatory conditions. The aim of this study is to evaluate the potential role of FLC as biomarker of inflammation and fibrosis in NAFLD/NASH.

Method: We enrolled 187 patients with metabolic liver disease at Liver Outpatient clinic at Policlinico A. Gemelli: 48 with NAFLD, 85 with NASH and 54 with cirrhosis. Diagnosis of NASH was histologically assessed. Medical and pharmacological anamnesis, anthropometric measurements and laboratory tests (FLC included, lambda and kappa) were obtained for all patients.

Results: Total FLC (lambda + kappa) were significantly higher in patients with cirrhosis than in patients with NAFLD or NASH (125.2 vs 32.7 mg/L, p < 0.01). Total FLC, lambda and kappa were higher in NASH patients than in NAFLD although non significantly (respectively 34.5 vs 32.4 mg/L, p = 0.2, 15.0 vs 13.2 mg/L, p = 0.2, 19.9 vs 19.1 mg/L, p = 0.8). In patients with NASH, total FLC are higher in patients with advanced fibrosis (F > 2, 39.0 vs 30.3, p = 0.03). Total FLC are associated to advanced fibrosis independently from age, sex, BMI and diabetes (OR 1.04, CI 1.00-1.08, p = 0.04).

Conclusion: In this study we highlight that FLC concentration is significantly higher in patients with cirrhosis than in patients with NAFLD or NASH. Increased FLC in NASH patients, advanced fibrosis is associated with higher serum concentration of total FLC. Serum FLC may represent a useful tool in grading and staging non-alcoholic fatty liver disease.

---

**Table 1**

<table>
<thead>
<tr>
<th>Treatment</th>
<th>Country</th>
<th>Incremental costs</th>
<th>Incremental utilities</th>
<th>Incremental cost effectiveness ratio (ICER)</th>
</tr>
</thead>
<tbody>
<tr>
<td>FLC</td>
<td>UK</td>
<td>£273</td>
<td>£0.077</td>
<td>£35.50</td>
</tr>
<tr>
<td></td>
<td>Germany</td>
<td>£30</td>
<td>£0.077</td>
<td>£6.658</td>
</tr>
<tr>
<td></td>
<td>Italy</td>
<td>£42</td>
<td>£0.077</td>
<td>£46.543</td>
</tr>
<tr>
<td></td>
<td>France</td>
<td>£41</td>
<td>£0.077</td>
<td>£6.183</td>
</tr>
<tr>
<td></td>
<td>Spain</td>
<td>£41</td>
<td>£0.077</td>
<td>£6.183</td>
</tr>
</tbody>
</table>

*UK* denotes England and Wales National Health Service (NHS)

Figure: Base case results when screening T2DM+ Fibrotic NASH patients aged 55 years.
Background and aims: Nonalcoholic fatty liver disease (NAFLD) is associated with inflammation and hepatocellular death, leading to activation of fibroblasts and progressive hepatic fibrosis—the single most important factor determining liver-related clinical outcomes and mortality. A range of non-invasive biomarker tests (NITs) are used in drug trials to measure biological response to therapy including routine biochemistry (ALT, AST), markers of necrosis/apoptosis (CK18-M65, and Fibrosis (ELF, PRO-C3, and Fibroscan (VCTE)). Although sustained weight loss >10% has been shown to improve histological fibrosis, little is known about its acute effects on NITs.

Method: 26 non-cirrhotic NAFLD patients were prescribed a 12-week very low calorie diet (VLCD) (800 kcal/day). Fasted blood samples were taken at weeks 0, 1, 3, 5, 7, 9 and 12 and VCTE measured at weeks 0 and 12. Routine labs as well as hyaluronic acid (HA), TIMP-1, PIIINP, PRO-C3, PRO-C4, PRO-C5, CK18-M65 were serially measured and ELF, ADAPT and FIB4 scores calculated. Patients were stratified by weight loss at 12 weeks into <5%, 5–7% and >7% of initial body weight and NIT change from baseline assessed.

Results: After 12-weeks VLCD, 4 patients had lost <5%, 4 had lost 5–7% weight and 18 had lost >7% body weight. No significant difference in NIT values were evident between weight loss groups at baseline. Rapid reductions in multiple collagen biomarkers were apparent after a week of VLCD. At 12-weeks, significant reductions in ELF (ANOVA p = 0.040, −5.3 ± 1.8% at >7% weight loss), driven by PIIINP (ANOVA p = 0.004, −23.7 ± 3.9% at >7% weight loss), and CK18-M65 (ANOVA p = 0.023, −43.5 ± 7.6% at >7% weight loss) were seen in patients who lost >7% weight. Similar trends were observed in ALT, AST, PRO-C3, and ADAPT but no difference was seen in FIB4 or VCTE.

Conclusion: A 12-week VLCD intervention induced significant weight loss of a level reported to reduce hepatic fibrosis if sustained.
Peripheral blood mononuclear cells mitochondrial copy number and adenosine triphosphate inhibition test in non-alcoholic fatty liver disease

Eileen Yoon1, Dae Won Jun1, Sang Bong Ahn2, Huiyul Park3, Hyo Young Lee4, Hyunwoo Oh5, Chul-min Lee6, Mi Mi Kim7, Bo-Kyeong Kang7, Joo Hyun Sohn8, Hanyang University College of Medicine, Department of Medicine, Seoul, Korea, Rep. of South; 2Nowon Eulji Medical Center, Eulji University School of Medicine, Department of Medicine, Seoul, Korea, Rep. of South; 3Uijeongbu Eulji Medical Center, Department of Family Medicine, Gyeonggi-do, Korea, Rep. of South; 4Uijeongbu Eulji Medical Center, Department of Medicine, Gyeonggi-do, Korea, Rep. of South; 5Hanyang University College of Medicine, Department of Radiology, Seoul, Korea, Rep. of South; 6Hanyang University Guri Hospital, Hanyang University College of Medicine, Department of Medicine, Gyeonggi-do, Korea, Rep. of South

Email: noshin@hanyang.ac.kr

Background and aims: Non-alcoholic fatty liver disease (NAFLD) is known to be associated with mitochondrial dysfunction. The purpose of this study was to develop biomarkers for the assessment of mitochondrial dysfunction in patients with NAFLD.

Method: Mitochondrion-associated transcriptome analysis was performed from the NAFLD and healthy control liver. Peripheral blood mononuclear cells obtained from 88 patients with NAFLD and healthy controls were used to measure mitochondrial DNA (mtDNA) copy number. Mitochondrial inhibition substrate test (ATP assay) was performed in HepG2 cells using patients’ serum. Cellular ATP concentration was measured in patient serum was applied at the same quantity as the media.

Results: Hepatic mRNA transcriptome analysis showed that patients with NAFLD exhibited upregulated expression of genes related to mitochondrial tricarboxylic acid (TCA) cycle (E2F1, E2F2, and ORC6) and those related to the mitochondrial envelope (E2F1, MAPPK4, and CYP2K6) compared to healthy controls. Gene set enrichment analysis revealed upregulated expression of genes related to the pathways of TCA cycle and DNA replication in patients with NAFLD as compared to that in healthy controls. The mtDNA copy number in the peripheral blood mononuclear cells was 1.28-fold lower in patients with NAFLD than in healthy controls (p < 0.0001). Cellular adenosine triphosphate (ATP) concentration decreased 1.2-fold times in NAFLD patients than in healthy controls (p < 0.0001). The mtDNA copy number and ATP inhibition test showed negative correlation with degree of hepatic steatosis. And ATP concentration showed positive correlation with mtDNA copy number.

Conclusion: Peripheral blood mononuclear cells mitochondrial copy number and ATP inhibition test can be used biomarkers for the assessment of mitochondrial dysfunction in patients with NAFLD.

Assessing the applicability of non-invasive diagnostic tests (NITs) in non-alcoholic fatty liver disease: an international qualitative study

Maja Thiele1, Sophie Péloquin2, Luca Valentí3, Patrice Lazure4, Mounia Hedid Masson5, Alina Allen6, Jeffrey Lazarus7, Mazen Noureddin8, Mary Rinella9, Frank Tack10, Suzanne Murray11, Emmanuel Toschatzis11, 1Center for Liver Research, Odense University Hospital and University of Southern Denmark, Odense, Denmark; 2AXDEV Group Inc., Canada; 3Università degli Studi di Milano, Fondazione IRCCS Ca’ Granda Ospedale Maggiore Policlinico, Milan, Italy; 4AXDEV Group Inc.; 5EASL, Geneva, Switzerland; 6Mayo Clinic, Rochester, MN, United States; 7Barcelona Institute for Global Health (ISGlobal), Hospital Clinic, University of Barcelona, Barcelona, Spain; 8Cedars Sinai Medical Center, Los Angeles, CA, United States; 9Northwestern University Feinberg School of Medicine, Chicago, IL, United States; 10Charité Universitätsmedizin Berlin, Dept. of Hepatology and Gastroenterology, Berlin, Germany; 11UCL Institute for Liver and Digestive Health, Royal Free Hospital and UCL, London, United Kingdom

Email: lazurep@axdevgroup.com

Background and aims: The use of non-invasive tests (NITs) in the field of non-alcoholic fatty liver disease (NAFLD), non-alcoholic steatohepatitis (NASH), and advanced fibrosis has the potential to improve patient care by simplifying the diagnostic process, providing comprehensive data, and reducing the need for biopsies. We assessed the challenges to implementation of NITs in Germany, Italy, the United Kingdom, and the United States.

Method: We conducted a two-phase qualitative assessment consisting of interviews (n = 29) followed by an expert workgroup discussion (n = 8). Interviews allowed for exploration of challenges with diabetologists, hepatologists, primary care providers (PCPs), patient advocates, clinical/basic researchers, and healthcare administrators/payers. The expert working group discussion included internationally recognized clinicians and researchers in NAFLD and liver fibrosis from the four selected countries. They were asked to review, validate, and expand on the identified challenges and collaboratively discuss potential solutions. Transcripts from both phases were analyzed thematically.

Results: The main challenges related to the implementation of NITs are shown in Figure 1. First, we identified a lack of awareness about NITs and the importance of early detection of NAFLD, NASH, and advanced fibrosis among PCPs and diabetologists. Second, respondents described a need for NITs with more specificity and for their automation to build effective and efficient referral pathways. Some
first phase participants reported that, in the absence of available therapeutic agents, there was no need for novel diagnostic tools. In the opinion of experts, more effort should be made to demonstrate the impact of early diagnosis through NITs. This would help in enhancing patient motivation for improved metabolic health, slowing or halting disease progression and establishing surveillance for the timely detection or prevention of liver related complications. Liver disease was reported to be of low priority among non-hepatologists. This challenge is unlikely to change unless the cost-effectiveness of the more costly NITs and their impact on patient outcomes can be demonstrated.

**Conclusion:** The results of this qualitative study should inform the development of awareness campaigns and targeted educational interventions focused on diagnosis and risk stratification with NITs. This will facilitate early diagnosis and care and help to raise NAFLD as a public health issue.

**FRI085**

**Evaluation of the performance of a novel digital pathology method for the continuous quantification of steatosis, ballooning and inflammation in liver biopsies and its correlation with NASH-CRN scores in patients with NASH**

Louise Petitjean1, Li Chen1,2, Aras Matti3, Mojgan Hosseini4, Michael Goedken2, Cynthia Behling4, Arun Sanyal5, Mathieu Petitjean1. 1PharmaNest, Princeton, United States; 2PharmaNest Inc, Princeton, United States; 3University of California San Francisco, San Francisco, United States; 4University of California San Diego, La Jolla, United States; 5Rutgers University, New Brunswick, United States; 6Virginia Commonwealth University, Richmond, United States

Email: mathieu.petitjean@pharmanest.com

**Background and aims:** We have previously shown that the Phenotypic Fibrosis Composite Score calculated by the FibroNest Quantitative Image analysis and AI methods correlate with the NASH-CRN histological fibrosis stages and steatosis grades established from collagen-stained histology slides. Here, we report the performance of the FibroNest method to quantify Ballooning, Inflammation and Steatosis from digital images of H&E human liver biopsy sections.

**Method:** This retrospective study comprised a cohort of 87 patients with NASH diagnosed by histologic assessment of liver biopsy according to the NASH-CRN criteria with Lobular Inflammation grades of 0 (N = 7), 1 (68), and 2 (12), hepatocyte ballooning grades of 0 (N = 31), 1 (43) and 2 (13), and steatosis grades of 0 (N = 2), 1 (40), 2 (30) and 3 (14). Formalin-fixed, paraffin embedded biopsy sections were H&E stained and imaged with an Opero CS2 scanner at 20X in white light. Quantitative image analysis was performed by FibroNest™ to extract individual features of inflammation (stained nuclei) and tissue texture quantitative layers from the calibrated and normalized images. A subset of 21 representative images was used to develop a machine learning (ML) predictive model using 2.3 K annotations for lobular inflammation, 5.62 K for portal and periporal inflammation, 1.41 for “false” lobular inflammation such as isolated ducts or microscopic necrosis, 1.08 for ballooning and 787 for balloon mimics made by 4 hepatopathologists familiar with the NAS scoring system. The predictive ML model established topographical probability maps for lobular, total inflammation, and hepatocellular ballooning. Confidence thresholds are defined to identify histological features of interest, which are then quantified by several continuous and normalized parameters (biopsy area ration, density count, and 200XFOV normalized count).

**Results:** The Lobular Inflammation composite score exhibits moderate correlation with the histological grades. Significant disagreement in the assessment of grade 1 lobular inflammation is driven by “confusion” with portal inflammatory features which degrades the specificity between grades 1 and 2 (p = 0.187). The mean values of the Ballooning Density correlate with the histological assessment, but p-values between grades are poor. The mediocre performance of the ML model is driven by the lack of agreement in the annotations provided by pathologists. The steatosis proportion area is in fair agreement with steatosis grades. Disagreement is driven by the fact that the NASH-CRN criteria is based on percent hepatocytes with fat rather than fat area ratio (in full tissue area).

**Conclusion:** As reported by other teams, liver biopsy Digital Pathology methods based on supervised ML and annotation provided by pathologists (H&E stains, Inflammation, Ballooning) result in continuous quantification methods of moderate performance.

**FRI086**

**Can combination of M2BPGi and APRI help endocrinologists refer patients with advanced hepatic fibrosis to hepatologists?**

Mi Mi Kim1, Bo-Kyeong Kang1, Chul-min Lee1, Huiyul Park2, Hyo Young Lee3, Hyunwoo Oh1, Sang Bong Ahn4, Dae Won Jun5, Eileen Yoon6, Joo Hyun Sohn6. 1Hanyang University College of Medicine, Department of Radiology, Seoul, Korea, Rep. of South; 2Uijeongbu Eulji Medical Center, Department of Family Medicine, Gyeonggi-do, Korea, Rep. of South; 3Uijeongbu Eulji Medical Center, Department of Medicine, Gyeonggi-do, Korea, Rep. of South; 4Nowon Eulji Medical Center, Eulji University School of Medicine, Department of Medicine, Seoul, Korea, Rep. of South; 5Hanyang University College of Medicine, Department of Medicine, Seoul, Korea, Rep. of South; 6Hanyang University Guri Hospital, Hanyang University College of Medicine, Department of Medicine, Gyeonggi-do, Korea, Rep. of South

Email: mmbogri@naver.com

**Background and aims:** Although the non-invasive tests (NITs, ex. FIB-4, NAFLD fibrosis score (NFS), AST to platelet ratio index (APRI)) are widely used to diagnose advanced hepatic fibrosis, there is a considerable intermediate zone and diagnostic performance decreased in diabetes subjects. The purpose of this study is to figure out whether combination of M2BPGi with various NITs can help endocrinologist screening for advanced hepatic fibrosis in clinic.

**Method:** A total of 1,129 subjects visiting endocrinology clinic of tertiary hospital and performed M2BPGi were included (mean age: 53.7 ± 14.8 years). NFS, FIB-4, and APRI were calculated for all subjects. Advanced fibrosis was defined by transient elastography (TE≥8.0 kPa). Sensitivity analysis was also performed.

**Results:** This study included 426 (37.7%) were diabetes and 703 (62.3%) were non-diabetes who visited the endocrinology clinic of tertiary hospital and performed M2BPGi were included (mean age: 53.7 ± 14.8 years). NFS, FIB-4, and APRI were calculated for all subjects. Advanced fibrosis was defined by transient elastography (TE≥8.0 kPa). Sensitivity analysis was also performed.

**Conclusion:** As reported by other teams, liver biopsy Digital Pathology methods based on supervised ML and annotation provided by pathologists (H&E stains, Inflammation, Ballooning) result in continuous quantification methods of moderate performance.
POSTER PRESENTATIONS

Results: NAFLD was diagnosed in 92 of 576 (16%) adolescents (52% male). Adolescents with NAFLD had higher body mass index (BMI), waist circumference, suprailiac skinfold thickness, alanine aminotransferase (ALT), gamma glutamyl transpeptidase, triglycerides, total and low density lipoprotein cholesterol, leptin and Homeostasis Model Assessment for Insulin Resistance (HOMA-IR), but lower high density lipoprotein cholesterol and adiponectin levels compared with those without NAFLD (p < 0.05 for all). Birth weight, gestational age, IUGR, SGA and LGA were not associated with NAFLD. Using multivariable logistic regression analysis, low-stable HC trajectory group 1 (OR 3.54; 95% CI, 1.21–10.35, p = 0.02), suprailiac skinfold thickness (OR 1.09, 95% CI 1.05–1.13, p < 0.001), ALT (OR 1.03, 95% CI 1.01–1.06, p = 0.02) and leptin (OR 1.03, 95% 1.02–1.05, p = 0.001) were associated with NAFLD.

Conclusion: The low–stable HC trajectory attributed with a persisting small HC through pregnancy, but not birth characteristics, was associated with increased risk of subsequent NAFLD in adolescents. The association of a low foetal HC trajectory with NAFLD in adolescence supports the Developmental Origins of Health and Disease (DOHaD) hypothesis linking early life events with subsequent disease.

FR1088
Liver stiffness assessed by transient elastography predicts clinical events in patients with T2DM and NAFLD
Jesús Rivera1, Monica Pons1, Alejandra Planas2, Raúl Simo Canonge2, Jordi Bañeras3, Ignacio Ferreira4, Joan Genesca1, Juan Manuel Pericás1, 1Vall d’Hebron Hospital Universitari, Liver Unit, Barcelona, Spain; 2Vall d’Hebron Hospital Universitari, Diabetes and Metabolism Research Unit, Spain; 3Vall d’Hebron Hospital Universitari, Cardiology Department, Spain
Email: jesusriveraest@gmail.com

Background and aims: Non-alcoholic fatty liver disease (NAFLD) and type 2 diabetes (T2DM) are intimately related entities. T2DM is a major predictor of cardiovascular events (CVE) in NAFLD patients, whereas the role of NAFLD on CVE in T2DM as well as the impact of T2DM on liver-related events (LRE) in NAFLD remain poorly known. The aim of this study was to evaluate the role of NAFLD on the onset of clinical outcomes among T2DM patients.

Method: Prospective cohort with case-control analysis comprising 200 T2DM subjects with no history of CV disease (CVD) and 60 non-diabetic subjects matched by age with available transient elastography (TE) data. Patients were selected from the Outpatient Diabetes Clinic of Vall d’Hebron Hospital and the Primary Healthcare centres within its catchment area (North Barcelona). Overall clinical events (CE) were composed by CVE (coronary, cerebrovascular or peripheral arteriopathy), LRE (liver decompensation or hepatocellular carcinoma) and all-cause mortality. NAFLD was defined as Controlled Attenuation Parameter (CAP) ≥275 dB/m and/or Fatty liver index (FLI) ≥60 after exclusion of the other liver diseases and alcohol consumption over 30 gr/day in males and 20 gr/day in females. A value of coronary arterial calcium score (CACs) ≥400 Agatston units (AU) was considered indicative of high risk of CVD. Cox regression analysis to predict CE was performed.

Results: Overall, 34 (18.2%) T2DM patients presented any CE vs 4 (7.0%) controls (p 0.042) during a median follow-up of 5.6 years. Among patients with T2DM and NAFLD (n = 134), 21 (28.4%) CVE were reported, being coronary events the most frequent outcome (11/134; 8.2%). One subject (0.7%) presented LRE and 8 (6%) patients died, 25% of which due to CVD and 37.5% each for malignancy and infectious diseases. T2DM-NAFLD patients with CE showed higher rates of diabetes complications (42.9% vs 22.1%; p 0.04 and 61.9% vs 34.2%; p 0.017 for diabetic retinopathy and nephropathy, respectively), high-risk CVD (CACs ≥400 52.6% vs 19.3%, p 0.002) and higher median liver stiffness (6.7 vs 5.4 kPa, p 0.007) than those without CE. No differences were found between groups in terms of T2DM control (fasting glucose; HbA1c) or metabolic syndrome determinants rates

Figure: Head Circumference trajectory groups: 1 Low-stable, 2 Average-falling, 3 Low-rising, 4 Average-stable, 5 High-stable. SDS-standard deviation scores, Dotted lines represent 95% confidence intervals, Percentages represent individual group membership.
(high blood pressure or obesity). In Cox analysis, development of clinical events among T2DM-NAFLD patients was associated with a higher liver stiffness (HR = 1.05; 95%CI 1.01–1.09, p = 0.003) and male gender HR = 4.02; 95%CI 1.29–12.50, p = 0.016). No statistical association was found for diabetes complications or CACs ≥400.

**Table 1. Cox regression analysis**

<table>
<thead>
<tr>
<th></th>
<th>Hazard Ratio</th>
<th>95% CI</th>
<th>p</th>
</tr>
</thead>
<tbody>
<tr>
<td>Liver stiffness</td>
<td>1.05</td>
<td>1.01–1.09</td>
<td>0.003</td>
</tr>
<tr>
<td>Male gender</td>
<td>4.02</td>
<td>1.29–12.50</td>
<td>0.016</td>
</tr>
<tr>
<td>Age</td>
<td>1.08</td>
<td>0.99–1.19</td>
<td>0.07</td>
</tr>
<tr>
<td>CAC ≥ 400 AU</td>
<td>0.42</td>
<td>0.14–1.19</td>
<td>0.10</td>
</tr>
<tr>
<td>Diabetic nephropathy</td>
<td>0.41</td>
<td>0.15–1.11</td>
<td>0.82</td>
</tr>
<tr>
<td>Diabetic retinopathy</td>
<td>0.46</td>
<td>0.17–1.24</td>
<td>0.12</td>
</tr>
</tbody>
</table>

**Conclusion:** Our results suggest that severity of NAFLD is associated with clinical events in patients with T2DM independently of CV disease or T2DM complications. TE might help stratifying T2DM patients with NAFLD at higher risk of developing clinical events and therefore shall be recommended in all T2DM patients.

**FRI089**

**Repeated noninvasive liver biopsy surrogate LIVERFAS$t$ correlates with BMI and liver enzyme improvements**

Marie Decraecker1, Hiriart Jean-Baptiste1, Marie Irles-Depe1, Faiza Chermak1, Juliette Foucher1, Victor de Lédinghen1, 1CHU BORDEAUX, Pessac, France

Email: marie.decr aecker@gmail.com

**Background and aims:** MAFLD-related morbi-mortality is increasing worldwide due to epidemics of obesity and type 2 diabetes (T2D). LIVERFAS$t$ (LF, Fibronostics, US) is a new point-of-care proprietary technology to assess quantitatively (score from 0.00 to 1.00) liver fibrosis (LF-Fib) in MAFLD pts, with prognostic value for liver-related events and overall mortality (Hepatology Suppl.2021).

To assess repeated LF-Fib performance for liver fibrosis regression rate (LF-R) reflected with significant improvement in clinical endpoints, body mass index BMI≥10% and liver enzymes ALT≥50% from baseline.

**Method:** Pts with repeated LF-Fib were prospectively included. Significant improvements in clinical endpoints were: BMI decrease of ≥10% and ALT decrease ≥50% from baseline. Half fibrosis stage improvement was considered with each 0.15 of LF-Fib score. Statistics were descriptive and FPR time dependent using hazard ratios HR (95%CI).

**Results:** 500 MAFLD patients from a tertiary center were pre-included with LF-Fib at baseline and 401 were included with at least one repeated LF-Fib during follow up; 87 pts had 7 repeated LF-Fib during 9.9 years follow up. 44.3% were female, median (range) age 56 (21–77) yrs, distribution of fibrosis 45%F0, 29%F1, 6%F2, 12%F3 and 8% F4, respectively. 13/401 (3.24%) regressed liver fibrosis as per LF-Fib ≥0.15 from baseline score. 109 (27.2%) patients had an ALT regression of ≥50% from baseline during FU. 75 (18.7%) experienced an improvement in BMI ≥10% during FU. Median LF-FIB was 0.27 and median (range) FU between baseline and last repeated LF-Fib was 3.57 yrs (3–9.9).

Occurrence of half-stage liver fibrosis improvement as per LF-Fib was more probable among those that achieved ALT regression of ≥50% from baseline: Cox Mantel Hazard Ratios [HR (95%CI)] 3.47 (1.08–11.19) versus 0.29 (0.09–0.93) in those without ≥50% ALT decrease (logrank probability level 0.02) (Figure 1).

HR (95%CI) for LF-Fib half-stage improvement (0.15 score) in the group with BMI improvement of ≥10% was 1.78 (0.38–8.39) vs 0.56 (0.12–2.64) in the group that not achieved a BMI improvement of ≥10% (logrank probability level = 0.37).

**Conclusion:** LF-Fib improvement of half-stage was significantly more prevalent in patients that achieved ALT decrease ≥50% from baseline and a trend was observed in patients that had ≥10% decrease in BMI from baseline. LF-Fib correlates with clinical endpoints and, therefore can be used for long-term monitoring of MAFLD patients.

**FRI090**

**Increased liver stiffness on vibration controlled transient elastography (Fibroscan) as a predictor of all-cause mortality in people with fatty liver disease**

Michael Braude1,2, Ammar Majeed 2,3, Stuart Roberts2,3, Stephen Bloom2,4, Paul Gow5,6, Anouk Dev1,2, William Sievert1,2, William Kemp2,3, 1Monash Health–Clayton Hospital Main Entrance, Gastroenterology and Hepatology, Clayton, Australia; 2Monash University Clayton Campus, Clayton, Australia; 3The Alfred, Melbourne, Australia; 4Eastern Health, Box Hill, Australia; 5Austin Hospital, Heidelberg, Australia; 6Melbourne University-Swanston St, Parkville, Australia

Email: mrbrau de@gmail.com

**Background and aims:** Fatty liver disease, which is often asymptomatic and progressive, is a multi-system, condition which is becoming the leading cause of liver-related morbidity, mortality, and liver transplant. Ascertaining liver disease severity is therefore important to guide management and prognosis. Several studies have shown a correlation between mortality and progressive liver fibrosis on both histopathology and blood-based fibrosis predictive tests. We aimed to assess vibration-controlled transient elastography (VCTE) as a predictor of mortality.

**Method:** VCTE studies for a primary indication of non-alcoholic fatty liver disease (NAFLD) were collated from consecutive outpatients across 4 Australian tertiary referral centres between July 2008 and April 2019. Patients with VCTE data were linked to Victorian Death Index (VDI) and the Victorian Admitted Electronic Dataset (VAED) via the Centre for Victorian Data Linkage (CVDL). Comorbidity data was derived from International Classification of Diseases 10th Revision (ICD-10) coding within the VAED. Cause of death (COD) was analysed using descriptive statistics. Liver stiffness measurement (LSM, kPa) was analysed as a predictor of all-cause mortality using Cox-proportional regression analysis with multivariable adjustment for age, gender, and comorbidities, including the Charlson Comorbidity Index (CCI).

**Results:** A total of 7079 individual VCTE records were identified, 6341 of which were matched via data linkage, and 5857 were represented in the VAED. The median follow-up period from VCTE to death/ censorship was 3.6 (IQR 2.1–5.5, range 0.2–11.0) years. Mean age at VCTE across the 7079-patient cohort was 55±13.6 years, median LSM was 6.1 kPa (IQR 4.7–9.3) and mean controlled attenuation
Background and aims: Liver fibrosis is the only histological feature predictive of nonalcoholic steatohepatitis (NASH) progression to cirrhosis and liver-related complications. Currently, the FDA requires the inclusion of patients with biopsy-proven NASH-related fibrosis for therapeutic trials. We aimed to assess the accuracy of simple and available magnetic resonance imaging (MRI) for the detection of NASH with fibrosis.

Method: We performed a cross-sectional international study that included subjects with NAFLD from three countries evaluated between 2017 and 2021. The training cohort included 138 consecutive patients with contemporaneous MRI and biopsy-proven NAFLD from Spain and Portugal and a validation cohort of 44 patients from USA. Patients with Fibrosis-4 index >4.63 and NAFLD fibrosis score >1.57 were excluded due to high pretest probability of cirrhosis (98% specificity). Disease severity was estimated using the histology NAFLD activity score (NAS), defining NASH as NAS≥4 and significant fibrosis as F≥2. Performance parameters of sensitivity, specificity, positive predictive value (PPV) and negative predictive value (NPV) were calculated.

Results: NASH was diagnosed on liver biopsy in 53% of the European and 59% of the US cohorts, while significant fibrosis was found in 50% and 82% patients in the two cohorts, respectively. In the training cohort, MRI-Proton Density Fat Fraction (MRI-PDFF; OR: 1.57; 95%CI 1.31–1.86) and MRI-determined waist circumference (WC; OR: 1.004; 95%CI 1.001–1.007) were imaging biomarkers independently associated with NASH (adjusted for sex, age, height, and liver fibrosis). A median MRI-PDFF >11% combined with a WC >96 cm in women and >107 cm in men, showed 86% sensitivity, 88% specificity, 89% PPV and 84% NPV for the diagnosis of NASH. Among patients that were above these cut-offs, 90% had fibrosis and 63% demonstrated significant fibrosis. In the validation cohort, the combined image biomarkers had 82% sensitivity, 83% specificity, 86% PPV, and 79% NPV for the diagnosis of NASH. All selected patients had fibrosis, including 81% with significant fibrosis.

Conclusion: An MRI-based composite biomarker of PDFF+WC identified patients with NASH and liver fibrosis with high specificity and PPV. This finding offers clinical utility in the management of NAFLD and patient selection for NASH clinical trials.
Patients in our cohort were classified according to the cut-off values obtained from another Meta-analysis of individual patient data (2.61 kpa for F1, 2.97 kpa for F2, 3.62 kpa for F3, 4.69 kpa for F4). We also made an analysis to identify those variables that could underestimate (MRE result lower than biopsy result), overestimate (MRE result higher than biopsy results) or achieve concordance (MRE result consistent with biopsy result). ANOVA, Kruskal-Wallis test were used for continuous variables and chi-square test or Fisher’s exact test for categorical variables. ROC (receiver operator characteristic) curves for diagnostic accuracy were evaluated, and Spearman’s correlation was performed to compare histologic liver fibrosis with MRE elastography and Fibroscan.

Results: The area under the ROC curve (AUROC) of MRE for ≥F2 was 0.886 vs Fibroscan AUROC 0.842 (p = 0.48). MRE AUROC for F3 was 0.887 vs Fibroscan AUROC 0.820 (p = 0.27). Spearman’s correlation coefficient of liver fibrosis and Fibroscan was 0.651 (p < 0.0001) whereas correlation coefficient of liver fibrosis and MRE elastography was 0.704 (p < 0.0001).

Variables that could overestimate MRE accuracy were AST (p = 0.0005), ALT (p = 0.0032) and inflammation activity (p = 0.008); BMI, weight, or DM did not affect diagnostic accuracy (p = 0.732, p = 0.816, p = 0.521, respectively).

Conclusion: MRE is an effective, non-invasive method for detecting/staging hepatic fibrosis in NAFLD. Although we did not reach statistical significance, MRE showed a higher diagnostic accuracy than transient elastography in discriminating significant and advanced fibrosis. The liver inflammation grade may affect the diagnostic accuracy of MRE in staging hepatic fibrosis in NAFLD patients, but BMI or DM did not.

FR1093 Aldafermin quantitatively improves inflammation in a 24-week clinical trial in patients with nonalcoholic steatohepatitis

Tian Lan1, Luong Ruiz2, Wenhen Liu1, Amir Ashique1, Harry Chen1, Jing Zha1, Alex DePaoli1, Igor Mikaelian1, Cynthia Guy3, Eugenia Henry4, Corinne Foo-Atkins5, William Chang6, Hsiao Lieu6.

1NGM Biopharmaceuticals Inc., Translational Science, South San Francisco, United States; 2Adagene Inc., Clinical Development, San Diego, United States; 3Duke University Medical Center, Pathology, Durham, United States; 4NGM Biopharmaceuticals Inc., Clinical Research, South San Francisco, United States

Email: tlan@ngmbio.com

Background and aims: Pathologist-based scores are the standard for assessing efficacy in nonalcoholic steatohepatitis (NASH) clinical trials, but are limited by variability in interpretation and insensitivity to small changes, especially for lobular inflammation. Lobular inflammation scores reflect the number of inflammatory foci per microscopic field, which are in part contributed by macrophages. Samples from a Phase 2 clinical trial with aldafermin (NGM282), an engineered fibroblast growth factor 19 analogue, were used to develop and test novel image analysis readouts for liver inflammation based on CD68, a macrophage lysosomal marker.

Method: Liver biopsies were from a 24-week clinical trial with aldafermin: NCT02443116 (Cohort 4, placebo (PBO), n = 18; 1-mg NGM282, n = 47). Biopsies and blood for non-invasive biomarkers were collected at baseline and at the end of treatment. A 6-plex immunohistochemistry (IHC) panel that included CD68 was developed to enable two image analysis endpoints: (1) "Type 1 macrophages" (M1 s) based on CD68 expression and cell shape; and (2) "Macrophage foci" to account for focal accumulations of M1 s.

Results: NGM282 decreased lobular inflammation measured by the NASH Clinical Research Network (CRN) criteria (p = 0.02) and the inflammation measured by the IHC macrophage foci (PBO vs. 1-mg, −0.39% vs. −1.41%, p = 0.04). The decrease of M1 s did not reach statistical significance in this relatively small study (p = 0.18). Inflammation reads by CRN criteria and by image analysis did not correlate robustly with the circulating biomarkers, including AST and ALT (r-squared ≈ 0.2).

Conclusion: Quantified IHC readouts can identify histological changes in an automated manner. These histological endpoints do not correlate well with current circulating biomarkers.
FRIO94
Clinical and economic evaluation of community-based preventative screening strategies for non-alcoholic fatty liver disease in people with Type-2 diabetes mellitus
Roberta Forlano1, Tijana Stanic2, Sahan Jayawardana2, Benjamin H. Mulish3, Michael Yee1, Mark Thursz1, Elias Mossialos2,3, Pinelopi Manousou1, 1Department of Metabolism, Digestion and Reproduction, Imperial college London, London, UK, United Kingdom; 2Department of Health Policy, London School of Economics and Political Science, London, UK, United Kingdom; 3Centre for Health Policy, The Institute of Global Health Innovation, Imperial College London, London, UK
Email: r.forlano@imperial.ac.uk

Background and aims: The exact prevalence of Non Alcoholic Fatty Liver Disease (NAFLD) in type 2 diabetes (T2DM) is unknown. We aimed to determine the prevalence and develop a risk stratification and cost analysis for a screening policy in T2DM in primary care. We compared the cost-effectiveness of 5 screening strategies vs standard of care (SoC).

Method: Consecutive T2DM patients underwent blood tests, ultrasound (US) and liver stiffness measurement (LSM). Significant fibrosis and advanced fibrosis were defined by LSM≥8.1 kPa and ≥12.1 kPa. Diagnosis of cirrhosis was clinical, histological or radiological. Markov model included 3 health states: NMD-: no NAFLD; NMD+: NAFLD with LSM<8.1 kPa; significant liver disease (SLD: LSM≥8.1 kPa); compensated cirrhosis (CC) (Fig 1).

The probability of progressing was assumed reduced for those at risk of NAFLD (NMD+) or diagnosed with SLD (SLD+) compared to those at lower risk (NMD−), or with undiagnosed disease (SLD−). The effect of earlier identification, diagnosis and treatment was based on the reduction of transition probabilities for NMD+/SLD+ vs NMD−/SLD−. The base-case analysis was conducted over a lifetime horizon and generated the cost per quality-adjusted life year (QALY) gained. We calculated average cost-effectiveness and the incremental cost-effectiveness ratio (ICER) vs SoC. Life expectancy, lifetime costs, and number of correct diagnoses were estimated. A cost-effectiveness threshold was set at £20,000/QALY gained, as per NICE.

Results: Of 300 patients enrolled, 287 were included; 13 withdrew: 184 (73%) had NAFLD, 28 (10%) other causes of liver disease (alcohol, HBV) and 75 (26%) no liver disease. Significant fibrosis and advanced fibrosis due to NAFLD were 17% (50/287) and 11% (31/287) respectively. The prevalence of cirrhosis was 3% (8/287). Based on predictors of significant fibrosis, the BIMAST score (BMI and AST) performed better for diagnosing significant (AUROC 0.81, p < 0.0001) and advanced fibrosis (AUROC 0.84, p < 0.0001) (Fig 2). Five screening strategies were compared: 1) US + liver function tests (LFTs), 2) FIB-4, 3) NAFLD fibrosis score, 4) BIMAST score, 5) fibroscan. In a Markov model, NAFLD screening improved the rate of correct diagnoses by 8–15%, with an exception of the NAFLD fibrosis score strategy, which led to a 2% decrease in correct diagnoses. All screening strategies were associated with QALY gains, ranging from 121–148 years, with fibroscan resulting in the most substantial gains. In all screening strategies, ICER compared to SoC was between £1,970 (BIMAST score) and £2,480 (fibroscan) per QALY gained (Tab 1).

Conclusion: Screening for NAFLD in T2DM improved diagnostic outcomes and was cost-effective in all evaluated scenarios within NICE’s cost-effectiveness threshold. Fibroscan followed by BIMAST was the screening strategy associated with the greatest clinical gains.

FRIO95
Confounding factors in diagnostic performance of magnetic resonance elastography for staging liver fibrosis in patients with non-alcoholic fatty liver disease: an individual patient data meta-analysis
JiaXu Liang2,3, Javier Ampuero1,2, Kento Imajo4, Mazen Noureddin5, Jaideep Behari6, Dae Ho Lee7, Richard L. Ehman8, Juan R. Lalalle9, Javier Castell10, Ferenc Mozes11,12, Quentin Ansee13, Steven Harrison14, Manuel Romero Gomez1,2,3, 1Virgen del Rocio University Hospital, Digestive Diseases Unit, Seville, Spain; 2Institute of Biomedicine of Seville (HUVR/CSIC/US), Seville, Spain, University of Seville, Seville, Spain; 3People’s Hospital of Zhengzhou, Radiology, Zhengzhou, China; 4Yokohama City University Graduate School of Medicine, Department of Gastroenterology, Yokohama, Japan; 5 Cedars-Sinai Medical Center, Fatty Liver Program, Karsh Division of Digestive and Liver Diseases, Comprehensive Transplant Program, Los Angeles, CA, United States; 6University of Pittsburgh Medical Center, Department of Medicine, Division of Gastroenterology, Hepatology and Nutrition, Center for Liver Diseases, Pittsburgh, United States; 7Gachon University Gil Medical Center, Gachon University College of Medicine, Departments of Internal Medicine, Incheon, Korea, Rep. of South; 8 Mayo Clinic College of Medicine, Department of Diagnostic Radiology, Rochester, United States; 9University of Seville, Biostatistics Unit, Department of Preventive Medicine and Public Health, Seville, Spain; 10Virgen del Rocio University Hospital, Radiology, Seville, Spain; 11Radcliffe Department of Medicine, University of Oxford, Oxford Centre for Clinical Magnetic Resonance Research, Division of Cardiovascular Medicine, United Kingdom; 12University of Oxford, Translational Gastroenterology Unit, United Kingdom; 13Faculty of Medical Sciences, Newcastle University, Translational and Clinical Research Institute, Newcastle upon Tyne, United Kingdom
Email: mromerogomez@us.es

Background and aims: We conducted an individual patient data meta-analysis to assess potential confounding factors influencing diagnostic accuracy of magnetic resonance elastography in staging liver fibrosis and to determine specific diagnostic cutoff values in patients with non-alcoholic fatty liver disease.

Method: A review of the literature identified studies containing MRE data for grading liver fibrosis in NAFLD patients with liver biopsy as reference standards. The original database was obtained in Excel form the corresponding authors. Pooled diagnostic cutoff value for the
various fibrosis stages were determined in a two-stage meta-analysis as the primary outcome. Multilevel modelling methods were used to analyses potential confounding factors influencing diagnostic accuracy of MRE in staging liver fibrosis.

**Results:** 6 independent cohorts comprising 483 patients were included in the meta-analysis, yielding liver stiffness cutoffs of 2.77 kPa (area under the receiver operating characteristic curve 0.86 [0.83–0.89]) for any fibrosis (≥F1), 3.09 kPa (0.90 [0.87–0.92]) for significant fibrosis (≥F2), 3.41 kPa (0.93 [0.91–0.96]) for advanced fibrosis (≥F3) and 4.10 kPa (0.91 [0.88–0.93]) for cirrhosis (F4). Notably, cases with mild fibrosis stage (F0–1) with moderate to severe inflammatory activity (A3–4) had exhibited greater stiffness than matched cases of the same fibrosis stage with none to mild inflammation activity. Similarly, higher liver inflammatory activity was an independent variable predicting reduced diagnostic accuracy of MRE (OR [95% CI] = 0.404 [0.220–0.740], p < 0.01), whereas steatosis degree, BMI, ALT, and AST did not affect the diagnostic accuracy of MRE (Table).

Table: GLMM (generalized linear mixed model) explore variables associated with prediction failure

<table>
<thead>
<tr>
<th>Variable</th>
<th>Estimate (SE)</th>
<th>Z-value</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>BMI</td>
<td>0.007 (0.002)</td>
<td>0.37</td>
<td>0.71</td>
</tr>
<tr>
<td>ALT</td>
<td>0.203 (0.075)</td>
<td>0.27</td>
<td>0.79</td>
</tr>
<tr>
<td>AST</td>
<td>0.003 (0.002)</td>
<td>0.41</td>
<td>0.68</td>
</tr>
<tr>
<td>Age</td>
<td>0.002 (0.002)</td>
<td>0.40</td>
<td>0.68</td>
</tr>
</tbody>
</table>

**Conclusion:** MRE has excellent diagnostic performance for determining significant, advanced fibrosis and cirrhosis in patients with NAFLD. Accuracy was not influenced by anthropometric, biochemical, or steatosis degree, but could be influenced by high inflammatory activity.

**FRI096**
Is it possible to identify nonalcoholic steatohepatitis and the associated degree of fibrosis by noninvasive methods in patients with MAFLD?

José López González1, Marta Casado1, Teresa María Jordan Madrid1, Almudena Porcel Martín1, José Luis Vega Sáenz1, Torrecárdenas University Hospital, Almería, Spain

Email: pepe_1993_17@hotmail.com

**Background and aims:** Non-alcoholic steatohepatitis (NASH) is a chronic and progressive form of metabolic associated fatty liver disease (MAFLD). NASH diagnosis requires histological evaluation after liver biopsy. Therefore, it is necessary to develop non-invasive diagnostic alternatives to identify NASH and the associated degree of fibrosis. The aim of this study is to analyze the presence of NASH and NASH with advanced fibrosis (AF) in patients with MAFLD and increased liver stiffness (LS), and to identify those associated factors with AF.

**Method:** We included a prospective cohort of all patients with clinical and ultrasound diagnosis of MAFLD, treated in our department since January 2019, with LS >8 kPa, measured by transient elastography. Presence of NASH and the degree of fibrosis, were evaluated after histological analysis of a liver biopsy. Epidemiological, clinical, analytical, elastographic and histological variables were collected. Patients were classified according to the presence of AF in the liver specimen (grade 3–4) or mild fibrosis (MF) (grade 1–2 or absence).

**Results:** Our study included 40 patients, whose characteristics are shown in Table 1. Histological analysis demonstrated NASH in 36 patients (90%), 14 patients with AF (35%), and two of them with F4 grade fibrosis. GGT and LS were significantly higher in patients with NASH and AF vs patients with MF (161.86 ± 115 vs 90.6 ± 56, p = 0.04, 15.9 ± 8.9 vs 10 ± 1.48, p = 0.02). 42% of patients with MF had APRI >0.5 and 57% had APRI between 0.5–1. No patient with MF had APRI >0.5. Likewise, 50% of patients with AF had APRI >0.5, and 50% of them, had APRI >1.5 (p = 0.026). All patients with APRI >1 and LS >12.1 kPa had AF, and only 29% of patients with AF did not meet both criteria (p = 0.037). In addition, all patients with APRI>1.5 and GGT>115.6 IU/ml had AF, compared to 29% of patients with AF who did not meet both analytical criteria (p = 0.037).

**VARIABLE** | **RESULTS (n = 40)**
<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>AGE</td>
<td>59.78 ± 8.5</td>
</tr>
<tr>
<td>SEX (%)</td>
<td>MALE 20 (50%)</td>
</tr>
<tr>
<td></td>
<td>FEMALE 20 (50%)</td>
</tr>
<tr>
<td>AHT (%)</td>
<td>30 (75%)</td>
</tr>
<tr>
<td>DIABETES (%)</td>
<td>27 (67.5%)</td>
</tr>
<tr>
<td>OBESITY (%)</td>
<td>40 (100%)</td>
</tr>
<tr>
<td>AST</td>
<td>47.4 ± 28.2 U/L</td>
</tr>
<tr>
<td>ALT</td>
<td>56.1 ± 33.5 U/L</td>
</tr>
<tr>
<td>GGT</td>
<td>115.6 ± 88 U/L</td>
</tr>
<tr>
<td>HEMOGLOBIN A1c</td>
<td>6.3 ± 1.27</td>
</tr>
<tr>
<td>CHOLESTEROL</td>
<td>202 ± 34.6 mg/dl</td>
</tr>
<tr>
<td>TRIGLYCERIDES</td>
<td>190.4 ± 95 mg/dl</td>
</tr>
<tr>
<td>ADVANCED FIBROSIS (%)</td>
<td>14 (35%)</td>
</tr>
<tr>
<td>LIVER STIFFNESS (kPa)</td>
<td>12.1 ± 5.8 kPa</td>
</tr>
<tr>
<td>CAP (n = 23)</td>
<td>334.4 ± 32.4</td>
</tr>
<tr>
<td>FIB-4 (%)</td>
<td>&lt;1.33 13 (32.5%)</td>
</tr>
<tr>
<td></td>
<td>1.33–2.66 22 (55%)</td>
</tr>
<tr>
<td></td>
<td>&gt;2.66 5 (12.5%)</td>
</tr>
<tr>
<td>FIB-4 (%)</td>
<td>1.8 ± 1.04</td>
</tr>
<tr>
<td>APRI (%)</td>
<td>&lt;0.5 18 (45%)</td>
</tr>
<tr>
<td></td>
<td>0.5–1.5 19 (47.5%)</td>
</tr>
<tr>
<td></td>
<td>&gt;1.5 3 (7.5%)</td>
</tr>
<tr>
<td>APRI</td>
<td>0.66 ± 0.49</td>
</tr>
</tbody>
</table>

**Conclusion:** Most patients with MAFLD and RH >8 kPa have NASH, one-third of them have AF. Increased GGT, APRI index, and LS were associated with a higher probability of having NASH with AF. LS and APRI combination or APRI and GGT combination, can identify patients with NASH and FA. Therefore, it seems possible to identify patients with MAFLD and high risk of NASH and NASH with AF with non-invasive methods. Nevertheless, further prospective studies are needed to confirm these preliminary results.

**FRI097**
The potential role of fatigue in identifying patients with NASH and advanced fibrosis who experience disease progression

Zobair Younossi1,2,3, Maria Stepanova1,2,4, Robert Myers5, Reem Al Shabeeb3, Issah Younossi4, Linda Henry1,2,4, Zobair Younossi1,2,3, Maria Stepanova1,2,4, Robert Myers5,1Inova Health System, Medicine Service Line, Falls Church, United States; 2Betty and Gay Beaty Center for Integrated Research, IHS, Falls Church, United States; 3Center for Liver Diseases, Department of Medicine, Falls Church, United States; 4Center for Outcomes Research in Liver Disease, Washington DC, United States; 5Gilead Sciences, Inc., Foster City, United States

Email: zobair.younossi@inova.org

**Background and aims:** Fatigue is common in patients with advanced liver disease. We aimed to investigate the association of fatigue with the risk of progression among patients with NASH and advanced fibrosis.

**Method:** In this post hoc cohort study, enrolled subjects were required to have a liver biopsy consistent with NASH and bridging fibrosis (F3) or compensated cirrhosis (F4), and were followed up for up to two years. Fatigue was quantified using the fatigue domain of the CLDQ-NASH instrument completed by subjects at baseline (score range 1–7, lower score indicates worse fatigue). Cox proportional hazard model was used to determine the relationship between the
baseline fatigue score and the time to liver-related clinical events (progression to histologic cirrhosis for F3, developing hepatic decompensation for F4).

**Results:** There were 1679 advanced NASH patients (N = 802 F3 and 877 patients F4, age 58 ± 9 years, 40% male, 74% type 2 diabetes). During median follow-up of 16 months (IQR 14–18 month, max 26 months), 123 (15%) of F3 patients and 31 (3.5%) F4 patients experienced liver-related clinical events. The mean baseline CLDQ-NASH fatigue score was 4.77 ± 1.36 in F3 and 4.56 ± 1.44 in F4. In both F3 and F4 cohorts, patients with liver-related events in follow-up had higher baseline AST, lower platelet count, and elevated non-invasive test scores for fibrosis (APRI, FIB-4, ELF, Fibrotest, NAFLD Fibrosis Score) in comparison to patients who remained stable in follow-up (all p < 0.01). Their baseline fatigue scores were also significantly lower: 4.47 ± 1.36 in progressed F3 vs. 4.83 ± 1.35 in stable F3 (p = 0.0091); 3.74 ± 1.31 in progressed F4 vs. 4.59 ± 1.43 in stable F4 (p = 0.0011). In multivariate analysis, the association of lower fatigue scores (more fatigue) with the risk of liver-related events was significant: hazard ratio (HR) per 1 fatigue point = 0.84 (0.75–0.93), p = 0.0012, in all patients; HR = 0.85 (0.75–0.96), p = 0.0088, in F3; HR = 0.67 (0.53–0.85), p = 0.0014, in F4. These associations remained significant after adjustment for clinico-demographic confounders: adjusted HR = 0.79 (0.70–0.89), 0.85 (0.74–0.97), and 0.62 (0.48–0.81), respectively (all p < 0.02).

**Conclusion:** Lower baseline fatigue scores were associated with adverse clinical events in patients with advanced NASH. A combination of baseline clinical and fatigue parameters can inform clinicians of which patients with advanced fibrosis due to NASH are at risk of adverse clinical outcomes.

**FRI029**
Novel digital pathology quantitative image analysis and AI method detects the treatment effects of NASH drug candidates with a performance that benchmarks imaging-based measurements

Li Chen1, Elizabeth Brown2, Anne Minnich2, Vipul Baxi2, Dimple Pandya2, Shuyu Du2, Edgar Charles3, Zachary Goodman2, Mathieu Petitjean1, Arun Sanyal4, PharmaNest, Inc, Princeton, United States; 1Bristol Myers Squibb, Princeton, United States; 2Inova Health Systems, Falls Church, United States; 3Virginia Commonwealth University, Richmond, United States

**Background and aims:** Manual histological evaluation of liver biopsy is the gold standard method for fibrosis and steatosis staging in Non-Alcoholic Steatohepatitis (NASH), but it is limited by its inter- and intra-reader variability. Quantitative Digital Pathology image analysis and AI (FibroNest™) as well as quantitative MRI signal analysis methods have the potential to overcome the current limitation of standards. This exploratory post-hoc analysis compared FibroNest digital pathology scoring methods with NASH-CRN categorical stages and imaging-based scores in patients with NASH from the phase 2b FALCON1 study (NCT248689).

**Method:** Eligible adults were 18–75 years of age (N = 197) with NASH diagnosed by histologic assessment of liver biopsy according to NASH CRN criteria and stage 3 fibrosis. During the 48-week double-blind treatment period, patient received 10 mg, 20 mg, or 40 mg PGBF subcutaneous or placebo once weekly. Liver biopsies were obtained six months before or during screening and at week 24. Most patients underwent imaging resulting in Mean Liver Stiffness (MRE) and Mean Proton Density Fat Fraction (MRI-PDFF) measurements. Formalin-fixed, paraffin embedded sections of the liver biopsies were stained with Masson Trichrome and imaged at 40X. Quantitative image analysis was performed to extract single-fiber quantitative traits (qFTs, N = 315) from the fibrosis histological phenotype. A previously validated selection of principal qFTs were normalized and combined into a fibrosis severity score (Ph-CFS, 1 to 10). The non-fibrotic/scar parenchymal tissue area fat ratio (A%) is measured, and its square root is used as an exploratory marker SQRT (A%). Each digital image was evaluated for quality along 20 dimensions (tissue processing, staining, and scanning) to generate a Digital Biopsy Adequacy Score (DBA).

**Results:** Patients with biopsies with a DBA lower than 5 (non-adecuate, ~10% of the cohort) were not included in the results. Groups sizes ranged from 27 to 45 patient per group. The quantification of the antifibrotic effect of the treatments was similar using the mean change from baseline of the Ph-CFS and MRE. SQRT (%) was highly correlated to PDFF (R^2 = 0.660, N = 334) and demonstrated same anti-steatotic effects as PDFF for each group (Fig. A). Responders were identified with a relative reduction from baseline of MRE, Ph-CFS, PDFF and SQRT (%) of ≥15%, ≥25%, ≥30% and ≥30% respectively, and with a 1-unit reduction for the histological stage. The agreement between quantitative digital pathology and imaging methods is illustrated in Fig. B, C.

**Conclusion:** Combined to AI algorithms, quantitative digital pathology image analysis generates continuous scores that enhance conventional histological staging methods. They detect the antifibrotic and anti-steatotic effect of treatment such as PGBF with a performance that benchmarks imaging-based measurements.

**FRI099**
Translational fibrosis phenotypes between the 3D human NASH spherical model and clinical NASH samples

Louis Petitjean1, Simon Ströbel2, Li Chen1,3, Francisco Verdeguer2,4, Radina Kostadinova2, Arun Sanyal5, PharmaNest, Inc, Princeton, United States; 1Bristol Myers Squibb, Princeton, United States; 2Inova Health Systems, Falls Church, United States; 3Virginia Commonwealth University, Richmond, United States; 4University of Zurich, Zürich, Switzerland; 5Virginia Commonwealth University, Richmond, United States

**Background and aims:** The use of 3D human spherical model for efficacy testing of anti-fibrotic compounds for Non-Alcoholic Steatohepatitis (NASH) has led to the need to understand the relevance of the fibrosis histological phenotypes and their clinical translational relevance. Here, a novel digital pathology quantitative image analysis and AI platform, FibroNest™, was used to measure quantifiable Fibrosis Traits (qFTs) in 3D human NASH models and natural cohort of patients diagnosed with NASH.

**Method:** 3D liver tissues were either treated for 10 days with free fatty acids and LPS or not to generate NASH (n = 14 tissues) and lean (n = 17 tissues) conditions respectively. The clinical cohort was retrospective and consisted of 104 patients with NASH diagnosed by histologic assessment of liver biopsy according to NASH CRN criteria by pathologists F0 (26), F1 (24), F2 (28), F3 (20), F4 (6). 4 μm FFPE spheroid and liver biopsies sections were stained with Picro Sirius Red, and scanned (40X and 20X) with bright-light whole slide imaging scanners. FibroNest™, was used to quantify the fibrosis histological phenotype including 32 traits for collagen content, fiber morphometry, and architecture, generating 315 qFT. Principal qFTs were automatically detected to best describe the progression of the fibrosis in both models. A Venn diagram approach was used to identify those traits that describe histological fibrosis severity in both models.

**Results:** The Venn Diagram identifies 97 shared traits between the two fibrosis progression models. qFTs are normalized to their initial
value and their folds describe relative levels of progression benchmarked from a model to another. 10 traits described collagen features such as collagen area ratio, assembled/fine collagen fibers area ratio, and density area ratio (Figure). 61 traits described common morphometric features, such as the proportion of long collagen fibers, the mean fiber skeleton length, and the mean fiber area. 26 traits described common architectural features. The 3D human NASH spheroidal model cannot be directly associated to a specific NASH CRN score, but specific qFTs can be associated with either F2 or F3 stages using their fold values.

Conclusion: We identified 97 histological traits of fibrosis severity phenotype that can be translated from the 3D NASH spheroid model to clinical F2 or F3 NASH CRN stages. These traits will be used to evaluate the anti-fibrotic compounds effect in 3D NASH model to predict their effect in human.

FRI100
Shear wave elastography, transient elastography and enhanced liver fibrosis test use in the assessment of non-alcoholic fatty liver disease (NAFLD) in real-world practices

Sean Felix1, Elena Younossi1,2, Thomas Jeffers2, Evis Hudson3, Nagashree Gundu Rao4, Z. Chris5, Amish Gandhi5, Maria Castillo-Catoni5, Maria Ramirez5, Meheen Husain5, Evangeline Delgado5, Ambika Baru5, Merica Shrestha5, Romona Satchi5, Yemrsach Gami5, Pegah Golabi5, Andrei Racila4, Fatema Nader4, Maria Stepanova5, Zobair Younossi5. 1Inova Fairfax Medical Campus, Department of Medicine, Falls Church, United States; 2Inova Fairfax Hospital, Falls Church, United States; 3Inova Health System, Medicine Service Line, Falls Church, United States; 4Inova Fairfax Medical Campus, Falls Church, United States; 5Center for Outcomes Research in Liver Diseases, Washington, United States

Email: zobair.younossi@inova.org

Background and aims: Risk stratification of NAFLD patients using non-invasive tests can be challenging. In this context, correlation of different radiologic and blood-based NITs to each other can be clinically informative. We aimed to assess the correlation of different NITs to identify high-risk NAFLD/NASH patients seen at real-world primary care provider (PCP) and endocrinology (ENDO) practices and link them to a GI or hepatology practice for specialized care.

Method: Using the electronic health records (EHRs), patients seen at PCP and ENDO clinics were screened for the presence of NASH risk factors. Patients with a diagnosis of type 2 diabetes or those with >2 other components of metabolic syndrome (hypertension, hyperlipidemia, or obesity) were eligible for the second round of assessment using FIB-4. Patients with FIB-4 score ≥1.45 were referred to a hepatology practice for transient elastography (TE) by FibroScan™ (Echosens, Paris, France: liver stiffness [LSM] and fat assessment by controlled attenuation parameter [CAP]), shear-wave elastography (SWE) by ACUSON Sequoia Ultrasound System (Siemens Healthineers, Erlangen, Germany: LSM by Point Shear Wave Elastography [pSWE] and ultrasound-derived fat fraction [UDFF]), and the Enhanced Liver Fibrosis (ELF) Test (Siemens Healthineers, Tarrytown, NY, USA).

Results: 13, 953 patients were screened (53% from ENDO practices, 47% from PCP). Of those, 4, 269 (30%) met the criteria for the second round of screening with FIB-4: 1, 286 (30%) agreed to enroll. Based on the FIB-4 risk cut-off, 328 (25%) patients were considered eligible for linkage to hepatology care, of whom 177 (53%) agreed to undergo linkage assessment. Patients who underwent linkage assessment were 67 ± 10 years of age, 52% male, 61% white, 23% black, 4% Hispanic, and 8% Asian, mean BMI was 31.6 ± 6.4 kg/m², 90% had clinical history of hyperlipidemia, 79% hypertension, 62% type 2 diabetes, and 23% reported having coronary artery or cardiovascular disease. Mean (SD) FIB-4 score: 1.95 ± 0.74; ELF score: 9.55 ± 0.83, LSM by TE: 7.0 ± 4.0 kPa, CAP 287 ± 64 dB/m, LSM by SWE: 3.98 ± 1.55 kPa, UDFF: 13.4 ± 8.6%, and FAST score: 0.25 ± 0.24. Of these patients, based on published or recommended by manufacturers cut-offs, 3% were considered high-risk by ELF, 17% by TE, and 8% by SWE; and additional 64% by ELF, 68% by TE, and 84% by SWE were considered low-risk. The correlations among the two stiffness measures (TE and SWE) and ELF were significant: Spearman’s rho = +0.51 (p < 0.0001) between stiffness by TE and SWE; +0.60 (p < 0.0001) between stiffness by SWE and ELF; +0.25 (p = 0.0028) between stiffness by TE and ELF.

Conclusion: High-risk NASH patients can be identified by applying a simple clinical algorithm using electronic health records and point-of-care NITs.
POSTER PRESENTATIONS

FR101
Diagnostic performance of AGILE 3+ score for identification of advanced fibrosis and prediction of liver-related events in patients with non-alcoholic fatty liver disease
Grazia Pennisi1, Ciro Celsa1, Marco Enea1, Alessandra Pandolfo2, Michela Antonucci3, Carla Ciccom1, Giuseppe Infantino1, Claudia La Mantia1, Stefanie Parisi1, Adele Tulone1, Vito Di Marco1, Antonio Craxi1, Calogero Camma1, Salvatore Petta2, 1Section of Gastroenterology and Hepatology, Department of Health Promotion, Mother and Child Care, Internal Medicine and Medical Specialties (PROMISE), University of Palermo, Italy; 2University of Palermo; 3University of Palermo, Dipartimento di Biomedicina, Neuroscienze e Diagnostica avanzata (BIND)
Email: salvatore.petta@unipa.it

Background and aims: We aimed to assess the diagnostic accuracy of AGILE 3+, a recently developed score based on the combination of AST/ALT ratio, platelet count, diabetes status, sex, age and LSM, respect to FIB-4 and LSM, for the diagnosis of advanced fibrosis and for the prediction of liver-related events (LRE) occurrence in patients with non-alcoholic fatty liver disease (NAFLD).

Method: 614 consecutive patients with biopsy-proven NAFLD or clinical diagnosis of NAFLD-related compensated cirrhosis were enrolled. LRE were recorded during follow-up. FIB-4, LSM by TE and AGILE 3+ were measured. The diagnostic performance of noninvasive criteria for advanced fibrosis and for the prediction of LRE was assessed by AUROC curve and by decision curve analysis (DCA).

Results: In patients with biopsy-proven NAFLD (n = 520), LSM and AGILE 3+ had higher AUROC than FIB-4 (0.88 for LSM and AGILE 3+ vs 0.78 for FIB-4; p < 0.001) for advanced fibrosis, and AGILE 3+ exhibited the lower rate of indeterminate area of the test (25.2% for FIB-4, vs 13.1% for LSM, vs 8.3% for AGILE 3+). In the entire cohort AGILE 3+ had significantly higher AUC for predicting LRE respect to LSM (36-month AUROC 0.95 vs 0.93, p = 0.008; 60-month 0.95 vs 0.92, p = 0.006; 96-month 0.97 vs 0.95, p = 0.001). DCA showed that all scores had modest net benefit for ruling-out advanced fibrosis at the risk threshold of 5%–10% of missing advanced fibrosis. At the risk threshold of 5% of false negative or false positive LRE at 36–, 60–, 96– and 120-month, AGILE 3+ outperformed both FIB-4 and LSM for ruling-out LRE.

Conclusion: AGILE 3+, according to resource availability, clinical setting and the risk scenarios is an accurate and valid alternative to FIB-4 and LSM for the noninvasive assessment of disease severity and prognosis in NAFLD patients.

FR102
Diagnostic accuracy of non-invasive tests for cirrhotic NAS-NASH-NASH on an individual participant data meta-analysis

Background and aims: Screening for non-alcoholic steatohepatitis with cirrhosis (NASH+F4), identified by regulators as an unmet medical need, is done by liver biopsy. Given the low prevalence of the condition in typical clinical populations, risk stratification using non-invasive tests (NITs) is desirable to reduce the number of unnecessary liver biopsies. The aim of this study was to evaluate the diagnostic performance of vibration-controlled transient elastography (LSM-VCTE), fibrosis-4 index (FIB-4) and NAFLD fibrosis score (NFS) as screening tests for NASH+F4.

Method: This was an individual participant data meta-analysis of studies evaluating NITs against liver histology. NASH was defined as NAS >4 with at least grade 3 in each of the components. Diagnostic accuracy was assessed by the area under the receiver operating curve (AUROC). The relationship between NIT cut-off and screen failure rate (SFR) and the number of patients that needed to be tested (NNT) to identify 1 positive case was explored visually. We report on cut-offs that achieved 90% sensitivity, 90% specificity and maximised the Youden-index as well as cut-offs that achieved screen failure rate of 50% and 60%. Sequential combinations of serum NITs followed by LSM-VCTE were also evaluated.

Results: We included 2738 individual patient data from 25 primary studies (43% female, median age 52 years, median BMI 29 kg/m2; 41% had type 2 diabetes; 57% had NASH, 6% had NASH + F4). LSM-VCTE had AUROC = 0.90, higher than 0.80 for FIB-4 and 0.78 for NFS (both p < 0.001). Cut-offs for 90% sensitivity, 90% specificity and maximum
Youden-index were 10.2 kPa (Sp 76%, SFR 80%, NNT = 18), 14.6 (Se 68%, SFR 69%, NNT = 24), and 10.4 kPa (Se 89%, Sp 77%, SFR 79%, NNT = 18) for LSM-VCTE; 1.16 (Sp 52%, SFR 89%, NNT = 18), 2.73 (Se 41%, SFR 79%, NNT = 39) and 1.35 (Se 88%, Sp 61%, SFR 87%, NNT = 18) for FIB-4; −1.637 (So 53%, SFR 89%, NNT = 18), 0.473 (Se 32%, SFR 82%, NNT = 50) and −0.878 (Se 77%, Sp 69%, SFR 86%, NNT = 21) for NFS (Figure 1). A cut-off combination of FIB4 1.16 or NFS −1.637 followed by LSM VCTE of 16 kPa yielded Se 59%, Sp 93%, SFR 62%, and NNT = 27 and only 10% of the entire patient group would have to undergo liver biopsy while also reducing the number of LSM-VCTE exams to 51%.

Conclusion: Only LSM-VCTE achieved SFR of 50% and 60% which was at the cost of high NNT. Sequential combinations can achieve similar diagnostic accuracy while potentially reducing the number of LSM-VCTE exams and biopsies being performed, which could have favorable cost implications.

Method: TARGET-NASH is a longitudinal study of patients managed for NAFLD in usual clinical practice. Data from patients enrolled in the US with ≥3 ALT measures were included. Liver transplant, cholecystitis, liver cancer, sepsis were excluded. ALT categories: normal (<30 U/L), slightly high (1–2X normal), high (2–3X normal), very high (>3X normal). Using available data, the transition between ALT categories was modelled using a recurrent neural network. 80%–20% data split into training-testing approach was utilized to fit the model and assess accuracy. Age, sex, body mass index (BMI), race/ethnicity, ALT date, hypertension, diabetes, cardiovascular disease and statin use were identified a priori.

Results: 3,664 adult patients were followed over a median of 38.2 months (range: 1.7–87) with 3.9 months (range: 0.5–54.2) between ALT measures. Median age: 59; non-Hispanic (85%), White (76%), BMI 32 kg/m², history of hypertension (74%), type 2 diabetes (54%), cardiovascular disease (22%), statin use (46%); diagnosed with NASH (44.3%), cirrhosis (40.4%), NAFLD (15.3%). Patients in higher ALT categories at baseline were younger with a greater percentage of Hispanic or Latino participants vs. lower ALT categories. At baseline, 33%, 38%,15%,14% of patients had normal ALT, slightly high, high, very high ALT levels, respectively. In the unadjusted model, 39% with normal ALT at baseline remained in that category during follow up. Among those with slightly high ALT at baseline, 18% remained within that stratum; 5% and 18% of those with high and very high ALT, respectively, at baseline remained in the same strata. Probability of transitioning from normal or slightly high to very high ALT level was 2% and 6%, respectively, suggesting that transition from low to high ALT levels is uncommon. Risk of transition was higher in NH Whites (24%) and Hispanics (24%), followed by NH Black (21%), Asians (19%). Statin use did not influence transition. Accuracy of the neural network on training and testing data sets was 99% and 82%, respectively. Accuracy of the testing data set improved when limiting to phenotype at baseline: 89% (NAFLD), 84% (NASH), 84% (cirrhosis).

Conclusion: Longitudinal ALT trajectories remained relatively stable among patients with NAFLD. Understanding the course of ALT fluctuations is important for helping to differentiate natural variation from potential hepatotoxic or beneficial effects of therapeutics. Next steps include exploration of ALT trends associated with probability of clinical outcomes.

Conclusion: Only LSM-VCTE achieved SFR of 50% and 60% which was at the cost of high NNT. Sequential combinations can achieve similar diagnostic accuracy while potentially reducing the number of LSM-VCTE exams and biopsies being performed, which could have favorable cost implications.

Background and aims: Serum alanine aminotransferase (ALT) is a biomarker used to monitor liver injury. Little is known about ALT fluctuations over short intervals or the influence of patient characteristics on ALT trajectory in patients with NAFLD. This study modelled longitudinal variability in ALT and estimated the probability of a patient transitioning from their baseline level.

Conclusion: Longitudinal ALT trajectories remained relatively stable among patients with NAFLD. Understanding the course of ALT fluctuations is important for helping to differentiate natural variation from potential hepatotoxic or beneficial effects of therapeutics. Next steps include exploration of ALT trends associated with probability of clinical outcomes.
Background and aims: Several genetic variants that associate with hepatic fat content in adults have been identified in genome-wide association studies. Their effects in children and adolescents remain unclear. The aims of this study were to test the effect of genetic variants known to associate with hepatic fat in adults, individually and combined as a genetic risk score (GRS), with cardiometabolic traits, and to investigate the predictive ability of the GRS for hepatic steatosis in children and adolescents.

Method: Children and adolescents with overweight/obesity from an obesity clinic cohort (n = 1, 843, median age 11.7 years, body mass index standard deviation score [BMI SDS] 2.85, 45.2% male) and a population-based cohort of children and adolescents (n = 2, 271, median age 11.6 years, BMI SDS 0.26, 40.1% male) were included. Anthropometrics and biochemical parameters were measured in both cohorts. Liver fat content was measured by magnetic resonance spectroscopy in 539 individuals. We calculated a weighted GRS based on eight genetic variants known to associate with hepatic fat content in adults. Associations of individual genetic variants and the GRS with cardiometabolic traits were tested using multiple linear and logistic regression models. Receiver operating characteristic (ROC) curve analysis was performed on models based on risk factors for hepatic steatosis, defined as hepatic fat ≥5%, and area under the curve (AUC) was calculated to evaluate model performance.

Results: Variants in PNPLA3, TM6SF2, GPM, and GCKR were significantly associated with higher liver fat content (p < 0.01) and with distinct patterns of circulating lipids. The GRS was associated with higher liver fat content and alanine transaminase (ALT), as well as lower LDL-cholesterol and triglycerides in the obesity clinic and with higher liver fat content and alanine transaminase (ALT), as well as significantly associated with higher liver fat content (p < 0.01) and with lower LDL-cholesterol and triglycerides in the obesity clinic and population-based cohorts. The GRS was not associated with adiposity or other metabolic traits. The GRS was associated with higher prevalence of hepatic steatosis (odds ratio [OR] per 1-unit GRS-increase: 2.18, p = 1E-8), and with lower prevalence of dyslipidemia (OR 0.90, p = 0.02). A prediction model for hepatic steatosis including GRS alone yielded cross-validated AUC of 0.76 (95% CI 0.69–0.83). The GRS was associated with higher liver fat content, liver enzymes and lipid profiles, but was not associated with adiposity and other metabolic traits in children and adolescents. The GRS could serve as a predictor of the risk for hepatic steatosis in addition to clinical risk factors and could be used for early preventative initiatives.

Conclusion: The adult-based GRS for hepatic fat was associated with liver fat content, liver enzymes and lipid profiles, but was not associated with adiposity and other metabolic traits in children and adolescents. The GRS could serve as a predictor of the risk for hepatic steatosis in addition to clinical risk factors and could be used for early preventative initiatives.
Conclusion: IL-32 expression in the liver shows the most robust and dynamic association to steatohepatitis and might constitute a useful biomarker for its detection and follow-up in patients.

FR106
NASH patient’s itinerary: Comparison of strategies for screening, referring and management
Manuel Romero Gomez1,2,3, Yolanda Sánchez2,4, Silvia García Rey2,4, Francisco Javier Atienza Martín5, Pablo Remón6, Carmen Lara Romero6,7, Maria C. Roque-Cuéllar2,4, Inmaculada Domínguez2, Ioanna-Panagiota Kalafati2, Sabine Kahl9, Pedro Pablo García-Luna10,11, Jörn Schattenberg6,11, Michael Roden11,12, George Dedoussis8, Jeffrey Lazarus13,9, George Dedoussis8, Jeffrey Lazarus13.

Background and aims: Non-alcoholic fatty liver disease (NAFLD) is a highly prevalent, underdiagnosed, health system burden and impacts on quality of life including comorbidities in the affected population. Cost-effective strategies focusing on clinical pathways to detect and refer patients to care are needed. The aim of this study is to build a stepwise algorithm combining non-invasive freely available methods (FIB-4, NFS, HFS alone or combined) and vibration-controlled transient elastography (VCTE) in diabetic patients from primary care and endocrinology units.

Method: One-hundred sixty-four diabetes patients were recruited from January 2021 to February 2022 and randomized to one of three arms: Arm A (n = 55) patients referred following standard of care; Arm B (n = 55) patients referred due to altered combined fibrosis score (CFS) (FIB>4.3 or NFS>1.156 or VCTE>8 KPa); and Arm C (n = 54) patients referred due to HFS>0.12 or VCTE>8 KPa. Patients at risk of confirmed NAFLD with description of sensitivity & specificity at diagnostic threshold were referred to the liver unit. Estimated cost for NAFLD patient referral to the liver unit was approximately €570, 78 (Sánchez-Torrijos et al. REED 2019). VCTE €120 and CFS €0.59 per patient with T2DM: cost in Arm A was €31, 392.9; cost in Arm B was €24, 90053 and in Arm C was €16, 215.12

Conclusion: The prevalence of advanced fibrosis in a diabetic cohort reached 7.3% confirmed by transient elastography and MRE. A stepwise algorithm in the management of patients with type 2 diabetes with combined score and VCTE was cost-effective, allowing to save 50% of the budget compared to the standard of care. Acknowledgement: Unrestricted grant from Gilead Sciences.

FR107
Performance of fibrometer-derived biomarker panels for assessment of fibrosis stage in NAFLD: NIMBLE stage 1 and the NASH CRN collaborative Study
Rohit Loomba1, Sudha Shankar2, Katherine Yates3, Clayton Dehn4, James Bolognese5, Brent Tetri6, Krist Wowley7, Raj Vuppulanchi8, Cynthia Guy9, James Tonascia3, Anthony Samir10, Claude Sirlin11, Sarah Sherlock12,13, Kathryn Fowler13, Helen Heymann13, Tania Kamphaus13, Roberto Calle14, Arun Sanyal15,1. University of California at San Diego, San Diego, United States; 2Astrazeneca, United States; 3Johns Hopkins University, Bloomberg School of Public Health, United States; 4P-value LLC, United States; 5Cytel, United States; 6Saint Louis University, Department of Gastroenterology and Hepatology, United States; 7Liver Institute Northwest, United States; 8Indiana University, Division of Gastroenterology and Hepatology, United States; 9Duke University, Department of Pathology, United States; 10Massachusetts General Hospital, Department of Radiology, United States; 11University of California at San Diego, Department of Radiology, United States; 12Pfizer, United States; 13Foundation for the National Institutes of Health (FNIH), United States; 14Regeneron Pharmaceuticals, United States; 15Viralogical Commonwealth University, Division of Gastroenterology, Hepatology and Nutrition, Department of Internal Medicine, United States.

Background and aims: The intent of the current collaborative study between NIMBLE & the NASH CRN was to further evaluate the performance of Fibrometer-based biomarker panels, including those developed for NAFLD or other liver diseases, with & without VCTE for identification of fibrosis strata in those with NAFLD. This cross-sectional study evaluated the diagnostic-test performance characteristics of four Fibrometer-based biomarker panels for assessing fibrosis in a well-characterized cohort of patients with biopsy-confirmed NAFLD with description of sensitivity & specificity at Youden’s cutoff for their intended diagnostic use in a large, multicenter US cohort of patients with NAFLD/NASH.

Method: The performance of Fibrometer Virus (FM-VIRUS), Cirrhotometer Virus (CM-VIRUS), Estimation of Fibrometer NAFLD (FM-NAFLD) & Fibrometer VCTE-Light (FM-VCTE-Light) was evaluated for the assessment of fibrosis. Blood-based parameters were tested from aliquots of the same blood sample from each patient obtained within 90 days of a liver biopsy demonstrating NAFLD of varying activity &
stages (Stages 0–4). VCTE measurements were performed in a subgroup of trial participants within this time window. In order to minimize spectrum bias, the cohort was selected a priori to have a similar distribution of fibrosis stages across its entire range. The primary hypothesis was that the AUROC for each panel for its intended use was numerically >0.7 & significantly superior to 0.5. The secondary hypothesis was that the AUROC for each panel for fibrosis was significantly greater than that for FIB-4 (as the common reference).

**Results:** 1073 patients with biopsy-proven NAFLD including NAFL (n = 220) & NASH (n = 853) were evaluated. The number of patients with fibrosis stages 0, 1, 2, 3 & 4 were 222, 114, 262, 277 & 198, respectively. The dataset for Fibrometer VCTE-Light was smaller as VCTE data were available in only 393 patients. The AUROCs, Youden’s cutoff with its sensitivity/specificity are provided below: All 4 panels met criteria for intended use for diagnosis of fibrosis stage ≥2, advanced fibrosis, & cirrhosis. Compared to FIB-4, FM-VIRUS & FM-NAFLD met criteria for diagnosis of advanced fibrosis but not for fibrosis stage ≥2 or cirrhosis, while CM-VIRUS was not superior to FIB-4 for any of the intended uses. In contrast, FM-VCTE-Light was significantly superior to FIB-4 for all three intended uses.

**Conclusion:** FM-VCTE-Light consistently outperformed FIB-4 for stratification of fibrosis across a spectrum of fibrosis stages. FM-VIRUS & FM-NAFLD appear to be better than FIB-4 for detecting advanced fibrosis but not for other fibrosis stages. These data will be helpful in informing trial design for future studies using these Fibrometer-based non-invasive tools across various intended use populations.
Sequential combinations of NITs could perform similarly to single NITs, with fewer individuals needing LSM-VCTE and liver biopsy. FIB-4 with cut-offs of 0.7 and 4.63 followed by LSM-VCTE with cut-offs of 6 and 20 kPa had Se 68%, Sp 59%, SFR 60%, NNT 5. NFS with cut-offs of 3.272 and 1.766 followed by LSM-VCTE with cut-offs of 6 and 20 kPa had Se 70%, Sp 56%, SFR 62%, NNT 5. 

Conclusion: The major benefit of employing a sequential testing strategy was the reduced number of liver biopsies. Additionally, we noticed no further gain in diagnostic accuracy for the upper threshold of NITs above a certain level, suggesting that a judicious choice of thresholds can lead to a reduction in testing costs. 

**FR109**

Multiparametric MRI biomarker corrected T1 as a prognostic marker in chronic liver disease

Naim Alkhouri1, Cayden Beyer2, Anneli Andersson2, Elizabeth Shumbayawonda3, Michael Pavlides3, Arjun Jayaswal3, Matt Kelly2, Stephen Harrison3.

1Arizona Liver Health, Fatty Liver Program, Chandler, United States; 2Perspectum, Innovation, United Kingdom; 3Oxford Centre for Magnetic Resonance (OCMR), Headington, United Kingdom

Email: cayden.beyer@perspectum.com

**Background and aims:** Liver biopsy is an imperfect reference test for non-alcoholic fatty liver disease (NAFLD) and non-alcoholic steatohepatitis (NASH), due to its invasive nature, 2.4% major complication rate, high intra- and inter-reader variability and sampling error. The utility of non-invasive technologies (NITs) as alternative tools for NASH prognosis are assessed by their ability to predict clinical outcomes. Non-invasive multiparametric magnetic resonance imaging (mpMRI) with LiverMultiScan, and specifically corrected T1 (cT1), has previously been shown to predict clinical outcomes. With this study we investigate the association of increasing cT1 thresholds with clinical outcomes.

**Method:** Imaging and outcomes data were collected at two tertiary centers in the UK between May 2011 and July 2017 from patients referred to clinically indicated biopsy or known liver cirrhosis diagnosis. Clinical outcomes data were collected as a composite endpoint comprising ascites, variceal bleeding, hepatic encephalopathy, hepatocellular carcinoma (HCC), liver transplantation and mortality, more details described by Jayaswal et al. Liver Intl (2020) and in NCT01543646. Cox proportional hazard analysis was used to calculate hazard ratios (HRs) for the continuous and grouped variables. Probability of clinical outcome for cT1 as a continuous variable was used as reference and the HRs for each cut-off were used as scaling factors.

**Results:** 182 patients, including 54% with NAFLD, with 620 years follow up were included in the analysis where 13 patients had liver event occurrences, suggesting the overall risk of complications of 7% within the <72 months follow-up time. The events were ascites (5), variceal bleeding (1), hepatic encephalopathy (2), HCC (3) and mortality (9), with some patients having multiple events. cT1 had a 0.7% increase in risk of clinical event for every 1 ms increase in cT1 (HR = 1.007, 95% CI: 1.003–1.011, p = 0.0010), which is equivalent to 91% increase of risk per 100 ms (HR 1.91). Patients with cT1 greater than 875 ms had 3.42 [95% CI: 1.05–11.11, p < 0.05] times higher risk to experience an event before those with cT1 below or equal to 875 ms. The cumulative probability of clinical events over time was higher for patients with cT1 of greater than 875 ms, compared to those with intermediate (800–875 ms) and low (<800 ms) cT1 (Fig. 1).

**Conclusion:** This study demonstrates that cT1 above 875 ms is not only able to identify high-risk NASH patients, but also predicts who is at higher risk for clinical events by evaluating patient health records and clinical outcomes. These results show the potential impact non-invasive mpMRI biomarkers can have to inform public health strategies and mitigate the impact of the growing burden of NAFLD.
Background and aims: The regulatory qualification of non-invasive tests (NITs) for liver fibrosis severity assessment is a major unmet need in non-alcoholic fatty liver disease (NAFLD). Ultrasound-based methods such as shear-wave elastography (SWE) and vibration-controlled transient elastography (VCTE) have the potential, through repeated use, to assess disease response and progression. However, this application has been limited by a paucity of reproducibility data across device manufacturers in the population at risk. The aim of this study from the imaging workstream of the FNIH NIMBLE consortium (NCT04828551), was to address this knowledge gap and contribute to the evidence needed for qualification of ultrasound-based methods.

Method: A prospective two-center study of adults with suspected or established NAFLD stratified by FIB-4 (≤1.3, >1.3 < 2.67, ≥2.67) to reduce spectrum bias was performed. Each participant underwent 6 examinations on different ultrasound systems and VCTE on two days, each day by a different operator, less than a week apart. Sonographers and clinical investigators were blinded and a pre-specified data chain of custody was maintained. For uniformity, VCTE and SWE measurements were reported and analyzed in units of meters per second by an independent statistician. The primary end point was pooled estimates are likely to inform ultrasound-based NIT qualification by (1) defining expected variability, (2) establishing that serial examination variability is lower when performed on the same vendor platform, and (3) informing future clinical trial design, including NIMBLE stage 2.

Conclusion: SWE demonstrated good RDC\textsubscript{DDD}, with slightly higher RDC\textsubscript{DDD} observed for VCTE. Considerably higher SWE variability is observed with measurements on different vendor platforms. These estimates are likely to inform ultrasound-based NIT qualification by (1) defining expected variability, (2) establishing that serial examination variability is lower when performed on the same vendor platform, and (3) informing future clinical trial design, including NIMBLE stage 2.

**FRI111**

**Independent association of physical activity with nonalcoholic fatty liver disease and alanine aminotransferase levels**

Jun Kyu Lee\textsuperscript{1}, Dongguk University Ilsan Hospital, Internal Medicine, Goyang, Korea, Rep. of South

Background and aims: The aim of the current study was to examine the independent association of physical activity with nonalcoholic fatty liver disease (NAFLD) and aminotransferases while adjusting for obesity and diet.

Method: A data from 32, 391 participants aged ≥20 years in the Korea National Health and Nutrition Examination Surveys (KNHANES) was analyzed by logistic regression models and general linear models. Physical activity was assessed from the questionnaire by health-enhancing physical activity (HEPA).

Results: The physical activity was negatively associated with NAFLD after adjustment for multiple factors with an odds ratio of 0.66 (95% CI, 0.57–0.76) comparing the most active (HEPA active) and the least active (inactive) participants. Among the participants with NAFLD, physical activity also showed an independent negative association with alanine aminotransferase (ALT) levels but not with aspartate aminotransferase levels. These independent associations were not observed when comparing the minimally active and inactive participants.

**Fig. 1. Flow diagram of participant inclusion and exclusion in the current study using data from Korea National Health and Nutrition Examination Surveys (KNHANES IV, V and VI).**

<table>
<thead>
<tr>
<th>Number of Observations</th>
<th>RDC\textsubscript{Conf}</th>
<th>Upper Confidence Bound</th>
<th>95% RDC\textsubscript{Conf}</th>
<th>Upper Confidence Bound</th>
<th>95%</th>
</tr>
</thead>
<tbody>
<tr>
<td>Vendor 1</td>
<td>24</td>
<td>31.9%</td>
<td>42.5%</td>
<td>19.0%</td>
<td>25.8%</td>
</tr>
<tr>
<td>Vendor 2</td>
<td>24</td>
<td>24.2%</td>
<td>35.1%</td>
<td>13.9%</td>
<td>18.3%</td>
</tr>
<tr>
<td>Vendor 3</td>
<td>24</td>
<td>29.9%</td>
<td>39.4%</td>
<td>14.2%</td>
<td>18.7%</td>
</tr>
<tr>
<td>Vendor 4</td>
<td>24</td>
<td>32.3%</td>
<td>42.5%</td>
<td>14.9%</td>
<td>19.6%</td>
</tr>
<tr>
<td>Vendor 5</td>
<td>24</td>
<td>34.3%</td>
<td>45.2%</td>
<td>35.0%</td>
<td>46.1%</td>
</tr>
<tr>
<td>Pooled SWE</td>
<td>60</td>
<td>30.7%</td>
<td>34.4%</td>
<td>21.0%</td>
<td>23.5%</td>
</tr>
<tr>
<td>VCTE</td>
<td>39</td>
<td>35.6%</td>
<td>43.9%</td>
<td>16.8%</td>
<td>24.1%</td>
</tr>
</tbody>
</table>
Conclusion: Physical activity is independently associated with the degree of hepatocellular injury in patients with NAFLD as well as the risk of NAFLD in the general population. Sufficiently active physical activity greater than a minimally active level may be needed to lower the risk of NAFLD and ALT levels.

FRI112

In a nonalcoholic steatohepatitis (NASH) clinical trial, baseline and screen failure magnetic resonance elastography (MRE) liver stiffness values calculated as weighted means were not different from values calculated as simple means

Michael Middleton¹,², Mark Becker³, Walter Henderson¹, Claude Sirlin¹, "University of California, San Diego, Radiology, San Diego, United States; ²Quantix Bio, Lewes, United States; ³Intercept Pharmaceuticals, Inc., San Diego, United States

Email: msm@ucsd.edu

Background and aims: Magnetic resonance elastography (MRE) liver stiffness, a quantitative imaging biomarker of hepatic fibrosis, is commonly used in nonalcoholic steatohepatitis (NASH) clinical treatment trials. Typically, four images are acquired through the liver, and means of liver stiffness, weighted based on region-of-interest size are calculated to generate a single representative liver stiffness value for each exam. This is an appropriate method to use in clinical trials, but anecdotally it has been suggested that obtaining simple, rather than weighted means for routine clinical care is easier and may suffice. The Quantitative Imaging Biomarker Alliance (QIBA) has considered this question as part of their efforts to provide guidelines on how MRE exams should be acquired and analyzed. Data from drug development clinical trials are in many ways ideal to study this kind of question, given that typically such studies are conducted at large numbers of clinical sites using a wide variety of MR scanners of different styles and field strengths, from different MR scanner vendors. Hence, we undertook an analysis of MRE baseline and screen failure imaging data from a clinical trial testing a potential new treatment drug for NASH (NCT03439254; in progress) to determine whether liver stiffness values differed as to whether weighted, or simple means were used to generate final liver stiffness values for each exam.

Method: 308 baseline and screen failure MRE exams were obtained between October 2017 and December 2019 from 49 imaging sites worldwide. 19 MR scanner styles were represented, including 1.5 T and 3 T scanners from GE, Siemens, and Philips, with each exam using either a 2D GRE or a 2D SE-EPI pulse sequence. After exclusion of 13/308 (4.2%) of exams that were not analyzable, and 6/308 (1.9%) of exams for which incorrect images were acquired, 289/308 (93.8%) of exams were included in this analysis. Weighted and simple liver stiffness means were calculated, and compared using regression, Bland Altman, and Student t test analyses.

Results: Weighted liver stiffness means were not different from simple means (5.51 ± 1.97 kPa vs. 5.50 ± 1.94 kPa, respectively; p = 0.11). On regression analysis, slope was 0.986, intercept was 0.07 kPa, and the R² value was 0.995. On Bland Altman analysis, weighted and simple means differed by 0.01 ± 0.14 kPa. This difference is small compared to typical variability due to inter-scanner reproducibility, and is not clinically meaningful.

Conclusion: In a multi-center NASH clinical trial in which sites were trained and site protocols qualified by a central analysis center before study exams were acquired, no difference was observed between baseline weighted and simple mean MRE liver stiffness values across four acquired slices. This data will help inform ongoing work by QIBA in qualifying MRE liver stiffness as a quantitative imaging biomarker of hepatic fibrosis.

FRI113

Influence of pregnancy on NAFLD-associated lipidomic signatures

Tatyana Kushner¹, Ibon Martinez-Arranz², Marco Arrese³, Mazen Noureddin¹, Rhoda Sperling¹, Keith Sigel¹, Scott Friedman¹, Pablo Ortiz², Cristina Alonso².

¹Icahn School of Medicine at Mount Sinai; ²OWL Metabolomics, Spain; ³Pontificia Universidad Catolica de Chile; ²Cedars Sinai

Email: tatyana.kushner@mssm.edu

Background and aims: Although NAFLD-associated lipidomic signatures have been defined in the general population, there is limited data on the influence of pregnancy on NAFLD-associated
lipidomic changes. In this study, we elucidate the deregulated lipidomic serum landscape of pregnant women with NAFLD.

**Method:** We prospectively screened for NAFLD at 18–22 weeks gestation in pregnant women. Pregnant woman with NAFLD (n = 6) and without NAFLD (n = 7) were matched 1:1 with retrospectively collected cases from non-pregnant woman with and without NAFLD (n = 13) based on age-, BMI- and disease-stage. Lipidomic analysis of serum samples collected under fasting conditions was performed using ultra-high performance liquid chromatography-mass spectrometry, covering lipid species across classes of glycerolipids, glycerophospholipids (phosphatidylcholin, acyl- and ether-linked phosphatidylethanolamine (PE) and phosphatidylcholine (PC)), sphingolipids (ceramides, monohexosylceramides and sphingomyelins), fatty acids and steroids (cholesteryl esters, steroids and bile acids). Lipidomic profiles in pregnant females with vs. without NAFLD and in pregnant females vs. non-pregnant matched female controls were compared.

**Results:** Pregnant women with NAFLD had higher PE, lysoPE and lower ceramides compared to non-pregnant women with NAFLD (see Figure). Pregnant women with NAFLD had lower triglycerides compared to non-NAFLD pregnant women; non-pregnant females with NAFLD had higher triglycerides compared to non-pregnant females without NAFLD. Pregnant women without NAFLD were significantly more likely to have lower saturated (SFA), monounsaturated (MUFA), and polyunsaturated fatty acids (PUFA) (p < 0.05), but significantly more likely to have lower saturated (SFA), monounsaturated (MUFA), and polyunsaturated fatty acids (PUFA) (p < 0.05). Non-NAFLD pregnant women also had lower ceramides and ether linked-lysoPC compared to non-pregnant women.

**Conclusion:** Our findings suggest that NAFLD associated lipidomic signatures may be significantly impacted by pregnancy. NAFLD in pregnancy appears to be associated with a depletion in serum triglycerides and ceramides. Further workup should evaluate pregnancy-trimester specific changes as well as the role these lipid changes may play on NAFLD-associated adverse pregnancy outcomes such as gestational diabetes or effects on the newborn.

**FR1114**

**Plasma sgp130 is an independent predictor of non-alcoholic fatty liver disease severity**

Aysim Gunes1,2,3, Laurent Bilodeau4, Catherine Huet4, Assia Belbiadia1, Cindy Baldwin1, Jeanne-Marie Girard1, Laurent Bierto6,2, Annie Lafortune6,2, Christian Couture6,8, Bich N. Guyen3, Eithan Galun10,11, Chantal Bemeur11,12, Marc Bilodeau12, Mathieu Laplante11,13, An Tang4, May Faraj1,2,3, Jennifer Estall1,2,3, 1Institut de recherches cliniques de Montréal (IRCM), Montréal, Canada; 2McGill University, Division of Experimental Medicine, Montréal, Canada; 3Montreal Diabetes Research Centre, Canada; 4Hôtel Dieu de Montréal-CHUM, Département de radiologie, Montréal, Canada; 5Hôtel Dieu de Montréal-CHUM, Département d’hépatologie, Montréal, Canada; 6University Institute of Cardiology and Respiratory of Quebec, Québec, Canada; 7Laval University, Département de chirurgie, Québec, Canada; 8Department of Molecular Biology, Medical Biochemistry and Pathology, Québec, Canada; 9University of Montreal, Département de pathologie et biologie cellulaire, Montréal, Canada; 10Goldyne Savad Institute of Gene Therapy, Israel; 11University of Montreal, Département de nutrition, Montréal, Canada; 12Research Center Du Chum, Labo HépatoNeuro, Montréal, Canada; 13Laval University, Centre de recherche sur le cancer de l’Université Laval, Québec, Canada

Email: a.gkizil@gmail.com

**Background and aims:** Nonalcoholic steatohepatitis (NASH) is a metabolic disease associated with liver failure and cancer. Monitoring of advancing NASH is challenging. Since liver inflammation is a main driver of fibrosis, we investigated relationships between circulating components of the interleukin-6 signaling pathway (IL-6, sIL-6R and sgp130) and liver pathology in subjects with NAFLD and NASH.

**Method:** Predictive performance of plasma IL-6, sIL-6R and sgp130 were investigated in two independent cohorts: 1) patients with biopsy-confirmed NASH (n = 49), where magnetic resonance spectroscopy (MRS), imaging (MRI) and elastography (MRE) assessed liver fat, volume and stiffness; and 2) patients with morbid obesity (n = 245) undergoing bariatric surgery where histological staging of steatosis, activity, and fibrosis assessed NASH severity. Correlations were evaluated between IL-6, sIL-6R, sgp130 and anthropomorphic characteristics, plasma markers of metabolic disease or liver pathology.

**Results:** In patients with NASH, plasma IL-6 and sgp130 strongly correlated with liver stiffness, which for sgp130 was independent of age, sex, BMI, diabetes, hyperlipidemia, hypertention or history of HCC. Plasma sgp130 was the strongest predictor of liver stiffness compared to common biomarkers and risk scores. Plasma sIL-6R correlated with liver volume independent of age, sex, and BMI. In stepwise regression analysis, plasma sgp130 followed by NAFLD fibrosis score and plasma globulin, predicted up to 74% of liver stiffness. In patients with morbid obesity, circulating sgp130 correlated with advanced liver fibrosis.

Figure: Heatmaps of lipidomic profiles in pregnant women (with and without NAFLD) compared to non-pregnant controls (with and without NAFLD).
**FRI115**

**FIB4 outperforms other serum non-invasive fibrosis tests in metabolic associated fatty liver disease**

Nikoletta Maria Tagkou1, Giulia Magini1,2, Laurent Spahr1, Francesco Negro1,3, Jean-Louis Frossard1, Nicolas Goossens1,2.

1Hôpitaux Universitaires de Genève (HUG), Division of Gastroenterology and Hepatology, Geneva, Switzerland; 2Hôpitaux Universitaires de Genève (HUG), Division of Transplantation, Geneva, Switzerland; 3Hôpitaux Universitaires de Genève (HUG), Division of Clinical Pathology, Geneva, Switzerland

**Email:** tagkounikoletta@gmail.com

**Background and aims:** Metabolic associated fatty liver disease (MAFLD) is a recently proposed terminology to replace non–alcoholic fatty liver disease (NAFLD) but non-invasive fibrosis scores have not been validated in this population. Additionally, MAFLD definition broadens the disease spectrum by including the overlap with alcohol related liver disease (MAFLD-ALD). We therefore aimed to determine the diagnostic performance of non-invasive fibrosis scores in MAFLD and whether the coexistence of alcohol abuse affects their performance.

**Method:** We retrospectively collected data of 409 consecutive MAFLD patients undergoing liver biopsy at our institution from 2007 to 2021. We stratified our patients by excessive alcohol consumption defined as >20 g/day in females and >30 g/day in males. The following scores were calculated with previously published cutoffs: NFS, FIB4, APRI and BARD. Advanced fibrosis was considered as F3–4 and cirrhosis as F4 fibrosis on liver biopsy. Diagnostic performance was assessed by analysis of the area under receiver operating characteristic curve (AUROC) and sensitivity/specificity calculations.

**Results:** Among 409 patients, 277 (66.4%) had pure MAFLD and 132 (31.7%) had MAFLD-ALD. Baseline characteristics in pure MAFLD vs MAFLD-ALD were: age (51.2 vs 58.2, p < 0.001), male sex (49.5 vs 87.9%, p < 0.001), BMI (36.9 vs 30.4 kg/m², p < 0.001), diabetes (51.1 vs 69.2%, p < 0.001), advanced fibrosis (27.7 vs 71.2%), cirrhosis (17.5 vs 63.6%), NASH (37.3 vs 32.6%, p = 0.406) and median steatosis proportion (50 vs 30%, p < 0.001). In pure MAFLD, the AUROCs of FIB4, NFS, APRI, and BARD for advanced fibrosis were 0.88, 0.74, 0.78 and 0.73, respectively (Table). The same AUROCs for predicting cirrhosis were 0.94, 0.82, 0.8 and 0.79, respectively. When comparing the AUROCs, FIB4 performed significantly better than the other non-invasive scores (p < 0.001) for the prediction of both advanced fibrosis and cirrhosis in pure MAFLD. However, FIB4 performed less well for the prediction of cirrhosis in patients with MAFLD-ALD compared to pure MAFLD (AUROC 0.83 vs 0.94, p = 0.005), while the other scores performed similarly.

**Table:** Comparison of the diagnostic performance of non-invasive fibrosis scores in MAFLD

<table>
<thead>
<tr>
<th>Score</th>
<th>AUROC 95% CI Cut-offs</th>
<th>Sensitivity (%)</th>
<th>Specificity (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Advanced fibrosis</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>FIB4</td>
<td>0.88 0.83–0.93 1.3</td>
<td>79</td>
<td>75</td>
</tr>
<tr>
<td>NFS</td>
<td>0.74* 0.66–0.81 −1.455</td>
<td>90</td>
<td>29</td>
</tr>
<tr>
<td>APRI</td>
<td>0.78* 0.72–0.84 0.5</td>
<td>68</td>
<td>72</td>
</tr>
<tr>
<td>BARD</td>
<td>0.73* 0.66–0.8</td>
<td>42</td>
<td>90</td>
</tr>
<tr>
<td>Cirrhosis</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>FIB4</td>
<td>0.94 0.92–0.97 1.3</td>
<td>92</td>
<td>72</td>
</tr>
<tr>
<td>NFS</td>
<td>0.82* 0.73–0.91 −1.455</td>
<td>94</td>
<td>28</td>
</tr>
<tr>
<td>APRI</td>
<td>0.8* 0.73–0.87 0.5</td>
<td>76</td>
<td>69</td>
</tr>
<tr>
<td>BARD</td>
<td>0.79* 0.71–0.86 2</td>
<td>91</td>
<td>41</td>
</tr>
</tbody>
</table>

*p < 0.05 significantly different to FIB4.

**Conclusion:** FIB4 performs better than other serum non-invasive tests for the prediction of advanced fibrosis and cirrhosis in MAFLD patients, however its performance for the prediction of cirrhosis is reduced in the presence of alcohol abuse.

**FRI116**

**Presence of auto-antibodies has no impact on histological parameters in non-alcoholic fatty liver disease**

Ajeet Singh Bhadoria1, Kavita Jain1, Archana Rastogi2, Chhagan Bhikha1.1 All India Institute of Medical Science Rishikesh, Community and Family Medicine, Rishikesh, India; 2Institute of Liver and Biliary Sciences, New Delhi, India

**Email:** ajeetsinghbhadoria@gmail.com

**Background and aims:** Presence of auto-antibodies have been documented with liver diseases like viral hepatitis, drug induced hepatitis and non-alcoholic fatty liver disease (NAFLD). However, significance and impact of these autoantibodies on histological severity of NAFLD yet needs to be explored. Previous reports on association of autoantibodies with histological severity in other cohorts have revealed inconsistent results. Therefore, this study was undertaken to document the impact of auto-antibodies on histological parameters of NAFLD.

**Method:** All cases with histological diagnosis of NAFLD during Jan 2016–Jan 2021 were included in the study. Laboratory parameters were recorded and histological assessment was done utilizing Ishak’s modified system. Positivity of autoimmune markers was defined as presence of either Anti-nuclear Antibody (ANA; titre of >1:80), anti-smooth muscle antibodies (ASMA), or anti-liver-kidney-microsomal antibodies (LKM-1; titre of >1:40). Demographic, biochemical, serologic and histological characteristics were compared between cases with and without any antibody positivity. Serum levels of CK18-M30 and PIIINP were evaluated by ELISA to assess the subtle changes in necro-inflammatory activity and fibrosis.

**Results:** Out of 1149 NAFLD cases screened, complete autoantibody status was known for 683 cases. Autoantibodies were present in 281/683 (41.1%, 95% CI 37.4–44.9) patients. ANA, ASMA, ANA plus ASMA was seen in 20.9% (95% CI 17.9–24.2), 14.5% (95% CI 11.9–17.4) and 5.7% (95% CI 4.1–7.7) cases, respectively. LKM-1 was not seen in any case. No significant difference was noted between the two groups in...
Meta-analysis of magnetic resonance versus histology—A systematic review and meta-analysis

Sami Qadri¹,², Kimmo Porthan ¹,², Anne Juuti³, Anne Penttilä³, Juhani DaBek¹,², Tiina E. Lehtimäki⁴, Wenla Seppänen⁴, Johanna Arola⁵, Perttu Arkkila⁶, Hannele Yki-Järvinen¹,².
¹University of Helsinki and Helsinki University Hospital, Department of Medicine, Helsinki, Finland; ²Minerva Foundation Institute for Medical Research, Helsinki, Finland; ³University of Helsinki and Helsinki University Hospital, Department of Gastrointestinal Surgery, Abdominal Centre, Helsinki, Finland; ⁴University of Helsinki and Helsinki University Hospital, Department of Gastrointestinal Surgery, Abdominal Centre, Helsinki, Finland; ⁵Helsinki University Hospital, HUS Medical Imaging Centre, Helsinki, Finland; ⁶University of Helsinki and Helsinki University Hospital, Department of Pathology, Helsinki, Finland; ⁷Helsinki University Hospital and University of Helsinki, Department of Gastroenterology, Abdominal Centre, Helsinki, Finland.

Email: hannele.yki-jarvinen@helsinki.fi

Background and aims: Magnetic resonance spectroscopy (MRS) and imaging (MRI) measure liver fat via the proton density fat fraction (PDFF), which reflects the tissue volume fraction of hepatic triacylglycerols. Intuitively, PDFF would be predicted to give lower values of steatosis compared to histology, which estimates the percentage of lipid droplet-laden hepatocytes out of all hepatocytes. We conducted a systematic review and meta-analysis of patient-level data to characterise the linearity and agreement between PDFF and histological steatosis across the full spectrum of fatty liver.

Method: Following the PRISMA guideline, we searched PubMed, Scopus, Web of Science, and the Cochrane Library until February 20, 2022, to identify all studies showing data on histological macrovesicular steatosis percentage and MRS/MRI-PDFF in adults with non-alcoholic fatty liver disease (NAFLD) or in living liver donor candidates. We invited authors to submit individual patient data for pooled analysis. Linearity between PDFF and histological steatosis was assessed using Pearson’s correlation, linear regression, and mixed-effects models. Agreement was assessed using Bland-Altman analysis and intraclass correlation coefficient (ICC) for continuous data and Cohen’s kappa for graded classification. Risk-of-bias was assessed using QUADAS-2.

Results: The eligible studies numbered 11 (3 with MRI-PDFF and 8 with MRS-PDFF; N=755). The relationship between PDFF and histological steatosis was highly linear (r=0.82, p<0.0001), and their values were fairly similar at low levels of liver fat (<5–10%). However, the higher the liver fat, the more PDFF underestimated steatosis as compared to histology (Fig. A). On the average, histological steatosis was 2.7-fold higher than PDFF, and the fractional underestimation by PDFF tended to increase from low to high levels of liver fat. A histological steatosis of 100% corresponded to an average PDFF of 33% (Fig. A). The ICC for absolute agreement between the measures was 0.43, denoting poor reliability, and for consistency between the measures 0.52, denoting moderate reliability. Use of the common NAFLD grading of steatosis (S0: <5%; S1: 5–33%; S2: 34–66%; S3: >66%) for PDFF resulted in gross misclassification of especially those patients with histological steatosis above grade S1 (kappa=0.32; Fig. B-C). Median PDFF values corresponding to each steatosis grade were 2.2% for S0, 8.0% for S1, 18.9% for S2, and 25.2% for S3.

Conclusion: Magnetic resonance and PDFF measurements of liver fat are fundamentally different. While they are in reasonable agreement at levels around the diagnostic threshold for NAFLD (~5%), histological steatosis far surpasses PDFF in patients with moderate-to-severe fatty liver. This difference should be acknowledged in guidelines for NAFLD to prevent misjudgement of the clinical status or treatment effect in patient care.

FRI117

Marked underestimation of liver fat content as measured by magnetic resonance versus histology—a systematic review and meta-analysis

Sami Qadri¹,², Kimmo Porthan ¹,², Anne Juuti³, Anne Penttilä³, Juhani DaBek¹,², Tiina E. Lehtimäki⁴, Wenla Seppänen⁴, Johanna Arola⁵, Perttu Arkkila⁶, Hannele Yki-Järvinen¹,².
¹University of Helsinki and Helsinki University Hospital, Department of Medicine, Helsinki, Finland; ²Minerva Foundation Institute for Medical Research, Helsinki, Finland; ³University of Helsinki and Helsinki University Hospital, Department of Gastrointestinal Surgery, Abdominal Centre, Helsinki, Finland; ⁴University of Helsinki and Helsinki University Hospital, Department of Gastrointestinal Surgery, Abdominal Centre, Helsinki, Finland; ⁵Helsinki University Hospital, HUS Medical Imaging Centre, Helsinki, Finland; ⁶University of Helsinki and Helsinki University Hospital, Department of Pathology, Helsinki, Finland; ⁷Helsinki University Hospital and University of Helsinki, Department of Gastroenterology, Abdominal Centre, Helsinki, Finland.

Email: hannele.yki-jarvinen@helsinki.fi

Background and aims: Magnetic resonance spectroscopy (MRS) and imaging (MRI) measure liver fat via the proton density fat fraction (PDFF), which reflects the tissue volume fraction of hepatic triacylglycerols. Intuitively, PDFF would be predicted to give lower values of steatosis compared to histology, which estimates the percentage of lipid droplet-laden hepatocytes out of all hepatocytes. We conducted a systematic review and meta-analysis of patient-level data to characterise the linearity and agreement between PDFF and histological steatosis across the full spectrum of fatty liver.

Method: Following the PRISMA guideline, we searched PubMed, Scopus, Web of Science, and the Cochrane Library until February 20, 2022, to identify all studies showing data on histological macrovesicular steatosis percentage and MRS/MRI-PDFF in adults with non-alcoholic fatty liver disease (NAFLD) or in living liver donor candidates. We invited authors to submit individual patient data for pooled analysis. Linearity between PDFF and histological steatosis was assessed using Pearson’s correlation, linear regression, and mixed-effects models. Agreement was assessed using Bland-Altman analysis and intraclass correlation coefficient (ICC) for continuous data and Cohen’s kappa for graded classification. Risk-of-bias was assessed using QUADAS-2.

Results: The eligible studies numbered 11 (3 with MRI-PDFF and 8 with MRS-PDFF; N=755). The relationship between PDFF and histological steatosis was highly linear (r=0.82, p<0.0001), and their values were fairly similar at low levels of liver fat (<5–10%). However, the higher the liver fat, the more PDFF underestimated steatosis as compared to histology (Fig. A). On the average, histological steatosis was 2.7-fold higher than PDFF, and the fractional underestimation by PDFF tended to increase from low to high levels of liver fat. A histological steatosis of 100% corresponded to an average PDFF of 33% (Fig. A). The ICC for absolute agreement between the measures was 0.43, denoting poor reliability, and for consistency between the measures 0.52, denoting moderate reliability. Use of the common NAFLD grading of steatosis (S0: <5%; S1: 5–33%; S2: 34–66%; S3: >66%) for PDFF resulted in gross misclassification of especially those patients with histological steatosis above grade S1 (kappa=0.32; Fig. B-C). Median PDFF values corresponding to each steatosis grade were 2.2% for S0, 8.0% for S1, 18.9% for S2, and 25.2% for S3.

Conclusion: Magnetic resonance and PDFF measurements of liver fat are fundamentally different. While they are in reasonable agreement at levels around the diagnostic threshold for NAFLD (~5%), histological steatosis far surpasses PDFF in patients with moderate-to-severe fatty liver. This difference should be acknowledged in guidelines for NAFLD to prevent misjudgement of the clinical status or treatment effect in patient care.

FRI118

Disease severity assessment of metabolic dysfunction-associated fatty liver disease in Taiwan

Jee-Fu Huang¹,²,³, Pei-Chien Tsai¹, Ching-I Huang³,³, Ming-Lun Yeh¹,³, Chung-Feng Huang¹,³, Chia-Yen Dai¹,³, Ming-Lung Yu¹,³, Wan-Long Chung¹,³, Kaohsiung Medical University Hospital, Hepatobiliary Division, Department of Internal Medicine, Kaohsiung, Taiwan; ²Kaohsiung Medical University Hospital, Hepatitis Center, Kaohsiung, Taiwan; ³Kaohsiung Medical University, Faculty of Internal Medicine, College of Medicine, Kaohsiung, Taiwan.

Email: waloch@kmu.edu.tw

Background and aims: Disease severity in metabolic dysfunction-associated fatty liver disease (MAFLD) has rarely been investigated in Asians. The study aimed to assess the fibrosis stages of MAFLD in a community-based cohort in Taiwan. We also aimed to compare the differences of features between different definitions as well as the interaction between metabolic factors and viral factors.

Method: The retrospective case-control study was performed in adult subjects participating liver disease screening in Southern Taiwan. The items of liver disease screening included HBsAg, anti-HCV, transaminases, and metabolic profiles in a voluntary basis. Abdominal sonography was performed for those who had viral hepatitis or elevated transaminase levels. According to the MAFLD diagnostic criteria we stratified the subjects into: group A for type 2 diabetes, group B for BMI≥23 kg/m², and group C of BMI<23 kg/m² subjects who carried at least 2 metabolic items, respectively. Disease severity was assessed by non-invasive Fibrosis-4 (FIB-4) Index. Advanced fibrosis was defined as FIB-4 value>3.25.

Results: From 2009 to 2020, there’re 5,180 subjects who had fatty liver index (FLI)>60 and has fatty liver on sonography. We recruited 1,948 subjects (mean age = 51.5 ± 13.4 years, females 52.1%) who met the diagnostic criteria of MAFLD and had completed results for fibrosis assessment. The study pool included 1,470 (75.5%) NBNC NAFLD subjects and 478 subjects possessing concomitant liver diseases such as viral hepatitis infections and alcoholism. There were 395 (20.3%) of Gr A, 1,818 (93.3%) of Gr B, and 44 (2.3%) subjects of Gr C, respectively. Advanced fibrosis on FIB-4 was observed in 79 (4.1%) subjects. The subjects of Gr C had a significantly higher percentage (p<0.001). Excluding those who had concomitant liver diseases, the subjects of Gr C still had a significantly higher percentage (p<0.001). Multivariate regression analysis demonstrated that HBV/HCV co-infection (OR = 16.74, 95% CI = 4.62–60.67, P<
HCV infection (OR = 8.83, 95% CI = 4.79–16.30, P < 0.001), Gr C (OR = 6.94, 95% CI = 2.65–18.15, P < 0.001), and age (OR = 1.08, 95% CI = 1.05–1.11, P < 0.001) were significant factors for predicting the subjects with advanced fibrosis.

**Conclusion:** Lean MAFLD Taiwanese subjects carrying metabolic abnormalities had a higher chance of advanced fibrosis than others in a community-based setting.

**FR119**

**Optical analysis of liver magnetic resonance images (MRI) 3 T to detect steatohepatitis features: the program DeMILI 3.0.**

Isabel Fernández-Lizaranzu1,2, Emilio Gomez-Gonzalez2, Sheila Cato Zambrano3, Rocío Montero-Vallejo1, Enrique Claudio Fernandez1, Juan Carlos Diaz Martin1, Rebeca Sigüenza4, Rocío Aller4, María Angeles Martin Prats5, Manuel Romero Gomez3, Instituto Biomedicina of Seville, Seville, Spain;2Universidad de Sevilla, Higher Technical School of Engineering (ETS), Group of Interdisciplinary Physics (GFI), Seville, Spain;3Virgen del Rocío University Hospital, Department of Radiology, Spain; Hospital Clínico Universitario de Valladolid, Spain;4Universidad de Sevilla, Department of Electronic Engineering, Spain;5Institute of Biomedicine of Sevilla, Seville, Spain

Email: ifernandez14@us.es

**Background and aims:** DeMILI in MRI 1.5 T has been proved as useful to detect steatohepatitis in patients with non-alcoholic fatty liver disease (NAFLD) (Gallego-Durán et al. Sci Rep 2016). The aim of this study was to evaluate the potential of optical processing methods applied to non-enhanced contrast liver 3 T MRI to predict steatohepatitis in NAFLD patients.

**Method:** Seventy-nine biopsy-proven NAFLD patients recruited between October 2019 and December 2021 at Virgen del Rocío University Hospital (HUVR, n = 68) and Valladolid Clinical University Hospital (HCUV, n = 11). Main characteristics: 50.6% female, 21.5% <45 years old and 32.9% >65 years old, 55.6% showed steatohepatitis in the liver biopsy. 3.0 T MRI was conducted using a whole-body Philips® scanner without contrast medium. 3 different sequences were performed in axial plane: SSFSE-T2 (Single Shot Fast Spin Echo T2-weighted), FAST-STIR (Fast Short inversion Time Inversion Recovery) and DYNAMIC. The entire liver was imaged and 6 consecutive slices, per each sequence, were manually selected covering the whole organ. 84 physical and mathematical feature descriptors (estimators) were computed from every image. Principal Component Analysis was performed to extract the main estimators related to steatohepatitis and two logistic regressions (LR) were built: The first one (DeMILI 3.0-v1) used estimators E63, E12 and E21, n = 43 HUVR patients for training, and n = 36 patients (25 HUVR + 11 HCUV) for validation. The second LR (DeMILI 3.0-v2) was built with estimators E70, E12 and E21 and the same cohort in different subsets: training n = 64 from HUVR, and validation n = 15 (4 HUVR + 11 HCUV). Receiver operating characteristic (ROC) curves were obtained.

**Results:** ROC curves for DeMILI 3.0-v1 and DeMILI 3.0-v2 are shown in Figure 1. The area under the ROC curves (AUROC) obtained were: i) for DeMILI 3.0-v1, AUROC = 0.7378 for training set and AUROC = 0.7307 for validation set, and ii) for DeMILI 3.0-v2, AUROC = 0.7958 for training set and AUROC = 0.6071 for validation set.

Figure: ROC curves for DeMILI 3.0.

**Conclusion:** Initial results with limited cohorts show that DeMILI 3.0 detects steatohepatitis in patients with NAFLD with a diagnosis accuracy of 0.73 (DeMILI 3.0-v1). Validation cohorts include patients from other center than training. DeMILI 3.0-v1 yields results close to DeMILI using 1.5 T MRI.

**FR1120**

The fibrosis-4 cut-off value for significant fibrosis is dependent on the type of non-alcoholic fatty liver disease patients

Leen Heyens1,2,3, Wouter Robaeys1,2, Christophe Van Steenkiste4,5, Sven Franqué6, Geert Robaeys1,2,7, Hasselt University, Faculty of Life Sciences and Medicine, Hasselt, Belgium; Ziekenhuis Oost-Limburg, Gastro-enterology and Hepatology, Genk, Belgium; Maastricht University, Faculty of Health, Medicine and Life Sciences, Maastricht, Netherlands; Maria Middelares, Gastro-enterology and Hepatology, Gent, Belgium; University of Antwerp, Gastro-enterology and Hepatology, Antwerp, Belgium; Antwerp University Hospital, Gastro-enterology and Hepatology, Edegem, Belgium; UZ Leuven Gastruisberg Campus, Gastro-enterology, Leuven, Belgium

Email: leen.heyens@uhasselt.be

**Background and aims:** Non-alcoholic fatty liver disease (NAFLD) has become the most frequent cause of chronic liver disease. The fibrosis stage has been identified as the most important predictor of prognosis. The Fibrosis-4 (FIB-4) is an easy-to-use non-invasive score to predict fibrosis based on routine blood parameters. However, we previously showed that the 1.3 FIB-4 cut-off value had a low performance to detect significant fibrosis (≥F2) in a primary care (PC) population. We aimed to determine whether NAFLD-group-specific optimal FIB-4 cut-off values can be determined to identify patients with a high likelihood of ≥F2, considered an at-risk population to be referred for further management.

**Method:** In a prospective study in the Belgian regions of Limburg, East-Flanders, and Antwerp, patients were screened in seven PC practices. Type 2 diabetes mellitus patients (T2DM) were screened in the hospital of Ziekenhuis Oost-Limburg. As a proxy of the fibrosis stage, liver stiffness was determined using Vibration Controlled Transient Elastography (VCTE) by FibroScan® (Echosens, France) and used as the reference method. The FIB-4 was calculated based on recent laboratory data from the electronic patient file. The Youden Index (J) was used to determine the optimal cut-off value for detecting ≥F2 (>7.9 kPa for the M-probe and >7.2 kPa for the XL-probe) in three populations: PC (unselected all-comers), T2DM screened in PC (T2DM-PC, PC subgroup), T2DM screened in a hospital (T2DM-H).
Results: Of the 816 (424 (52.0%) PC, 103 (12.6%) T2DM PC, and 289 (35.4%) T2DM-H) screened patients, 534 (65.4%) had FIB-4 values and no other causes of steatosis but NAFLD. Of these, 275 (51.5%) were male, median age was 63 (26–71) years, median BMI 29.8 (26.2–33.46) kg/m², median waist circumference 104.0 (97.0–113.0) cm for men and 80.8 (86.1–110.0) cm for women, and 276 (51.9%) had T2DM. The number of patients with ≥F2 was 30 (11.8%), 20 (30.3%), and 96 (45.7%) for the PC, T2DM-PC, and T2DM-H cohorts. Using logistic regression, both FIB-4 (p < 0.05) and the type of NAFLD-group significantly (p < 0.05) contributed to ≥F2. The area under the operating curve (AUROC) of the model was 0.76 compared to an AUROC of 0.61 using only FIB-4. The maximum J was 0.40461 and corresponded to a sensitivity of 0.61 and specificity of 0.80. Using the linear predictor, the optimal cut-off value per population was 4.3 for the PC cohort, 2.3 for the T2DM-PC, and 0.66 for the T2DM-H cohort. These cut-off values were not influenced by age or the grade of steatosis as measured by controlled attenuation parameter (CAP).

Conclusion: The optimal cut-off value of the FIB-4 score for detecting NAFLD-associated significant fibrosis depends on the patient groups’ characteristics, potentially resulting from the different prevalence of the condition in the respective groups. However, the cut-off values were not influenced by age or the severity of the steatosis.

FRI121
Developing an algorithm to predict NAFLD in clinical trial volunteers-interim report NCT04873258
Jörg Täubel1,2,3, Dominic Pimenta4, Aviva Petrie5, Lydia Sulaiman6, Ulrike Lorch1, Kevin Moore5.

Background and aims: Non-alcoholic fatty liver disease (NAFLD) affects around 1 in 4 of the global adult population, and ranges in severity from benign fatty liver infiltration, to hepatitis, cirrhosis and hepatocellular carcinoma. NAFLD has important implications for clinical trial volunteers as an occult co-morbidity. NAFLD may modulate drug metabolism, and studies have suggested that Grade III/IV liver reactions are 4x commoner in healthy volunteers with probable NAFLD than without. We therefore aimed to develop a non-invasive tool, utilizing new technology, to predict NAFLD in this population. This is our interim report (NCT04873258)

Method: This is an ongoing observational cross-sectional study design. Volunteers attend the unit for a single day of biomarker assessment, including bioimpedance vector analysis (%visceral fat, total body fat% and skeletal muscle %), anthropometric measurement (BMI, waist circumference), and lab bloods. A FibroScan is performed as a pragmatic gold standard ‘outcome’ for NAFLD, and E (fibrosis) and CAP (steatosis) scores are recorded. Traditional multivariable linear and logistic regression is performed, correlating biomarkers with linear E and CAP scores, and ‘significant’ disease (≥F2, E > 7.5 kPa and ≥S2, Cap ≥ 260 dB) respectively. Alongside this machine learning models are trained (Python {sklearn, TensorFlow}) and performance compared.

Results: Interim results: 290 individuals (of extended target 1500) with demographics as follows; 61% male, 51.5% Caucasian, average age of 39.4 years, 40% of the cohort had diabetes. The overall prevalence of significant fibrosis (E score ≥ 7.5 kPa) was 11.4% and the prevalence of significant steatosis (CAP ≥ 260 dB) was 35.6%. A logistic regression model was trained for E and CAP scores, identifying key features in the dataset as waist circumference and GGT. A prototype clinical score was derived, with an AUC of 0.81 for E and 0.89 for CAP scores. Machine learning models were compared, with the best performing model being Gaussian Naive Bayes for E (AUC 0.82) and Decision Tree for CAP (0.79). A clinical tool based on a score derived from logistic regression coefficients was created (Figure) for use by physicians to gauge the risk of NAFLD in volunteers, using two variables (GGT and waist circumference), with high sensitivity and acceptable specificity (E score sensitivity 90%, specificity 45%, CAP score sensitivity 85.9%, specificity 81.9%).

Conclusion: Our early interim analysis shows promising results, sufficient to prototype a clinical tool with high sensitivity and acceptable specificity for screening out individuals in clinical trials at high probability of occult NAFLD and/or fibrosis. Future work to develop the underlying model, advance machine learning models to further improve performance, and deliver to clinic is underway.

FRI122
Correlation of ultrasound derived fat fraction (UDFF) with MRI (PDFF): possibilities and analysis of confounding factors
Reinhard Kubale1,2, Marcin Krawczyk3,4, Paul Lessenich1, Arno Bücker1, Aaron Engel5, Andrzej Milkowski5, Guenther Schneider1,2, Saarland University Hospital, Homburg, Germany;2Saarland University, Saarbrücken, Germany;3Saarland University Hospital, Department of Internal Medicine II- Gastroenterology, Hepatology, Endocrinology, Diabetology, and Nutritional Medicine, Homburg, Germany;4Innere II, Homburg/Saar, Germany;5Siemens Healthineers, Forchheim, Germany

Background and aims: Ultrasound derived fat fraction (UDFF) is a non-invasive tool to screen for NAFLD, and E (fibrosis) and CAP scores are recorded. Traditional multivariable linear and logistic regression is performed, correlating biomarkers with linear E and CAP scores, and ‘significant’ disease (≥F2, E > 7.5 kPa and ≥S2, Cap ≥ 260 dB) respectively. Alongside this machine learning models are trained (Python {sklearn, TensorFlow}) and performance compared.

Method: This is an ongoing observational cross-sectional study design. Volunteers attend the unit for a single day of biomarker assessment, including bioimpedance vector analysis (%visceral fat, total body fat% and skeletal muscle %), anthropometric measurement (BMI, waist circumference), and lab bloods. A FibroScan is performed as a pragmatic gold standard ‘outcome’ for NAFLD, and E (fibrosis) and CAP (steatosis) scores are recorded. Traditional multivariable linear and logistic regression is performed, correlating biomarkers with linear E and CAP scores, and ‘significant’ disease (≥F2, E > 7.5 kPa and ≥S2, Cap ≥ 260 dB) respectively. Alongside this machine learning models are trained (Python {sklearn, TensorFlow}) and performance compared.

Results: Interim results: 290 individuals (of extended target 1500) with demographics as follows; 61% male, 51.5% Caucasian, average age of 39.4 years, 40% of the cohort had diabetes. The overall prevalence of significant fibrosis (E score ≥ 7.5 kPa) was 11.4% and the prevalence of significant steatosis (CAP ≥ 260 dB) was 35.6%. A logistic regression model was trained for E and CAP scores, identifying key features in the dataset as waist circumference and GGT. A prototype clinical score was derived, with an AUC of 0.81 for E and 0.89 for CAP scores. Machine learning models were compared, with the best performing model being Gaussian Naive Bayes for E (AUC 0.82) and Decision Tree for CAP (0.79). A clinical tool based on a score derived from logistic regression coefficients was created (Figure) for use by physicians to gauge the risk of NAFLD in volunteers, using two variables (GGT and waist circumference), with high sensitivity and acceptable specificity (E score sensitivity 90%, specificity 45%, CAP score sensitivity 85.9%, specificity 81.9%).
consecutive patients (112 male, 82 female), who received a liver MRI for clinical reasons.

Results: In the pilot study (Study I) PDFF of the whole liver (10.3 ± 9.4%), was significantly higher than in the corresponding ROI (8.65 ± 9.6%). The correlation of PDFF-measurements with scan heads (5C1, DAX, 6C1) were r = 0.94/0.91 and 0.85. Repeated measurements showed values of r = 0.99/0.97 and 0.89 with best reproducibility of the DAX. Measurements before, 1, 3 and 5 hours after meal showed no significant differences between the time points (Friedmann-Test).

The main study shows a significant difference in PDFF-measurement of the whole liver (11.6 ± 9.1%) and the ROI (8.9 ± 9.5%). Although AC and BSC are not linear related to PDFF the model with both parameters shows a significant correlation between UDFF and PDFF of the whole liver and the corresponding ROI and Voxel for all patients r = 0.80/0.7 and 0.6 (6C1). Bland-Altman shows, that main confounding factors are severe liver cirrhosis with a small RLL, chemotherapy/lipiodol application, sarcoidosis and amyloidosis. Problems in MRI arose in severe Hemochromatosis, patients over 150 kg due to artifacts.

Conclusion: UDFF shows a strong positive correlation with PDFF. Confounding factors could be identified hypothetically allowing for improvement in the future. UDFF could be a screening tool for early diagnosis of NAFLD and a biomarker for therapy control.

FRI123
ELF to identify NASH and fibrosis in non-alcohol related fatty liver disease
Richard Parker1, Peter Eddowes2, Natasha McDonald3, Phillip N. Newsome2, Gideon Hirschfield4, Jonathan Fallowfield3, Ian Rowe5. 1Leeds Teaching Hospital Trust, Leeds Liver Unit, Leeds, United Kingdom; 2University of Birmingham, Centre for Liver Research, Birmingham, United Kingdom; 3University of Birmingham, Centre for Liver Research, Birmingham, United Kingdom; 4MRC/University of Edinburgh Centre for Inflammation Research, Queen’s Medical Research Institute, Edinburgh, Edinburgh, United Kingdom; 5University of Toronto, Division of Gastroenterology, Toronto, Canada; 6University of Leeds, Leeds Institute for Medical Research, Leeds, United Kingdom
Email: richardparker@nhs.net

Background and aims: The current paradigm for eligibility for trials in NAFLD requires the presence of NASH and fibrosis of particular severity. We examined whether the ELF score could be repurposed to predict both NASH and fibrosis.

Method: A cohort of 240 patients with biopsy-proven NAFLD was used. Treatment threshold was NAS ≥4 (as per the FLIP algorithm) and fibrosis grade of greater than 2. The cohort was split 60:40 into modelling and validation groups. Internal validation of modelling was done using 2000 bootstrapped samples. Test performance was evaluated with AUROC analysis. Low and high cut-offs at 90% sensitivity or specificity respectively were calculated in the modelling cohort, and negative and positive predictive values (NPV, PPV) and positive and negative diagnostic likelihood ratios (PDLR, NDLR)
calculated. The model was calibrated graphically in the validation cohort and test performance confirmed. All statistical tests were done in R using pROC, rms and geepack packages.

Results: The average age of the cohort was 55 years, 117 (66%) were male. All components of the ELF score correlated with NAS and were significantly different between patients with NAS <4 or ≥4. A model (‘ELF-t’) that included all of the ELF parameters (HA, P3P and TIMP-1) performed best to identify cases suitable for trials or treatment (AUROC 0.74). At a low cut-off ELF-t had a NPV of 91% and the high cut-off gave a PPV of 92%. NDLR was 0.27 (0.12–0.607), PDLR 2.47 (1.15–5.31). Calibration was good in the validation cohort with similar test performance (AUC 0.79, NPV 91%, PPV 93%).

Conclusion: The constituent markers of the ELF test can be repurposed to assess the likelihood of NAFLD with sufficient activity and scarring to meet common eligibility criteria for clinical trials, which are likely to translate into a paradigm for treatment as new drugs come to market. This provides a non-invasive method for assessing patients as an alternative to liver biopsy.

FR1124
Performance of the Steatosis-Associated Fibrosis Estimator (SAFE) to predict F2 fibrosis and higher in a cohort of South Korean patients with non-alcoholic fatty liver disease (NAFLD)
Vivek Churu1, Allison Kwong1, Ajitha Mallathara1, Eileen Yoon2, Dae Won Kim2, W Ray Kim3, 1Stanford University School of Medicine, Stanford, United States; 2Hanyang University College of Medicine, Korea, Rep. of South
Email: vcharu@stanford.edu

Background and aims: The Steatosis-Associated Fibrosis Estimator (SAFE) score is a recently developed scoring system to categorize NAFLD patients by their risk of having significant liver fibrosis (F2 or higher). Here we evaluate the performance of the SAFE score in predicting F2 fibrosis based on transient elastography (FibroScan) measurements in a cohort of South Korean patients with NAFLD.

Method: We identified a cohort of adult patients with a clinical diagnosis of NAFLD who underwent FibroScan at Hanyang University from 2020 to 2022. Using the available laboratory information, we calculated SAFE, Fibrosis-4 (FIB-4) and the NAFLD fibrosis score (NFS) for each patient. Our outcome of interest was F2 fibrosis or higher, and a FibroScan threshold of greater than 7 kPa was used. We computed the area under the receiver operating curves (AUROC) to quantitate the performance of each non-invasive score to predict F2 fibrosis or greater. We calculated the sensitivity, specificity, positive predictive value and negative predictive values of the SAFE score using an apriori determined threshold of greater than or equal to 100.

Results: We identified 749 patients with a clinical diagnosis of NAFLD who underwent FibroScan testing with clinical/laboratory data to generate SAFE, FIB-4 and NFS scores (Table). SAFE, FIB-4 and NFS were strongly correlated with each other in this cohort (pairwise Spearman’s correlations: SAFE-FIB4: 0.83; SAFE-NFS: 0.80; FIB4-NFS: 0.84). We estimated the AUROC for each fibrosis estimator (Table), and found that the AUROC for the SAFE score (0.76) was significantly higher than that for FIB-4 (0.64) and NFS (0.63) (p-values for DeLong’s tests: SAFE-FIB4, <2.2e-16; SAFE-NFS, 6.352e-16). FIB-4 and NFS scores had similar AUROC (0.64 and 0.63, p-value for DeLong’s test: 0.5822). Using a threshold for the SAFE score of greater than 100 to identify high-risk patients would result in a sensitivity of 0.66 (95%CI: 0.58–0.73), specificity of 0.74 (95%CI: 0.70–0.78), positive predictive value of 0.42 (95%CI: 0.36–0.48) and negative predictive value of 0.88 (95%CI: 0.85–0.91) for predicting F2 fibrosis or higher based on FibroScan measurements.

Conclusion: In a cohort of Korean adults with NAFLD, the SAFE score performs better than FIB-4 or NFS to predict F2 fibrosis or higher based on FibroScan measurement. A SAFE threshold of greater than 100 has reasonable, but not perfect, negative predictive value for identifying F2 fibrosis or greater in this cohort (0.88). Evaluating the performance of the SAFE score in additional diverse cohorts is essential to assess its utility in identifying patients at low risk of having clinically significant fibrosis.

FR1125
FIB-4 combined with positron emission tomography biomarkers detects fibrotic NASH
Sean Romeo1, Connie Chan2, Blake Shaw3, Karen Matsukuma4, Michael Corwin1, Victoria Lyo5, Shuai Chen3, Guobao Wang3, Souvik Sarkar1, 1University of California, Davis, Internal Medicine/Gastroenterology and Hepatology, United States; 2UC Davis School of Medicine, Sacramento, United States; 3University of California, Davis, Public Health Sciences/Biostatistics, United States; 4University of California, Davis, Pathology and Laboratory Medicine, United States; 5University of California, Davis, Radiology, United States; 6University of California, Davis, Surgery, United States; 7Florida Research Institute, Lakewood Ranch, United States
Email: ssarkar@ucdavis.edu

Background and aims: Non-alcoholic steatohepatitis (NASH) is a severe form of non-alcoholic fatty liver disease (NAFLD) that is associated with liver cirrhosis and hepatocellular cancer. Methods for diagnosing NASH without liver biopsy are limited, therefore presenting an urgency to noninvasively detect NASH by characterizing features: steatosis, inflammation, and fibrosis. We combined the well-established non-invasive fibrosis-4 (FIB-4) measurement with a recent 18F-fluorodeoxyglucose (FDG) positron emission tomography/computed tomography (PET/CT) imaging approach for NASH to elucidate imaging determinant of fibrotic NASH.

Method: The study was approved by the institutional review board. Patients ≥18 years with NAFLD who had undergone liver biopsy were enrolled. FDG transport rate (K1) by dynamic PET and CT Hounsfield units (CTHU) were determined from liver regions-of-interest (ROI) as previously defined, while FIB-4 was calculated from serum by an established criterion. Liver biopsies were scored per NASH-CRN (Clinical Research Network) criteria. Fibrotic NASH was defined as NAFLD activity score (NAS) ≥4 with Kleiner fibrosis stage ≥2. Severe fibrotic NASH was defined as NAS ≥5, plus fibrosis stage ≥3. Correlations among parameters were calculated using the
Spearman correlation. Receiver operating characteristics (ROC) analyses were performed with cut-off selected based on Youden’s index, where FIB-4, K1, and CTHU were combined using logistic regression.

**Results:** Of 45 enrolled patients, 31 were female, 54 ± 13 years, and BMI 34.0 ± 5.7 kg/m²; 16% of patients had inflammation >3, while 58% had NAS ≥4 and 29% with fibrosis ≥3. FIB-4 correlated with fibrosis significantly (r = 0.58, p < 0.001), as expected, but not with NAS (r = 0.2, p = 0.178). K1 and CTHU showed significant correlations with NAS. As shown prior, the dual-variate model of K1+CTHU could detect clinical NASH but not fibrotic NASH. When FIB-4 score was combined in the model it was able to detect fibrotic NASH with an AUC of 0.781 (Figure 1) and severe fibrotic NASH with an AUC of 0.845. The triple variate model of 1.46001*K1 – (Figure 1) and severe fibrotic NASH with an AUC of 0.845. The triple variate model of 1.46001*K1–0.04009*CTHU + 1.27309*FIB-4 ≥1.574408, was able to predict fibrotic NASH with a specificity of 93% and a specificity of 64%. While 3.27447*K1 + 0.00597*CTHU + 0.99330*FIB-4 ≥−1.296305 predicted severe fibrotic NASH with a sensitivity of 91% and specificity 68%.

**Conclusion:** Combination of non-invasive serum and imaging tests enabled detection of clinical fibrotic NASH. Studies in larger and diverse cohorts will enable establishing this tool for determination of clinical changes in NAFLD patients.

**FR1146**

Hepatic angiocrine HGF attenuates liver fibrogenesis via modulation of PDK1/AKT axis

Jianye Wang1, Sarah Schulze1, Victor Olsavszky2, Kai Schledzewski2, Cyrill Géraud2, Helmut Fries1, Norbert Hueser1, Daniel Hartmann1.

1 Klinikum rechts der Isar der Technischen Universität München, München, Germany; 2 Medical Faculty Mannheim, Heidelberg University, Mannheim, Germany

Email: jianye.wang@tum.de

**Background and aims:** Hepatocyte growth factor (HGF) is a complete hepatic mitogen and is believed to play a role in liver fibrogenesis and hepatocarcinogenesis. Liver sinusoidal endothelial cells (LSEC) can recruit inflammatory cells by releasing angiocrine signals to produce hepatic mitogen and is believed to play a role in liver fibrogenesis and cirrhosis, but the precise contributions of HGF from LSEC to liver fibrosis remain elucidated.

**Method:** To investigate the effects of hepatic angiocrine HGF on liver fibrogenesis, Stab2-CreER HGFfl/fl (HGF-Sec-KO) mice, in which HGF is specifically switched off in LSEC, were used. Carbon tetrachloride (CCL4) injection was performed in these mice and the kinetics of the ratio of liver to body weight, immunohistochemistry for liver fibrosis, Western blot and RT-PCR for fibrotic markers, HGF/c-MET signaling pathways and cell cycle-associated genes were determined after initiation of cirrhosis.

**Results:** We found that HGF-Sec-KO mice showed no difference in the liver-to-body-weight ratio compared to the control group after early-stage CCL4 treatment. After fibrogenesis, HGF-Sec-KO mice had a higher expression of collagen 1A1 and alpha-SMA and the proliferation of hepatocytes was significantly impaired in HGF-Sec-KO mice. In addition, the LSEC-specific HGF deficiency reduced the c-met level and thus deactivated the PD1 (3-phosphoinositide-dependent protein kinase-1)/Akt pathway while hepatic angiocrine HGF did not alter immune cell infiltration.

**Conclusion:** The hepatic angiocrine HGF signaling pathway plays a crucial role in the early stages of liver fibrogenesis. The hepatic angiocrine HGF signaling pathway is essential not only for liver fibrosis.
recovery during fibrogenesis, but also for the growth of the liver and even the entire organism.

**Key words:** hepatocyte growth factor (HGF), liver sinusoidal endothelial cells (LSEC), hepatocytes, liver, fibrogenesis, liver cirrhosis

**FR1147**

Bisphosphonate-loaded nanogels attenuate liver fibrosis by repolarization of M2-type macrophages

Leonard Kaps1, Anne Huppertzberg2, Niklas Choteschovsky1, Adrián Kletenza1, Feyza Durak2, Barbara Schoers3, Mustafa Diken3, Emma Eicher1, Sebastian Rosigleit1, Sascha Schmitt2, Christian Leis4, Friedrich Foerster1, Ernesto Bockamp1, Bruno Degeest5, Federico Marini6, Kalioi Koynov7, Stefan Tenzer4, Detlef Schuppan1, Lutz Nuhn8

1University Medical Center Mainz, Institute of Translational Immunology and Research Center for Immune Therapy, Mainz, Germany; 2Max Planck Institute for Polymer Research, Mainz, Germany; 3University Medical Center Mainz, TRON-Translational Oncology, Mainz, Germany; 4University Medical Center Mainz, Institute of Immunology, Mainz, Germany; 5Ghent University, Department of Pharmacology and Cancer Research Institute Ghent (CRIG), Belgium, Belgium; 6University Medical Center Mainz, Institute of Medical Biostatistics, Epidemiology and Informatics, Mainz, Germany; 7Max Planck Institute for Polymer Research, Mainz

Email: nuhn@uni-mainz.de

**Background and aims:** In liver fibrosis, M2-type macrophages promote the replacement of functional parenchyma by collagen-rich scar tissue. Bisphosphonates impaired the polarization towards M2-type macrophages and demonstrated an anti-fibrotic-tumor effect in murine models of mesothelioma and liver cancer [V. JD et al., Br J Cancer. 2010; T. L. Rogers et al., J Transl Med. 2011]. But, pharmacokinetics of bisphosphonates are poor for liver targeting as they are rapidly excreted by the kidneys after intravenous (iv) application. Here, we aimed to treat liver fibrosis by repolarizing liver M2-type macrophages towards an antifibrotic M1-type via a biocompatible, pH-degradable, nanogel carrier system conjugated to the bisphosphonate alendronate (AL).

**Method:** In primary murine macrophages, AL/NP (30 μM AL) induced no cytotoxic effect and repolarized M2-type polarized macrophages towards a M1-type, increasing the expression of the M1-type related markers TNF-α, CCL-2 and downregulated the M2-type markers IL-10 and chitinase YM-1 on the transcript and protein level as determined via qPCR and flowcytometry (FACS).

**Results:** After iv injection in CCL4 fibrotic Balb/c mice, more than 80% of near-infrared fluorescence labeled (CS800)-AL/NP rapidly accumulated in the liver, whereas CS800-AL were instantly cleared via the kidneys. On the cellular level, CS800-AL/NP were effectively engulfed by non-parenchymal cells (e.g. liver macrophages), while the AL/NP’s uptake was significantly lower in parenchymal cells (hepatocytes) as determined by FACS. CS800-AL/NP were well tolerated and showed no overt toxicity. For fibrosis induction, Balb/c mice were gavaged with CCL4 for 5 weeks. At week 4, mice received two iv injections of AL/NP (2 mg/kg or 4 mg/kg AL) per week while control groups received equal concentrations of AL or NP respectively. At the end of week 5, mice were sacrificed and liver collagen and the surrogate marker α-SMA were significantly reduced by physiological levels in AL/NP treated vs. control mice as determined by HYP quantification, Sirius Red readout and immunohistochemistry, while free AL and NP had no significant effect. Transcriptomic and proteomic data from total liver tissue of AL/NP (~4 mg/kg AL) treated vs. control mice (n = 3) revealed an upregulation of proinflammatory pathways and an enrichment of M1-type macrophages related genes in the treated mice, suggesting that AL/NP treatment triggers a switch from M2- to M1-type macrophages. In addition, we showed a downregulation of the M2-type markers YM-1, CD206 and IL-10 in the treated vs. control fibrotic liver both on the transcript and protein expression level.

**Conclusion:** This nanogel platform and the presented delivered drug conjugate AL/NP may serve as a novel, highly effective tool to treat liver fibrosis and possibly other diseases that are dominated by M2-type macrophages.

**FR1148**

Preclinical evaluation of the calpain inhibitor BLD-3051 as a therapeutic strategy for liver fibrosis

C. Wong1, J.-X. Huang1, W. Yu1, P. Ibrahim1, Ravi Rajagopalan1, 1Blade Therapeutics, Inc, South San Francisco, United States

Email: rrajagopalan@blademed.com

**Background and aims:** Calpains are a family of non-lysosomal intracellular calcium-dependent cysteine proteases that perform limited proteolytic cleavage of its substrates that in turn modulate a variety of signaling pathways controlling phenotypic effects like cell proliferation, migration, differentiation, and apoptosis. Elevated dimeric calpain activity levels are implicated in a variety of disease pathologies including fibrotic diseases. Additionally, calpain knockouts and small molecule dimeric calpain inhibitors are efficacious in animal models of fibrosis. We have generated multiple calpain inhibitors with significantly improved potency, protease selectivity, and ADMET properties that may represent important new anti-fibrotic agents. Here, we describe the properties of BLD-3051, a small molecule dimeric calpain inhibitor and characterize its activity in a therapeutic model of liver fibrosis.

**Method:** 8-week-old C57BL/6 mice were fed a choline-deficient, L-amino acid, high fat diet (CDAHFD) for the entire 10-week study duration. Oral gavage dosing of BLD-3051 was initiated on week 5 of CDAHFD and continued for 6 weeks. Once daily (QD) doses of 60 and 200 mg/kg were evaluated. Body and liver weight and liver enzyme panel data were collected. Histopathology by modified NAFLD activity score (NAS) and liver hydroxy-proline levels were used to assess anti-fibrotic efficacy.

**Results:** BLD-3051 reduced NAS scores and liver hydroxy-proline levels in a dose-dependent manner with BID dosing being more efficacious. The lowering of NAS by BLD-3051 is largely driven by an anti-fibrotic effect.

**Conclusion:** BLD-3051 is a potent, selective, orally bioavailable calpain inhibitor that when dosed therapeutically shows robust anti-fibrotic effects against multiple endpoints in a CDAHFD induced model of liver fibrosis. BLD-3051 is currently in preclinical development.

**POSTER PRESENTATIONS**
FR1149
Experimental fibrosis alters matrix-bound vesicles cargo that do not revert after histologic recovery
Toshifumi Sato1,2, Bashar Matour3, Jiang Li4, Michael Merchant4, Daniel Wilkey4, Kenichi Bejjimal5, Stephen Badylak1,5, George Hussey5,6, Melanie Scott3,7, Gavin Arteel2,7,1 Juntendo University Hospital, Gastroenterology, Bunkyo City, Japan; 2University of Pittsburgh-Department of Medicine, Gastroenterology, Pittsburgh, United States; 3University of Pittsburgh, Surgery, Pittsburgh, United States; 4University of Louisville, Medicine, Louisville, United States; 5University of Pittsburgh, McGowan Institute for Regenerative Research, Pittsburgh, United States; 6University of Pittsburgh, Pathology, Pittsburgh, United States; 7Pittsburgh Liver Research Center, University of Pittsburgh, Pittsburgh, United States
Email: tosato@juntendo.ac.jp

Background and aims: Although it is now understood that hepatic fibrosis can resolve, potential therapies to enhance fibrosis resolution are lacking. MBV are nanometer-sized vesicles bound within the ECM collagen network. Changes in MBV cargo may contribute, at least in part, to the phenotypic changes driven by fibrosis and recovery.

Method: Fibrosis was induced by injecting male C57Bl/6j mice with CCl4 (1 ml/kg 2 x /wk 4wk); animals were sacrificed 1–28 days later. Liver injury and fibrosis was monitored by chemical, histology and gene expression. MBV were extracted from the livers of mice and the trypsinized MBV proteome cargo was analyzed by LC-MS/MS analysis using a Proxeon EASY-nLC 1000 UHPLC and nanoelectrospray ionization into an Orbitrap Elite mass spectrometer. Feature data were extracted and analyzed using Proteome Discoverer v2.4. Hierarchical clustering of significantly-changed MBV proteins was performed using StringDB and KEGG classification. To investigate the effect of MBV on the recovery of liver fibrosis, normal MBV from porcine urinary bladder (30 mg/mouse i.p.) were injected for up to 2 weeks after cessation of CCl4.

Results: Fibrosis caused by CCl4 rapidly resolved after cessation, reverting to almost normal histology and expression after 28 d recovery. The amount and type of proteins associated with the MBV tended to decrease in fibrosis, which was not reversed even after fibrosis recovery. StringDB and KEGG analysis indicated that the proteins lost in fibrosis/recovery were predominantly RNA-binding proteins associated with the ribosome, which may also impact the RNA cargo of the MBV. Some mice injected with normal MBV accelerated the fibrotic resolution.

Conclusion: Liver MBV alter their protein cargo in response to experimental fibrosis. Importantly, these changes do not revert to baseline levels even after almost complete histological recovery of fibrosis. These data suggest MBV may be a novel prospect for mechanistic insight into hepatic disease progression and recovery.

FR1150
Hepatocyte cell-specific deletion of cathepsin D does not affect liver inflammation and fibrosis during cholestatic-induced liver fibrosis
Maria Fernandez-Fernandez1,2, Paloma Ruiz-Blazquez2,3, Valeria Pistorio1,2, Susana Núñez2,3, M. Carmen Garcia-Ruiz2,5,6,7, José Fernandez-Checa2,5,6,7, Anna Moles2,3,6,1 Institute of Biomedical Research of Barcelona (IBB-CISC), Experimental Pathology, Barcelona, Spain; 2CiberEHD, Spain; 3Institute of Biomedical Research of Barcelona (IBB-CISC), Experimental Pathology, Barcelona, Spain; 4University of Naples Federico II, Italy; 5Institute of Biomedical Research of Barcelona (IBB-CISC), Cell Death and Proliferation, Barcelona, Spain; 6DIBAPS, Barcelona, Spain; 7USC Research Center for ALPD, United States
Email: anna.moles.fernandez@gmail.com

Background and aims: During liver fibrosis proteolytic activity is regulated in a timely manner in infiltrating and liver-resident cells depending on the cellular demands and controls not only matrix turnover but also, the activation and repression of growth factors and chemokines. Despite our growing understanding of the roles played by lysosomal proteases, cathepsins, in liver fibrosis, our knowledge of their specific targets and signaling networks remains limited. Thus, the aim of this study was to analyse cathepsin D (CtsD) cell-specific role in hepatocytes during liver fibrosis.

Method: To study the cell-specific role of CtsD we generated a novel knock-out mouse strain by breeding Albumin Cre (hepatocytes) mice with CtsD floxed mice. CtsD cell-specific deletion was confirmed by CtsD WB in primary mouse hepatocytes and dual IF (F4/80-CtsD) in liver sections. Fibrosis was established using bile duct ligation (BDL) for 14 days or chronic administration of CCl4 (0.5 μl/g) twice a week for 8 weeks in CtsDΔF and CtsDΔstep mice. Liver damage was determined by serum ALT and H&E staining in liver sections. CtsD was assessed by enzymatic activity assay and RTPCR. Fibrosis was analysed by Sirius Red staining, α-SMA and CtsD ΔF. Liver inflammation was determined by F4/80 and TNF-α, CCL2 and CCL3 RTPCR.

Results: First we determined CtsD expression in mouse fibrotic livers, demonstrating CtsD presence in hepatocytes and macrophages. CtsD cell-specific deletion in hepatocytes was validated by CtsD WB in primary mouse hepatocytes and dual IF (F4/80-CtsD) in liver section from CtsDΔF and CtsDΔstep mice. Of note, CtsD expression remained unaffected in liver non-parenchymal cells. In addition, adult unchallenged CtsDΔstep mice displayed normal liver damage determined by ALT and H&E staining in liver sections. Next, fibrosis was established for 14d using BDL. CtsD deletion in CtsDΔstep livers was confirmed by CtsD activity assay and gene expression. CtsD deletion in hepatocytes, did not affect liver damage (ALT) and liver fibrosis as determined by Sirius red staining, α-SMA IHP and hepatic α-SMA, Col1A1 and TGF-beta gene expression. Furthermore, liver inflammation was also not significantly affected in CtsDΔstep mice after BDL as assessed by NIMP and F4/80 IHP and TNF-α, CCL2 and CCL3 gene expression. In agreement, no significant changes in liver damage, fibrosis and inflammation were observed after chronic CCl4 administration between CtsDΔF and CtsDΔstep mice supporting our results in the BDL model.

Conclusion: CtsD expressed in hepatocytes does not play an essential contribution to liver fibrosis development after cholestatic-induced liver injury.

FR1151
The therapeutic potential of alpha v integrins in liver fibrosis
Syedia Rahman1,2,6, Guruprasad Alitha1,2, Jane Grove1,3, K. Tao Pun4, James Koper7, Andrew Bennett1,2,3, NHR Nottingham Biomedical Research Centre, Nottingham University Hospitals NHS Trust and University of Nottingham, Nottingham, United Kingdom; 2FRAME Alternatives Laboratory, University of Nottingham Medical School, Life Sciences, Nottingham, United Kingdom; 3Nottingham Digestive Diseases Centre, Medicine, Nottingham, United Kingdom; 4GlaxoSmithKline, Novel Human Genetics Research Unit, United Kingdom
Email: syedia.rahman@nottingham.ac.uk

Background and aims: Hepatic stellate cells (HSC) are the primary effector cells in liver fibrosis and they secrete inactive transforming growth factor beta (TGFbeta) which, when activated through proteins known as alpha v integrins, contributes to liver fibrosis. These integrins are composed of beta 1, 3, 5, 6 and 8 subunits. Specific inhibitors which target alpha v integrins and their particular beta subunit have shown to reduce fibrosis progression in mouse models but their role has not been explored in human liver disease. We aimed to assess integrin expression on activated human HSCs and the level of integrin expression in human liver samples from patients with varying degrees of fibrosis. Subtype selective integrin inhibitors were tested to determine their capability to inhibit HSC activation and their effect on TGFbeta activity. This has previously never been performed before using human samples.

Method: HSCs were isolated from healthy individuals, integrin gene and protein expression was measured using qPCR and western blot. Tissue expression of integrins on fibrotic human liver tissue was
examined using a novel technique known as RNAscope®. To assess TGFbeta activity in HSCs, HSCs were co-cultured with mink lung epithelial TGFbeta reporter cells which were used to detect levels of active TGFbeta.

**Results:** There was gene and protein expression of alpha v, beta 1, 3 and 5 integrins with the exception of beta 6 on activated human HSCs. There was high gene expression of alpha v, beta 1, 3, 5 and 8, normalized to beta-actin. We show, for the first time, an identical pattern of integrin expression observed in fibrotic human liver tissue which showed increased expression compared to healthy controls. In co-culture assays, antibodies to alpha v, beta 1 and beta 3 integrins inhibited the increase in active TGFbeta, while antibodies to beta 5 and beta 6 integrins did not have any effect. From the subtype selective compounds tested, a beta 1 inhibitor, prevented the TGFbeta increase in a dose-dependent manner while a beta 6 inhibitor did not.

**Conclusion:** In activated HSCs, there was gene and protein expression of integrins beta 1, 3 and 5 with similar integrins expressed on fibrotic human liver tissue, not reported previously. A beta 1 integrin inhibitor compound successfully inhibited TGFbeta activation in a dose-dependent manner. This shows the exciting potential of beta 1 integrin specifically being a successful treatment target for liver fibrosis.

**FRI152**

**Dual inhibition of integrins alpha-v/beta-6 and alpha-v/beta-1 decreases portal pressure and liver fibrosis in rats with biliary cirrhosis**

Philipp Königshofer, Benedikt Hofer, Oleksandr Petrenko, Hubert Scharnagl, Tatjana Stojaková, Philipp Schwabi, Eric Lefebvre, Scott Turner, Thomas Reiberger, Benedikt Simbrunner, Filip Hlava, Benedikt Huber, Hubert Scharnagl, Tatjana Stojaková, Philipp Schwabi, Eric Lefebvre, Scott Turner, Thomas Reiberger.

**Background and aims:** Transforming growth factor-beta (TGF-beta) signalling is a key driver of liver fibrosis. In primary sclerosing cholangitis (PSC), integrins overexpressed on injured cholangiocytes (alpha-v/beta-6) and myofibroblasts (alpha-v/beta-1) regulate TGF-beta activity; they bind and activate latent TGF-beta thereby promoting liver fibrosis. We investigated the effects of PLN-75068, a tool alpha-v/beta-6 and alpha-v/beta-1 inhibitor compound, on liver fibrosis and portal hypertension in rats with cholestatic biliary cirrhosis.

**Method:** Male Sprague Dawley rats underwent bile duct ligation (BDL) or sham operation (SHAM). Two weeks post-surgery, BDL rats received PLN-75068 100 mg/kg (BDL-LOW), 300 mg/kg (BDL-HIGH), riociguat (RIO: positive control) 0.5 mg/kg or vehicle (VEH), and SHAM rats received VEH (SHAM-VEH) twice daily via oral gavage for 2 weeks. Portal pressure (PP), mean arterial pressure (MAP), heart rate and splanchnic/portal blood flow were measured at end of treatment. Alanine transaminase (ALT), aspartate transaminase (AST), alkaline phosphatase (ALP) and bilirubin (BIL) were assessed. Fibrosis was quantified by automated morphometry of collagen proportionate area (CPA) on Picro-Sirius red-stained full liver lobe sections and assessment of hydroxyproline (HP).

**Results:** Cirrhotic vehicle control rats (BDL-VEH) showed significantly higher values of PP (12.2 ± 1.9 vs 6.8 ± 0.9 mmHg; p < 0.001) and CPA (13.8 ± 4.3 vs 1.1 ± 0.2%; p < 0.001) compared with SHAM-VEH. Elevated PP in BDL rats was lowered with treatment: BDL-LOW (−10%; p = 0.009), BDL-HIGH (−9%; p = 0.26) and BDL-RIO (−10%; p = 0.02). MAP was significantly reduced in all treated groups (BDL-LOW: −22%; BDL-HIGH: −27%; BDL-RIO: −24%; all p < 0.001) vs BDL-VEH. CPA was decreased with treatment: BDL-LOW (−28%; p = 0.04), BDL-HIGH (−41%; p = 0.003) and BDL-RIO (−29%; p = 0.03) compared with BDL-VEH (Figure). HP levels were comparable across all BDL rats (VEH: 489 ± 163 ug/g; LOW: 508 ± 111 ug/g; HIGH: 473 ± 114 ug/g; RIO: 476 ± 174 ug/g). ALT was significantly lower with treatment: BDL-LOW (63 ± 10 U/L; −26%), BDL-HIGH (58 ± 12 U/L; −32%) and BDL-RIO (59 ± 9 U/L; −31%) all p < 0.001, compared with BDL-VEH (85 ± 17 U/L). Treatment with RIO significantly reduced AST (p = 0.03), but ALP and BIL remained unchanged in all treated animals compared with BDL-VEH. Weight loss was observed in BDL-HIGH but was not statistically significant.
Conclusion: In rats with biliary cirrhosis, dual alpha-v/beta-6 and alpha-v/beta-1 inhibition by PLN-75068 ameliorated portal hypertension, exerted dose-dependent anti-fibrotic effects as assessed by CPA and significantly reduced ALT levels. A multinational Phase 2a evaluation of PLN-74809 in participants with PSC is ongoing (INTEGRIS-PSC; EudraCT: 2020–001428–33; NCT04480840).

FR153 Dual roles of PSMP/MSMP in the progression of hepatic fibrosis and hepatocellular carcinoma
Shaoping She1, Liying Ren2, Pu Chen1, Dongbo Chen1, Hongsong Chen1, 1Peking University People’s Hospital, Peking University Hepatology Institute, Beijing Key Laboratory of Hepatitis C and Immunotherapy for Liver Diseases, Beijing, China; Affiliated Hospital of Guilin Medical University, Laboratory of Hepatobiliary and Pancreatic Surgery, Guilin, China
Email: chenhongsong@bjmu.edu.cn

Background and aims: Chemokines are a family of cytokines that orchestrate the migration and positioning of immune cells within tissues and are critical for the function of the immune system. PC3 secreted microprotein (PSMP) or microprotamine (MSMP) is a novel chemotactic cytokine discovered through genome-wide bioinformatics analysis and chemoattractant platform screening, which can act as a CCR2 ligand to recruit peripheral blood monocytes and lymphocytes. CCR2 participates in liver pathology, including acute liver injury, chronic hepatitis, fibrosis/cirrhosis and tumor progression, by mediating the recruitment of immune cells to inflammation and tumor sites. In the present study, we investigated the expression of PSMP in liver fibrosis/cirrhosis and hepatocellular carcinoma (HCC).

Method: PSMP expression was studied in patients and murine models of fibrosis/cirrhosis and HCC. The role of PSMP in vivo was evaluated in PSMP gene knockout mice. The direct effects of PSMP on macrophages, hepatic stellate cells and tumor cells were studied in vitro.

Results: In this study, we found that PSMP is highly expressed in fibrotic/cirrhotic tissues from patients with multiple etiologies. PSMP is also overexpressed in human liver cancer-adjacent tissues, and its expression level is positively correlated with patients’ survival. PSMP deficiency (Psmp−/−) resulted in a marked amelioration of hepatic fibrosis, but promoted liver tumor growth in mice. Damage-associated molecular patterns molecules HMGB-1 and IL-33 significantly induced hepatocytes to produce PSMP. In CCl4-induced hepatic injury, the infiltration of CCR2+ monocytes and macrophages into the liver is significantly decreased in Psmp−/− mice. In HCC, knockout of PSMP can inhibit the infiltration of tumor-infiltrating CD8+ lymphocytes and promote M2-polarization of tumor-associated macrophages (TAMs) in mice. At the cellular level, we found that PSMP can directly promote the M1 polarization of bone marrow-derived macrophages and the activation of LX-2 cells, and also inhibit the proliferation and migration of HCC cells.

Conclusion: In conclusion, PSMP can promote liver fibrosis, while inhibit liver carcinogenesis. These results indicate that PSMP may play different or even opposite functions in different stages of liver disease, suggesting that PSMP is a potential target for the treatment of chronic liver disease and HCC.

FR154 NKT cells promote both type 1 and type 2 inflammatory responses in the non-obese diabetic inflammation and fibrosis (NIF) mouse model
Julia Nilsson1, 2, Maria Hörnberg3, Kajsa Linde1, Dan Holmberg1, 2, Sofia Mayans1, 1Inficure Bio AB, Umeå, Sweden; 2Lund University, Experimental Medical Science, Malmö, Sweden
Email: sofia.mayans@inficurebio.com

Background and aims: Sterile liver inflammation and fibrosis are associated with many liver disorders of different etiologies. Both type 1 and type 2 inflammatory responses have been reported to contribute to liver pathology and the mechanisms controlling the balance between these responses are largely unknown. Here we use the non-obese diabetic inflammation and fibrosis (NIF) mouse model for chronic liver inflammation and fibrosis to investigate the role of NKT cells in the different phases of sterile liver inflammation.

Method: Transgenic mice overexpressing a NKT cell population in the presence or absence of an adaptive immune system was analyzed and the role of this population in the generation of chronic liver inflammation and fibrosis was examined.

Results: We demonstrate that transgenic NKT cells, when developing in an immunodeficient Rag2−/− genetic background (the NIF mouse), expresses a mixed Th1/Th2 cytokine profile, which induces IL-1β production through the NLRP3 pathway that initially result in the development of chronic liver inflammation. This phase is followed by the development of a type 2 inflammatory response including the
Conclusion: Our data illustrates how plasticity in NKT cells can drive an initial type 1 inflammatory response and promote the transition into a type 2 inflammatory response thus overlapping key cellular and molecular events characterizing human liver diseases such as e.g. NAFLD/NASH. Further, the data suggests that this process is controlled by some component(s) of the adaptive immune system. The observed mechanistic overlap with human liver disease suggest that the NIF mouse model represents a unique tool for drug efficacy tests in liver inflammation and/or fibrosis with large translational potential as illustrated in the figure.

FR155
Using qFibrosis analysis to predict disease and survival outcome of patients with hepatocellular carcinoma after curative treatment
Chih-Yang Hsiao1,2, Dean Tai2, Yayun Ren3, Kai-Wen Huang1,2, 1National Taiwan University Hospital, Department of Surgery, Taipei, Taiwan; 2National Taiwan University, Graduate Institute of Clinical Medicine, College of Medicine, Taipei, Taiwan; 3HistoIndex Pte Ltd, Research, Singapore, Singapore

Background and aims: Stromal remodelling in tumor microenvironment plays an important role in cancer progression. It is featured by collagen realignment in the stromal compartment, collagen fibers and basal membrane. There remains a lack of studies addressing the stromal background and fibrosis features and its prognostic value in liver cancer. qFibrosis is a system of second harmonic generation and two photon emission (SHG/TPE) microscopy which can identify, quantify and visualize the fibrosis features from biopsy samples. qFibrosis has been validated for its application in diagnosis and staging of liver fibrosis.

Method: Total of 198 patients with HCC underwent curative tumor resection were included. Their disease status, survival time, and clinical outcomes of whether portal vein thrombosis (PVT) and metastasis (Meta) developed during follow-up after surgery were analyzed. Liver tissue and liver tumor from the 198 patients were imaged and assessed using qFibrosis system, and generated a total of 33 and 156 collagen parameters from liver tissue and tumor part, respectively. We used these collagen parameters to build two models, PVT-index and Meta-index, to differentiate the patient’s clinical outcome of PVT and Meta, respectively. The models were validated using leave-one-out method.

Results: Both developing PVT and metastasis were significant indicators for poor prognosis. Seven parameters were selected from the parameters of liver tissue and tumor part to build the PVT-index and Meta-index, respectively. The PVT-index well differentiates patients developing PVT (p < 0.001 for training, p = 0.030 for validation, Figure), and the Meta-index also well differentiate patients developing metastasis during follow-up (p < 0.001 for training, p = 0.024 for validation, Figure).

Conclusion: Prognostic estimation models consist of collagen parameters in qFibrosis system could be built to predict HCC patient’s clinical outcomes of developing PVT and Meta during follow-up after radical treatment. Our results demonstrated the potentials of using qFibrosis system to transform the histopathological features into quantifiable data that could be used to correlate with patient outcome as other clinical biomarkers.

FR156
Multi-target engagement effect of a novel long-acting Glucagon/GIP/GLP-1 triple agonist, HM15211, in animal model of NASH/fibrosis
Jong Suk Lee1, Jung Kuk Kim1, Seonmyeong Lee1, Yohan Kim1, Jaehyuk Choi1, Hyunjoo Kwon1, Eun Jin Park1, Sung Min Bae1, Sang Hyeon Lee1, In Young Choi1. 1Hanmi Pharm.Co., Ltd., Seoul, Korea, Rep. of South Korea

Background and aims: Although its benefits were confirmed for NASH resolution, semaglutide failed to improve fibrosis in human. Recently, benefits of glucagon and GIP in addition to GLP-1 have been suggested beyond metabolism such as fibrosis. Thus, optimal use of these incretins simultaneously could be a promising strategy for NASH and fibrosis treatment. For this purpose, a novel long-acting Glucagon/GIP/GLP-1 triple agonist, HM15211, was developed. Here, beneficial effect of HM15211 via multi-target engagement was evaluated in animal models of NASH/fibrosis.

Method: AMLN-diet induced NASH mice and CDA-HFD induced nash.fibrosis mice were administered either with HM15211 or acylated GLP-1, GLP-1/GIP, or GLP-1/Glucagon agonist. Choline-deficient, L-amino acid-defined, and high fat diet (CDA-HFD)
induced NASH and fibrosis mice were also utilized. After treatment for 8 ~ 12 weeks, histologic analysis including NAFLD Activity Score (NAS) and hepatic hydroxyproline (HP) were determined. Liver transcriptome analysis was performed to investigate differentially expressed genes (DEGs) for diverse biological pathways.

**Results:** In AMLN mice, HM15211 treatment led to greater reduction in each component and composite NAS (6.1, 4.9, 3.6, 4.9, 2.0 for vehicle, acylated GLP-1, GLP-1/GIP, GLP-1/Glucagon, HM15211) than incretin analogs, and more NASH resolution achievement were confirmed for HM15211. In CDA-HFD mice, HM15211 treatment was consistently associated with greater reduction of NAS than incretin analogs. More reduction in hepatic HP and collagen contents (~4.2, ~10.0, 7.1, and ~26.5% vs. vehicle for acylated GLP-1, acylated GLP-1/GIP, acylated GLP-1/Glucagon, and HM15211) than incretin analogs were confirmed, indicating potential benefits of HM15211 for liver fibrosis. To understand underlying mechanisms for improved therapeutic effects of HM15211 on NASH and fibrosis, DEG analysis was performed and compared to acylated GLP-1, HM15211 treatment was associated with more favourable DEG signature in diverse pathways including bile acid metabolism, inflammation and fibrosis in addition to lipid metabolism, highlighting its multi-targeting MoA for the treatment of NASH and fibrosis. To induce liver injury and liver fibrosis, escalating doses of thioacetamide-induced mouse model of liver injury and fibrosis was associated with more favourable DEG signature in diverse pathways including bile acid metabolism, inflammation and fibrosis in addition to lipid metabolism, highlighting its multi-targeting MoA for the treatment of NASH and fibrosis. Human study is ongoing to assess the clinical relevance of these findings.

**Conclusion:** Notably, DEG analysis supports the basis for multi-target engagement of HM15211 treatment significantly reduced HP content (<0.01), Sirius red positive area (26.5%) and subsequent cytokine secretion were significantly attenuated by HM15211 treatment was associated with robust reduction across pro-inflammatory cytokines such as TNF-alpha, IL-1beta, IL-6, and etc. Significant reduction in blood level of enzyme activities was also confirmed. Mechanistically, PMA/LPS-induced THP-1 cell adhesion and subsequent cytokine secretion were significantly attenuated by HM15211. TGF-beta-induced collagen production was also reduced in LX2 cell. Based on in vitro results, observed benefits in TAA mice might primarily results from direct anti-inflammatory and -fibrotic effects of HM15211.

**Conclusion:** HM15211 markedly improved liver inflammation and fibrosis in TAA mice, and related MoAs were elaborated by in vitro studies. Together with previous results, generalized anti-inflammatory and -fibrotic effects of HM15211 were corroborated. Thus, HM15211 could be a novel therapeutic option for fibrosis due to NASH. Human study is ongoing to assess the clinical relevance of these findings.

**FR158**

**Loss of bile salt export pump (BSEP/ABC11) protects mice from development of carbon tetrachloride (CCl4) induced hepatic fibrosis**

Claudia Fuchs 1, Emmanuel Daoud Dixon 1, Philipp Königshofer 1,2,3,4,5, Veronika Militz 1, Hubert Scharnagl 6, Tatjana Stojakovic 7, Thomas Reiberger 1,2,3,4,5, Michael Trauner 1, 1Medical University of Vienna, Division of Gastroenterology and Hepatology, Internal Medicine III, Vienna, Austria; 2Medical University of Vienna, Vienna Experimental Hepatic Hemodynamics lab (HEPEX); 3Medical University of Vienna, Christian Doppler laboratory for Portal Hypertension and Liver Fibrosis; 4, Ludwig Boltzmann Institute for Rare and Undiagnosed Diseases (LB-RUD); 5CeMM Research Center for Molecular Medicine of the Austrian Academy of Sciences; 6Medical University of Graz, Clinical Institute of Medical and Chemical Laboratory Diagnostics; 7University Hospital Graz, Clinical Institute of Medical and Chemical Laboratory Diagnostics

**Background and aims:** Loss of BSEP/ABC11 was shown to protect mice from acquired cholestasis due to preconditioning with a hydrophilic bile acid (BA) pool, with tetrahydroxylated BAs as the most prominent species. In this study we aimed to investigate whether loss of BSEP and subsequent increase in hydroxylation/ detoxification of BAs protects mice from development of carbon tetrachloride (CCl4) induced hepatic fibrosis.

**Method:** BSEP WT and KO mice were injected every other day with CCl4 for 8 weeks as model of hepatic fibrosis. In vitro, the hepatic stellate cell line LX2 was challenged with TGF-beta with and without cotreatment of tetrahydroxylated BAs. RNA profiling was performed by RT-PCR. Liver histology/immunohistochemistry (IHC), immunofluorescence (IF) and immunoblot were assessed.

**Results:** In contrast to WT mice, serum parameter ALT and AST were not elevated in BSEP KO mice by CCl4 injection. In line, mRNA expression of inflammatory markers Cxcl1, Cxcl2, Ccl2, Ccl5 remained unchanged in BSEP KO mice injected with CCl4 while in WT CCl4 mice these markers were significantly increased (3fold, 20fold, 20fold, 26fold, respectively). Accordingly, numbers of MAC-2 positive cells were significantly lower in BSEP KO CCl4 injected mice when compared to CCl4 WT mice. Fibrotic markers Col1a1, Col1a2 as well as Sirius red were significantly reduced in BSEP KO CCl4 mice compared to WT CCl4 mice (by 40%, 60%, 65% respectively). Accordingly, alph-SMA (marker of activated hepatic stellate cells) (IF) remained at basal levels in BSEP KO CCl4 mice. Mechanistically, we could demonstrate that hepatic protein expression of pJNK (known to be involved in development of CCl4 induced hepatic fibrosis) was reduced in BSEP KO CCl4 mice in comparison to challenged WT mice. In vitro, activated phenotype of LX2 cells was ameliorated with treatment of tetrahydroxylated BAs, as reflected by significant reductions of alpha-SMA and Col1a1 gene expression.

**Conclusion:** Loss of BSEP and subsequent hydroxylation of the bile pool protects mice from CCl4 induced hepatic fibrosis via suppression of hepatic pJNK signalling and attenuation of HSC activation.

Journal of Hepatology 2022 vol. 77(S1) | S389–S664

S469 POSTER PRESENTATIONS
Background and aims: The expression of the receptor tyrosine kinase Axl and the release of its cleavage product soluble Axl (sAxl) are highly elevated in hepatocellular carcinoma (HCC), advanced fibrosis, and cirrhosis. Recent studies suggest that the expression of Gas6, the high affinity ligand of Axl, is also enhanced during liver fibrogenesis and HCC. In this study, we evaluated the diagnostic accuracy of sAxl and Gas6 in a large cohort of patients with HCC, liver fibrosis and end-stage liver disease.

Method: Levels of sAxl and Gas6 were analyzed by enzyme-linked immunosorbent assays (ELISAs) in serum samples of patients with HCC, cholangiocarcinoma, colorectal liver metastases, chronic liver disease of all fibrosis stages, end-stage liver disease, and healthy controls from five centers in Europe. ELISAs were optimized to maximally detect sAxl and Gas6 levels. Results: A total of 1111 patients (median age 57.8y, 67.3 % male) was included in the study. sAxl, Gas6 as well as their albumin (alb) ratios showed high diagnostic accuracy for the detection of HCC in comparison to healthy controls (AUC 0.765–0.942). sAxl/alb was confirmed as an accurate biomarker of advanced liver fibrosis and cirrhosis, and was even outperformed by Gas6/alb, which showed good accuracy (AUC 0.818–0.897) comparable to ELF™ test for the detection of liver cirrhosis. sAxl, Gas6 and their albumin ratios detected hepatic decompensation (Gas/alb: AUC 0.878), and were predictors of transplant-free survival.

Conclusion: Gas6/alb shows high accuracy for the detection of significant to advanced fibrosis and liver cirrhosis, as well as compensated liver cirrhosis superior to sAxl/alb.

Background and aims: Despite availability of direct-acting antivirals, viral hepatitis C (HCV) still impacts ~58 million people world-wide and ~70% progress to chronic infection. Chronic hepatitis develops after the virus restricts pro-inflammatory macrophage activation necessary to control infection, contributing to T cell dysfunction and viral persistence. Intrahepatic macrophages represent ~20% of non-parenchymal cells and greatly impact the hepatic microenvironment, host immune response to liver injury and the development of fibrosis. We hypothesized that variations in the heterogeneity of macrophages determine disease progression in HCV + patients.

Method: We used multispectral imaging to phenotype and quantify resident Kupffer cells (CD68 +), monocyte-derived macrophages (Mac387 +), pro-fibrogenic macrophages (CD163 +), and co-expression of pro-inflammatory (CD14) and anti-inflammatory (CD16) in patients with minimal (fibrosis stage: 0/6; n = 5) or advanced (fibrosis stage: 6/6; n = 6) fibrosis. Next, we compared differences in the spatial distribution of the identified phenotypes (i.e., enrichment or depletion) within the hepatic microenvironment. Multiplex stained liver biopsies were scanned with a spectral imaging microscope (Vectra 3, Akoya Biosciences) and multi-component TIFF images and cell_seq_data files were analyzed to determine the heterogeneity of these various cell phenotypes. Both phenotype matrices and t-distributed stochastic neighbour embedding plots (t-SNE) were used (Visiopharm®; MATLAB 2020a, MathWorks inc.).

Results: Phenotype matrix analysis revealed the enrichment of unique pathogenic macrophage phenotypes (CD163 + CD16 +, CD68 +, CD68 + MAC387 +) in the HCV + patients with advanced fibrosis (p <0.05). Increased CD68 +, CD68 + MAC387 + macrophage populations, in certain individuals, correlated with poor clinical outcome (increased prothrombin time and decreased platelet counts). Spatial analysis showed significant (p <0.05) enrichment of CD14 +, CD68 + CD14 + CD163 +, CD68 + MAC387 +, and MAC387 + macrophage populations near CD68 + cells and depletion of CD163 + CD16 + population to CD14 + cells. Enriched interactions between MAC387 + and CD163 + MAC387 + positive macrophages were exclusively observed in the HCV + patients with advanced fibrosis.

Conclusion: Multispectral imaging with spatial analysis enabled detailed evaluation of intrahepatic macrophages and their relationship with neighbouring cells phenotypes. Unique phenotypes and interactions were observed among HCV patients with advanced fibrosis and in those that had disease progression. This approach identified novel potential targets for inhibiting fibrosis development and development of future personalized medicine approaches.
Neutrophil-specific NLRP3 activation triggers liver inflammation and fibrosis

Benedikt Kaufmann¹,², Yanfang Peipei Zhu¹, Aleksandra Leszczyńska¹, Agustina Reca¹, Laela M. Booshehri¹, Alexander Wree¹, Helmut Friess², Daniel Hartmann², Hal M. Hoffman¹, Ben Croker¹, Ariel Feldstein¹. ¹Department of Pediatrics, University of California San Diego, La Jolla; ²Department of Surgery, TUM School of Medicine, Klinikum rechts der Isar, Technical, University of Munich; ³Charité, Campus Virchow Klinikum and Charité, Campus Mitte, Department of Hepatology and Gastroenterology, Universitätsmedizin Berlin

Email: benedikt.kaufmann@hotmail.com

Background and aims: Neutrophils have a key role in the acute inflammatory response during liver inflammation and fibrosis and are hypothesized to promote chronic inflammation and liver fibrosis if they are not efficiently cleared by macrophages. The NLRP3 inflammasome is crucial in liver inflammation and fibrogenesis. In this study the role of neutrophil-specific NLRP3 inflammasome over-activation in liver pathobiology was investigated.

Method: Neutrophil-specific mutant NLRP3 knock-in mice were generated by crossing Nramp3 knock-in mouse strains with the presence of an intronic floxed neomycin resistance cassette with mice expressing Cre recombinase under the control of Calcium-binding protein A8. Liver tissue and bone marrow were analysed by immunohistochemistry, flow cytometry, and real-time quantitative polymerase chain reaction.

Results: Mutant mice with neutrophil-specific NLRP3 activation showed shortened survival, poor growth, and severe liver inflammation. Furthermore, neutrophil-specific NLRP3 activation resulted in systemic changes in hematopoiesis and an accumulation of inflammatory neutrophils, the key cells in the initial phase of inflammation, in the liver. Infiltrative inflammatory neutrophils were identified by elevated CD162 (PSGL-1) and increased expression of CD16/32 myeloperoxidase staining in the liver of mutant mice. Inflammation of liver tissue in mutant mice resulted in a decrease of resident macrophages evident by reduced CLEC4f and F4/80 expression in both IHC staining and qRT-PCR. In contrast, pro-inflammatory macrophage population was increased in mutant mice demonstrated by Ly6C staining and upregulation of inducible nitric oxide synthase 2 (iNOS2). Sirius Red staining revealed liver fibrosis in mutant mice, whereas WT mice showed a healthy liver. The expression of the pro-fibrotic genes metalloproteinasines 1 (TIMP1) and connective tissue growth factor (CTGF) was upregulated in the liver tissue of mutant mice.

Conclusion: Neutrophil-specific NLRP3 overactivation resulted in severe liver inflammation with accumulation of inflammatory neutrophils and pro-inflammatory macrophage polarization. Furthermore, it induced liver fibrosis and a pro-fibrotic gene expression pattern. This data provides novel insights into the complex relationship between liver neutrophil-driven inflammation, macrophage polarization and liver fibrosis.

Imaging of fibrosis in metabolic associated liver disease by a radiolabeled affibody targeting PDGFRB

Oliveia Wegrzyniak¹, Johanna Rokka², Bo Zhang³, Maria Rosestedt¹, Bogdan Mitran¹,², Pierre Cheung³, Emma Pauwouli³, Sofie Ingvast³, Frederik Ponten⁴, Frederik Frejd⁴, Olle Korsgren⁴, Jonas Eriksson¹,³, Olof Eriksson¹,²,³ Uppsala University, Department of Medical Chemistry, Uppsala, Sweden; ²Uppsala University, Department of Public Health and Caring Sciences, Uppsala, Sweden; ³Antaros Medical AB, Mölndal, Sweden; ⁴Uppsala University, Department of Immunology, Genetics and Pathology, Uppsala, Sweden; ⁵Affibody AB, Solna, Sweden; ⁶Uppsala University Hospital, PET Center, Uppsala, Sweden; ⁷Antaros Tracer AB, Mölndal, Sweden

Email: olivia.wegrzyniak@ilu.uu.se

Background and aims: The pathological formation of fibrosis, is an important feature in liver in Metabolic Associated Fatty Liver Disease (MAFLD) as well as in many different other diseases. Platelet-derived growth factor receptor beta (PDGFRB) is a known biomarker of activated hepatic stellate cells, and thus play a key role in fibrosis in MAFLD. Today, the treatment and monitoring of hepatic fibrosis is hampered by the lack of suitable methods for detecting and diagnosing the disease. Therefore, it is of crucial importance to develop non-invasive methods in order to detect, diagnose, stage and study fibrosis. Herein, we report the preparation, characterization, and evaluation of fluorine-18-labelled Affibody molecule Z09591, in a mouse model of non-alcoholic steatohepatitis (NASH).

Method: Affibody molecule Z09591 was labelled with fluorine-18 via tetratrace/transpose-cyclooctene click chemistry. ¹⁸F-TZ-Z09591 was evaluated in a 6 weeks CCl₄ treatment mouse model of liver fibrosis by a PET study, including ex vivo biodistribution and autoradiography. Binding results were correlated to staining and PDGFRB immunohistochemistry (IHC) on post-mortem biopsies.

Results: Affibody molecule Z09591 was successfully radiolabelled with fluorine-18 with high purity and reproducible yield. PET studies demonstrated that liver uptake of ¹⁸F-TZ-Z09591 was higher in mice with induced hepatic fibrosis compared to healthy liver (Figure). The liver binding could also be blocked by pre-treatment with Z09591 in excess, indicating receptor specific binding. Ex vivo autoradiography demonstrated high signal intensity in positive hepatic sinusoids affected by fibrosis, as confirmed by Sirius red staining and PDGFRB IHC.

Conclusion: We describe the radiolabelling and evaluation of the PDGFRB binding affibody Z09591. ¹⁸F-TZ-Z09591 exhibited specific binding to hepatic fibrotic lesions. ¹⁸F-TZ-Z09591 is a promising tool for PET imaging of fibrosis in MAFLD. The use of such a tracer clinically could represent a non-invasive diagnostic, prognostic as well as predictive tool for MAFLD patients.
FR1163
Liver complications in greek patients with sickle cell disease: a multicenter retrospective analysis from eight thalassemia and sickle cell units across Greece
Konstantinos Manganas1, Sophia Delicou1, Aikaterini Xydaki1, Alexandra Kourakili2, Loukia Evlati3, Euthimia Vlakaki4, Evangelos Klonromos5, Michail Diamantidis6, Ioannis Lafiatis1, Antonis Kattamis1, Ioannis-Georgios Koskina1,1Ipokrateio General Hospital of Athens, Athens, Greece; 2General University Hospital of Patras, Rio, Greece; 3Evangelismos General Hospital, Athens, Greece; 4Ipokrateio-General Hospital of Thessaloniki, Thessaloniki, Greece; 5Venizeleio General Hospital, Heraklion, Greece; 6General University Hospital of Larissa, Larissa, Greece; 7General Hospital of Mytilene, Mytilene, Greece; 8Agia Sofia Children’s Hospital, Athens, Greece
Email: kmagaganas92@gmail.com

Background and aims: Sickle cell disease (SCD) is one of the most common monogenic disorders worldwide and liver complications, acute and chronic, are common in this group of patients. Our study aims to highlight the prevalence and predisposing factors of liver fibrosis in SCD patients.

Method: Eight Thalassemia and Sickle Cell Units across Greece and 219 patients enrolled in our study and history of liver related disease complications was recorded, as well as a full laboratory and imaging analysis concerning their liver function. Patients were divided in two groups, those with indications of advanced liver fibrosis (Fibroscan >13.5 kPa or FIB-4 > 3.25 or APRI >1.5) and those without indications of advanced liver fibrosis.

Results: The prevalence of significant liver fibrosis in SCD patients in our study was 10.7%. The presence of liver fibrosis was significantly correlated with advanced age, male gender, cholelithiasis and higher LDH, γ-GT, INR, direct and indirect bilirubin levels. Noteworthy, patients with advanced liver fibrosis had suffered significantly more acute liver crises, acute liver sequestration crises and acute intrahepatic cholestasis in the last five years, while these patients were also receiving transfusion therapy more often and for a longer period of time and had higher Liver Iron Concentration (LIC) levels, but without statistical significance. No correlation was observed with ultra-sound findings of right hearth failure or previous viral hepatitis.

Conclusion: Our study shows that advanced liver fibrosis is a significant cause of morbidity in patients with SCD and is primarily associated acute vaso-occlusive phenomena and chronic intravascular hemolysis of the disease itself.

FR1164
Hemodynamic, molecular, and histological characterization of a toxic liver fibrosis regression model
Philipp Königshofer1,2,3,4,5, Ksenia Brusilovskaya1,2,3,4,5, Benedikt Hofer1,2,3,4,5, Benedikt Simbrunner1,2,3,4,5, Oleksandr Petrenko1,2,3,4,5, Hubert Scharngli6, Tatjana Stojakovic6, Michael Trauner1, Philipp Schwabl1,2,3,4,5, Stefan Günther Kauschke7, Larissa Pfisterer7, Thomas Reiberger1,2,3,4,5, 1Division of Gastroenterology and Hepatology, Department of Internal Medicine III, Medical University of Vienna, Vienna, Austria; 2Vienna Experimental Hepatic Hemodynamic lab (HEPEX), Medical University of Vienna, Vienna, Austria; 3Christian Doppler laboratory for Portal Hypertension and Liver fibrosis, Vienna, Austria; 4Ludwig Boltzmann Institute for Rare and Undiagnosed Diseases (LBI-RUD), Vienna, Austria; 5CeMM Research Center for Molecular Medicine of the Austrian Academy of Sciences, Vienna, Austria; 6Clinical Institute of Medical and Chemical Laboratory Diagnostics, University Hospital Graz, Graz, Austria; 7Boehringer Ingelheim Pharma GmbB, Biberach, Germany
Email: thomas.reiberger@meduniwien.ac.at

Background and aims: Portal hypertension (PH) results from ‘static’ liver fibrosis and ‘dynamic’ vascular components. Liver disease regression depends on cessation of liver injury to allow liver fibrosis regression and functional regeneration. We aimed to establish a toxic liver disease regression model to investigate the ‘regressive’ course of PH and fibrosis.

Method: Male C57BL/6J mice were exposed to CCL4 for eight (8 w) or twelve (12 w) weeks (2 μL/g in olive oil, 3x/week, per oral), respectively, to induce moderate (8 wC) and severe liver fibrosis (12 wC)-followed by one (+R1) or two (+R2) weeks of regression period, respectively (Figure). Healthy control groups received olive oil only (OO), Portal pressure (PP) was measured at end of each timeline. Blood parameters were assessed. Fibrosis was quantified by collagen proportionate area (CPA) in % Matrix- and inflammation-related gene-expression was measured in bulk liver tissue.

Conclusion: Our study shows that advanced liver fibrosis is a significant cause of morbidity in patients with SCD and is primarily associated acute vaso-occlusive phenomena and chronic intravascular hemolysis of the disease itself.
Results: Diseased animals developed PH with PP (8wC: 8.5 ± 1.3 mmHg vs OO: 4.9 ± 0.8 mmHg; 12wC: 10.0 ± 1.2 mmHg vs OO: 5.2 ± 0.2 mmHg; all p < 0.001) and liver fibrosis with CPAS (8wC: 8.5 ± 5.0 % vs OO: 16 ± 0.9 %; 12wC: 16.9 ± 3.9 % vs OO: 0.8 ± 0.2 %; all p < 0.001). In both models, PP regressed after one (8wC + R1: −31 %, p < 0.001; 12wC + R1: −16 %, p = 0.01) and after two weeks (8wC + R2: −29 %, p < 0.001; 12wC + R2: −21 %, p = 0.002), respectively. Fibrosis regressed in the 8-weeks (8wC + R1: −1 %, p < 0.001; 8wC + R2: −37 %, p = 0.24) and significantly in the 12-weeks (12wC + R1: −16 %, p = 0.002; 12wC + R2: −21 %, p < 0.001) setting. AST and ALT levels significantly decreased after 1 week of regression (8wC/12wC+R1: −85/−91 %; 12wC + R1/2: −83/−74 %), Tgf-beta (8wC + R1/2: −71/−80 %; 12wC + R1/2: −62/−72 %), and alpha-Sma (8wC + R1/2: −86/−85 %; 12wC + R1/2: −70/−42 %). Matrix-metalloproteinase activity was promoted by decreased Timp1 (8wC + R1/2: −94/−95 %; 12wC + R1/2: −92/−85 %) expression. Pro-inflammatory Tnf-alpha (8wC + R1/2: −69/−74 %; 12wC + R1/2: −70/−69 %) expression was also decreased.

Conclusion: The characterization of this toxic model of liver disease regression suggests that the two-week regression period following 12-weeks of CCl4 exposure includes a suitable therapeutic window to ameliorate advanced fibrogenesis in diet- and toxicity-induced NASH. Of great interest, the 11betaHSD1 resulted in reprogramming of hepatic stellate cell (HSC) and fibrosis through depolarizing of hepatic stellate cell in NASH. Inhibition of 11beta-hydroxysteroid dehydrogenase type 1 (11betaHSD1) is a key enzyme that catalyses the intracellular conversion of cortisone to physiologically active cortisol. Although 11betaHSD1 has been implicated in numerous metabolic syndromes, such as obesity and diabetes, the functional roles of 11betaHSD1 during progression of nonalcoholic steatohepatitis (NASH) and consequent fibrosis have not been fully elucidated.

Method: The effects of J2H-1702 on steatosis and fibrogenesis were investigated in both multicellular hepatic spheroids (MCHSs) in vitro systems and in vivo mouse models.

Results: We found that pharmacological and genetic inhibition of 11betaHSD1 resulted in reprogramming of hepatic stellate cell (HSC) activation via inhibition of p-SMAD3, alpha-SMA, Snail, and Col1A1 in a fibrotic environment and in multicellular hepatic spheroids (MCHSs). We also determined that 11betaHSD1 contributes to the maintenance of NF-kappaB signalling through modulation of TNF, TLR7, ITGB3, and TWIST, as well as regulating PPAR-alpha signalling and extracellular matrix accumulation in activated HSCs during advanced fibrogenesis in MCHSs. Of great interest, the 11betaHSD1 inhibitor J2H-1702 significantly attenuated hepatic lipid accumulation and ameliorated liver fibrosis in diet- and toxicity-induced NASH mouse models.

Figure: Frequency of fibrosis according to aetiology between both ALT groups.

POSTER PRESENTATIONS

FR166
Inhibition of 11beta-hydroxysteroid dehydrogenase 1 relieves fibrosis through depolarizing of hepatic stellate cell in NASH
Su-Yeon Lee1, Hyung Chul Rhu2, Sanghwa Kim1, Yeonhwa Song1, Inhee Choi1, Namjeong Kim1, Jee Woong Lim2, Hyo Jin Kang2, Jason Kim2, Haeng Ran Seo1. 1Institut Pasteur Korea, Advanced Biomedical Research Lab, Seongnam-si, Korea, Rep. of South; 2J2H Biotech Inc., R&D Center, Suwon-si, Korea, Rep. of South

Background and aims: 11-beta-hydroxysteroid dehydrogenase type 1 (11betaHSD1) is a key enzyme that catalyses the intracellular conversion of cortisone to physiologically active cortisol. Although 11betaHSD1 has been implicated in numerous metabolic syndromes, such as obesity and diabetes, the functional roles of 11betaHSD1 during progression of nonalcoholic steatohepatitis (NASH) and consequent fibrosis have not been fully elucidated.

Method: The effects of J2H-1702 on steatosis and fibrogenesis were investigated in both multicellular hepatic spheroids (MCHSs) in vitro systems and in vivo mouse models.

Results: We found that pharmacological and genetic inhibition of 11betaHSD1 resulted in reprogramming of hepatic stellate cell (HSC) activation via inhibition of p-SMAD3, alpha-SMA, Snail, and Col1A1 in a fibrotic environment and in multicellular hepatic spheroids (MCHSs). We also determined that 11betaHSD1 contributes to the maintenance of NF-kappaB signalling through modulation of TNF, TLR7, ITGB3, and TWIST, as well as regulating PPAR-alpha signalling and extracellular matrix accumulation in activated HSCs during advanced fibrogenesis in MCHSs. Of great interest, the 11betaHSD1 inhibitor J2H-1702 significantly attenuated hepatic lipid accumulation and ameliorated liver fibrosis in diet- and toxicity-induced NASH mouse models.

Conclusion: There is a significant proportion of patients with ALT 31–55 U/L who have underlying liver disease or fibrosis. Lowering the ULN of ALT has increased the detection rate of liver disease and fibrosis in these patients.

FR1165
The upper limit of normal of alanine aminotransferase (ALT) in diagnosing liver disease and fibrosis by the Intelligent Liver Function Test (iLFT system)
Jeremy Lee1, John Dillon1, Iain Macpherson1. 1University of Dundee, School of Medicine, Dundee, United Kingdom

Email: jslee@dundee.ac.uk

Background and aims: There is an increasing prevalence of liver disease in the UK, and mortality from liver disease continues to rise. Liver function tests (LFTs) are often used to investigate for liver disease, but there remains a significant number of patients with undiagnosed liver disease who could benefit from early detection and intervention. The intelligent LFT (iLFT) system is designed to cascade further tests in patients with abnormal LFTs, generating a probable liver diagnosis. This increased the rate of diagnosis of liver disease by 43%. One parameter used by iLFT is serum alanine aminotransferase (ALT) level, using an upper limit of normal (ULN) of 30 U/L, given recent evidence suggesting a lower ULN of ALT to diagnose liver disease. This study aims to determine the frequency of liver disease and fibrosis at ALT level 31–55 U/L, using an upper limit of normal (ULN) of 30 U/L, in the iLFT system.

Method: A retrospective analysis was done on patients undergoing iLFT in 2018–19, comparing ALT levels to iLFT and fibrosis outcomes.

Results: 672 iLFT diagnoses were made in the ALT 31–55 U/L group, with 148 (22.0%) alcoholic liver disease (ALD) diagnoses, 74 (11.0%) non-alcoholic fatty liver disease (NAFLD) diagnoses, 30 (4.5%) combined NAFLD and ALD diagnoses, 15 (2.2%) hepatitis B or C diagnoses, 74 (11.0%) metabolic or autoimmune liver diseases. 1041 diagnoses were made in the ALT >55 U/L group, which is significantly higher (p < 0.05) compared to the ALT 31–55 U/L group. There were 137 (20.4%) fibrosis diagnoses in the ALT 31–55 U/L group, which is significantly higher (p < 0.05) compared to the ALT >55 U/L group.
Conclusion: Together, our data indicate that J2H-1702 is a promising new clinical candidate for the treatment of NASH.

**FR167**

**Anti-fibrotic effects of microRNA-9-5p and microRNA-122**

Dana Eidelshtein¹, Eithan Galun¹, Jonathan Axelrod¹. ¹Hadassah University Hospital-Ein Kerem, The Goldyne Savad Institute of Gene and Cell Therapy, Jerusalem, Israel

Email: dana.eidelshtein@mail.huji.ac.il

**Background and aims:** Liver fibrosis is the final consequence of many chronic liver injuries and is an increasingly crucial health problem. MicroRNA's (miR's) are short single-stranded RNAs that regulate post-transcriptional mRNA expression by binding to complementary mRNA sequences, resulting in translational repression and gene silencing. In this *in vitro* study, we sought to identify potential miRNAs that could serve as potential therapeutic targets through which to ameliorate liver fibrosis. We identified and validated fibrosis-reducing miRNAs based on their ability to suppress two key fibrogenic pathways: 1) NADPH Oxidase 4 (NOX4), which maintains stellate cells activation by generation of reactive oxygen species (ROS)-induced oxidative stress and DNA damage; and 2) TGF-beta, a central molecular signaling pathway in fibrosis.

**Method:** Potential miR candidates were identified by bioinformatics screening for miR seed sequences in the NOX4 3′ UTR. Candidate miRNA’s were evaluated for anti-fibrotic activity by transfection of synthetic mimic-miRs into LX-2 cells, an established activated human stellate cell (HSC) line, and assessed for reduction of smooth muscle actin (alpha-SMA) protein levels by flow cytometry. Target-sequence specificity of candidate miRs was validated by co-transfection into LX-2 or HEK293 cells of mimic-miRs with a PmiRGLO vector (Promega) containing a cloned NOX4-3′ UTR (PmiRGLO-Nox4) or mutant control (PmiRGLO-mutNox4) sequence and analysis of luciferase activity.

**Results:** Bioinformatics screening identified miR-9-5p and miR-96-5p miRs as having the highest predicted binding potential to NOX4 3′ UTR seed sequences and highest potential for NOX4 expression inhibition. miR-9-5p was also predicted to target TGF-beta receptor (TGFbR2) as was miR-122, an important regulator of hepatic metabolism. Co-transfection experiments in HEK293 demonstrated that mimic-miR-9-5p, but neither miR-96-5p nor miR-122, effectively suppressed PmiRGLO-Nox4 directed luciferase expression, but not that of PmiRGLO-mutNox4. miR-96-5p transfection similarly suppressed both NOX4 and TGFbR2 mRNA levels in LX-2 cells. In contrast, both miR9-5p and miR-122, but neither miR96-5p nor a scrambled control-miR, effectively suppressed alpha-SMA expression in transfected LX-2 cells. Preliminary evidence suggests that LX-2 cells may also inherently express and perhaps secrete both miR-9-5p and miR-122.

Figure: miR-9-5p and miR-122 suppress alpha-SMA in HSCs in vitro. Transfection of LX-2 cells with miRNAs, miR-9-5p and miR-122 decreases alpha-SMA protein expression. *p < 0.05 by two-way Student’s t test.

**Conclusion:** In *vitro* findings demonstrate an anti-fibrotic therapeutic potential of miR-9-5p and miR-122 in activated human stellate cells and liver fibrosis.

**FR168**

**Higher daily Aramchol dose results in higher effect size in fibrosis improvement in the ARMOR study open label part**

Vlad Ratziu¹, Yusuf Yilmaz², Don Lazas³, Scott Friedman⁴, Liat Hayardeny⁵, Shaul Kadosh⁶, Tali Gorfine⁷, Arun Sanay⁸.

¹Sorbonne Université, Institute for Cardiometabolism and Nutrition (ICAN) and Hôpital Pitié-Salpêtrière, INSERM UMR5 1138 CRC, Paris, France; ²Liver Research Unit, Institute of Gastroenterology, Marmara University, and Department of Gastroenterology, School of Medicine, Marmara University, Istanbul, Turkey; ³ObjectiveGI, Inc., Nashville, United States; ⁴Icahn School of Medicine at Mount Sinai, New York, United States; ⁵Calmed Pharmaceuticals Ltd., Tel Aviv-Yafo, Israel; ⁶Stateexcellence Ltd., Israel; ⁷Virginia Commonwealth University, Department of Gastroenterology, Richmond, United States

Email: vlad.ratziu@inserm.fr

**Background and aims:** Aramchol is a partial inhibitor of hepatic stearoyl-CoA desaturase (SCD1) with direct anti-fibrotic activity demonstrated in pre-clinical models. In a 52-week phase 2b study, improvement in fibrosis by ≥1 stage without NASH worsening was observed in 17.5%, 21.3% and 29.5%, in the placebo, Aramchol 400 and 600 mg, respectively. A 53% higher exposure is achieved when dividing 600 mg QD Aramchol to 300 mg BID. Since this higher exposure was expected to improve efficacy, Aramchol 300 mg BID was selected for a phase 3 study in patients with NASH and fibrosis. An Open-Label Part is designed to explore the kinetics of histological outcome measures and non-invasive tests as a function of treatment duration.

**Method:** 150 patients with histologically confirmed NASH and fibrosis are being enrolled to receive Aramchol 300 mg BID in the Open-Label Part of the study. Patients are randomized 1:1:1 to perform a post-baseline liver biopsy at weeks 24, 48 or 72. The primary efficacy endpoints are the kinetics of fibrosis improvement without NASH worsening and NASH resolution without fibrosis worsening. Biopsies are read by 3 independent pathologists, followed by a consensus reading.

**Results:** Herein we report the results from the first 20, F1-3 patients that received Aramchol in whom the scheduled post-baseline biopsy was performed. At baseline, mean age ± SD was 58.5 ± 8.7 years; 70% were females; 75% White; mean BMI 33.5 ± 3.6 kg/m²; 90% had type 2 diabetes; 13 patients had stage 3 fibrosis; 4 stage 2, and 3 stage 1; Mean NAS was 4.8 ± 1.3. Post-baseline biopsies were performed for 9 patients at 24 weeks, 9 at 48 weeks and 2 at 72 weeks. Altogether 12/20 patients (60%) showed fibrosis improvement by ≥1 stage (5/9 after 24 weeks, 6/9 after 48 weeks and 1/2 after 72 weeks). 19/20 patients were either stable or reduced fibrosis measured by liver biopsy. In 5 patients, fibrosis was reduced by 2 points. In 9/20 (45%) patients there was fibrosis improvement without NASH worsening. Statistically significant reductions in ALT, AST and biomarkers associated with liver fibrosis Fib-4 and Proc-3 were also observed corroborating the histological effects. Reductions of a similar magnitude are seen in a cohort of the first 20 patients for which paired biopsy have been analyzed, a cohort of 50 patients for which biomarker data was analyzed (ARCON Cohort) and a cohort of 139 of which ALT, AST and FIB-4 were analyzed. Aramchol showed excellent safety and tolerability. Updated data from the open label study will be presented.

**Conclusion:** 60% of the 20 patients treated with Aramchol 300 mg BID showed fibrosis improvement. Data is corroborated by congruent changes in fibrosis biomarkers and by a biochemical response in aminotransferases. The data presented here, albeit preliminary, is aligned with the hypothesis that higher Aramchol exposure results in an improved efficacy profile and a direct anti-fibrotic effect may be manifested as early as 24 weeks.
**FR169**

**Development of a high precision liver biopsy method to improve the accuracy of fibrosis staging and collagen profiling**

Morten Christensen¹, Ida Villesen¹, Mette Juul Nielsen¹, Morten Karsdal¹, Diana Leeming¹, Nordic Bioscience, Fibrosis Research, Herlev, Denmark

Email: moc@nordicbio.com

**Background and aims:** Liver biopsy is the gold standard for diagnosis and staging of hepatic fibrosis, however it is associated with limitations such as the pathologist’s inter-variability, small sample size, and patient discomfort. Currently, liver biopsy is required as a primary regulatory outcome in clinical trials on non-alcoholic steatohepatitis (NASH), which has increased the need for regulatory approved biomarkers as clinical endpoints. Additionally, hepatic fibrosis is characterized by the excessive accumulation of extracellular matrix (ECM) proteins such as collagens. Quantifying the ECM might improve the precision of fibrosis staging in the liver biopsy. The aim of this proof-of-concept study was to develop a high precision biopsy method to effectively quantify the fibrosis in the liver of bile duct ligated (BDL) rats using serological collagen degradation biomarkers.

**Method:** Sprague Dawley rats underwent BDL surgery and were terminated after 2 weeks. Post termination, 160 μg of snap frozen liver tissue was cleaved with matrix metalloproteinase (MMP)-2 and -9 for 3, 24, and 72 hours, and protease activity halted by addition of 1 μM EDTA. MMP-2 and -9 degradation fragments of type III, IV, and VI collagen were measured in the tissue extract by neo-epitope specific competitive ELISAs (C3M and C6M, respectively) based on monoclonal antibodies. The activity of MMP-2 and MMP-9 was confirmed by their ability to cleave carboxymethylated transferrin and visualized by Coomassie blue staining.

**Results:** Conditioned medium C3M increased significantly with increasing incubation time with MMP-2, thus a 78-fold increase at 24 hours, 150-fold at 72 hours. This was significant when compared to tissue extract with no MMP added (p < 0.0001). A significant increase was also seen in C6M levels at incubation times of 24 hours (MMP2: 66-fold and MMP9: 103-fold) and 72 hours (MMP2: 14-fold and MMP9: 46-fold) (p < 0.0001). MMP-2 and MMP-9 proved successful in cleaving carboxymethylated transferrin.

**Conclusion:** A proof-of-concept high precision ex vivo model was established in BDL treated rodents showing MMP-2 and MMP-9 degraded collagen type III and VI was released from the liver tissue to the conditioned medium as assessed by C3M and C6M. The high precision biopsy holds potential to improve the current liver biopsy evaluation by providing a quantifiable measurement of liver fibrosis.

---

**FR170**

**MAIT cell inhibition promotes liver fibrosis regression by reprogramming macrophage phenotype**

Morgane Mabire¹, Hegde Pushpa¹, Hammoutene Adel¹, JingHong Wan¹, Manon Allaire¹, Al Sayeghi Rola¹, Tristan-Thibault-Sogorb¹,², Emmanuel Weiss¹,², Valérie Paradis¹,², Pierre-Laurent Stefèn², Azéma-Gilgenkrantz³, Sophie Lotersztajn¹,²,¹ Université de Paris, Centre de Recherche sur l’Inflammation (CRI), INSERM, U1149, PARIS 18, France;² Département d’Anesthésie et Réanimation, Hôpital Beaujon, Assistance Publique-Hôpitaux de Paris, 92110, Clichy, France; Clichy, France;³ Département de Pathologie, Hôpital Beaujon, Assistance Publique-Hôpitaux de Paris, 92110, Clichy, France; GenoSplice Technology, Paris, France

Email: morgane.mabire@insERM.fr

**Background and aims:** Mucosal-Associated Invariant T (MAIT) cells are non-conventional T cells restricted by the non-classical MHC-1b molecule MR1 that display altered functions during chronic liver diseases. We recently reported that hepatic MAIT cells are activated during fibrosis in human liver samples and in mice models and display profibrogenic properties (Nat Commun 2018). Here, combining studies in human precision-cut liver slices (PCLS) and experimental models, we investigated whether and how targeting MAIT cell activation may impact fibrosis regression.

**Method:** Liver PCLS were generated from patients with end-stage fibrosis and cultured ex vivo with or without the MAIT cell antagonist Acetyl-6-formylpterin (Ac-6-FP) for 48 hrs. Fibrogenic and inflammatory gene expression was evaluated by RT-qPCR and α-SMA by immunostaining. Liver fibrosis was induced in mice by repeated carbon tetrachloride (CCL4) injections for 4 weeks. For fibrosis regression, CCl4 injections were discontinued and mice were daily administered with Ac-6-FP for up to 4 days. Comparison of genes differentially regulated by Ac-6-FP in Ly6Chigh profibrogenic macrophages and Ly6Clow restorative macrophages was performed by RNA sequencing.

**Results:** Human PCLS from patients with end-stage fibrosis exposed to Ac-6-FP showed significant reduction in the expression of fibrogenic genes such as TGFβ, ACTA2, COL1A1 and COL1A2. Concordantly, the number of α-SMA+ cells was reduced in PCLS exposed to Ac-6-FP. Moreover, inhibiting MAIT cells decreased CCL2 and its receptor CCR2 expressions. Mice chronically exposed to CCL4 and daily injected with Ac-6-FP showed accelerated fibrosis regression associated with a decrease in CCR2+ Ly6Chigh and an increase in Ly6Clow macrophages. RNAseq analyzes performed on Ly6Chigh and Ly6Clow macrophages in Ac-6-FP- and vehicle-exposed mice showed reprogramming of macrophage signature by Ac-6-FP. Apoptosis was the most significant pathway deregulated by Ac-6-FP with upregulation of apoptotic genes in Ly6Chigh macrophages while induction of survival genes was mainly observed in Ly6Clow. Genes of the autophagy pathway, an anti-inflammatory and antifibrogenic mechanism in the liver, were also induced in both populations by Ac-6-FP, together with an increase in the number of LC3II+cells.

**Conclusion:** Inhibiting MAIT cell activation may offer new perspectives for antifibrogenic therapy, by promoting fibrosis resolution via reprogramming of macrophage profile.
The derivation cohort included 463 patients, 75% male, with a median age of 57 years (IQR 14). The majority (197/463, 55%) had significant liver fibrosis (≥F2), and 94 (20%) had advanced liver fibrosis (≥F3). The LiverPRO score diagnosed significant fibrosis with good diagnostic accuracy (AUC 0.84; 95% CI 0.81–0.88), similar as the ELF-test (AUC 0.84; 0.80–0.88), and superior to the FIB-4 (AUC 0.77; 95% CI 0.73–0.83). The same was observed for advanced fibrosis (LiverPRO AUC 0.92; 0.88–0.95 versus ELF-test AUC 0.92; 0.89–0.95 versus FIB-4 AUC 0.84; 95% CI 0.79–0.89).

The validation cohort included 4,722 participants, 49% male, median age 57 years (IQR 11), and 299 (6%) had a TE ≥ 8 kPa, of those 50% had risk factors for ALD, 46% for NAFLD and 4% had no risk factors for fatty liver disease. In this low prevalence cohort, the LiverPRO score detected TE ≥ 8 kPa with moderate accuracy (AUC 0.75; 95% CI 0.72–0.77), comparable to the ELF test (AUC 0.74; 95% CI 0.71–0.78) and superior to FIB-4 (AUC 0.64; 95% CI 0.59–0.68).

**Conclusion:** The LiverPRO score accurately predicts significant and advanced liver fibrosis in both a high prevalence and a low prevalence cohort. Combined with a very low cost of the routine liver blood markers and an easy interpretable score from 0 to 100%, the score may be a useful screening tool and decision aide for primary care referral pathways.
Macrophage MerTK promotes a profibrogenic cross-talk with hepatic stellate cells via soluble mediators

Mirella Pastore1, Chiara Raggi1, Nadia Navari1, Benedetta Piombanti1, Giovanni Di Maio1, Elisabetta Rovida1, Marie-Pierre Piccinni1, Letizia Lombardelli1, Federica Logiodice1, Cristina Rombouts2, Salvatore Petta3, Fabio Marra1.1University of Florence, Firenze, Italy; 2University College London, United Kingdom; 3Università degli Studi di Palermo, Palermo, Italy
Email: fabio.marra@unifi.it

Background and aims: Activation of Kupffer cells and recruitment of monocytes are key events in fibrogenesis. These cells release soluble mediators which induce the activation of hepatic stellate cells (HSC), the main fibrogenic cell type within the liver. Mer tyrosine kinase (MerTK) signaling regulates multiple processes in macrophages and has been implicated in the pathogenesis of NASH-related fibrosis. In this study, we explored if MerTK activation in macrophages influences the profibrogenic phenotype of HSCs.

Method: M2c-like (MerTK+/CD206+/CD163+/CD209−) macrophages were differentiated from peripheral blood monocytes using M-CSF and IL-10. The role of MerTK was assessed by stimulation with the ligand Gas-6 and by pharmacologic inhibition with UNC569.

Results: MerTK+ macrophages exhibited activation of STAT3, ERK1/2, and p38 and increased expression of VEGF-A. Exposure of MerTK+ macrophages to Gas-6 increased activation of MerTK and downstream pathways. These events were reverted by pretreatment with UNC569. MerTK and Gas-6 mRNA levels were gradually increased during macrophage polarization towards a M2c-like phenotype and were significantly greater in Kupffer cells than in peripheral blood monocytes. Gas-6 was released both by M2c-like macrophages and Kupffer cells. Activation of MerTK in macrophages induced a secretome which caused a significant increase in migration, proliferation, viability and expression of profibrogenic factors in HSCs. Conditioned medium of Gas-6-stimulated MerTK+ macrophages also induced a significant increase in phosphorylation of STAT3 and p38 in HSCs, and upregulation of IL8 expression. These effects were specifically related to MerTK activity in macrophages, as indicated by pharmacologic inhibition.

Conclusion: MerTK activation in M2c-like macrophages modifies the secretome to promote HSC profibrogenic features, indicating that this receptor may be implicated in the pathogenesis of hepatic fibrosis.

FR174

Comparative fibrosis-reducing activities of farnesoid X receptor (FXR), peroxisome-proliferator activated receptor delta (PPARδ) and thyroid hormone receptor (THR) agonists in the carbon tetrachloride mouse model

Edward Cable1, Jeffrey Stebbins1, Yun-Jung Choi1, Jiangao Song1, Prasad Manchem2, Sanjay Pandy2, Charles McWherter1. 1CymaBay Therapeutics Inc., Newark, United States; 2Triangulum Biopharma, Carlsbad, United States
Email: ecable@cymabay.com

Background and aims: Fibrogenesis is a key first step toward cirrhosis in the liver, independent of etiology. A limited number of nuclear receptor agonists that have been tested in diseases with liver fibrosis. The AIM of the current study is to test three of these agonists in established fibrosis in the mouse CCl4 model. These three selected agonists are: the FXR agonist, obeticholic acid; the PPARδ agonist, seladelpar, and the THRβ agonist, resmetirom. This model can be used to attempt to answer these questions and build on the findings that PPARδ agonists reduce established fibrosis in the dietary NASH mouse, the foz/Shf mouse, and the NIF mouse models.

Method: Male C57B/6 mice were treated with 1 mL of CCl4 per g BW via IP injection twice per week for 8 weeks. Concurrent with treatment initiation at week 5, a set of animals (n = 10) was sacrificed to assess the fibrosis levels. Animals (n = 20/group) were dosed daily with OCA (30 mg/kg), seladelpar (10 mg/kg), resmetirom (1 mg/kg) or vehicle in 0.5% CMC, PO for an additional 3 weeks while continuing CCl4 administration. Liver histology assessments (H&E and PSR) and hydroxyproline content were analyzed as measures of liver fibrosis. Results: Average hydroxyproline content at treatment start was 253 mg/g liver. Additional 3 weeks of CCl4 treatment increased the average hydroxyproline to 290 mg/g. Neither FXR nor THR agonists decreased hydroxyproline content (277 and 291 mg/g, respectively) while PPARδ decreased hydroxyproline to 215 mg/g. In addition to the reduction in total hydroxyproline, the PSR staining demonstrated a reduction in bridging fibrosis with seladelpar compared to both the vehicle at 8 weeks and the starting levels at 5 weeks. No apparent changes in fibrosis staining were observed with the other treatments.

Conclusion: The CCl4 mouse model may be used to test for molecular targets that will reduce established fibrosis. The combination of total biochemical and histologic measurements are important to assess the topographic changes. Reduction of the PSR positive fibrotic cords between the veins is generally considered beneficial and readily observable in this model. We believe that this 8-week model can be used to dissect some of the molecular mechanisms for fibrogenesis, fibrolysis after cessation of CCl4 and fibrosis in the presence of CCl4. Is treatment-related fibrosis in the presence of CCl4 just a reduction in the CCl4 mediated fibrogenesis or are there separate processes? This model can be used to attempt to answer these questions and build on the findings that PPARδ agonists reduce established fibrosis in the dietary NASH mouse, the foz/Shf mouse, and the NIF mouse models.

FR175

A novel role for serine protease Kallikrein 8 in liver fibrosis through cleaving complement C3 and hepatic macrophage polarization

Cichun Wu1, Yao Liu1, Ying Li1, Wei Zhang1, Lei Fu1, Xin Ni2, Shifang Peng1. 1Xiangya Hospital Central South University, Department of Infectious Diseases, Changsha, China; 2Xiangya Hospital Central South University, International Collaborative Research Center for Medical Metabolomics, Xiangya Hospital Central South University, Changsha, China
Email: sfp1988@csu.edu.cn

Background and aims: Kallikrein 8 (KLK8), an emerging serine protease in the family of Kallikrein-related peptidases (KLKs), has been implicated in myocardial and renal fibrosis. To date, it remains unknown whether and how KLK8 is involved in liver fibrosis. In this study, we aimed to determine the role of KLK8 in liver fibrosis and the underlying molecular mechanisms.

Method: KLK8 expression and localization were examined in liver tissues from fibrotic human subjects and rodent models. In vivo and in vitro silencing or overexpression of KLK8 was used for functional
Proposed mechanisms. During liver injury, KLK8 secreted by hepatocytes releases the active fragment C3a by shearing complement C3, which in turn activates macrophages to secrete TGFβ1 and promotes the development of liver fibrosis through the TGFβ1/smads2/3 signaling pathway.

Conclusion: This study has delineated a novel role for KLK8 in liver fibrosis. As such, the new findings may advance our understanding of KLK8, and eventually help unleash its therapeutic potential in the development of novel treatments.

FRI176
The modulation of NADPH oxidases by tyrosol-derived phenolic compounds prevents hepatic fibrogenesis

Daniela Gabbi1, Sara Carpi1,2,3, Samantha Sarcognato1, Ilaria Zanotto1, Beatrice Polini2, Katia Sayaf2, Paola Nieri2, Francesco Paolo Russo5, Maria Guido4, Sara De Martin1. 
1University of Padua, Department of Pharmaceutical and Pharmacological Sciences, Padova, Italy; 2University of Pisa, Department of Pharmacy, Pisa, Italy; 3CNR PISA, NEST, Pisa, Italy; 4University of Padua, Department of Medicine, Padova, Italy; 5University of Padua, Department of Surgery, Oncology and Gastroenterology, Padova, Italy
Email: sara.demartin@unipd.it

Background and aims: Hepatic NADPH oxidases (NOXs) are devoted to the production of reactive oxygen species (ROS), thus regulating inflammatory and fibrotic processes. Exaggerated NOX expression and activation, particularly of NOX1 and NOX4, have been related to the activation of hepatic stellate cells (HSCs) and the trigger of fibrogenesis. Therefore, compounds modulating the expression and activity of NOXs may represent promising agents for the management of hepatic fibrosis. In this study we investigated the antifibrotic and antioxidant action of the two phenolic compounds tyrosol and hydroxytyrosol, known for their cardioprotective activity, with the aim of unravelling their effect in vitro and in vivo on NOX-related fibrogenetic pathways.

Method: We evaluated tyrosol and hydroxytyrosol activity by means of LX2 and HepG2 cells, used as in vitro models of HSCs and hepatocytes, respectively. A mouse model of liver fibrosis was induced by a 4-week IP CCl4 administration to 6 Balb/C mice; 6 untreated mice were used as controls. Tyrosol and hydroxytyrosol were administered daily by oral gavage. Levels of hepatic NOX1/4, alphaSMA, COL1A1, IL-6, IL-10 were assessed by qPCR and Western blot. Hepatic miR-181-5p, miR-221, miR-29b-3p and miR-101 were measured by qPCR.

Results: Tyrosol significantly decreased the production of ROS by HepG2 cells, and the mRNA levels of NOX1/4, alphaSMA and COL1A1 in TGFβ1-activated LX2 cells, displaying an antifibrotic and antioxidant activity comparable to the prototypical NOX1/4 inhibitor GKT136901. An increase of hepatic ROS (p < 0.0001), alphaSMA, NOX1/4, alphaSMA, COL1A1, IL-6 and IL-10 mRNA levels (p < 0.05) were observed in fibrotic mice, as well as a slight increase in NOX1/4 expression. Tyrosol and hydroxytyrosol were able to counteract these effects, by significantly downregulating alphaSMA, COL1A1, NOX1/4, IL-6 and IL-10 with respect to fibrotic mice. The profibrotic miRNAs miR-181-5p and miR-221 were downregulated by tyrosol, whereas the expression of antibibrotic miRNAs miR-29b-3p and miR-101 was restored to physiological level by both tyrosol and hydroxytyrosol. Liver histology confirmed a reduction of fibrosis in treated mice.

Conclusion: The phenolic compounds tyrosol and hydroxytyrosol ameliorate hepatic fibrosis by reducing hepatic oxidative stress and inflammation and modulating the hepatic expression of miRNAs involved in fibrogenesis. Tyrosol-derived molecules should be evaluated as promising antifibrotic candidates.
FR1177
Exploring gender-related differences in liver fibrosis and regeneration through a new experimental carbon tetrachloride protocol in mice
Katia Sayaf1, Ilaria Zanotto2, Daniela Gabbia3, Dafne Alberti3, Giulia Pasquali1, Sara De Martin3, Francesco Paolo Russo3. 1University of Padova, Department of Surgery, Oncology and Gastroenterology, Padova, Italy; 2University of Padova, Department of Pharmaceutical and Pharmacological Sciences, Padova, Italy; 3University of Padova, Department of Surgery, Oncology and Gastroenterology, Padova, Italy
Email: francescopaolo.russo@unipd.it

Background and aims: The incidence of chronic liver diseases (CLDs) is two-fold higher in men than women and they display clinically relevant differences. Thus, understanding the mechanistic gaps between females and males by pre-clinical studies is fundamental to increase the awareness on gender influence in the pathophysiological and regenerative mechanisms underlying liver fibrosis.

Method: A new experimental protocol based on increasing doses of carbon tetrachloride (CCL4) has been developed and performed in female and male Balb/C mice, by intraperitoneal injections for 12 weeks, followed by a washout period of 8 weeks. Mice were sacrificed at different timepoints (6, 12 and 20 weeks). Flow cytometry experiments were performed on fresh liver tissues to evaluate the amount of recruited monocytes-derived macrophages (MoMFs). Liver histology was assessed by Masson’s trichrome staining, and liver function was evaluated by the hydroxyproline assay. The gene and protein expression of collagen, growth factors, and pro-inflammatory elements were evaluated by qPCR and immunohistochemistry, respectively.

Results: Both female and males developed a progressive liver fibrosis during CCL4 treatment and showed liver regeneration during the washout period. After 6 weeks of treatment, male mice showed more fibrotic areas (p < 0.05) and more activated stellate cells (HSCs) than female mice (p < 0.05). Furthermore, a higher inflammatory status within male liver was confirmed during the acute damage by the intensive recruitment of pro-inflammatory Ly6Chigh F4/80+CD11bhigh MoMFs, together with higher levels of gene expression of pro-inflammatory growth factors than females. On the other hand, females developed a worse hepatic condition after 12 weeks of CCL4 treatment, showing a higher hydroxyproline content, more activated HSCs than males, and elevate amounts of Ly6Chigh F4/80+CD11bhigh MoMFs. During the washout period, female mice showed less fibrotic areas than males (p < 0.05) and the presence of small amounts of MoMFs, while some activated HSCs but no pro-inflammatory MoMFs were detected in males.

Conclusion: This new model of fibrosis obtained with increasing doses of CCL4 led to the development of liver damage without adaptive responses of the liver to the injury. We observed gender-related differences in liver damage and regeneration, due to the fact that gender influences the recruitment of pro-inflammatory MoMFs and the activation of hepatic stellate cells.

FR1178
Multicenter external validation of FIB-6: a novel, machine-learning, simple bedside score to rule out severe liver fibrosis and cirrhosis in patients with MAFLD
Gamal Shiba1, Reham Soliman1, Nabil Mikhail2, Khalid Alswal3, Ayman Abdo3, Faisal Sana1, Necati Ormeci5, George Dalekos6, Amir Anushiravani7, Mai Mabrouk8, Samir Marzouk9, Katia Sayaf1, Ilaria Zanotto2, Daniela Gabbia2, Dafne Alberti3, Gamal Shiha1, Reham Soliman1, Nabiel Mikhail2, Khalid Alswal3, Ayman Abdo3, Faisal Sana1, Necati Ormeci5, George Dalekos6, Amir Anushiravani7, Mai Mabrouk8, Samir Marzouk9. 1Egyptian Liver Research Institute and Hospital (ELRIAH), Gastroenterology and Hepatology, Egypt; 2Egyptian Liver Research Institute and Hospital (ELRIAH), Biostatistics and Cancer Epidemiology, Egypt; 3College of Medicine, King Saud University, Medicine, Saudi Arabia; 4King Abdulaziz Medical City, Gastroenterology, Saudi Arabia; 5Ankara University School of Medicine, Gastroenterology, Turkey; 6National Expertise Center of Greece in Autoimmune Liver Diseases, Medicine and Research Laboratory of Internal Medicine, Greece; 7Tehran University of Medical Sciences, Digestive Disease, Iran; 8Misr University for Science and Technology (MUST), Biomedical Engineering, Egypt; 9Arab Academy for Science and Technology (AASTMT), Basic and Applied Science Department, Egypt
Email: g.shiha@hotmail.com

Background and aims: Non-invasive tests (NITs) are urgently required to evaluate hepatic fibrosis in MAFLD. We previously developed and validated a non-invasive diagnostic index based on routine laboratory parameters for predicting the stage of hepatic fibrosis in patients with chronic hepatitis C (HCV) called FIB-6 through machine learning with random forests algorithm using retrospective data of 7238 biopsy proven chronic hepatitis C (CHC) patients. Our aim is to validate this novel score in patients with MAFLD.

Method: Performance of the new score was externally validated in cohorts from one site in Egypt (n = 674) and in 5 different countries (n = 1798) in Iran, KSA, Greece, Turkey and Oman). Biopsy samples were scored by experienced pathologists who used the META VIR scoring system. Results were also compared with three established tools (FIB-4, APRI, and AAR).

Results: In this study, 2472 patients met the criteria, and their liver biopsy results were included for analysis. Using the optimal cutoffs in the data of FIB-6 indicated a reliable performance in diagnosing cirrhosis, severe fibrosis, and significant fibrosis. Results indicated good sensitivity and NPV. Sensitivity = 70.5%, specificity = 62.9%, PPV = 15.0% and NPV = 95.8% for diagnosis of cirrhosis. For diagnosis of severe fibrosis (F3 and F4), the results were 86.5%, 24.0%, 15.1% and 91.9% respectively, while for diagnosis of significant fibrosis (F2, F3 and F4), the results were 87.0%, 16.4%, 24.8% and 80.0%. Comparing of the results of FIB-6 rule-out cutoffs with those of FIB-4, APRI, and AAR showed that in ruling out severe fibrosis and cirrhosis, FIB-6 gave the highest sensitivity and NPV (97.0% and 94.7%), as compared to FIB-4 (71.6% and 94.7%), APRI (36.4% and 90.7%), and AAR (61.2% and 90.9%).

Table: (abstract: FR1178): Diagnostic performance of FIB-6 optimal cutoffs in all cohorts compared to the liver biopsy results

<table>
<thead>
<tr>
<th></th>
<th>Cutoff</th>
<th>Sensitivity</th>
<th>Specificity</th>
<th>PPV</th>
<th>NPV</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cirrhosis (F4 vs. F0123)</td>
<td>2.3159</td>
<td>70.5 (64.0–76.2)</td>
<td>62.9 (60.9–64.9)</td>
<td>15.0 (12.9–17.4)</td>
<td>95.8 (94.7–96.7)</td>
</tr>
<tr>
<td>Severe fibrosis (F34 vs. F012)</td>
<td>1.8992</td>
<td>86.5 (82.5–89.8)</td>
<td>24.0 (22.3–25.9)</td>
<td>15.1 (13.6–16.8)</td>
<td>91.9 (89.4–93.9)</td>
</tr>
<tr>
<td>Significant fibrosis (F234 vs. F01)</td>
<td>1.7720</td>
<td>87.0 (84.1–89.5)</td>
<td>16.4 (14.8–18.1)</td>
<td>24.8 (23.0–26.7)</td>
<td>80.0 (75.7–83.7)</td>
</tr>
</tbody>
</table>
Table: Diagnostic performance of FIB-6 rule-out cutoffs for severe fibrosis (F3) or cirrhosis (F4) in all cohorts compared with that of FIB-4, APRI, and AAR

<table>
<thead>
<tr>
<th>Cutoff</th>
<th>Sensitivity</th>
<th>NPV</th>
</tr>
</thead>
<tbody>
<tr>
<td>FIB-6</td>
<td>1.5023</td>
<td>97.0 (94.6–98.4)</td>
</tr>
<tr>
<td>FIB-4</td>
<td>1.45</td>
<td>71.6 (66.6–76.2)</td>
</tr>
<tr>
<td>APRI</td>
<td>0.70</td>
<td>36.4 (31.5–41.7)</td>
</tr>
<tr>
<td>AAR</td>
<td>1.00</td>
<td>61.2 (55.9–66.3)</td>
</tr>
</tbody>
</table>

Conclusion: FIB-6 score is an accurate, simple, noninvasive test for ruling out advanced fibrosis and liver cirrhosis in patients with MAFLD better than APRI, FIB-4 and AAR.

FR1180
Clinical and genetic factors associated with regression of fibrosis in ACLD after etiologic therapy
Yuly Mendoza1,2, Mojgan Masoodi3, Sofia Tsouka3, Jaime Bosch4, Annalisa Berzigotti1,2, 1Department of Visceral Surgery and Medicine, Inselspital, Bern University Hospital, University of Bern, Switzerland; 2Department for BioMedical Research, Visceral Surgery and Medicine, University of Bern, Switzerland; 3Institute of Clinical Chemistry, Bern University Hospital, Bern, Switzerland
Email: yuly.mendozajaimes@insel.ch

Background and aims: Liver fibrosis is the main determinant of clinical outcomes in advanced chronic liver disease (ACLD) of any etiology. The introduction of effective etiological therapies has shown that liver fibrosis and even cirrhosis is reversible after eliminating the cause of ACLD. However, not all patients experience fibrosis regression, evidencing that other factors modulate this process. In order to better understand the genetic and molecular mechanisms controlling fibrosis regression we analysed the genetic and transcriptional pathways in ACLD with or without regression of fibrosis using high-throughput technologies.

Method: We conducted a case-control pilot study of 60 patients with ACLD of different etiology, 30 with histological and/or clinical evidence of regression (Regressors, Re) and 30 without (Non-regressors, NRe), after a minimum of 24 months of etiological therapy. In all patients we performed genotyping (TaqMan assay) of gene variants associated with liver fibrosis (PNPLA3, TM6SF2, SERPIN1A, GCKR, TIMC4, HSD17B13). Transcriptomic analysis (RNAseq) was done in 30 frozen paired liver biopsies (before and after therapy) of 15 patients. Differentially Expressed Genes (DEGs) analysis were determined using DESeq2 and selected for FDR <0.05. The enrichment of biological pathways was determined with KEGG.

Results: Lack of regression was associated with higher frequency of GCKR-rs1260326 CT-Allele (NRe 63.3% vs Re 36.7%; OR: 0.240, p = 0.020), obesity (63.7% vs. 36.7%, p = 0.041) and higher liver stiffness (33.3 vs. 21.8 kPa, p = 0.032). These three factors remained independently associated with lower likelihood of ACLD regression on multivariate analysis (Figure). RNAseq data comparing Re vs. NRe in the post-therapy samples disclosed 109 significantly DEGs out of 17,243 genes. Downregulated DEGs in Re showed significant enrichment for the Hippo signaling pathway (p < 0.05). Other pathways identified included the PI3K-Akt signaling pathways, ECM-receptor interaction, focal adhesion and relaxin signaling pathways, already known to be involved in liver fibrosis.

Conclusion: Presence of obesity, high LSM and GCKR-rs1260326 CT-Allele decrease the likelihood of fibrosis regression of ACLD. The liver transcriptome analysis suggests that the Hippo signaling pathway, a pathway driving hepatic stellate cell activation, is involved in fibrosis...
regression and may represent a novel potential therapeutic target to reverse liver fibrosis in ACLD.

FR181
Addressing the heterogeneity of fibrosis in liver biopsy specimens with qFibrosis – a new paradigm for an old problem
David E. Kleiner1, Pik Eu Jason Chang2, Dean Tai3, Elaine Chng4, Yayun Ren5, Feng Liu4, Huiying Rao6, Lai Wei5, Arun Sanyal6.
1Laboratory of Pathology, Center for Cancer Research, NCI, MD, USA; 2Department of Gastroenterology and Hepatology, Singapore General Hospital, Singapore; 3HistolDx Pte. Ltd., Singapore; 4Peking University People’s Hospital, Peking University Hepatology Institute, Beijing Key Laboratory of Hepatitis C and Immunotherapy for Liver Diseases, Beijing, China; 5Hepatopancreatobiliary Center, Beijing Tsinghua Changgung Hospital, Tsinghua University, Beijing, 102218, China; 6Virginia Commonwealth University, Richmond, Virginia, USA
Email: kleinerd@mail.nih.gov

Background and aims: A 1-stage fibrosis improvement is key for therapeutic benefit assessment in NASH trials. But in trials with a 48-week duration, most patients do not change their fibrosis stage according to the CRN system. This is due to either insufficient change in collagen amount or fibrosis distribution. qFibrosis can analyze these differential changes which has been shown to provide insights on drug effects. The generalisability in this approach beyond NASH has not been established. In this exploratory analysis, a cumulative drug effects. The generalisability in this approach beyond NASH has not been established. In this exploratory analysis, a cumulative

Method: Paired biopsies from 35 patients assessed to have achieved sustained virological response. Paired biopsies from 35 patients assessed to have achieved sustained virological response. Paired biopsies from 35 patients assessed to have achieved sustained virological response.

Results: The baseline staging of the HCV patients were F0 (n = 1); F1 (n = 2); F2 (n = 2); F3 (n = 7); F4 (n = 9); F5 (n = 2); F6 (n = 12). This cohort was reclassified by qF-TWS as those with progression (n = 9), with qFibrosis

Conclusion: qF-TWS can differentiate subjects with fibrosis progression and regression post-treatment who were determined as no-change by pathologists’ assessment. The ability of qFibrosis to assess fibrosis heterogeneity on a continuous scale provides the potential of detecting subtle fibrosis changes that cannot be captured by current system. A separate study is planned to establish correlation to clinical outcomes.

Figure: qF-TWS of 3 patients who have no change in fibrosis before and after treatment. E.g., patient A showed increase in fibrosis (normalized) in 5 regions: 0.11 to 0.22 for portal, 0.17 to 0.30 for PP, 0.18 to 0.21 for PC, 0.21 to 0.33 for bridging, 0.48 to 0.36 for PS.

FR182
Characterisation of the novel Galectin-3 inhibitor GB1107 on CCl4-induced liver fibrosis in mice
Alison MacKinnon1, Ross Mills2, Fredrick Zetterberg3, Rob Slack4.
1Galecto Inc, Edinburgh, United Kingdom; 2University of Edinburgh, Centre for Inflammation Research, Edinburgh, United Kingdom; 3Galecto Inc. Copenhagen, Denmark
Email: AM@galecto.com

Background and aims: Galectin-3 (Gal-3) is a pro-fibrotic β-galactoside binding lectin highly expressed in fibrotic liver (1) and implicated in hepatic fibrosis (2). GB1107 is a novel orally active anti-Gal-3 small molecule inhibitor that has high affinity and selectivity for galectin-3 as well as high oral bioavailability in mice (3).

Method: Liver fibrosis was induced by administration of CCl4 (1:3 CCl3:olive oil) at 1 microlitre per g or olive oil control twice weekly by intraperitoneal injection in male C57Bl/6 mice for 8 weeks. GB1107 or vehicle control was administered once daily orally (10 mg/kg) for the last 4 weeks of CCl4 treatment. Livers were removed and fibrosis assessed by Sirius red staining of liver sections and gene sequencing. Total RNA was extracted and libraries were prepared using the NEBNEXT Ultra II Directional RNA Library Prep kit and the Poly-A mRNA magnetic isolation module. Paired-end sequencing with a read length of 100 bp was performed using a single P3 flowcell on the NextSeq 2000 platform. The raw reads were aligned to the mouse reference genome assembly GRCm39 using STAR. Pathway enrichment analysis was performed to determine enrichment of differentially expressed genes (DEGs) within Reactome pathways and Gene Ontology (GO) terms.

Results: GB1107 significantly reduced CCl3-induced liver fibrosis (Sirius red, CCl4-vehicle 2.70 ± 0.24%; CCl4-GB1107 1.99 ± 0.10% (p = 0.009)). Using a false discovery rate-adjusted statistical threshold (FDR-adjusted p < 0.05) and a 2-fold change in expression cutoff, 1, 659 DEGs were identified with CCl4 treatment compared to control. Comparing GB1107 treatment with CCl4 vehicle mice 1147 DEGs were identified. Pathways strongly enriched in up-regulated genes in the CCl4 group included those related to the extracellular matrix, and collagen biosynthesis and assembly, cell cycle and the immune system whilst pathways related to fatty acid or lipid metabolism were enriched in the down regulated genes. Principal component analysis revealed that GB1107 overlapped significantly with the control group and effectively reversed the CCl4-induced gene changes.

Conclusion: GB1107 inhibited CCl4-induced liver fibrosis and reversed CCl4-induced gene changes. Small molecular weight and orally active inhibitors of galectin-3 show promise as potential new oral anti-fibrotic agents for the treatment of liver fibrosis. A first-in-human study with GB1211, an analogue of GB1107, has shown it to be both safe and well tolerated in man, demonstrating a PK profile that supports twice daily dosing (NCT03809052). GB1211 has now progressed to a phase II study in patients with liver cirrhosis (NCT05009680).

References

FR183
Quantitative digital pathology of 3D human NASH models establish continuous scores to evaluate the anti-fibrotic effects of Selensertib, Firsocostat and Resmetinib
Louis Petitjean1, Simon Ströbel2, Li Chen2, Eva Thomà3, Radina Kostadinova3, 1PharmaNest, Inc, Princeton, United States; 2PharmaNest Inc, Princeton, United States; 3InSphero AG, Schlieren, Switzerland
Email: louis.petitjean@pharmanest.com

Background and aims: Human in-vitro 3D NASH tissue model have the potential to accelerate the discovery of new anti-fibrotic
Conclusion: The combination of FibroNest™ imaging analysis for automated quantification of histological fibrosis severity phenotype within vitro 3D InSight™ human NASH model provide powerful platform for anti-fibrotic drug-candidates response evaluation.

FRI184
Etiology-independent fibrosis severity scoring by quantitative digital pathology image analysis
Adam Watson1, Louis Petitjean2, Mathieu Petitjean2, Michael Pavlides1.1 University of Oxford, Oxford, United Kingdom; 2PharmaNest, Inc, Princeton, United States
Email: mathieu.petitjean@pharmanest.com

Background and aims: While fibrosis is the common end point of many chronic liver disease, little is known about the possible subtle histological differences between etiologies and the related performance of existing fibrosis staging system. Here, we used quantitative Digital Pathology image analysis and quantitative AI to quantify the phenotype of liver fibrosis using histological traits to describe collagen content, collagen fiber morphometry and fibrosis architecture. The aim of this study as to identify histological traits common to a variety of liver disease aetiologies and use these to develop a new quantitative etiology-independent fibrosis severity score.

Method: Patients who had undergone liver biopsy for the assessment of diffuse liver disease were included. Liver biopsy histology slides stained with Sirius Red were digitally scanned and categorised as mild (F0–2; n = 28), moderate (F3–4; n = 17) or severe (F5–6; n = 35) fibrosis using the Ishak staging system. Disease etiology was classified as alcohol related liver disease (ARLD; n = 25), non-alcoholic fatty liver disease (NAFLD; n = 17), viral (chronic hepatitis B or C; n = 20), or autoimmune (PBC, PSC or autoimmune hepatitis; AIH; n = 18). FibroNest™ was used to describe the fibrosis phenotype of each etiological group according to quantitative fibrosis traits parameters (qFTs; n = 220) from three phenotypic layers: collagen content, fibers morphometry and fibrosis architecture. For each etiological group, qFTs that showed significant variation (>20%; p < 0.05) between the mild and severe groups of fibrosis were combined to produce an etiology-specific score for fibrosis severity. We also combined qFTs common to all four aetiological groups (n = 77) to produce etiology-independent score for fibrosis severity, morphometry, and architecture.

Results: Our etiology-independent fibrosis phenotypic score (2nd row of Figure 1) correlates with fibrosis stage and distinguishes mild from severe fibrosis with acceptable performance. The etiology-specific phenotypic score (1st row of Figure 1) has a superior performance for mild fibrosis. For each etiology [NAFLD, Viral, Autoimmune, AR-SH], group mean values are comparable for the Mild [2.63;2.67;2.64;3.03], Moderate [3.03;3.04;3.04;2.90] and Severe [4.17;4.26;4.33;4.47] stages. The morphometric and architectural scores (and their related qFTs) can be used to further enrich the understanding of fibrosis phenotypes.

Conclusion: Our data shows that quantitative digital pathology image analysis can phenotype fibrosis and quantify severity in multiple liver disease aetiologies. We used this technology to develop an etiology-independent score to assess the severity of fibrosis from liver biopsies.
**FRI185**

**Liver stiffness and autoimmune profile in a cohort of patients with systemic sclerosis**

Davide Di Benedetto, Maria Lorenza, Francesca Baorda, Giulia Francesca Manfredi, Antonio Acquaviva, Carla De Benedittis, Cristina Rigamonti, Mattia Bellan, Davide Di Benedetto, Pascu Ariana, Ioan Sporea.

**Background and aims:** Systemic sclerosis (SSc) is characterized by skin fibrosis and involvement of esophagus, lungs, heart and kidneys. Liver involvement in SSc is considered rare, but reports addressing this issue are scarce. Here, we evaluated the prevalence of liver fibrosis and hepatic autoimmunity in a cohort of SSc patients.

**Method:** A retrospective observational study was performed on 97 patients diagnosed with SSc or mixed connective tissue disease with scleroderma manifestations who underwent transient elastography evaluating liver stiffness (LS) and controlled attenuation parameter (CAP) due to clinical indication; a biochemistry assessment and major antibodies associated to liver autoimmunity were recorded whether performed together to clinical and demographic data.

**Results:** Among the 97 patients included, 16 (16.5%) had LS performed together to clinical and demographic data.

**Conclusion:** Among SSc patients, the prevalence of biomarkers of hepatic fibrosis and AMA is relatively high, suggesting the opportunity of performing a transient elastography and a screening for hepatic autoimmunity at diagnosis and/or along the course of the disease.

**FRI186**

**Performance of a p-SWE method implemented on a new ultrasound system for predicting advanced liver fibrosis**


**Background and aims:** Ultrasound based elastography techniques became in the last years reliable tools to predict the severity of liver fibrosis in chronic hepatopathies. Usually, these techniques are integrated in high-end US machines but recently they became available in medium-range ones. To evaluate the performance of p-Shear-Wave Elastography from Siemens, implemented on the new ACUSON Juniper Ultrasound System, for the non-invasive assessment of liver fibrosis, and to identify liver stiffness (LS) cut-off value for predicting advanced fibrosis, using Transient Elastography (TE) as the reference method.

**Method:** We included 201 consecutive subjects (80% men, mean BMI = 28.7 ± 4.9 kg/m², mean age 59 ± 18.4 years) with or without chronic hepatopathies in whom LS was evaluated in the same session by means of 2 elastography techniques: TE and p-SWE from Siemens. Reliable LS measurements were defined for TE as the median value of 10 measurements with an interquartile range/median (IQR/M) <30%, and for p-SWE as the median value of 10 measurements acquired in a homogenous area and an IQR/M <30%. A cut-off of ≥9.5 kPa by TE was used to define advanced fibrosis (F ≥3).

**Results:** Valid liver stiffness measurements (LSM) were obtained in 97.5% of patients using both elastography methods. Therefore, 196 subjects were included in the final analysis (27.8% with TE ≥9.5 kPa). A moderate positive correlation was found between the LS values obtained by the 2 methods: r = 0.68, p < 0.0001 (Spearman correlation). LS values obtained by p-SWE were significantly lower than those obtained by TE: 8.3 kPa vs. 10.12 kPa (p < 0.0001). The best p-SWE cut-off value for advanced fibrosis (F ≥3) was 7.4 kPa (AUC-0.95; Se-81.5%; Sp-98%; PPV-95.7%; NPV-93.3%) (fig 1).

**Conclusion:** Using the new US system, the best p-SWE cut-off value for predicting advanced fibrosis was 7.4 kPa.

**FRI187**

**Inhibition of tumour progression locus 2 (TPL2) halts the progression of liver fibrosis in a stringent long term choline deficient high-fat diet (CdHFD) rat model**


**Background and aims:** Chronic inflammatory stimuli exacerbate liver damage and contribute to the development of fibrosis and NASH. Inhibition of TPL2, a serine-threonine kinase downstream of pattern recognition receptors, could halt or reverse NASH and liver fibrosis. Previously reduced hepatic inflammation and fibrosis was observed with a TPL2 inhibitor (TPL2i) in the rat CDHFD model. Here we explored the effect of TPL2i in an extended disease model.

**Method:** Male Wistar rats on CdHFD for 8 weeks were treated with TPL2i (100 mg/kg, BID), ACC inhibitor (ACCI, 10 mg/kg, QD), cenicriviroc (CVC, 100 mg/kg BID) or combinations of ACCi + TPL2i, and ACCi + FXR agonist cilofexor (CIL: 30 mg/kg BID) for 10 weeks (n = 10–15/group). Liver fibrosis was assessed by picrosirius red (PSR) and αSMA staining. Hepatic immune cell and cytokine content were assessed by immunohistochemistry and ELISA, respectively. CCR2γ and Foxp3γ expression was assessed.

Figure 1: Performance of p-SWE for predicting advanced fibrosis (F ≥3).
cells were measured by immunofluorescence and quantified using Visiopharm.

**Results:** TPL2i reduced PSR by 48% and αSMA by 50% vs. vehicle (both p < 0.001). The combination TPL2i + ACCi reduced PSR by 63% and αSMA by 72% vs. vehicle. No improvement in these endpoints was observed with either ACCi or CVC. TPL2i reduced the expression of fibrogenic genes and hepatic content of macrophages and T-cells compared to vehicle (p < 0.001), but no further reductions were observed with the TPL2i + ACCi combination. A reduced number of CCR2+ cells and increased proportion of TRegs were observed in liver from TPL2i-treated rats vs. vehicle. As expected, CVC reduced macrophage number (by 22%, p < 0.01) but did not alter T-cells. TPL2i reduced TNF-α by 64%, KC/GRO by 47% and IL-1β by 46% (vs vehicle, all p < 0.01). Further reductions in TNFα and KC/GRO were observed with ACCi + TPL2i combination. CVC reduced TNF-α by 48%, KC/GRO by 32%, and IL-1β by 34% (vs. vehicle, all p < 0.05). As a clinically relevant benchmark, the ACCi + CILO combination reduced PSR and αSMA (by 30% and 52% vs. vehicle, both p < 0.001), as well as macrophages and T-cells (by 28% and 32% vs. vehicle, both p < 0.001).

**Conclusion:** TPL2i improved fibrotic and inflammatory endpoints in this extended rat CDHFD model, with greater or equivalent efficacy compared to the clinically validated combination of ACCi + CILO. These results provide rationale for inhibition of TPL2 for the treatment of NASH and suggest potential for its use in novel combination therapies.

**FRI188**

**Evaluation of the antifibrotic effects of naringenin, asiatic acid and icariin by using precision-cut liver slices of mouse and human**

Ke Luo1, Yana Geng1, Vincent de Meijer2, Dorenda Oosterhuis1, Peter Olinga1. 1University of Groningen, Department of Pharmaceutical Technology and Biopharmacy, Groningen, Netherlands; 2University of Groningen, University Medical Center Groningen, Department of Surgery, Groningen, Netherlands

Email: p.olinga@rug.nl

**Background and aims:** Fibrosis is an exaggerated wound healing response defined by excessive accumulation of extracellular matrix, which may lead to organ dysfunction or even organ failure. Therapies for liver fibrosis are lacking. Naringenin (NRG), asiatic acid (AA) and icariin (ICA) are three compounds that were reported to exert antifibrotic effects in both in vitro and in vivo animal models of liver fibrosis. However, no human data is available. Our objective was to investigate the potential antifibrotic effects of these three compounds by using the ex vivo mouse and human precision-cut liver slices (PCLS) model.

**Method:** PCLS prepared from mouse liver tissue (mPCLS), healthy human liver tissue (hhPCLS) and cirrhotic human liver tissue (chPCLS) were cultured for 48 h with or without different concentrations of the three compounds. The viability was assessed by evaluating the ATP content of PCLS to study the toxicity of the three compounds. Gene expression of the fibrotic markers alpha-1 type I collagen (COL1a1), heat shock protein 47, alpha-smooth muscle actin, connective tissue growth factor, plasminogen activator inhibitor-1, and inflammatory markers interleukin-1 beta, interleukin-6, tumor necrosis factor alpha were determined by qPCR. Pro-collagen 1α1 (Pcol1α1) excreted by PCLS into the culture medium was determined by an ELISA assay.

**Results:** NRG concentration-dependently inhibited Pcol1α1 gene expression in mouse and human PCLS. The highest non-toxic concentration of NRG (300 μM in mPCLS, 200 μM in hhPCLS and chPCLS) suppressed fibrosis and inflammation related genes and reduced the Pcol1a1 in the culture medium by 54 ± 21 % (mPCLS), 34 ± 23 % (hhPCLS), and 75 ± 23 % (chPCLS). The highest non-toxic concentration of AA (30 μM) decreased only in hhPCLS Pcol1a1 and Pcol1a1 by 34 ± 17 %, and downregulated fibrosis-related gene expression. 25 μM of ICA, the highest non-toxic concentration, only suppressed in mPCLS Pcol1a1 gene expression, while decreasing inflammation related genes in all PCLS types.

**Conclusion:** NRG showed the most promising antifibrotic potency in both mouse and human PCLS, with more profound effects in chPCLS than in the early-on-set of fibrogenesis in hhPCLS. Antifibrotic effects of AA were only shown in hhPCLS. ICA only exerted antifibrotic effects on fibrosis related genes in mPCLS.

**FRI189**

**Diagnostic efficacy of Mac-2 binding protein glycosylation isomer for predicting liver fibrosis in patients with metabolic associated fatty liver disease**

Se Young Jang1, Dae Won Jun2, Hoon Gil Jo3, Ki Tae Yoon4, Young Youn Cho5. 1School of Medicine, Kyungpook National University, Kyungpook National University Hospital, Internal Medicine, Korea, Rep. of South; 2Hanyang University College of Medicine, Internal Medicine, Korea, Rep. of South; 3Wonkwang University Hospital, Wonkwang University School of Medicine, Internal Medicine, Korea, Rep. of South; 4Pusan National University Yangsan Hospital, Internal Medicine, Korea, Rep. of South; 5Chung-Ang University Hospital, Internal Medicine, Korea, Rep. of South

Email: gongori1004@gmail.com

**Background and aims:** The definition of metabolic associated fatty liver disease (MAFLD) has newly been proposed. We aimed to investigate the efficacy of Mac-2 binding protein glycosylation isomer (M2BPGi), non-invasive fibrosis marker, for discriminating significant and advanced fibrosis, and cirrhosis, respectively according to MAFLD and NAFLD definitions.

**Method:** Serum M2BPGi levels were collected and analyzed from 950 fatty liver patients in a tertiary hospital. Liver fibrosis was graded by transient elastography. Diagnostic efficacy of serum M2BPGi and other serum markers including liver fibrosis markers [fibrosis index based on four factors (FIB-4) and NAFLD fibrosis score (NFS)] was evaluated using correlation analysis and area under the ROC curve (AUC).

**Table 1:** 

<table>
<thead>
<tr>
<th>AUC (95% CI)</th>
<th>Cut-off value</th>
<th>Sensitivity (%)</th>
<th>Specificity (%)</th>
<th>PPV (%)</th>
<th>NPV (%)</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>F &gt;1</td>
<td>0.706 (0.657–0.755)</td>
<td>1.15</td>
<td>48.6</td>
<td>81.2</td>
<td>35.9</td>
<td>88.0 &lt;0.001</td>
</tr>
<tr>
<td>F &gt;2</td>
<td>0.719 (0.662–0.776)</td>
<td>1.19</td>
<td>50.5</td>
<td>80.4</td>
<td>24.6</td>
<td>92.8 &lt;0.001</td>
</tr>
<tr>
<td>F &gt;3</td>
<td>0.843 (0.774–0.912)</td>
<td>1.31</td>
<td>73.7</td>
<td>85.6</td>
<td>20.1</td>
<td>98.5 &lt;0.001</td>
</tr>
<tr>
<td>FIB-4</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>F &gt;1</td>
<td>0.703 (0.650–0.756)</td>
<td>1.61</td>
<td>68.8</td>
<td>66.2</td>
<td>30.6</td>
<td>90.7 &lt;0.001</td>
</tr>
<tr>
<td>F &gt;2</td>
<td>0.709 (0.643–0.774)</td>
<td>1.63</td>
<td>70.3</td>
<td>65.9</td>
<td>20.7</td>
<td>94.6 &lt;0.001</td>
</tr>
<tr>
<td>F &gt;3</td>
<td>0.796 (0.713–0.878)</td>
<td>2.40</td>
<td>65.8</td>
<td>82.8</td>
<td>15.8</td>
<td>98.0 &lt;0.001</td>
</tr>
<tr>
<td>NFS</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>F &gt;1</td>
<td>0.660 (0.608–0.713)</td>
<td>–0.72</td>
<td>62.5</td>
<td>65.8</td>
<td>28.3</td>
<td>89.0 &lt;0.001</td>
</tr>
<tr>
<td>F &gt;2</td>
<td>0.682 (0.616–0.748)</td>
<td>–0.72</td>
<td>68.1</td>
<td>64.4</td>
<td>19.5</td>
<td>94.4 &lt;0.001</td>
</tr>
<tr>
<td>F &gt;3</td>
<td>0.787 (0.711–0.863)</td>
<td>–0.70</td>
<td>84.2</td>
<td>63.5</td>
<td>10.2</td>
<td>98.6 &lt;0.001</td>
</tr>
</tbody>
</table>

S484 Journal of Hepatology 2022 vol. 77(S1) | S389–S664
Results: There were 810 patients and 687 patients by the MAFLD and NAFLD definition, respectively. Serum M2BPGi level and other liver fibrosis markers showed a positive correlation with fibrosis grade. The AUC values of M2BPGi were 0.698, 0.698, and 0.828 for predicting fibrosis (F) >1, F >2, and F >3, respectively in NAFLD group. The AUC values of M2BPGi were 0.706, 0.719, and 0.843 for predicting F >1, F >2, and F >3, respectively in MAFLD group. The AUC values of M2BPGi for predicting severity of fibrosis were greater than those of serum based liver fibrosis markers (Table 1).

Conclusion: M2BPGi showed better diagnostic efficacy for diagnosing the severity of liver fibrosis in MAFLD patients.

FR190 Multispectral imaging analysis of liver biopsies from patients with non-alcoholic steatohepatitis reveals enrichment of pathogenic macrophage phenotypes associated with disease progression

Joseph Gosnell1, Omar Saldarriaga1, Santhoshi Krishnan2, Morgan Oneka2, Arvind Rao2, Daniel Millian1, Timothy Wanninger1, Jingjing Jiao2, Laura Beretta3, Heather Stevenson3. 1UTMB Health-University of Texas Medical Branch at Galveston, Pathology, Galveston, United States; 2Rice University, Houston, United States; 3University of Michigan, Ann Arbor, United States; 4The University of Texas MD Anderson Cancer Center, Houston, United States

Background and aims: Non-alcoholic steatohepatitis (NASH) affects 3–6% of the US population and risk factors include obesity, dyslipidemia, metabolic disease, and type 2 diabetes. While many patients diagnosed with NASH will not progress to cirrhosis, identifying which patients will develop advanced fibrosis is a challenge. Intrahepatic macrophages are critical gatekeepers in the hepatic microenvironment that assist in maintaining immune tolerance. Upon activation, they can promote a pro-fibrotic hepatic microenvironment. We hypothesized that patient variation in intrahepatic macrophage phenotypes could predict disease progression in patients with NASH.

Method: We used multiplex staining followed by multispectral imaging to phenotype and quantify resident liver macrophages (CD68+), monocyte-derived macrophages (Mac387+), pro-fibrogenic macrophages (CD163+), and their co-expression of pro-inflammatory (CD14) and anti-inflammatory (CD16) markers in the context of hepatic architecture. We compared differences in spatial distribution (i.e., in enrichment and/or depletion) of macrophage populations in patients with NASH and either minimal (n = 6; fibrosis stage: 0–1) or advanced (n = 5, fibrosis stage: 4/4) fibrosis. First, multiplexed stained liver biopsies were scanned with a multispectral microscope (Vexta 3, Akoya Biosciences). We then determined the heterogeneity of these various macrophage populations in the study groups using phenotype matrices and t-distributed stochastic neighbor embedding plots (t-SNE) (Visiopharm®; MATLAB 2020a). Phenotypes that were significantly increased in the patients with advanced fibrosis were selected for spatial proximity analysis using G-function equations.

Results: Phenotype matrix analysis revealed the enrichment of unique pathogenic macrophage phenotypes (MAC387+, MAC387+ CD163+, MAC387+ CD163 + CD68+, MAC387+ CD163 + CD16 + CD14+, MAC387+ CD163 + CD16 + CD14 + CD68+) in NASH patients with advanced fibrosis when compared to those with minimal fibrosis. Pathogenetic macrophage populations (MAC387+, CD163 + MAC387+, CD163+ CD68+ CD163+) correlated with poor clinical outcome (increased prothrombin time and decreased platelet counts) in two of the patients with minimal fibrosis. In patients with advanced fibrosis, spatial analysis also showed significant (p < 0.05) infiltration of MAC387+ macrophages near CD68+ Kupffer cells.

Conclusion: Multispectral imaging combined with spatial analysis allows characterization of distinct macrophage subpopulations that may be able to predict fibrosis progression in patients with NASH. The ability to identify at-risk patients by the presence of pathogenic intrahepatic macrophages may also lead to future precision medicine approaches.

FR191 Diabetes, but not prediabetes, is associated with significant liver fibrosis

Byung Ik Kim1, Yong Kyun Cho1, Won Sohn1, 1Kangbuk Samsung Hospital Email: hand0827@naver.com

Background and aims: This study aimed to assess the risk of liver fibrosis between no glucose intolerance, prediabetes and diabetes in the general population.

Method: A cross-sectional study was conducted based on a cohort from a health examination program which included a magnetic resonance elastography (MRE). The participants were classified into three subgroups according to glucose tolerance: no glucose intolerance, prediabetes and diabetes mellitus. Liver fibrosis was evaluated by liver stiffness measurement (LSM) value using 2-dimensional real-time MRE. The risk of liver fibrosis was compared after adjusting for confounding factors including the presence of liver disease (non-alcoholic fatty liver disease, significant alcohol consumption and viral hepatitis).

Results: A total of 2, 090 subjects was included: no glucose intolerance (n = 889); prediabetes (n = 985); and diabetes (n = 216). The mean age was 50.6 years. The mean values of LSM in no glucose intolerance, prediabetes, and diabetes were 2.37 ± 0.43 kPa, 2.41 ± 0.34 kPa, and 2.65 ± 0.70 kPa, respectively (p < 0.001). The proportion of significant fibrosis (LSM ≥2.97 kPa) in no glucose intolerance, prediabetes, and diabetes was 3.1%, 4.4%, and 16.7%, respectively (p < 0.001). Compared with no glucose intolerance, the risk of significant fibrosis was higher in diabetes (adjusted odds ratio [aOR] 3.37, 95% confidence interval [CI] = 1.78–6.40, p < 0.001). However, there was no difference between prediabetes and no glucose intolerance (aOR 0.94, 95% CI = 0.54–1.64, p = 0.940). A subgroup analysis also showed that prediabetes is not associated with significant fibrosis unlike diabetes in subjects with or without liver disease.

Conclusion: Diabetes but not prediabetes is a risk factor for significant liver fibrosis regardless of the presence of liver disease.

FR192 Lysophosphatidylycerine may stimulate liver fibrosis

Takako Nishikawa1, Makoto Kurano2, Hitoshi Ikeda2, Nobutake Yamamichi1, Yutaka Yatomi2, Kazuhiko Koike3, Mitsuhiko Fujishiro3. 1The University of Tokyo Hospital, Center for Epidemiology and Preventive Medicine, Tokyo, Japan; 2The University of Tokyo, Clinical Laboratory Medicine, Tokyo, Japan; 3Graduate School of Medicine, the University of Tokyo, Japan, Department of Gastroenterology, Tokyo, Japan

Email: kuranoma-int@h.u-tokyo.ac.jp

Background and aims: Lysophospholipids (LPLs), such as lysophosphatidic acid and sphingosine 1-phosphate are had an interest as second-generation lipid mediators. Lysophosphatidylycerine (LysoPS), a phosphatidylglycerine-derived LPL, has recently been identified as a specific receptor, such as GPR34 and GPR174, P2Y10, and has begun to attract attention as a novel lipid mediator. In this study, we report the effect of LysoPS on liver fibrosis and their physiological roles in vitro.

Method: (1) The hepatic myofibroblast-like stellate cell line, CFSC-88 (CFSC), derived from a CCl4-induced cirrhotic rat liver was utilized. The cells were incubated with the medium added various concentrations of 18: 0 and 18: 1 LysoPS. Expressions of alfa-smooth muscle actin (α-SMA) determined by western blotting. (2) Liver fibrosis was induced by intraperitoneal injection of carbon tetrachloride (CCl4) two times a week for 8 weeks in mice. (3) The tissue of liver with hepatocellular carcinoma in patient with hepatitis B virus and the plasma in patients with liver dysfunction was utilized. Expressions of
GPR34 and GPR174, P2Y10 receptor and LysoPS levels in the plasma were examined.

**Results:** (1) When the cells were incubated with LysoPS for 24 hours, expressions of alfa-smooth muscle α-SMA were up-regulated by 10 μM of 18: 0 and 18: 1 LysoPS treatment. Expressions of α-SMA were inhibited by inhibitors of Smad3, p38 mitogen-activated Protein kinase and Rho-associated kinase. (2) Expressions of GPR34 and GPR174, P2Y10 receptor were up-regulated along with CCl4 treated mice. 16:1 and 20:4 LysoPS levels in the plasma were increased in CCl4 treated mice. (3) Expressions of GPR34 and PGR174, P2Y10 receptor, derived from a hepatic myofibroblast-like stellate cell, were up-regulated along fibrous capsule of hepatocellular carcinoma in patient with hepatitis B virus. 16:0 and 18:2 LysoPS levels and phosphatidylserine (PS) levels, as precursor of 16:0 LysoPS, in the plasma were increased in patients with liver fibrosis.

**Conclusion:** In this study, it was suggested that LysoPS is involved in liver fibrosis in vitro. In vivo study, upregulation of LysoPS receptor were observed in hepatic myofibroblast-like stellate cells, suggesting that LysoPS may also be involved in liver fibrosis. Furthermore, an increase in LysoPS of some fatty acid molecular species was observed in mouse plasma, suggesting the possibility of laboratory medical application of LysoPS as a marker of liver fibrosis.

**FR193**

**Quantitative assessment of liver fibrosis in NASH patients**

Luong Ruiz1, Tian Lan1, Wenhui Liu1, Amir Ashique1, Harry Chen1, Jiping Zha2, Alex DePaoli1, Igor Mikaelian1, Cynthia Guy1, Eugenia Henry1, William Chang1, Corinne Foo-Atkins1, Hsiao Lieu1, 1NGM Biopharmaceutical Inc., Translational Sciences, South San Francisco, United States; 4Adagene Inc, San Diego, United States; 2Duke University Medical Center Greenspace, Department of Pathology, Durham, United States

Email: lruiz@ngmbio.com

**Background and aims:** The success of clinical trials for the treatment of nonalcoholic steatohepatitis (NASH) is dependent on the efficacy evaluation of the liver fibrosis endpoint. Fibrosis is currently assessed visually using the NASH Clinical Research Network (CRN) staging scheme. However, the NASH CRN scheme evaluates patterns of fibrosis that are not related by a linear relationship to the quantified abundance of pathologic collagen deposition. Samples from a Phase 2 clinical trial with aldefarmin (NGM282), an engineered fibroblast growth factor 19 analogue, were used to develop a novel image analysis readout for liver fibrosis.

**Method:** Liver biopsies were from a 24 week clinical trial with aldefarmin (NGM282): NCT02443116 (placebo (PBO), n = 22; 1 mg, n = 49). Biopsies and blood for non-invasive biomarkers were collected at baseline and at the end of treatment. A 6-plex immunohistochemistry panel that included Collagen 1A1 (COL1A1) was developed. The image analysis method for COL1A1 area utilized morphological operations to eliminate normal collagen, adaptive thresholding to alleviate uneven signal intensities, and morphological erosion to remove edge effects. Parameters for the methods were tuned on a subset of images and then applied to the whole dataset.

**Results:** Fibrosis CRN reads correlated robustly with COL1A1% area (Kendall’s τ = 0.644, p-value <0.001). In addition, image analysis identified patients with decreases in COL1A1 area despite no changes in the CRN score. As a consequence, the COL1A1 area identified a statistically significant proportion of responders in the treatment arm (p = 0.037), which represented a 24% decrease in COL1A1 area compared to the PBO group, and which was not reflected by the CRN score (p = 0.12). The COL1A1% area and the CRN score correlated similarly to the non-invasive end points of serum N-terminal type III collagen propeptide and Enhanced Liver Fibrosis (ELF) score (Kendall’s τ = 0.3 with p <0.001). Finally, the coefficient of variation for COL1A1 in consecutive liver sections was 7%.

**Conclusion:** In summary, immunohistochemistry-based quantitative pathology endpoints may identify drug effects that are not captured by categorical CRN endpoints.
Efficacy and safety of prolonged released pirfenidone in patients with compensated cirrhosis. A placebo controlled multicenter study in Mexico

Linda Muñoz1, Aldo Torre2, Laura Esthela Cisneros Garza3, Israar Montalvo4, René Malé Velazquez5, Scherezada Mejia6, Juan Ramón Aguilar7, Javier Lizardí8, Maru Izaza9, Frida Gasca9, Larissa Hernandez10, Paula Cordero-Pérez11, Luis Chi-Cervera12, Lilian Torres Made13, Graciela Tapia14, Poo Jorge15.

Background and aims: Advanced liver fibrosis (ALF) is a common finding in many chronic liver diseases and considering its predictive value for adverse outcomes new therapies are mandatory. Therefore, we aimed to evaluate efficacy and safety of prolonged release pirfenidone tablets (PR-PFD) in a placebo controlled multicenter study.

Method: 171 patients with ALF were blindly allocated to 3 groups to study.

Results: 150 patients were eligible for efficacy and 171 for safety analyses. At baseline, demographic, etiology, cirrhosis stage, Child-Pugh class or MELD score, Quality of Life or Fatigue scales, as Liver fibrosis staging, varices evaluation at baseline, and at 12, and 24 mos. 21) and 14 SAEs (5, 6, and 3), in groups 1, 2, and 3, respectively. Differences were not significant. Albumin (4.1 ± 0.07 versus 4.4 ± 0.05, p = 0.000), platelets (117 ± 7.9 versus 141 ± 9.2, p = 0.000), and quality of life (80.7 ± 2.2 versus 87.8 ± 2.5, p = 0.006) increased in group 1. Adverse events were mild and affected mainly the GI tract (41, 21 and 5), and skin (14, 9, and 21) and 14 SAEs (5, 6, and 3), in groups 1, 2, and 3, respectively.

Conclusion: PR-PFD at doses of 1200, and 1800mg/day significantly decreased indirect markers of liver fibrosis at 24mos, and improved albumin, platelets and quality of life in patients with compensated cirrhosis. No liver toxicity was detected.

FRI196

Endothelin receptor A antagonist functionalized magnetic nanoparticles as a promising approach for the treatment of liver fibrosis

Marit ten Hove1, Andreas Smyris1, Carsten Höltke2, Ruchi Bansal3.

1University of Twente, Translational Liver Research, Enschede, Netherlands; 2University of Münster, Department of Clinical Radiology, Münster, Germany

Background and aims: Hepatic injuries, caused by various etiologies such as excessive alcohol intake, fatty liver disease, viral hepatitis, or metabolic disorders, can lead to development of hepatic fibrosis. Hepatic stellate cells (HSCs) activated upon hepatic injury, that proliferate and secrete an excess of extracellular matrix (ECM), remain an attractive target for the treatment of hepatic fibrosis. During liver injury, endothelin-1 (ET-1) levels are upregulated and activate HSCs by interacting with endothelin A (ETA) receptor, which is upregulated on activated HSCs upon hepatic injury. Several studies also indicate that HSCs regulate the sinusoidal blood flow and portal hypertension via ET-1, and hence antagonism of the endothelin pathway using endothelin receptor antagonist (ERA) may offer promising results. However, antagonism of ET pathway using small-molecule ERAs can result in adverse systemic effects since high or frequent dosing will be required to achieve desired therapeutic effects.

In this study, we conjugated ERA to superparamagnetic iron oxide nanoparticles (SPIONS) to improve pharmacokinetics of endothelin receptor antagonist (ERA) and to increase hepatic uptake thereby reducing the high/frequent dosing, reducing the systemic side effects while increasing the therapeutic efficacy. SPIONS are also biocompatible and have magnetic properties, therefore can be detected using magnetic resonance imaging (MRI), making them suitable for theranostic applications.

Method: First, we analyzed the association of ET-1 and ETA with HSCs in vitro. We then conjugated ERA on the surface of SPIONs via a thiol-disulfide exchange reaction. Second, we studied the in vivo biodistribution and therapeutic efficacy of conjugated ERA in a murine model of liver fibrosis.

Conclusion: ERA conjugated to SPIONS showed improved biodistribution and therapeutic efficacy in murine models of liver fibrosis, making them promising candidates for future clinical trials.
Results: We confirmed the overexpression of ET-1 and ETA in vitro in activated HSCs, and human and murine liver fibrosis. ERA dose-dependently inhibited TGF-β1-induced HSCs, collagen-I expression and contractility in vitro. ERA-SPIONs were synthesized and attenuated TGF-β1-induced HSCs activation, ECM production, contractility via antagonizing the endothelin pathway. In CCL4-induced liver fibrosis mouse model, ERA-SPIONs treatment, compared to ERA treatment, significantly reduced liver weight, ALT levels and inhibited collagen-I deposition indicating attenuation of liver fibrosis.

Conclusion: In this study, we demonstrate that the delivery of ERA using SPIONs is a promising therapeutic approach for the treatment of liver fibrosis that increases the therapeutic efficacy of ERA in vitro and in vivo.

FR197

3D human NASH model as a screening-based discovery approach for selecting and prioritizing drug candidates

Radina Kostadinova1, Simon Ströbel1, Jana Rupp1, Katia Fiaschetti1, Agnieszka Pajak1, Katarzyna Sanchez1, Mathieu Petitjean2, Li Chen2, Manuela Bieri1, Armin Wolf1, Sue Grepper1, Francisco Verdeguer1.

1InSphero, Schlieren, Switzerland; 2PharmaNest, Princeton, United States

Email: radina.kostadinova@insphero.com

Background and aims: Non-alcoholic fatty liver disease (NAFLD) is a chronic liver disease, which includes hepatic steatosis that often progresses into steatohepatitis (NASH), characterized additionally by inflammation and fibrosis. We have modeled NASH using 3D human liver microtissues as a high-throughput tool for drug discovery. We present here a novel 3D human NASH model, which incorporates primary hepatocytes, kupffer cells, liver endothelial cells, and hepatic stellate cells for high-throughput-compatible drug efficacy testing.

Method: We generated liver microtissues by culturing human primary hepatocytes, kupffer cells, liver endothelial cells, and hepatic stellate cells in InSphero plates. Upon exposure to defined lipotoxic and inflammatory stimuli, including free fatty acids and LPS in media containing high levels of sugar and insulin, this 3D NASH model displayed pathophysiological hallmarks within 10 days of treatment. The accumulation of intracellular triglycerides (biloumin-escent assay), secretion of pro-inflammatory cytokines/chemokines (Luminescent), and pro-collagens type I and III (HTRF/ELISA) were measured. Quantification of fibrosis based on Sirius Red-stained tissue slices was performed using the PharmaNest imaging platform.

Results: We observed increases in intracellular triglyceride content and the secretion of proinflammatory (e.g. IL-6, IL-1b, TNF-a) and profibrotic (e.g. IL-10, GRO-a, IP-10, MCP-1) cytokines/chemokines in the NASH-treated tissues as compared to the untreated controls. Further, we detected increased fibril collagen deposition, and increased secretion of procollagen type I/III peptides under NASH conditions. Whole transcriptome analysis of NASH-treated tissues versus control revealed activation of pathways and differential regulation of genes associated with lipid metabolism, inflammation, and fibrosis induction. Treatment with the anti-TGF-β antibody and ALK5i (TGF-βR inhibitor) concentration dependently decreased secretion of procollagen type I/III. Decreased deposition of fibril collagens based on quantification of fibrosis of Sirius Red-stained tissues was observed in the presence of anti-TGF-β antibody and ALK5i. The efficacy results of drug clinical candidates Selonsertib and Firsocostat were in line with clinical observations.

Conclusion: In summary, this high-throughput and compatible 3D human NASH model represents a promising approach for NASH drug candidate efficacy selection early within the drug discovery process.
FR199

Discovery of AMS-III-1086, a novel LPA1 antagonist for the treatment of liver fibrosis and liver cirrhosis

Nakcheol Jeong1, Peppi Prasit1, Jung-Hye Kim1, Misun Lee1, Bo-Yeong Pak2, Sojin Ahn1, Gil Won Lee1, Seohyun Min1, Sanghyeok Lee1, Yeup Yoon3,4,5, Wonseok Kang6,6, Hyeree Kim1,7,1, JAM Sciences, Seoul, Korea, Rep. of South; 2AM Sciences, Seoul, Korea, Rep. of South; 3Samsung Advanced Institute for Health Sciences and Technology, Sungkyunkwan University, Department of Health Science and Technology, Korea, Rep. of South; 4Institute for Future Medicine, Samsung Medical Center, Korea, Rep. of South; 5Samsung University, Department of Biopharmaceutical Convergence, Korea, Rep. of South; 6Samsung Medical Center, Sungkyunkwan University School of Medicine, Division of Gastroenterology, Department of Medicine, Korea, Rep. of South; 7Institute for Future Medicine, Samsung Medical Center, Korea, Rep. of South

Email: njeong@amsiences.co.kr

Background and aims: Activation of the lysophosphatidic acid 1 (LPA1) receptor has been implicated in a various tissue fibrosis. LPA1 receptor antagonists have shown efficacy in a wide range of animal fibrosis models. Recently a human proof of concept in idiopathic pulmonary fibrosis (IPF) was obtained with the first generation of LPA1 antagonist in a 6-month Phase 2 clinical trial. But the compound was withdrawn from clinical development because of hepatobiliary toxicity, which was unrelated to LPAR1 antagonist but to the inhibition of bile salt export pumps (BSEP). AMS-III-1086 is a novel LPA1 antagonist designed to have a reduced risk of hepatobiliary liability by minimizing bile acids transport inhibition while its efficacy both in vitro and in vivo was improved thus providing a larger therapeutic index.

Method: The potency and selectivity of AMS-III-1086 for LPA1 receptors were determined in vitro by calcium flux and cell chemotaxis assays using B103 cells stably expressing LPA receptors and A2058 cells. LX2 cells were used for evaluating anti-fibrotic activities. Pharmacokinetic (PK) properties were assessed in rodent and non-human primates. N-nitrosodiethyamine (DEN)-induced rat fibrosis model was used for in vivo efficacy studies. BSEP inhibition was determined by BIOIVT. In vivo liver toxicity was evaluated in the cynomolgus monkeys. Human hepatotoxicity was ascertained by in vitro model using Hurel micro liver.

Results: AMS-III-1086 inhibited LPA-stimulated intracellular calcium release (IC50 = 5.3 nM) from B103 cells stably expressing human LPA1 and LPA-induced chemotaxis (A2058 cells; IC50 = 5.7 nM). AMS-III-1086 showed selective antagonism on LPA1 over the other LPA receptors. Treatment with LPA in LX2 cells induced the expressions of the LPA1 gene as well as fibrotic genes, but these were significantly reduced by AMS-III-1086. Functionally, AMS-III-1086 inhibited LPA-induced chemotaxis of LX2 cells. PK results showed good systemic exposure and high oral bioavailability in multiple species. BSEP inhibition was markedly improved, IC50 (20 uM) compared to the first-generation clinical candidates (IC50 = 5 uM). In a DEN-induced rat model of fibrosis and hepatocarcinogenesis, the therapeutic treatment of AMS-III-1086 (oral administration at 10 mg/kg once daily) resulted in the attenuation of fibrogenesis as well as the prevention of cirrhosis after 4 weeks of treatment. There were no significant changes in the levels of AST and ALT in the cynomolgus monkeys. Moreover, a cytotoxicity study using Hurel micro liver predicted that AMS-III-1086 had reduced risk of drug-induced liver injury which was corroborated in vivo in cynomolgus monkey.

Conclusion: AMS-III-1086 is a newly identified LPA1 antagonist which shows a good therapeutic index with increased efficacy and improved hepatobiliary toxicity and a favorable preclinical profile.

FR120

Integrated spatial-temporal mathematical liver lobule model for simulation of fibrotic wall formation

Seddik Hammad1, Jieliang Zhao2,3, Mathieu de Langlard2, Yueyi Li1, Jan G. Hengstler3, Dirk Drasdo2,3, Steven Dooley4,5,6

1Heidelberg University, Molecular Hepatology Section, University Medical Center Mannheim, Medical Faculty Mannheim, Mannheim, Germany; 2Institute National de Recherche en Informatique et en Automatique, (INRIA), Salacy, France; 3Leibniz Research Centre for Working Environment and Human Factors at the Technical University Dortmund, Dortmund, Germany

Email: steven.dooley@medma.uni-heidelberg.de

Background and aims: Upon different liver injuries, distinct patterns of fibrosis arise i.e. extracellular matrix (ECM) septa (fibrotic walls) connecting pericentral areas due to toxic drugs, or periporal compartments in cholestasis. Organ fibrosis is a highly coordinated and complex multi-cellular process that is difficult to capture with experimental models.

Method: We stepwise developed a computational two liver-lobule model that is continuously refined by iteration between modelers and experimentalists. The model permits to assess the role of biomechanics in the formation of the fibrotic scar. It for the first time integrates the orchestration of hepatocytes and non-parenchymal cells (NPC) during fibrosis development, including their interaction with the ECM network mechanics.

We stepwise developed a computational two liver-lobule model for simulation of fibrotic wall formation, including their interaction with the ECM network mechanics. The model is continuously refined by iteration between modelers and experimentalists. The model permits to assess the role of biomechanics in the formation of the fibrotic scar. It for the first time integrates the orchestration of hepatocytes and non-parenchymal cells (NPC) during fibrosis development, including their interaction with the ECM network mechanics.

Results: Model predictions are quantitatively confirmed with experimental data. Pattern-characterizing model parameters, e.g. the density of hepatic stellate cells (HSC) and macrophages (Mph) were determined through analysis of experimental 2D and 3D images. A model of the ECM network, NPC and their intercellular communication were integrated as new elements into the existing computational model of the basic liver micro-architecture that already included hepatocytes, sinusoids, central and portal veins. The newly advanced model was applied to test possible mechanisms how the fibrotic scar may form during fibrosis in space and time.

Conclusion: Using this strategy, we propose a scenario that distinguishes regeneration after a single acute toxic injury without scarring versus repeated toxic exposure leading to formation of (etiologic dependent) characteristic fibrotic scar patterns, as follows: (i) The spatial pattern of CYP2E1 (key metabolizing enzyme) expressing hepatocytes determines the location of ECM deposition (collagen). The tissue response is thereby mediated by the spatial-temporal pattern of certain signaling molecules provided the CYP2E1-positive damaged hepatocytes (DAMPs), leading to activation and attraction of HSC and Mph. (ii) Surviving (CYP2E1-negative) hepatocytes surrounding the CYP2E1 positive (and now damaged) region proliferate and compress the deposited collagen network into the scar like shape. The model may in the future permit us to propose targeted manipulations to reduce scar formation and the transition to cirrhosis.
Background and aims: Telomeres are structures at the end of linear chromosomes constituted by repetitive 5′-TTAGGG-3′ sequences associated to protecting proteins. Human patients with germline pathogenic variants in telomere-biology genes present critically short telomeres and usually develop bone marrow failure, but a considerable percentage also manifest pulmonary fibrosis and liver cirrhosis, although the mechanisms for disease development are still unclear. Here, we aim to investigate whether immune-mediated responses are skewed in telomerase-“knockout” (KO) mice challenged with Schistosoma mansoni-induced liver fibrosis.

Method: Liver fibrosis was induced by inoculation of approximately 100 cercariae to Terc−/− (n = 16), Tert−/− (n = 10) and wild-type (WT; n = 8) C57Bl/6 mice, which were euthanized after 12 weeks, along with a non-infected group (Terc−/− n = 7, Tert−/− n = 16 and WT n = 11). Telomere length (TL) in leukocytes and liver fragments was determined by qPCR. Liver tissue samples were stained with haematoxylin-eosin (HE) and Picro-Sirius Red. Immunohistochemical (IHC) staining to F4/80, iNOS and CD206 was determined by qPCR. Liver tissue samples were stained with haematoxylin-eosin (HE) and Picro-Sirius Red. Immunohistochemical (IHC) staining to F4/80, iNOS and CD206 was performed using diaminobenzidine. Bone-marrow derived macrophages (BMDM) were isolated from a second group of animals (n = 12; 4/each genotype), cultured for 7 days in RPMI and stimulated with lipopolysaccharide (LPS) or interleukin-4 (IL-4) for 24 hours. The polarization to M1 or M2-like phenotypes was determined by nitrite levels and gene expression (IL-6, MMP9, TNF-alpha, CD206 and ARG1).

Results: TL was significantly shorter in both KO groups (p < 0.01). Infected animals presented hepatosplenomegaly and multiple inflammatory foci in the liver and tissue darkening. Histopathology showed the presence of granulomas surrounding S. mansoni eggs trapped within the tissue. Terc−/− and Tert−/− mice developed less fibrotic areas when compared to the WTs (p < 0.05). IHC staining revealed less macrophage infiltration within the tissue in KO animals. BMDM assay showed that the telomerase KOs impair the classical activation of macrophages, as indicated by nitrite concentrations and the differential expression of TNF-alpha, IL-6, and MMP9.

Conclusion: Our results suggest that the absence of telomerase causes a limited immune response following S. mansoni infection in mice, which mitigates the fibrotic process and cell activation. These findings also reveal that functional telomerase is critical for adequate immune response and, in patients harboring mutations in telomere-biology genes, fibrogenesis must be modulated by other inflammation signaling pathways, which deserves further investigation.
FRI203
Sex and diagnosis-specific differences in liver elastography and attenuation
Zhi Tan1, Marcelle Scagliotta1, Crystal Connelly1, Wendy Lam1, Oyekoya Ayonrinde1,1 Fiona Stanley Hospital, Gastroenterology and Hepatology, Murdoch, Australia
Email: oyekoya.ayonrinde@uwa.edu.au

**Background and aims:** Liver stiffness measurement (LSM) using Transient Elastography (TE), combined with liver attenuation measurement using controlled attenuation parameter (CAP), allows rapid, non-invasive assessment of liver fibrosis and steatosis. We examined the usefulness of TE and CAP for assessment of liver disorders in an adult hepatology outpatient population.

**Method:** In this cross-sectional study, we investigated the duration and findings of TE and CAP in adult outpatients with known or suspected chronic liver disease, between 2012 and 2021. LSM and CAP were measured using a FibroScan® model 502 Touch. Each procedure was performed by a hepatology nurse with experience of over 500 examinations. Patient age, sex, assessment indication, duration, LSM, CAP, and accuracy of the examination was recorded.

**Results:** There were 5645 examinations performed on patients with various liver disorders, mean age 55.9 (standard deviation 12.9) years, and 60.7% male. Of these, a medium (M) probe was used for 4212 (74.6%), extra-large (XL) probe for 1422 (25.2%), and small (S) probe without CAP in 11 (0.2%). The most common indications were chronic hepatitis C (CHC, 46%), chronic hepatitis B (CHB, 22%), non-alcoholic fatty liver disease (NAFLD, 15%), and alcohol-related liver disease (ALD, 6%). Median LSM in the cohort was 6.8 (IQR 4.9–11.8) kPa and CAP 252 (IQR 204–307.5) dB/m. Both LSM and CAP were higher in males, compared with females; (LSM 7.1 [5.3–12.2] kPa vs. 6.1 [4.6–10.7] kPa, p < 0.001) and (CAP 255 [208–309] dB/m vs. 241 [196–298], p < 0.001) respectively. Also, median LSM was highest with ALD (14.5 [7.5–35.3]), compared with CHC (7.6 [5.4–12.5]), NAFLD (7.6 [5.3–13.3]) and CHB (5.4 [4.3–71]). Median CAP was highest with NAFLD (315 [261–361] dB/m), compared with ALD (263 [211–329] dB/m), CHC (245 [203–293] dB/m) and CHB (233 [189–283] dB/m). There were sex-differences in CAP, LSM and duration of the examination, across different liver disorders (Table 1).

**Conclusion:** Across various liver disorders, CAP was significantly higher in males overall, suggesting more severe hepatic steatosis. LSM was higher in males with CHC and CHB, compared with females. Severity thresholds for CAP and LSM should consider these differences.

---

FRI204
Progression of liver disease among patients with a new diagnosis of protease inhibitor ZZ alpha-1 antitrypsin deficiency
Harmeet Malhi1, Tiffany Wu1, May Hagiwara2, Gregory Donadio3, Esteban Gnass3, Will Treem2, Kaili Ren2, Ed G. Marinis2, Chitra Kirk2.
1Mayo Clinic, Rochester, United States; 2Takeda Pharmaceutical Company Limited, Cambridge, United States; 3Inference, Cambridge, United States
Email: malhi.harmeet@mayo.edu

**Background and aims:** Few studies have characterized disease progression in patients (pts) with alpha-1 antitrypsin deficiency-associated liver disease protease inhibitor ZZ (AATD-LD PiZZ) genotype, who may progress variably with time and may remain asymptomatic despite advanced liver fibrosis. We examined the relationship between progression of disease and LD-related clinical events (LD events) over time in this population.

**Method:** Data were extracted from the nference database (a proprietary electronic medical record database from the Mayo Clinic Healthcare System) between January 2004 and September 2021. Pts with AATD were defined by the presence of structured diagnosis (dx) codes for AATD, or an alpha-1 antitrypsin serum level of <100 mg/dL. LD was defined based on structured dx codes and surrogate measures. PiZZ genotype was defined by genotype results or unstructured data through natural language processing. Index date was defined as the first date of dx of LD. Fibrosis stage (F0–F4) was assessed at baseline (index date ± 90 days) and during follow-up using a hierarchical approach: liver biopsy (META VIR staging), magnetic resonance elastography, Fibroscan, APRI and FIB-4. Pts with <90 days of follow-up were excluded. LD events were defined as development of ascites, spontaneous bacterial peritonitis, variceal bleeding, hepatic encephalopathy, hepatocellular carcinoma and need for liver transplantation. Outcomes were analyzed using descriptive statistics and Kaplan-Meier analysis for time-to-event.

**Results:** Of 685 000 pts, 6315 had a dx of AATD; of these 501 had the AATD PiZZ genotype, and 316 qualified for the study. Among pts with AATD-LD PiZZ, the mean age was 50.5 years (y), 58.4% were male, 100% were White, and 37.7% were diagnosed with chronic obstructive pulmonary disease, chronic bronchitis, bronchiectasis, or emphysema. At baseline, 197 pts had fibrosis stage: F0/F1, 53%; F2, 24; F3, 33%; and F4 with compensated cirrhosis (F4cc), 87 (119 pts were not categorized owing to a lack of available data). Of 316 patients with 7.4 y of median follow-up, 17.4% underwent a liver transplant; 2%, 4%, 12% and 44% among pts with baseline stage F0/F1, F2, F3 and F4cc, respectively. Disease progression (≥1 fibrosis stage) occurred in 31 pts at ≤2y (F0/F1, 22%; F2, 5%; F3, 36%) and in 53 pts at >2y (F0/F1, 49%; F2, 38%; F3, 55%) (Figure A). At any time during follow-up (median 7.4 years), LD events occurred in 50.1% of pts, with a higher number of events recorded for pts with baseline stage F4cc (98.2%) compared with F3 (68.3%) and F2 (61.0%) (Figure B).

**Conclusion:** Across various liver disorders, CAP was significantly higher in males overall, suggesting more severe hepatic steatosis. LSM was higher in males with CHC and CHB, compared with females. Severity thresholds for CAP and LSM should consider these differences.
Perihepatic implantation of matrix-embedded endothelial cells (MEECs) display anti-inflammatory and anti-fibrotic activity in liver fibrosis. This study highlights the potential therapeutic utility of MEECs for chronic liver disease.

**Method:** Fibrosis was induced in BALB/c mice (n = 12) by i.p. injection of CCl4 diluted 1:8 v/v in corn oil twice a week for 8 weeks. Acellular matrices or MEECs were surgically implanted between the median and the right lobe in fibrotic mice. After one week, relative fibrosis area was analyzed by Sirius Red staining. Liver function was evaluated in serum samples. The expression of pro-inflammatory genes (nitric oxide synthase 2 (NOS2), cyclooxygenase-2 (COX-2), interleukin 1 beta (IL-1β)), anti-inflammatory genes (arginase 1 (ARG1), mannose receptor C-type 1 (MRC1), resistin (RETN1A)), hepatic stellate cell (HSC) activation factors (oncostatin M (OSM), platelet derived growth factor-BB (PDGFBB), transforming growth factor-beta (TGF-β)), and genes related to the extracellular matrix turnover (collagen-I (COL-I), alpha smooth muscle actin (ALPHA-SMA), tissue inhibitor of metalloproteinases-1 (TIMP1)) was quantified by Real-time PCR.

**Results:** Implantation of MEECs for seven days promoted a 21% reduction in the hepatic fibrosis area compared with fibrotic livers implanted with acellular matrices. These anti-fibrotic effects translated into a significant improvement of liver function reflected by the reduction of serum transaminases (ALT, 153.3 ± 15.8 vs 100.6 ± 14.5 U/L, p < 0.05; AST, 477 ± 50.4 vs 288 ± 54 U/L, p < 0.05). Perihepatic implantation of MEECs significantly reduced the hepatic expression of pro-inflammatory genes (COX-2, 1.0 ± 0.1 vs 0.6 ± 0.1 fold change (fc), p < 0.05; NOS2, 1.1 ± 0.3 vs 0.5 ± 0.1 fc, p < 0.01; IL-1β, 1.1 ± 0.1 vs 0.5 ± 0.1 fc, p < 0.01) and increased the hepatic expression of anti-inflammatory genes (ARG1, 1.0 ± 0.1 vs 1.6 ± 0.1 fc, p < 0.05; MRC1, 1.0 ± 0.1 vs 1.4 ± 0.1 fc, p < 0.05; RETN1A, 1.1 ± 0.1 vs 14.8 ± 4.8 fc, p < 0.01) on fibrotic mice. Our results also revealed that MEECs promoted a significant decrease in well-known stimulators of HSC (OSM, 1.0 ± 0.2 vs 0.35 ± 0.06 fc, p < 0.05; PDGFBB, 1.0 ± 0.1 vs 0.57 ± 0.08 fc, p < 0.01, TGF-β, 1.0 ± 0.1 vs 0.69 ± 0.05 fc, p < 0.05). This reduction was associated with a fall in the hepatic expression of genes related to HSC activation (COL-I, 1.0 ± 0.1 vs 0.49 ± 0.06 fc, p < 0.01; ALPHA-SMA, 1.1 ± 0.2 vs 0.63 ± 0.08 fc, p < 0.05, TIMP-1 1.0 ± 0.2 vs 0.56 ± 0.07 fc, p < 0.05).

**Conclusion:** Perihepatic implants of MEECs display anti-inflammatory and anti-fibrotic activity in liver fibrosis. This study highlights the potential therapeutic utility of MEECs for chronic liver disease.

**FR1206**

LncRNA XR_592974.2 and circRNA _2599 regulated hypoxic stress response in hepatic stellate cells by targeting the miRNA-145/JMY/P53 pathway

Dan Zhu1, Jing Gao2,3, Xiaojun Wang4, Yujin Li5, Hong Chen6, Liting Zhang1.

1The First Hospital of Lanzhou University; 2Department of Medicine, Karolinska Institute, Stockholm, Sweden; 3University of Helsinki, Heart and Lung Centre, Helsinki, Finland; 4Gansu Provincial Hospital; 5Capital Medical University, China; 6Xi’an International Medical Center, China

Email: lcheneye@163.com

**Background and aims:** Non-coding RNAs contribute to the activation of hepatic stellate cells (HSCs) and the progression of liver fibrosis. Hypoxia serves as a pivotal microenvironmental factor that facilitates the activation of HSCs. Our previous study demonstrated differentially expressed mRNAs and miRNAs in hypoxia-induced HSCs. Here, we investigated the interactions among lncRNAs/circRNAs, miRNAs, and miRNAs in HSCs under hypoxic stress.

**Method:** Hypoxia-induced HSCs model were treated with 400 μmol/L CoCl2 in HSC-T6 cells. The differentially expressed mRNAs, miRNA, circRNAs, and lncRNAs in hypoxia-induced HSCs were identified using whole-genome sequencing. Next, we constructed the ceRNA network based on the interactions among lncRNAs/circRNAs, miRNAs, and miRNAs in hypoxia-induced HSCs. The functional analyses were performed by the gene ontology analysis and the Kyoto Encyclopedia of Genes and Genomes pathway analysis. Finally, we performed the pathway analysis based on the public database and literature.
Results: A total of 1423 mRNAs, 54 miRNAs, 288 IncRNAs, and 60 circRNAs were differentially expressed in hypoxia-induced HSCs compared to the controls. Combined with our previous identified miRNA-miRNA regulation network in HSCs under hypoxic stress, the results presented that up regulation IncXR_592974.2 and up regulation circRNA_2599 regulated in down regulation miRNAs (miRNA-145-3p and novel 500 mature) -up regulation mRNA (Junction Mediating and Regulatory Protein (JMY, P53 Cofactor)) network, respectively. These ncRNAs/circRNAs-miRNAs- mRNAs were involved in P53 signaling pathway (Figure 1).

Conclusion: Our results showed the IncRNAs XR_592974.2/ circRNA_2599-miR-145-3p/novel 500 mature -Jmy-p53 regulatory axis that might participate in activated HSCs and might carry potential therapeutic targets for restraining hypoxic stress.

FRI207
Magnetic resonance elastography (MRE) demonstrate the strongest correlation with digital pathology and NASH CRN fibrosis assessments, compared to transient elastography and other assessed non-invasive tests (NITs)
Miljen Martic1, Dean Tai2, Nikolai Naoumov3, Elaine Chng2, Clifford Brass4, Juergen Loeffler5, Jossy George Kochuparampil6, Jia Ling Chong2, Shenglin Ma6, Andreas Sailer5, Dominique Brees5, Zachary Goodman7, Marcos Pedrosa5, Quentin Anstee8,9.

Background and aims: Correlation of a non-invasive test (NIT) with histology-based readouts is one of the key aspects of NIT inclusion in clinical trials and their adoption and impact on patient care. This sub-study aimed to explore correlation of different NITs with liver histology endpoints assessed by standard histology (NASH-CRN) and quantitative digital pathology (HistoIndex, HI-QDP).

Method: As part of the TANDEM NASH Phase 2 trial [NCT 03517540], the cross-sectional pre-treatment data has been collected from 269 patients with NAFLD (138 screen-failed and 131 randomized subjects). Key trial inclusion criteria were based on liver biopsy (NASH with F2 or F3 fibrosis). Only subjects who signed additional research ICF have been included in this analysis. Liver biopsies were evaluated by a central reader using NASH-CRN scoring system and analyzed by HI-QDP algorithm. ALT, AST, ELF, GGT, FIB-4 and Pro-C3 were analyzed by central laboratory, Fibroscan liver stiffness measurement (LSM) was assessed by a clinical site, while MRE LSM was assessed by a central imaging reader.

Results: Statistical analysis on the entire cohort (n = 269) revealed that MRE had the strongest correlation with both fibrosis assessments (NASH CRN and HI-QDP qFibrosis), followed by a MRI-aspartate aminotransferase (MAST) score (Figure). As MRE and MRI imaging were performed in a random subset of subjects, the MRE based dataset is smaller than for Fibroscan and soluble biomarkers. Interestingly, when correlating with qFibrosis, third and fourth ranked biomarkers were Pro-C3 and ELF, compared to FIB-4 and ELF when correlating with CR fibrosis assessment. In both cases, Fibroscan LSM and FibroScan-AST (FAST) score ranked fifth and sixth.

Conclusion: MRE LSM and MAST score had the strongest correlation with liver fibrosis staging (both NASH CRN and by HI-QDP qFibrosis). Additional evaluation of other individual biomarkers, as well as combination of imaging and soluble biomarkers is still ongoing and will also include separate correlations for randomized and screen failed subjects.

FRI208
Autoantibodies to apolipoprotein A-1 in chronic hepatitis C infection: a role in hepatic fibrosis and cirrhosis?
Simon Bridge1, Sabrina Pagano2, David Sheridan3, John Lodge1, Matthew Camp4, Simon Taylor-Robinson2, Dermot Neely5, Nicolas Vuilleumier2, Margaret Bassendine7, Simon Bridge1, Sabrina Pagano2, David Sheridan3, John Lodge1, Matthew Camp4, Simon Taylor-Robinson2, Dermot Neely5, Nicolas Vuilleumier2, Margaret Bassendine7.

Background and aims: Approximately 40–70% of chronic HCV (CHC) patients develop an autoimmune extrahepatic disorder. IgG auto-antibodies against apolipoprotein A-1 (AAA1) are a robust biomarker

Conclusion: MRE LSM and MAST score had the strongest correlation with liver fibrosis staging (both NASH CRN and by HI-QDP qFibrosis). Additional evaluation of other individual biomarkers, as well as combination of imaging and soluble biomarkers is still ongoing and will also include separate correlations for randomized and screen failed subjects.
of cardiovascular disease and predict all-cause mortality [1]. We previously reported the presence of AAA1 in 14/27 CHC patients [2]. Here, we evaluated AAA1 in a larger cohort of CHC patients to explore associations between AAA1, lipoproteins and severity of liver disease.

**Method:** Serum samples were obtained from 126 treatment naïve CHC subjects (61 genotype (GT) 1 and 65 GT3) and assayed for AAA1 and lipoprotein profiles. Subjects were classified as cirrhotic by liver imaging and/or histological assessment. Area under receiver operating characteristic curves (AUROC) were calculated for AAA1 and HDL-related parameters and used for predicting patients with cirrhosis. Fibronectin (FN) and messenger RNA (mRNA) were measured in human hepatic stellate cells (LX2) in the presence or absence of AAA1.

**Results:** Fifty-nine (47%) CHC patients were AAA1 positive. Twenty-one (70%) of 30 cirrhotic patients were AAA1 positive and the median magnitude of AAA1 was also significantly higher than non-cirrhotic patients (48% vs. 31%; p < 0.001). The AUROC for AAA1, ApoA-1 and HDL-C for predicting cirrhosis was 0.72 (p < 0.001), 0.65 (p = 0.01) and 0.64 (p = 0.02) (Figure A, B & C respectively). After 48 hours in the presence of AAA1, LX2 cells showed significantly increased levels of FN compared to LX2 cells alone (p = 0.02) and the LX2/IgG control (p = 0.0016). This was further confirmed by quantitating FN mRNA, LX2 cells and AAA1 showed an 80% increase in FN mRNA compared to LX2 cells alone (p = 0.035) and the LX2/IgG control (p = 0.028).

**Conclusion:** AAA1 are found in a subgroup of CHC patients and are found with higher incidence and magnitude in patients with advanced liver fibrosis. AAA1 are robust biomarkers for predicting cirrhosis. Human hepatic stellate cells in the presence of AAA1 showed a fibrotic phenotype. Further studies are warranted to define the role of AAA1 in the development of fibrosis and cirrhosis.

**References**


**FRI209 Selectivity matters: novel ROCK2 inhibitor down-regulates established liver fibrosis via concurrent targeting of inflammatory, fibrotic and metabolic pathways**

Alexandra Zanin-Zhorov1, Wei Chen1, Melanie Nyuydzefe1, Julien Moretti1, Iris Zhorov1, Rashmi Munshi1, Malavika Ghosh2, Kelli MacDonald3, Bruce Blazar4, Sam Waksal1.1Graviton Biosciences, B.V., Translational Medicine, Amsterdam, Netherlands; 2Aragen Biosciences, Morgan Hill, United States; 3QIMR Berghofer Medical Research Institute, Brisbane, Australia; 4University of MN, Masonic Cancer Center, Division of Blood & Marrow Transplant & Cellular Therapies, Minneapolis, United States

**Email:** alexandra.zanin-zhorov@graviton.bio

**Background and aims:** The pathogenesis of hepatic fibrosis is caused and driven by dysregulated metabolism precipitated by chronic inflammation. Rho-associated coiled-coil-containing protein kinases (ROCKs) have been implicated in these processes, however the ability of selective ROCK2 inhibition to target simultaneously profibrotic, pro-inflammatory and metabolic pathways was not demonstrated yet.

**Method:** We used the thioacetamide (TAA)-induced liver fibrosis model in combination with or without high fat diet to examine the efficacy of administration of the highly selective ROCK2 inhibitor GV101 to treat liver fibrosis, and its impact on inflammatory, fibrotic, and metabolic pathways in tissues.

**Results:** We found that therapeutic administration of GV101, a novel ROCK2 inhibitor with more than 1000-fold selectivity over ROCK1, attenuated established liver fibrosis induced by TAA alone or in combination with high fat diet in mice. GV101 treatment significantly reduced hydroxyproline levels in liver and serum AST/ALT ratio, which was associated with downregulation of pCofilin (pro-fibrotic), pSTAT3 (pro-inflammatory), while the levels of pSTAT5 (anti-inflammatory) and pAMPK (anti-metabolic) were increased in tissues of treated mice. In vitro experiments have shown that pharmacological selective ROCK2 inhibition, but not pan-ROCK inhibition down-regulates STAT3-dependent pro-inflammatory cytokine secretion in T cells as well as adipogenesis of both 3T3L1 mouse cells and primary human preadipocytes via AMPK-dependent mechanism.
Aldafermin rebalances collagen turnover in patients with NASH and liver fibrosis in the ALPINE 2/3 study

**Background and aims:** The most common method of evaluating liver fibrosis in clinical studies is by microscopic analysis of biopsies stained with Masson’s trichrome or sirius red—an approach that may be too simplistic and not able to specifically differentiate among the many different collagen molecules. Recent research has demonstrated that not all collagens are created equal, and that an array of collagen-derived molecules has emerged with novel functions. Whereas the interstitial matrix collagens are increased with more severe disease, the basement membrane collagens are important for regeneration of hepatic tissue (Villesen et al., AASLD 2021). Aldafermin, an engineered analog of the human hormone FGF19, inhibits bile acid synthesis and has improved liver histology in advanced fibrosis (Villesen et al., AASLD 2021). Our results revealed novel insights into aldafermin biology in reducing the fibrogenesis of type 3 collagen in the interstitial matrix, while strengthening type 8 collagen in the basement membrane. Given the invasive and heterogeneous nature of liver biopsy, these novel, non-invasive fibrosis markers may have the potential to obviate the limitations of liver biopsy by providing important information regarding the state of the liver and extracellular matrix turnover.

**Conclusion:** Aldafermin rebalanced interstitial matrix collagen turnover, as measured by Pro-C3 and Pro-C8, and basement membrane collagen turnover, as measured by Pro-C6, in patients with NASH and liver fibrosis in the ALPINE 2/3 study. Aldafermin did not reach statistical significance on the dose-dependent improvement in fibrosis on liver biopsy (19%, 31%, 15% and 30% of the patients in the placebo, 0.3 mg, 1 mg and 3 mg groups, respectively, achieved fibrosis improvement of ≥1-stage without NASH worsening).
patient management. The aim was to investigate if the ELF score could be used safely and effectively as a rule out test for cirrhosis and advanced fibrosis within the iLFT pathway.

Method: Outcomes for all patients who received an ELF test via the iLFT pathway between July 2020 and April 2021 were collected and analysed to compare ELF scores with the incidence of cirrhosis and advanced fibrosis diagnoses. A further analysis of all patients who had undergone ELF testing since its introduction in NHS Tayside, regardless of involvement with iLFT, was undertaken to compare ELF score with Transient Elastography (TE) reading.

Results: 634 patients were included in the study; 62.3% of the patients were male, with a mean age of 62.5 years and mean BMI of 31. 419 (66%) had a ‘high’ ELF score (≥9.8) and 219 had a ‘low’ ELF score. Median ELF score was 10.2 (IQR 9.5–11.1). 139 patients received TE, with a median ELF score of 10.7 (IQR 9.9–11.4).

Conclusion: The high sensitivity and NPV of the ELF test for cirrhosis and advanced fibrosis confirms the safe implementation of ELF as an additional fibrosis ‘rule-out’ within the iLFT pathway. It allows for a streamlined, triaged referral system, ensuring that patients requiring secondary care involvement are picked up, whilst reducing unnecessary referrals amongst lower risk patients who can be safely managed in primary care.

FRI215
Comparison of CT, blood test, elastometry and their combination for non-invasive staging of liver fibrosis
Paul Cales1, Anita Paisant1, Clémence M. Canivet1, Jerome Lebigot1, Lannes Adrien1, Carole Vitelli1, Julien Chaigneau1, Frédéric Oberti1, Isabelle Fouchard1, Sophie Michalak1, Jerome Boursier1, Christophe Aubé1.1Angers University, HIFIH Laboratory, Angers, France

Background and aims: The EASL 2021 guidelines on non-invasive diagnosis state that imaging does not discriminate initial stages of liver fibrosis. We sought to evaluate whether liver computed tomography (CT) imaging could discriminate Metavir fibrosis (F) stages.

Method: 111 patients with Metavir F stage by liver biopsy, CT, liver stiffness measurement (LSM), blood test (FM) or their combination (EFM) were retrospectively included. CT was prospectively evaluated by a) an expert radiologist according to the 7 usual signs of cirrhosis + CT-F stage, equivalent to Metavir; b) semi-automated quantitative morphometry (43 signs); c) 70 hepatogastroenterologists according to CT F-stage in 10 patients (2 per Metavir F stage) for whom 4 independent diagnostic methods agreed for fibrosis stages (method without gold standard). We developed multivariate scores predictive of Metavir F stages using CT signs assessed by the expert radiologist (expert score) or by morphometry (morpho score) and by all non-invasive methods (mixed score including EFM, expert and morpho scores).

Results: 1) Characteristics in all 111 patients were, age: 54.2 ± 12.8 years, male: 60.4%, BMI: 31.2 ± 6.6 kg/m², NAFLD: 75.7%, Metavir: F0: 15.3%, F1: 34.2%, F2: 18.0%, F3: 14.4%, F4: 18.0%. Spearman correlation coefficients (Rs) with Metavir F stages were, expert score: 0.605, FM: 0.648, CT-F stage: 0.661, morpho score: 0.705, LSM: 0.737, EFM: 0.750, mixed score: 0.783. Obuchowski indexes for Metavir F stage discrimination were, expert score: 0.683, FM or CT-F stage: 0.683, morpho score: 0.855, LSM: 0.881, EFM: 0.889, mixed score: 0.909. Concerning discrimination between adjacent Metavir F stages, a significant difference was observed for the following tests, F0 vs F1: FM, LSM, EFM, expert score; F1 vs F2: all tests; F2 vs F3: LSM, EFM; F3 vs F4: CT-F stage, FM, EFM, expert and mixed scores. 2) In the 10 patients evaluated with multiple F references: the Metavir F stages were well-discriminated by CT-F stage with Rs: 0.914, Obuchowski index: 0.950 and significant differences (p<0.001) between all adjacent Metavir F stages (Figure).

Conclusion: A CT expert score discriminates Metavir F0 to F2 stages. The best single test to discriminate all Metavir F stages from each other is a combination of a blood test and elastometry. However, combined methods (blood test, LSM and CT) offer better discrimination. Using multiple concordant F references, a simple CT semiology discriminates between all Metavir F stages very well.
FRI216
Reliability criteria of non-invasive tests for liver fibrosis
Paul Cales1, Clémence M. Canivet2, Lannes Adrien1, Hunault Gilles2, Frédéric Oberli1, Valérie Moal1, Isabelle Fouchard1, Sophie Michalak1, Jerome Boursier1, 1Angers University, HIFIH Laboratory, Angers, France; 2Angers University Hospital, Hepatology, Angers, France; 3Angers University Hospital, Hepatology, Angers, France; 4Angers University Hospital, Hepatology, Angers, France
Email: paul.cales@univ-angers.fr

Background and aims: The need for reliability studies on non-invasive tests (NITs) was underlined in the 2021 EASL guidelines. Recently, we developed intrinsic blood test reliability criteria. We sought to validate these criteria and apply them to other NITs.

Method: 6858 patients with chronic liver disease (etiologies: virus, NAFLD, alcohol) were recruited in one (cross-sectional) derivation and two (cross-sectional and longitudinal) validation sets. The main fibrosis measurements were: blood test (FibroMeter FM2G), liver stiffness measurement (LSM), Metavir F (liver biopsy) and survival. We developed a reliability score (RS) for FM2G with Metavir F as reference. It included FM2G markers + etiology and comprised 3 classes: low, fair and high reliability.

Results: 1/In the derivation set, RS estimated FM2G accuracy for fibrosis staging well (agreement coef: 0.96). Thus, cirrhosis AUROCs were, low RS: 0.686, fair RS: 0.824, high RS: 0.924, all: 0.883 (p < 0.001 vs each class); accuracy is detailed in the figure. 2/In the cross-sectional validation set, these significant differences were confirmed. Moreover, FM2G RS was well-correlated with the LSM AUROC (Rp: 0.83). Thus, the FM2G RS discriminated the cirrhosis AUROC of LSM better than did reliability criteria based on LSM and the IQR/LSM ratio. Also, the FM2G RS discriminated well the cirrhosis AUROCs of other blood tests (APRI, Fib4, Fibrotest, Hepascore, ELF); e.g. for Fibrotest, low RS: 0.569, fair RS: 0.680, high RS: 0.894 (p < 0.001 vs low). The FM2G and LSM reliability classes were complementary. Thus, we developed a sequential algorithm using first FM2G in high RS and otherwise LSM combined with FM2G. The algorithm accuracy was, according to its reliability classes, low (0.6% of patients): 22.2%, high: 86.0%, p < 0.001 (Figure). Its overall accuracy was 85.6% vs FM2G: 78.3% or LSM: 81.1% (p < 0.001).

3/In the longitudinal validation set, FM2G RS discriminated survival accuracy. Thus, logrank tests for Kaplan-Meier survival estimates of fibrosis stages were, low RS: p = 2.10−6, fair RS, p = 1.10−18, high RS: 3.10−92. RS was thus validated independently of Metavir F.

Conclusion: A blood test reliability score estimates remarkably its own diagnostic and prognostic accuracies and discriminates diagnostic performances of other NITs. The combination of blood test and elastometry reliability criteria dramatically reduces unreliable NIT prevalence (≤1%), improves accuracy and better individualizes patients with under-accuracy.

FRI217
Metabolic profiling of capillary dry blood samples for the differential diagnoses of hepatocellular carcinoma and liver diseases
Philipp Brunnbauer1, Jennifer Kirwan2,3, Can Kamali1, Christian Benzing1, Katrin Splith1, Karl Hillebrandt1, Johann Pratschke1, Moritz Schmelzle1, Felix Krenzien1, 1Charité-Universitätsmedizin Berlin, Corporate Member of Freie Universität Berlin and Humboldt Universität zu Berlin, Department of Surgery, Experimental Surgery, Berlin, Germany; 2Berlin Institute of Health, Core Unit Metabolomics, Berlin, Germany; 3Max Debrück Center for Molecular Medicine, Metabolomics, Berlin, Germany
Email: philipp.brunnbauer@charite.de

Background and aims: Hepatocellular carcinoma (HCC) remains the second most common tumour-associated cause of death globally, in part, due to a lack of viable screening options, non-specific clinical presentation and late diagnosis. In fact, alpha-fetoprotein (AFP), the biomarker of choice, is of low diagnostic utility (sensitivity of 41–65%, specificity of 80–94%), which further deteriorates in the presence of cirrhosis or hepatitis. Herein, we present promising preliminary results of an untargeted metabolomics biomarker-discovery study, based on dry blood sampling, demonstrating robust classification accuracy, discriminating HCC (including HCC in cirrhosis) from severe fibrosis or cirrhosis.

Method: Capillary blood samples (10 uL) were collected from the earlobe of patients using a volumetric absorptive microsampling (VAMS) device. Metabolic analysis was performed using liquid chromatography (LC) coupled to an electrospray ionisation mass spectrometry (ESI-MS). Raw LC/ESI-MS data were processed using a standard metabolomics workflow and peaks were annotated using an internal database of m/z and retention time with a 30 ppm mass accuracy. Data were further corrected for technical variation and background effects, followed by batch correction and data filtering in MATLAB (R2021a). Random forest classification was conducted in MetaboAnalyst 5.0.

Results: Having analysed dried blood samples from individuals with liver disease and healthy controls, we obtained 297 metabolites from 483 samples (162 patients), deemed suitable for statistical analysis. Although some patients presented with both, for the purpose of classification, we separated preoperative samples into two mutually exclusive groups: HCC (including HCC in cirrhosis, n = 36) and severe fibrosis/cirrhosis (F3F4, n = 25). From 43 significantly altered metabolites (fold-change ratio = 2.0, evaluated via t-test with p < 0.05), we selected a panel of three metabolites (IDs available on request), achieving an AUROC of 0.892 (95% CI: 0.777–0.983, Figure A), and promising predicted class probabilities and confusion matrix (Figure B).
Conclusion: Dry blood sampling can identify promising biomarker candidates that could improve HCC time-to- and stage-at-diagnosis. While our findings will be confirmed in a prospective study, focusing on age and risk factor stratification, we aim to translate our findings into an easy-to-use, low-cost population screening tool for HCC. MS&FK share senior authorship.

POSTER PRESENTATIONS

**FRI218**

**Stable rates of cirrhosis diagnosed by Fibroscan despite changing trends in liver disease epidemiology: a single centre retrospective cohort study**

Joan Ericka Flores1,2, Anne Craigie1, Lucy McDonald1, Amy Edwards1, Tim Papaluca1,2, Michael MacIsaac1, John Gough1, Kate New1, Susanne Glasgow1, Bradley Whitton1, Paul Desmond1,2, Marno Ryan1,2, Thai Hong1, Zina Valaydon2, Jacinta Holmes1,2, Barbara Demediuk1, Catherine Croagh1, David Iser1, Kumar Visvanathan1,2, Swee Lin Chen Yi Mei1, Alexander Thompson1,2, Jessica Howell1,2. 1St. Vincent's Hospital Melbourne, Fitzroy, Australia; 2University of Melbourne, Parkville, Australia

Email: ericka@flores.com.au

**Background and aims:** Data for cirrhosis prevalence in Australia are urgently needed to plan health resourcing for hepatocellular carcinoma (HCC) surveillance and liver disease prevention programs. The aim of this study was to describe the prevalence of cirrhosis diagnosed by Fibroscan within an urban tertiary health network and linkage to specialist care.

**Method:** This retrospective cohort study was conducted at St Vincent’s Hospital Melbourne, Australia. Raw Fibroscan data files were extracted from three machines (one static, two portable) used in hospital and community sites, and Fibroscan database. Cirrhosis was defined by aetiology specific cut offs and ≥12.5 kPa where aetiology was not available. Individuals with cirrhosis range Fibroscans were cross referenced with hospital record data to describe the proportion of patients referred for follow up. Median time intervals were reported in months (IQR). Proportions of Fibroscans in cirrhotic range and aetiologies compared with Chi square test.

**Results:** 10,622 Fibroscans were performed in 8727 individuals from 9 April 2010 to 27 April 2021. Fibroscan data from 2012 was not available. Peak number of Fibroscans in 2016, coincided with availability of hepatitis C DAAs. Recorded liver disease aetiologies: 38% chronic hepatitis C (3358/8798), 25% hepatitis B (2231/8798), 15% fatty liver disease (1297/8798) and 10% alcohol (837/8798). 15% (1595/10622) of Fibroscan records were in cirrhosis range. Proportion of Fibroscans with cirrhosis range were similar over time, ranging between 15 and 19% without significant variation (p = 0.68) (Figure 1a). Proportion of fibroscans with cirrhosis due to most common aetiologies showed significant downtrend with chronic hepatitis C and chronic hepatitis B (p = 0.018 and p = 0.012, respectively). An uptrend with MAFLD (p = 0.35) and alcohol was observed, but only statistically significant for alcohol (p = 0.009).

**Conclusion:** The proportion of patients with cirrhosis diagnosed by Fibroscan has remained stable over time, with changing trends of chronic liver disease aetiology from viral hepatitis to fatty liver disease and alcohol related liver disease. Despite this, linkage to care

1045 patients with cirrhotic Fibroscan range had hospital records: 56% (584/1045) were known to the liver clinic at the time of Fibroscan, 20% (205/1045) were referred following Fibroscan and 24% (252/1045) had no referral. 3% (32/1045) required multiple referrals until patient attendance was recorded and 1% (13/1045) patients never attended liver clinic. Median time from Fibroscan to liver clinic referral was 13 months (IQR 3–34).

**Conclusion:** The proportion of patients with cirrhosis diagnosed by Fibroscan has remained stable over time, with changing trends of chronic liver disease aetiology from viral hepatitis to fatty liver disease and alcohol related liver disease. Despite this, linkage to care

1045 patients with cirrhotic Fibroscan range had hospital records: 56% (584/1045) were known to the liver clinic at the time of Fibroscan, 20% (205/1045) were referred following Fibroscan and 24% (252/1045) had no referral. 3% (32/1045) required multiple referrals until patient attendance was recorded and 1% (13/1045) patients never attended liver clinic. Median time from Fibroscan to liver clinic referral was 13 months (IQR 3–34).

**Conclusion:** The proportion of patients with cirrhosis diagnosed by Fibroscan has remained stable over time, with changing trends of chronic liver disease aetiology from viral hepatitis to fatty liver disease and alcohol related liver disease. Despite this, linkage to care
of people with cirrhosis remains suboptimal. These data are limited by focusing on one hospital's liver clinic and no data of follow-up at other health services, but suggest greater resourcing streamlining and linkage of people diagnosed with cirrhosis by Fibroscan into specialist care is warranted.

**FRI219**

**Comparative assessment of noninvasive methods (NIMs)-LIVERFAS**t, liver stiffness measurement (LSM) with transient elastography (TE, Fibroscan) ELF and FIB-4 in a prospective cohort with chronic liver diseases (CLD) from a tertiary liver center

Kawin Tangvoraphonkhal1, Tanita Suttichaimongkol2, Prakasit Sangiamwibool1, Wattana Sukeepaisarnjaroen4, Churaiat Kularkaeaw1, 1Khon Kaen University, Faculty of Medicine, Division of Gastroenterology, Department of Medicine, Thailand; 2Khon Kaen University, Division of Gastroenterology, Department of Medicine, Thailand; 3Khon Kaen University, Department of Pathology, Thailand; 4Khon Kaen University, Department of Pathology, Faculty of Medicine, Thailand

*Email: kawin_tang@hotmail.com*

**Background and aims:** CLD-related mortality in Thailand is increasing due to high prevalence of obesity and not eradicated chronic viral hepatitis B (CHB) and C (CHC). LIVERFAST (LF, Fibronostics, US) is a new point-of-care proprietary technology to assess quantitatively liver fibrosis (LF-Fib) and steatosis (LF-Ste), (Hepatology Suppl. 2020) In NAFLD pts, LF-Fib predicted liver-related events and overall mortality (Hepatology Suppl. 2021).

To assess: 1/LF-Fib performance for advanced (AF) and bridging fibrosis (BF) vs LSM, FIB-4 and ELF in a prospective tertiary cohort with CLD and LB. 2/LF-Ste performance for mild (≥S1), moderate (≥S2) and marked steatosis (S3) vs. imaging methods (CAP) in NAFLD pts, including a CHC/CHB control group without steatosis (S0).

**Method:** Pts with simultaneous LB, blood biomarkers (LF, FIB4 and ELF) and LSM using TE were prospectively included. LB staging was as per METAIR for CHB/CHC and NASH-CRN for NAFLD. Statistics were descriptive and using binary area under ROC [BinAUROC (95%CI)].

**Results:** 157 patients had ELF determined along with LF and other SOC. Main descriptive and using binary area under ROC [BinAUROC (95%CI)]. ELF) and LSM using TE were prospectively included. LB staging was as follows: 26.4% NAFLD, 23.9% CHB, 49.8% CHC, BMI 34.9 kg/m², HbA1c 5.5, LSM 4.9 kPa, LF-Fib 0.29, LF-Act 0.29, LF-Ste 0.35, 49.5% severe NAFL, 50.2% stratifying the severity of the disease.

**Conclusion:** LIVERFAST is a blood biomarker for fibrosis/steatosis staging with similar performances to TE/CAP in a tertiary cohort with CLD. In NAFLD pts, LF can be an alternative to imaging methods (e.g. CAP and LSM) for stratifying the severity of the disease.

**FRI220**

**Diagnostic accuracy of non-invasive imaging modalities for the diagnosis of liver cirrhosis compared to histological assessment in a clinical setting**

Liv Hetland1, Mira Thing1, Thit Kronborg1, Beth Hæsted Olsen2, Nina Kimer1, Lise Lotte Gluud1, 1Hvidovre Hospital, Gastro Unit, Hvidovre, Denmark; 2Hvidovre Hospital, Department of Radiology, Hvidovre, Denmark; 3Copenhagen University, Department of Clinical Medicine, København, Denmark

*Email: livelinehetland@gmail.com*

**Background and aims:** Diagnostic imaging including abdominal ultrasound (US) and computed tomography (CT) are important tools in the initial evaluation of patients with liver disease. We evaluated the accuracy of US and CT in diagnosing liver cirrhosis using a prospective design with histological assessment as the gold standard.

**Method:** This study included 369 patients from three prospective cohort studies between January 2017 and November 2021 who underwent diagnostic imaging (US or CT) and a liver biopsy based on clinical indication. Two cohorts (ProDoc, n = 34; StatLiver, n = 78) included patients with suspected cirrhosis and one cohort (FLINC, n = 257) included patients with non-alcoholic fatty liver disease (NAFLD). US and CT scans were performed by experienced radiologists and the results were re-evaluated by a second radiologist in case of inconclusive findings.

**Results:** The cohorts include 369 patients who underwent a liver biopsy and an US (n = 279) and/or CT scan (n = 129). In addition, 291 patients underwent a Fibroscan. In total 143 patients had histologically confirmed cirrhosis (38.7%). Of patients who underwent US, 78 were correctly diagnosed as having cirrhosis and 159 as correctly being non-cirrhotic; the sensitivity was 0.72, specificity 0.89, positive predictive value (PPV) 0.88 and negative predictive value (NPV) 0.84. Of patients who underwent CT scan, 61 were correctly diagnosed as having cirrhosis and 46 as correctly being non-cirrhotic, giving a sensitivity of 0.75, specificity of 0.96, PPV 0.97 and NPV 0.70. The PPV and NPV for Fibroscan was 0.71 and 0.91.

**Conclusion:** This study demonstrates that both US and CT provide important diagnostic information for ruling in cirrhosis. However, this study includes a relatively high proportion of patients with cirrhosis and the findings should therefore be re-evaluated in low risk groups.

**FRI221**

**Use of Fibrosis-4 (FIB-4) in liver fibrosis screening: which thresholds to choose?**

Denis Ouzan1, Jeremie Corneille2, Guillaume Penaranda3, Jean Marie Dubertrand4, 1Arnault Institute Tzacq, Saint-Laurent-du-Var, France; 2BIOGROUP BIOESTEREL-Laboratoire Mougin's-Les-espérance, Mouins, France; 3BIOGROUP ALPHABIO-Laboratoire Européen, Marseille, France; 4BIOGROUP BIOESTEREL-Laboratoire Mandelieu-Passerio, Mandelieu-la-Napoule, France

*Email: denis.ouzan@wanadoo.fr*

**Background and aims:** Rationale: Screening for liver fibrosis in the general population is a major public health issue. We have shown in a previous study (EASL 2020, Abs FRI225) that FIB-4, a simple score combining age, ALT/AST activity and platelet count, can detect liver fibrosis in general practice and identify a possible cause of chronic liver disease. But the optimal FIB-4 threshold that detects hepatic fibrosis remains to be defined. The FIB-4 thresholds recently proposed by a single study (1) are age-dependent: low risk if <1.30 (<65 years) and <2 (>65 years), intermediate risk between 1.3 and 2.67 (<65 years) and between 2 and 2.67 (>65 years), and high risk if >2.67. The aim of our work is to explore the simpler, age-independent FIB-4 threshold of 2 by performing a second-line ELF (Enhanced Liver Fibrosis) score after automatic calculation of FIB-4.

**Method:** The FIB-4 score has been automatically generated since January 1, 2020 by all city analysis laboratories in the Alpes-Maritimes French area as soon as ALT/ASAT and platelets are
prescribed. The FIB-4 results, calculated by 80 laboratories, were analyzed. The FIB-4 thresholds used are a function of age as defined above. The ELF score was performed in the second line in a group of 183 patients at intermediate or high risk of fibrosis.

**Results:** During the first 3 months of the implementation of the automatic calculation of the FIB-4, 131, 861 subjects were screened, an automatic calculation of the FIB-4, 131, 861 subjects were screened, and the distribution of fibrosis risk observed by the FIB-4 according to age was as follows: low risk for 107, 148 subjects (81.3%), intermediate risk for 16, 297 subjects (12.4%), and high fibrosis risk for 8, 416 subjects (6.4%). An ELF score >9.8 indicative of advanced fibrosis was observed in 14/54 subjects (26%) of those with a FIB-4 score between 1.3 and 2 and in 102/129 (79%) of those with a FIB-4 ≥2 (p < 0.001).

**Conclusion:** The automatic calculation of the FIB-4 showed in a large cohort, a risk of hepatic fibrosis in almost 19% of the subjects: intermediate risk 12.4% and high risk of fibrosis 6.4%. The ELF test performed in the second line significantly more often confirmed the intermediate fibrosis risk 12.4% and high risk of fibrosis 6.4%. The ELF test performed in the second line significantly more often confirmed the intermediate fibrosis risk 12.4% and high risk of fibrosis 6.4%. The ELF test performed in the second line significantly more often confirmed the intermediate fibrosis risk 12.4% and high risk of fibrosis 6.4%.

**Reference**

**FRI222**
Plasma cell-free DNA methylation as biomarker for hepatocellular carcinoma
María Gárate-Rascón1, Miriam Recalde1, Idobia Bilbao2, Fabrice Daian3, María Elizalde1, María Azkona1, José María Herranz1,4, Carla Rojo1, Mercedes Íñarrairea4,2,4, Itziar Abete6, María A. Zulet6, Bruno Sangro2,4,2, Maite G. Fernandez-Barrena4,2,4,2, Loreto Boix7, María Reig7, Andrea Casadei Gardini8, Matías A. Avila1,4,2, Manuel F. Landecho2, Carmen Berasain1,4,2, María Arechederra1,5,1,5,1,5
1Center of Applied Medical Research (CIMA), Program of Hepatology, Pamplona, Spain; 2Navarra University Clinic, Hepatology Unit, Pamplona, Spain; 3Developmental Biology Institute of Marseille (IBDM), Marseille, France; 4National Institute for the Study of Liver and Gastrointestinal Diseases (CIBERehd, Carlos III Health Institute), Madrid, Spain; 5Navarra Institute for Health Research (IdiSNA), Pamplona, Spain; 6Food Sciences and Physiology and Center for Nutrition Research, Department of Nutrition, Pamplona, Spain; 7Barcelona Clinic Liver Cancer (BCLC), Hospital Clinic de Barcelona, IDIBAPS, Liver Unit, Barcelona, Spain; 8BCCS-San Raffaele Scientific Institute, Unit of Oncology, Milan, Italy
Email: macalderon@unav.es

**Background and aims:** Hepatocellular carcinoma (HCC) is a global health concern with increasing impact on our societies. Nowadays, there are limited diagnostic methods and most patients are diagnosed at advanced stage when current treatments have little effectiveness. Moreover, although patients in early and intermediate stages might benefit from potentially curative treatments, there is a high rate of recurrence. It is therefore essential to identify new non-invasive reliable biomarkers for the detection of HCC at an early stage and the prediction of recurrence-progression to improve patient survival. In this regard, recent advances have demonstrated that circulating tumor DNA (ctDNA) methylation has a great potential to serve as a blood-based biomarker for early diagnosis and precision treatment. In this project, we aim to identify and validate new ctDNA methylation markers for early HCC detection and HCC recurrence-progression monitoring.

**Method:** For in silico analyses we used available tissue methylation data on control and HCC patients, focusing on CpG islands and lncRNA promoter regions. We set up the protocol to isolate ctDNA from 1 ml of plasma, to treat ctDNA with bisulfite and to perform targeted sequencing. Plasma from control and HCC patients were used for validations.

**Results:** Using available tissue methylation data on HCC (n = 670) and control (n = 135) samples from three different studies (GSE45688, GSE54503 and TCGA-LIHC) as well as from blood leukocyte samples of healthy individuals (754 samples, GSE40279) and deep learning approaches we defined a blood-based HCC Methyl Diagnostic panel (HepaMet Panel) consisting on 27 CpG marks located within CpG islands and 2 located within IncRNA promoter regions. HepaMet Panel revealed a robust performance (accuracy of 97.3%) for control and HCC patient classification. In silico validation of HepaMet Panel in three independent HCC cohorts (GSE60753, GSE89852 and GSE157341) showed a sensitivity range of 97%–100%. We first set up conditions to analyze 16 of these 29 marks. Validation of this sub-panel using ctDNA from 7 early stage HCCs, 22 advanced HCCs as well as 11 healthy controls succeeded to classify 76% of HCC patients (71% early and 77% advanced).

**Conclusion:** We have identified a blood-based HCC Methyl Diagnostic panel that effectively classify control and HCC patients. Ongoing analyses will determine HepaMet Panel utility in the early diagnosis of HCC and HCC recurrence-progression monitoring.

**FRI223**
A derivation and validation study of paired liver and plasma proteomics in 659 individuals reveals circulating biomarkers for alcohol-related liver disease
Lili Niu1, Maja Thiele2,3, Philipp Geyer1, Ditlev Nytoft Rasmussen2, Henry Emanuel Webel1, Alberto Delgado1, Rajat Gupta3, Florian Mei1, Maximilian Strauss1, Maria Kjærgaard4, Katrine Priør Lindvig4,5, Mads Israelsen1,3, Simon Rasmussen1, Torben Hansen4, Matthias Mann1, Aleksander Krag1,6, 7University of Copenhagen, Center for Protein Research, Copenhagen, Denmark; 2Center for Liver Research, Odense University Hospital, Department of Gastroenterology and Hepatology, Odense, Denmark; 3University of Southern Denmark, Faculty of Health Sciences, Department for Clinical Research, Odense C, Denmark; 4University of Copenhagen, Center for Basic Metabolic Research, Denmark
Email: maja.thiele@rsyd.dk

**Background and aims:** Alcohol-related liver disease (ALD) is the most common cause of liver-related mortality, but diagnosis is often delayed due to lack of accurate, circulating biomarkers. We aimed to develop and validate diagnostic and prognostic protein marker panels of fibrosis, hepatocyte injury with inflammation, and steatosis, using paired liver and plasma proteomics.

**Method:** We included 459 patients with early ALD in a prospective derivation cohort, used mass spectrometry to measure plasma and liver proteome, and integrated them to determine the tissue origin of circulating proteins. We used machine learning with feature selection to derive three proteomic panels of significant fibrosis (≥F2), mild activity (sum of ballooning and lobular inflammation ≥2) and any steatosis (≥S1), and validated their ability to rule out or rule in disease in 137 healthy, age- and gender-matched controls, and 63 liver-biopsied ALD patients from an independent screening cohort. Finally, we evaluated the proteomic biomarkers’ ability to predict liver-related events and all-cause mortality, and compared their diagnostic performance with 15 best-in-class existing tests.

**Results:** The derivation cohort consisted of 76% males, age 57 ± 13 years, 44% significant fibrosis (≥F2), 46% mild activity, 44% steatosis (≥S1). 717 unique proteins were dysregulated during disease progression, accounting for 13% of the measured liver proteome, but only half of liver proteome changes were transmitted to the circulation. Integrative analysis revealed 46 co-dysregulated proteins, representing mostly the downregulation of metabolic functions and upregulation of fibrosis signaling and immune response (figure). Feature selection found that 22 unique plasma proteins could be used in different combinations to derive three proteomic biomarker panels. The panels performed better than all comparators (including elastography, ELF, FIB-4, cytoketatin-18) for detecting significant fibrosis (AUC 0.92) and mild activity (AUC 0.87). The ≥F2 proteomic
Panel ruled out significant fibrosis in 99% of the healthy controls and had the highest prognostic accuracy for liver-related events and all-cause mortality (Harrell’s C 0.90 and 0.79). We successfully reproduced the excellent proteomics performance in the independent validation cohort (AUC 0.87 for significant fibrosis, and AUC 0.81 for mild activity).

**Conclusion:** Plasma proteomics has a great potential for the diagnosis and prognosis of overall liver health in people with a history of harmful drinking.

**Background and Aims:** Noninvasive and accurate methods are needed to identify patients with clinically significant portal hypertension (CSPH). This study aims to explore the variations of hepatic vascular geometries in patients with CSPH and investigate the capability of using CT/MRI angiographic imaging-based vascular geometrical model (VGM) to identify CSPH in patients with cirrhosis.

**Method:** The portal vein (PV), hepatic vein (HV), hepatic artery (HA) and inferior vena cava (IVC) were segmented using a pre-trained attention-based convolutional neural network (CNN). A total of 64 vascular geometrical parameters were automatically extracted from those segmented vessels and then fed into the VGM to identify CSPH patients. A total of 853 consecutive liver cirrhosis patients from two centers who underwent contrast enhanced MRI/CT scans within 14 days of transjugular catheterization for hepatic venous pressure gradient (HVPG) measurement were included in this study. The model was trained and validated in a CT cohort (#1) containing 256 patients with cirrhosis and 267 age-matched participants without a history of chronic liver diseases, and tested on another centers including a CT cohort (#2) with 106 patients and an MRI cohort (#3) with 224 patients. CSPH was defined as HVPG ≥ 10 mmHg.

**Results:** In PV, significant increase of vessel diameter (from 1.50 ± 0.91 to 2.20 ± 0.69 cm) and branch vessel diameter (from 0.41 ± 0.15 vs 0.73 ± 0.56 cm) were observed in CSPH patients. In contrast, significant decrease of PV volume (from 31.01 ± 12.93 to 23.89 ± 9.68 cm³) and tortuosity (from 0.17 ± 0.05 to 0.13 ± 0.04°) were observed in CSPH patients. In HV, significant decrease of vessel volume (from 66.52 ± 16.91 to 33.31 ± 28.05 cm³) and length (from 812.42 ± 284.55 to 349.21 ± 185.87 mm) were observed in CSPH patients. In HA, significant increase of vessel length (from 77.26 ± 64.31 to 143.38 ± 57.2 mm) were observed, which indicates significant disruption of hepatic vascular system in CSPH patients. The AUC, accuracy, sensitivity and specificity were 0.90 ± 0.02 (95% CI, 0.88–0.93), 0.84 ± 0.01 (95% CI, 0.84–0.85), 0.87 ± 0.05 (95% CI, 0.80–0.92) and 0.83 ± 0.04 (95% CI, 0.80–0.89) for Cohort #1; 0.84 ± 0.12 (95% CI, 0.67–1), 0.88 ± 0.10 (95% CI, 0.75–1), 0.88 ± 0.10 (95% CI, 0.73–1) and 0.88 ± 0.09 (95% CI, 0.76–1) for Cohort #2; and 0.87 ± 0.11 (95% CI, 0.74–1), 0.91 ± 0.08 (95% CI, 0.8–1), 0.90 ± 0.09 (95% CI, 0.77–1) and 0.92 ± 0.08 (95% CI, 0.82–1) for Cohort #3.

**Conclusion:** Plasma proteomics has a great potential for the diagnosis and prognosis of overall liver health in people with a history of harmful drinking.
The diagnostic accuracy of ElastQ 2-D shear wave elastography for liver fibrosis risk assessment in a mixed etiology, multinational cohort

David J. M. Bauer, Annalisa De Silvestri, Laura Maiocchi, Giovanna Ferraöi, Thomas Reiberger, Medical University of Vienna, Division of Gastroenterology and Hepatology, Department of Medicine III, Wien, Austria; Medical University of Vienna, Vienna Hepatic Hemodynamic Lab, Division of Gastroenterology and Hepatology, Department of Medicine III, Wien, Austria; University of Pavia, Fondazione IRCCS Policlinico San Matteo, Pavia, Italy; Victor Babes University of Medicine and Pharmacy, Department of Internal Medicine II, Division of Gastroenterology and Hepatology, Center for Advanced Research in Gastroenterology and Hepatology, Timișoara, Romania

Background and aims: The 2-D shear wave elastography technique ElastQ (Philips) shows promise for evaluating liver fibrosis risk assessment.

Method: We prospectively recruited 875 patients for simultaneous liver stiffness measurements (LSM) by ElastQ and Vibration Controlled Transient Elastography (VCTE) in 3 European centers. IQR/median ≥ 30% was used as a reliability criterion. The correlation of ElastQ-LSM to VCTE-LSM was assessed by Pearson correlation. The fibrosis stage was classified by VCTE: no significant fibrosis VCTE <6 kPa, grey area/significant fibrosis VCTE 6–12 kPa, severe fibrosis/cirrhosis VCTE >12 kPa (EASL CPG 2021). This classification served as a basis for the ROC analysis and definition of 90%-specific rule-in, and 90%-sensitive rule-out cutoffs for ElastQ.

Results: Among 875 participants, ElastQ failed in 26 (2.97%) and 90%-sensitive rule-out cutoffs for ElastQ.

Conclusion: This prospective, multicentric study shows a moderate correlation of ElastQ-LSM to VCTE-LSM, with better correlations at VCTE-LSM ≤ 30 kPa. ElastQ-LSM rules out significant fibrosis at <5.3 kPa and rules in advanced fibrosis/cirrhosis at >10.2 kPa.

Reference

FRI226
Machine learning models for prediction of severe portal hypertension in patients with compensated cirrhosis

Oleksandr Petrenko, Jifi Reinis, Benedikt Simbrunner, Benedikt Hofer, Pierre-Emmanuel Rautou, Lucile Moga, Jonel Trebicka, Wenyi Gu, Philip Georg Ferstl, Lise Lotte Gluud, Flemming Bendtsen, Sören Møller, Agustin Albillos, Luis Téllez, Sven Francé, Wilhelms Kwanten, Juan Carlos Garcia Pagan, Valeria Perez, Virginia Hernandez-Gea, Filippo Schepis, Dario Saltini, Cândid Villanueva, Anna Brujats, Mattias Mandorfer, Thomas Reiberger, CeMM Research Center for Molecular Medicine of the Austrian Academy of Sciences, Vienna, Austria; Ludwig Boltzmann Institute for Rare and Undiagnosed Diseases (LBI-RUD), Vienna, Austria; Vienna Hepatic Hemodynamic Lab (HEPEX), Division of Gastroenterology and Hepatology, Department of Internal Medicine III, Medical University of Vienna, Vienna, Austria; Christian Doppler Laboratory for Portal Hypertension and Liver Fibrosis, Medical University of Vienna, Vienna, Austria; Service d’Hépatologie, DMU Digest, Hôpital Beaujon, AP-HP, Clichy, France; Department of Internal Medicine I, Goethe University Clinic, Frankfurt, Germany; European Foundation for the Study of Chronic Liver Failure, EFCLIF, Barcelona, Spain; Gastro Unit, Medical Section, Hvidovre Hospital and Department of Clinical Medicine, University of Copenhagen, Copenhagen, Denmark; Department of Clinical Physiology and Nuclear Medicine, Center for Functional and Diagnostic Imaging and Research, Faculty of Health Sciences Hvidovre Hospital, University of Copenhagen, Hvidovre, Denmark; Department of Gastroenterology, Hospital Universitario Ramón y Cajal, IRYCIS, CIBERehd, Universidad de Alcalá, Madrid, Spain; Department of Gastroenterology and Hepatology, University Hospital Antwerp, Antwerp, Belgium; Laboratory of
Background and aims: Hepatic venous pressure gradient (HVPG) is the gold standard for evaluation of the severity of portal hypertension (PH). In this multicenter study, we investigated the diagnostic value of different machine learning models trained on standard laboratory parameters to predict severe PH in compensated advanced chronic liver disease (cACLD) patients.

Method: The training cohort included cACLD patients recruited from the prospective VICIS study (NCT03267615). Regression and classification-based prediction models were applied to identify patients with severe PH (i.e., HVPG ≥16 mmHg) based on 52 widely available laboratory parameters. After feature selection, the models were applied to an external multicenter validation cohort using a cross-validation approach with the AUC reported as the median value across 75 cross-validations.

Results: The VICIS cohort included 139 cACLD patients (35.2% with HVPG ≥16 mmHg), main etiologies were viral hepatitis (32.4%), alcohol-related liver disease (ALD; 21.6%), and non-alcoholic fatty liver disease (NAFLD; 16.5%). The external validation cohort included 834 cACLD patients (36.7% with HVPG ≥16 mmHg), with the most prevalent etiologies being viral hepatitis (38.6%), NAFLD (24.2%), and ALD (20.6%). Recursive feature elimination identified three and five parameters as most suitable for the models.

In the VICIS cohort, internal training-validation with the 5-parameter (platelets, bilirubin, cholinesterase, GGT, aPTT) logistic regression model outperformed the other models with AUC of 0.898 for prediction of HVPG ≥16 mmHg (Figure-A).

The best 3-parameter model included platelets, bilirubin, and aPTT. After being applied to the external validation cohort, and following the training-validation split, logistic regression resulted in the highest AUC of 0.751 (Figure-B). The other 3-parameter models yielded median AUC of 0.681 (XGBoost), 0.726 (Random Forest), 0.748 (Support Vector Machine), and 0.750 (Multilayer Perceptron). When trained on the VICIS cohort first and then applied to the external cohorts, the 3-parameter model with logistic regression resulted in AUC spread from 0.472 to 0.872 in the different centers’ cohorts.

Conclusion: The VICIS-trained 5-parameter and 3-parameter model performed well to identify HVPG ≥16 mmHg in ‘local’ cACLD patients. However, the external applicability of the 3-parameter logistic regression model to predict HVPG ≥16 mmHg is limited—likely due to differences in laboratory assays and patient characteristics. Training and applying of the models in the subsets of the same cohort resulted in more sustained AUC. Invasive HVPG measurements are hence still needed to reliably identify cACLD with HVPG ≥16 mmHg.

FRI227 Reproducibility and applicability of spleen stiffness measurement by vibration controlled transient elastography in patients with and without chronic liver disease

Cristina Rigamonti1,2, Micol Cittone1,2, Giulia Francesca Manfredi1,2, Andrea Sorge1, Riccardo Molai, Maria Francesca Donato, Gianluca Gaidano1,2, Mirella Fraquelli1,2, Università del Piemonte Orientale, Department of Translational Medicine, Novara, Italy; 3AOU Maggiore della Carità, Division of Hematology, Italy; 4Fondazione IRCCS Ca’ Granda-Ospedale Maggiore Policlinico, Gastroenterology and Endoscopy Unit, Milan, Italy; 5AOU Maggiore della Carità, Division of Internal Medicine, Novara, Italy; 6Fondazione IRCCS Ca’ Granda-Ospedale Maggiore Policlinico, Gastroenterology and Hepatology Unit, Italy

Background and aims: Spleen stiffness measurement (SSM) by vibration controlled transient elastography (VCTE) has emerged as a promising non-invasive tool with good diagnostic accuracy for predicting the degree of portal hypertension in patients with advanced chronic liver disease (CLD). This study investigated intra-observer and inter-observer agreement and factors influencing SSM reproducibility.

Method: In this prospective multicentre study 297 patients with CLD of different aetiology (187 in Novara and 110 in Milan; 32 cirrhotics) and 123 controls (63 patients with Philadelphia negative (Ph-) myeloproliferative neoplasms in Novara and 60 healthy volunteers in Milan) consecutively underwent VCTE examination for SSM and liver stiffness measurement (LSM). SSM was blindly performed twice by two different operators. Intra-observer and inter-observer agreement was calculated using the intraclass correlation coefficient (ICC) in relationship with different patient-related covariates.

Results: A total of 922 VCTE examinations for SSM were performed in Novara and 680 in Milan, respectively, with an overall failure rate of 3.2% and 3.6%.

In CLD patients from Novara (33% cirrhotic, 26% with splenomegaly) median SSM was 24.9 kPa (IQR 20.6–36.1) and LSM was 6.8 kPa (IQR 4.9–11.3). In CLD patients from Milan (31% cirrhotics, 40% with splenomegaly) median SSM was 29.2 kPa (IQR 16.7–34.5) and median LSM 8.3 kPa (IQR 7.1–10.8). Median SS value was 26.6 kPa (IQR 24.3 to 36.1) in the overall CLD group, 26.3 kPa (IQR 22.3–33.6) in MPN patients and 16.1 kPa (IQR 14.6–18.7) in healthy volunteers.

In whole CLD group, SSM was significantly correlated with LSM (r = 0.67), spleen longitudinal diameter (r = 0.58), presence of cirrhosis (r = 0.54), and BMI (r = 0.24) (p < 0.0001 for all comparisons).

In CLD patients the overall inter-observer agreement ICC was 0.90 (0.88–0.92) and factors associated with a reduced agreement were: absence of splenomegaly (ICC 0.87 vs 0.91), BMI >25 kg/m² (ICC 0.91 vs 0.88) and absence of cirrhosis (ICC 0.84 vs 0.90). Intra-observer agreement ICC for rater 1 and rater 2 respectively were 0.93 (95% CI 0.91–0.95) and 0.96 (95% CI 0.95–0.97) in Novara and 0.91 and 0.94 (95% CI 0.91–0.96) (95% CI 0.87–0.93) in Milan.

Conclusion: SSM is a highly reproducible and feasible technique for assessing SSM in patients with CLD.
Validation of the continuous controlled attenuation parameter (CAPc) using the MRI-PDFF as reference

Nathalie Ganne-Carrié1, Olivier Chazouille1, Olivier Seror2, Yves Menu3, Olivier Serox4, Edouard Bardou-Jacquet5, 1Avicenne Hospital (AP-HP), Department of Hepatology, Bobigny, France; 2Hospital Saint-Antoine Ap-Hp, Department of Hepato-gastroenterology, Paris, France; 3Angers University Hospital Center, Department of Hepato-Gastroenterology and Digestive Oncology, Angers, France; 4IAP, University Hospital Center, Department of Radiology, Angers, France; 5Hospital Saint-Antoine Ap-Hp, Department of Radiology, Paris, France; 6Jean-Verdier Hospital Ap-Hp, Department of Radiology, Bondy, France; 7CHU Rennes-Pontchaillou Hospital, Department of Radiology and Medical Imaging, Rennes, France; 8CHU Rennes-Pontchaillou Hospital, Department of Liver Diseases, Rennes, France

Email: edouard.bardou.jacquet@chu-rennes.fr

Background and aims: Controlled Attenuation Parameter (CAP) was first introduced on the FibroScan (FS) device (Echosens, France) in 2010 and has been shown to be well correlated with liver steatosis in patients with various chronic liver diseases [PMID:28039099]. A new acquisition method for CAP (continuous CAP, CAPc) has recently been introduced in order to decrease the intra-examination measurement variability (IEMV) [ILC2020; poster FRI073]. The aim of this interim analysis of an ongoing study is to compare the diagnostic performances and the IEMV between CAP and CAPc.

Method: Consecutive patients, all etiologies combined, underwent FS, Magnetic Resonance Imaging (MRI) within 21 days and CAPs obtained by both methods (standard and continuous). A central reading of the MRI images was performed to assess the Proton Density Fat Fraction (PDFF) which was used as the reference to assess the steatosis grades (S >0: PDFF >5% and ≤10%; S >1: PDFF >10%). The CAPs standard deviations (SD) were compared using the unilateral Wilcoxon signed-rank test. The agreement between CAP and CAPc was assessed with the average bias, the Pearson coefficient of correlation (CC) and the absolute agreement intraclass coefficient (AA-ICC). The CAPs performances versus the PDFF were estimated with operating characteristics curves (ROC), and their areas under the curves (AUC). AUCs were compared with Delong's bilateral test.

Results: 157 patients were included (41% female, mean BMI = 28.4 ± 5.5 kg/m², mean age = 55.0 ± 13.4 years, Prevalence of S >0 and S >1 were 61% and 22%, respectively). The median CAPc SD (13.1 dB/m²) was significantly lower to median CAP SD (28.4 dB/m²) (p < 0.0001). The median reduction in IEMV was 50% (Fig). The average bias between the CAP and CAPc was 7.9 dB/m. The CC and AA-ICC were 61% and 22%, respectively. The median CAPc SD (13.1 dB/m²) was significantly lower to median CAP SD (28.4 dB/m²) (p < 0.0001). The average bias between the CAP and CAPc was 7.9 dB/m. The CC and AA-ICC were 61% and 22%, respectively. The median reduction in IEMV was 50% (Fig). The average bias between the CAP and CAPc was 7.9 dB/m. The CC and AA-ICC were 61% and 22%, respectively. The median reduction in IEMV was 50% (Fig). The average bias between the CAP and CAPc was 7.9 dB/m. The CC and AA-ICC were 61% and 22%, respectively. The median reduction in IEMV was 50% (Fig). The average bias between the CAP and CAPc was 7.9 dB/m. The CC and AA-ICC were 61% and 22%, respectively. The median reduction in IEMV was 50% (Fig). The average bias between the CAP and CAPc was 7.9 dB/m. The CC and AA-ICC were 61% and 22%, respectively. The median reduction in IEMV was 50% (Fig). The average bias between the CAP and CAPc was 7.9 dB/m. The CC and AA-ICC were 61% and 22%, respectively. The median reduction in IEMV was 50% (Fig). The average bias between the CAP and CAPc was 7.9 dB/m. The CC and AA-ICC were 61% and 22%, respectively. The median reduction in IEMV was 50% (Fig). The average bias between the CAP and CAPc was 7.9 dB/m. The CC and AA-ICC were 61% and 22%, respectively. The median reduction in IEMV was 50% (Fig).

Conclusion: By using the continuous method, the intra-examination measurement variability of the CAP is decreased with a factor 2, keeping the global performance of the CAP algorithm. Furthermore, the results of CAP and CAPc examinations are strongly correlated and in agreement. Performances of CAP and CAPc are good for S >0 and S >1.

A novel non-invasive index for the prediction of liver fibrosis in chronic hepatitis B patients with concurrent nonalcoholic fatty liver disease

Jian Wang1, Jiacheng Liu2, Yiguang Li2, Li Zhu3, Minxin Mao2, Weimao Ding2, Yuanwang Qui2, Chuanwu Zhu4, Jie Li2, Rui Huang1, Chao Wu1, Nanjing Drum Tower Hospital, The Affiliated Hospital of Nanjing University Medical School, Department of Infectious Diseases, Nanjing, China; 2Nanjing Drum Tower Hospital Clinical College of Traditional Chinese and Western Medicine, Nanjing University of Chinese Medicine, Department of Infectious Diseases, Nanjing, China; 3The Fifth People’s Hospital of Wuxi, Department of Infectious Diseases, Wuxi, China; 4The Affiliated Infectious Diseases Hospital of Soochow University, Department of Infectious Diseases, Suzhou, China; 5Huai’an No. 4 People’s Hospital, Department of Hepatology, Huai’an, China

Email: dr.wu@nju.edu.cn

Background and aims: Few accurate non-invasive indexes are available to evaluate liver fibrosis in chronic hepatitis B (CHB) patients with nonalcoholic fatty liver disease (NAFLD). We aimed to establish a predictive index for advanced fibrosis in CHB patients with NAFLD.

Method: A total of 267 treatment-naïve CHB patients with NAFLD underwent liver biopsy were enrolled from four hospitals and randomly divided into a derivation set (n = 134) and a validation set (n = 133). Receiver operating characteristic (ROC) curve was used to compare predicting accuracy of different indexes.

Results: In the derivation set, alanine aminotransferase, aspartate aminotransferase (AST), prothrombin time, presence of hypertension, and type 2 diabetes were significantly associated with advanced fibrosis (≥S3). Based on these parameters, a novel index namely AAPHD for predicting advanced fibrosis was developed. The areas under the ROC curves (AUROCs) of AAPHD index in predicting advanced fibrosis was 0.88 (95%CI:0.82–0.94). The optimal cut-off value of AAPHD was ~2.870, with a sensitivity of 72.73% and a specificity of 90.10%. The predicting accuracy of AAPHD for advanced fibrosis was significantly superior to AST-to-platelet ratio index (APRI) (AUROC = 0.70), fibrosis-4 score (FIB-4) (AUROC = 0.69), and NAFLD fibrosis score (NFS) (AUROC = 0.68). In the validation set, the AUROCs of AAPHD (AUROC = 0.88) remains significantly higher than that of FIB-4 and NFS, while it was comparable with APRI for predicting advanced fibrosis.

Figure: Receiver operating characteristic (ROC) curves of non-invasive tests for predicting advanced liver fibrosis in derivation set (A) and validation set (B).

AAPHD = −17.102 + 1.706 × hypertension (yes = 1, no = 0) + 1.974 × diabetes (yes = 1, no = 0) + 0.041 × AST (UL) + 0.965 × PT (s) - 0.064 × ALT (UL)
Conclusion: AAPHD is a promising non-invasive index for predicting advanced fibrosis with high accuracy in CHB patients with NAFLD. The application of AAPHD may reduce the necessary for liver biopsy in CHB patients with NAFLD.

FRI230
Comparison between two 2D-SWE techniques using transient elastography as a reference method for liver stiffness assessment
Alina Popescu1,2, Camelia Foncea1,2, Raluca Lupusoru1,2,3, Roxana SirilT2, Felix Bende1,2, Alexandru Popa1,2, Victor Baldea1,2, Radu Cotrua1,2, Fasuc Arianal1,2, Ioan Sporea1,2. 1Department of Gastroenterology and Hepatology, Department of Internal Medicine II, “Victor Babes” University of Medicine and Pharmacy Timisoara, Romania; 2Center for Advanced Research in Gastroenterology and Hepatology “Victor Babes” University of Medicine and Pharmacy Timisoara, Romania; 3Center for Advanced Hepatology Research of the Academy of Medical Sciences, Timisoara; 4Center for Modeling Biological Systems and Data Analysis, Department of Functional Sciences, “Victor Babes” University of Medicine and Pharmacy Timisoara, Romania
Email: foncea.camelia@gmail.com

Background and aims: Ultrasound-based liver elastography techniques are non-invasive methods used for the assessment of liver stiffness (LS). In addition to Transient Elastography (TE), new methods were developed. To compare the performance of 2D-SWE technique implemented on two different ultrasound probes from different vendors for the assessment of liver stiffness measurements (LSM) using transient elastography (TE) as reference method.

Method: A prospective study was conducted in which LSM were performed in 201 consecutive patients with or without chronic liver disease, evaluated in the same session by 2D-SWE and TE implemented on the following systems: Siemens ACUSON Sequoia (SC-1 convex transducer and Deep Abdominal Transducer–DAX), Aixplorer Mach 30 (C2-1X convex transducer) and FibroScan Compact M 530 (M and XL probes). Reliable measurements were defined as the median value of 10 measurements and an IQR/M < 0.3. For significant fibrosis a cut-off value for TE of 7 kPa was used, for advanced fibrosis 9.5 kPa and for liver cirrhosis 12 kPa.

Results: From 201 patients, 198 patients had reliable measurements in all techniques and were included in the final analysis, mean age 54.8 ± 13.3 years, mean BMI 28.8 ± 5.0, 58% (116/198) men. 58.5% had advanced fibrosis and 21.2% had liver cirrhosis. For significant fibrosis the performance was slightly better for 2D-SWE.SSI (AUROC = 0.89, p < 0.0001, >7.3 kPa, Se = 85.1%, Sp = 87.9%) followed by 2D-SWE.5C1 (AUROC = 0.79, p < 0.0001, >6.9 kPa, Se = 33.7%, Sp = 96.7%) and 2D-SWE.DAX (AUROC = 0.78, p < 0.0001, >6.3 kPa, Se = 36.4%, Sp = 96.7%), p = 0.01. For advanced fibrosis the best performance was slightly better by 2D-SWE.SSI (AUROC = 0.92, p < 0.0001, >8.8 kPa, Se = 92.5%, Sp = 91.9%), and by 2D-SWE.DAX (AUROC = 0.86, p < 0.0001, >7.6 kPa, Se = 38.8%, Sp = 99.3%), followed by 2D-SWE.5C1 (AUROC = 0.84, p < 0.0001, >8.6 kPa, Se = 38.8%, Sp = 95.5%), p = 0.02. For liver cirrhosis the performances were similar: 2D-SWE.SSI (AUROC = 0.91, p < 0.0001, >10.3 kPa, Se = 92.8%, Sp = 90.3%), followed by 2D-SWE.DAX (AUROC = 0.90, p < 0.0001, >10 kPa, Se = 93.8%, Sp = 98.7%) and 2D-SWE.5C1 (AUROC = 0.84, p < 0.0001, >9.9 kPa, Se = 93.3%, Sp = 96.7%), p = 0.10. The cut off values for predicting different stages of fibrosis ranged from 6.3–7.3 kPa for F2, 7.6–8.8 kPa for F3 and 9.9–10.3 for F4.

Conclusion: The performance of the evaluated 2D SWE techniques for liver stiffness assessment was similar.
Conclusion: In patients with acute liver failure syndromes, shear wave elastography can help in the early clinical assessment at admission in intensive care. Plasma vWF is highly correlated RLSM and it can be speculated that the presence of platelets aggregates can be responsible of the increased values. Moreover histological analysis showed high degree of intrahepatic cholestasis in ACLF. Further studies are needed to definitely explain the high level of stiffness reported in these patients.

FRZ232
A novel simple and reliable 2D-shear wave elastography (SWE) and ultrasound-guided coefficient attenuation parameter (SCAP) technique for patients with chronic liver disease
Christiane Stern1, An Ngo2, Cristiane Villela-Nogueira3, Dominique Thabut1, Vlad Ratziu1. 1Hôpital Pitié-Salpêtrière, Service d’Hépato-gastroentérologie, Paris, France; 2Hôpital Pitié-Salpêtrière, Service d’Hépato-gastroentérologie, Paris, France; 3Federal University of Rio de Janeiro, Serviço de Hepatologia, Rio de Janeiro, RJ, Brazil
Email: christiane.stern@gmail.com

Background and aims: Different non-invasive methods are now widely used for first line assessment of liver fibrosis and steatosis in patients with chronic liver disease. The detection of advanced fibrosis using 2D-shear wave elastography (SWE) and significant steatosis using ultraSound-guided CAP (SCAP) measured by Aixplorer MACH 30 (SS) is simple, safe and overcomes several limitations of transient elastography (TE) and CAP measured by FibroScan (FS). Nevertheless, reliability criteria have not been well described for SS. The aims of this study were to define the optimal technical procedure, the performance for the detection of fibrosis and steatosis and the reliability criteria using SS.

Method: 215 consecutive patients with chronic liver disease that underwent non-invasive tests were included. Clinical, biological and histological data within 6 months were collected. TE and CAP were performed by 2 experienced operators using the classical technique of 10 measurements at the midaxillary line. Measurements of SWE and SCAP were performed in triplicate at the mid (MAL), posterior (PAL) and anterior axillary lines (AAL) (total of 9 values). The technique the simplest to perform and most reliable has been analyzed. Performances of SWE and SCAP for the diagnosis of advanced fibrosis and significant steatosis have been defined using TE (≥9.5 kPa) and CAP (≥275 dB/m) as reference. Factors associated with discordance have been evaluated.

Results: FS and SS data from 203 patients were analyzed (12 patients excluded due to FS and/or SS failure). Baseline characteristics: mean age 56 ± 14 years; male 58%; MAFLD 59%, viral hepatitis 24%; mean BMI 28.3 ± 5.9 kg/m². Median TE and CAP were 6.5 kPa (2.5–66.9) and 272 dB/m (141–400). Table 1 shows the performances of SCAP according to different technique methods. The median of 3 SWE values and 3 SCAP values (1st measurement at MAL, PAL and AAL) had an AUROC of 0.96 [CI95%: 0.93–0.98] and 0.91 [CI95%: 0.86–0.95] for the diagnosis of advanced fibrosis and significant steatosis, and considered as the best technique. The accuracy of cut-off values for SWE (≥8.5 kPa) and SCAP (≥0.44) were analyzed in 54 patients with liver biopsy. There was only 1 false-negative for fibrosis (PPV = 50%, NPV = 97%) and 2 false-negatives for steatosis (PPV = 69%, NPV = 87%). The factors associated with discordance were skin-to-liver distance (SLD) ≥2.4 cm (p < 0.001), depth ≥5.5 cm (p < 0.001), stability index <70% (p = 0.009) and viscosity ≥2.4 (p = 0.026). In logistic regression, the only factor associated with discordance was SLD (p = 0.012).

Conclusion: A quick and reliable non-invasive diagnosis of advanced fibrosis and significant steatosis can be obtained with the median of 3 measurements (1 mid, 1 posterior and 1 anterior axillary line) using SS. The only non-reliable criterion is skin-to-liver distance ≥2.4 cm.
Abstract withdrawn

FRI234
Dynamics of liver stiffness predicts hepatocellular carcinoma and ascites occurrence in patients with hepatitis C virus related cirrhosis treated with direct-acting antiviral agents
Alberto Nicoletti1, Maria Elena Ainora1, Marco Cintoni2, Matteo Garcovich1, Martina De Siena1, Barbara Funaro1, Francesca Ponziani1, Antonio Grieco3, Laura Riccardi1, Maurizio Pompili1, Antonio Gasbarrini1, Maria Assunta Zocco1.
1Fondazione Policlinico Universitario "A. Gemelli" IRCCS, Università Cattolica del Sacro Cuore-Rome, Internal Medicine and Gastroenterology, Rome, Italy; 2Fondazione Policlinico Universitario "A. Gemelli" IRCCS, Università Cattolica del Sacro Cuore-Rome, Clinical Nutrition, Rome, Italy; 3Fondazione Policlinico Universitario "A. Gemelli" IRCCS, Università Cattolica del Sacro Cuore-Rome, Internal Medicine and Liver Transplant, Rome, Italy
Email: mariaazocco@hotmail.com

Background and aims: The achievement of a sustained virologic response (SVR) with direct-acting antivirals (DAAs) has been shown to prevent liver-related events (LREs) in patients with chronic hepatitis C virus (HCV)-related cirrhosis. Bidimensional shear wave elastography (2D-SWE) is an effective and easy to perform technique for the early assessment of liver fibrosis during DAA treatment. The main aim of the study was to evaluate changes in liver stiffness (LS) using 2D-SWE in patients with HCV-related cirrhosis undergoing DAA therapy. Secondary endpoint was to identify any correlation between LS, ultrasound and clinical parameters that predict the occurrence of LREs.

Method: We enrolled 229 consecutive patients who received DAAs based regimens for HCV-related cirrhosis between December 2014 and September 2016. Standard ultrasound, 2D-SWE measured LS, and clinical and laboratory data were assessed before treatment (baseline), 24 weeks after end of treatment (EOT) (T1) and 48 weeks after EOT (T2). Patients were followed up every 6 months according to international clinical practice guidelines. Any LRE was registered during follow-up. Uni- and multi-variate Cox regression analysis was performed to determine parameters associated with the development of LREs.

Results: At baseline, mean LS was 18.1 ± 6.6 kPa. Levels of LS decreased to a mean of 13.6 ± 6.1 kPa and 12.5 ± 6.1 kPa at T1 (p < 0.0001) and T2 (p < 0.0001), respectively. The median follow-up was 3.25 years (range 0.2–4.7). HCC was the most frequent LRE (30 patients, 13.1%), 13 patients (5.7%) developed ascites, 11 (4.8%) portal vein thrombosis (PVT), 8 (3.5%) hepatic encephalopathy (HE), 8 (3.5%) infections and 5 (2.2%) variceal bleeding. 9 patients died (3.9%) and 5 were transplanted (2.2%).

Male gender, bilirubin, international normalized ratio (INR), Model for End-stage Liver Disease (MELD) score, prior history of harmful alcohol intake, LS, portal velocity and a change in LS less than 20% at T2 (1-y Delta-LSM) were associated with HCC occurrence by univariate analysis. By Cox regression multivariate analysis, only MELD score (HR 1.16; CI 95% 1.01–1.33; p = 0.026) and 1-year Delta LSM <20% (HR 2.98; CI 95% 1.01–8.1; p = 0.03) were independently associated with HCC risk. Interestingly, 1-year Delta LSM <20% was independently associated with the development of ascites with significant hazard ratio (HR 5.08; CI 95% 1.03–25.14; p = 0.04).

Since the variables maintained their predictive value over time, we combined their HR in a simple model to estimate the probability of HCC occurrence at 24, 36, 48 and 60 months after EOT.

Conclusion: Alone and in association with clinical and biochemical variables, dynamic changes of 2D-SWE-measured LS after DAA therapy for HCV may be a useful tool to predict HCC and ascites occurrence in cirrhotic patients.

FRI235
The concordance within one blood test improves reliability evaluation of liver fibrosis
Paul Cales1, Clémence M. Canivet1, Lannes Adrien1, Frédéric Oberti1, Isabelle Fouchard1, Jerome Boursier1. 1Angers University Hospital, Hepatology, Angers, France
Email: paul.cales@univ-angers.fr

Background and aims: The improved reliability of non-invasive tests of liver fibrosis is defined by agreement between a patented blood test and liver stiffness measurement (LSM) by transient elastography (TE) in 2021 EASL guidelines. The inconvenience is to require two different tests adding cost and reducing availability. Our aim was to apply this agreement rule to a single blood test targeted either for significant fibrosis (FibroMeterV2G: FM2G) or cirrhosis (CirrhoMeterV2G: CM2G) using the same markers.

Conclusion: Alone and in association with clinical and biochemical variables, dynamic changes of 2D-SWE-measured LS after DAA therapy for HCV may be a useful tool to predict HCC and ascites occurrence in cirrhotic patients.

Figure: Predictive model for HCC occurrence.

Abstract withdrawn
POSTER PRESENTATIONS

Method: Patients with chronic liver disease of multiple untreated etiologies, with liver biopsy using Metavir F within 6 months of blood test, were included in a derivation (n = 2159) and a validation (n = 1476 with LSM by TE) sets. Agreement grade was calculated as the absolute difference (AD) between fibrosis (FM) classifications of FM2G and CM2G. The main outcome was severe fibrosis (Metavir F ≥ 3). Outcome measures were AUROC and accuracy (correct diagnosis).

Results: In the derivation set, FM2G accuracy (and prevalences) were according to agreement grade: high (FM AD ≤ 0.5): 83.1% (78.6%), fair (FM AD = 1): 70.2% (16.3%), poor (FM AD >1): 50.0% (5.1%), p < 0.001. CM2G accuracy was, respectively 83.1%, 67.6%, 50.9% (p < 0.001). Then, agreement was classified as concordant or not for Metavir F ≥ 3. FM2G accuracy (and prevalences) were, concordant: 83.9% (85.9%), discordant: 51.3% (14.1%), p < 0.001. FM2G AUROC were, respectively: 0.866 and 0.519, p < 0.001. The overall accuracy of FM2G (79.3%) and CM2G (79.0%) were not different (p = 0.688) but they were complementary (kappa: 0.573). So, a CM/FM algorithm was constructed. Its accuracy was significantly increased to 82.2% (p < 0.001) vs FM2G or CM2G and different between concordant (85.1%) and discordant (64.1%, p < 0.001) blood tests. In the validation set, previous results were confirmed, e.g. CM/FM accuracy was, concordant blood tests: 79.9%, discordant: 60.5% (p < 0.001). The concordance prevalence was higher for FM2G vs CM2G (84.9%) than vs LSM (70.9%, p < 0.001). Accuracy was globally, LSM: 78.8% vs CM/FM: 77.0% (p = 0.173) or FM2G: 75.5% (p = 0.011) but in the 70.9% of concordant FM2G/LSM it was, respectively: 88.0% vs 87.4% (p = 0.210) or 88.0% (p = 1). The accuracy in discordant tests was however higher in FM2G agreement vs LSM than vs CM2G, e.g. CM/FM: 88.0% vs 79.9% (p < 0.001).

Conclusion: The concordance within a blood test significantly increased the concordance prevalence. The limit was a reduced accuracy; the advantages were a reduced cost and liver biopsy recourse by half, and a simpler use (single time and greater ubiquity).

FR1236
Novel and accurate measurement of differential protease activity in diagnosed HCC patients compared to non-HCC cirrhotic patients

Amit Singal1, Tram Tran2, Ben Holmes2, Chris Gulk2, Anatóly Myaskovsky2, Andrea Shepard 2, Mackenzie Rowe2, Sophie Cazanave2, Facyal Touti2, Jina Lee2, Alejandro Balbin2, Wendy Winckler2, ‘UT Southwestern Medical Center, Department of Internal Medicine, Dallas, United States; 2Glympse Bio, Cambridge, United States

Background and aims: The incidence of hepatocellular carcinoma (HCC) is rising worldwide and projected to continue increasing through 2030. HCC surveillance using ultrasound with or without AFP has suboptimal sensitivity, missing over one-third of HCC at an early stage. We previously showed a panel of biosensors that interrogate biological pathways implicated in HCC pathogenesis (tumor invasion of extracellular matrix, matrix remodeling, inflammation, and fibrogenesis) was highly effective at differentiating patients with HCC from healthy controls, with AUCs >0.94. The aim of this study was to assess accuracy of protease biosensor biomarker panel to distinguish patients with HCC from those with cirrhosis without HCC.

Method: Retrospective plasma samples were obtained from patients diagnosed with HCC (cases) and those with cirrhosis without HCC (controls). Protease biosensor cleavage was assayed from plasma by fluorimetry. The relative signal was used for classification by regularized logistic regression using 100 cross-validation (80% train, 20% validation splits). The maximum point from the Youden’s J index in the training set was used to define the optimal cut-off, which was used to calculate sensitivity and specificity for HCC detection in the validation sets.

Results: Plasma protease activity was assessed in 43 HCC cases (65% male, mean age 58 years, 45% HBV/7% HCV/44% unknown etiology) and 26 cirrhosis controls (30% male, mean age 57 years, 100% NASH etiology). Nearly three-fourths (72%) of the cases had early-stage tumors (TNM stage I or II). The most significant biosensors in the classification of HCC vs cirrhosis were substrates of MMPs, DPP4, ANPEP, ARTS-1, KLK14 and Cathepsins (L, S, K, B) and ADAM17. The panel of protease biosensors had high accuracy for differentiating patients with HCC vs those with cirrhosis (AUC = 0.93 [CI 0.86–0.98]) (Figure). Using the Youden’s cut-off, sensitivity and specificity of the protease biosensor panel for HCC detection were 0.84 and 0.85, respectively.

Conclusion: Novel non-invasive biosensors measuring protease activity accurately differentiate HCC from cirrhosis and, if validated in larger biomarker studies, may serve as an alternative surveillance tool to improve early HCC detection.

FR1237
FIB-4 predicts severe hematological toxicity and 6-month mortality in older patients with cancer: ELCAPA-LIVER

Victoire De Salins1, Antoine Morel2, Claudia Martinez-Tapia2, Pierre-Emmanuel Rautou2, Florence Canoui-Poitrine2, Elena Paillaud4, Johanne Poisson3, 1AP-HP, Service de Gériatrie, Hôpital Européen George Pompidou, Paris, France; 2University Paris Est Creteil, INSERM, IRMB, F-94010 Créteil, France, Clinical Epidemiology and Ageing Unit, Institute Mondor de Recherche Biomédicale, Paris-East University, F-94000 Créteil, France; 3Université Paris–Cité, AP-HP, Hôpital Beaujon, Service d’Hépatologie, DMU DIGEST, Centre de Référence des Maladies Vasculaires du Foie, FILIOFIE, ERN RARE-LIVER, Centre de recherche sur l’inflammation, Inserm, UMR 1149, Paris, France; 4Université Paris–Cité, AP-HP, Service de Gériatrie, Hôpital Européen George Pompidou, Paris, France, Clinical Epidemiology and Ageing Unit, Institute Mondor de Recherche Biomédicale, Paris-East University, F-94000 Créteil, France; 5Université Paris–Cité, AP-HP, Service de Gériatrie, Hôpital Européen George Pompidou, Centre de recherche sur l’inflammation, Inserm, UMR 1149, Paris, France, France

Background and aims: The current increased life expectancy is associated with an increasing incidence of cancer in older patients. Geriatric assessment has improved the management of this heterogeneous population with thorough evaluation of physiologic systems

Conclusion: Novel non-invasive biosensors measuring protease activity accurately differentiate HCC from cirrhosis and, if validated in larger biomarker studies, may serve as an alternative surveillance tool to improve early HCC detection.
Reactive Protein (aHR = 1.55 (1.10–3.22), p = 0.02).

In addition, a FIB-4 index >2.67 was predictive for 6-month mortality independently of cancer site, metastasis, chronic heart failure, and C-Reactive Protein (aHR = 1.55 (1.10–2.20), p = 0.028).

Conclusion: A FIB-4 index >2.67 was an independent predictor for 6-month mortality and severe hematologic toxicity in older patients treated for cancer. This shows the importance of evaluating liver status to improve decision making in older patients with cancer.

Background and aims: Weight gain after liver transplantation (LTX) is common, contributing to the development of new-onset obesity at 2- and 3-years post-LTx in 22% and 38% of patients. These significant weight gains prompt the question of how patients cope with this increase of weight. Unfortunately, few studies examined the patients’ perspective. This study aimed to explore how patients’ experienced their weight gain after LTx.

Method: Individual interviews followed a guideline with open-ended questions. Transcripts were analyzed according to the six phases of the reflexive thematic analysis approach by Braun and Clarke.

Results: The 12 participants gained 11.5 kg weight (median) over a median of 23 months after LTx. The constitutive theme “The main thing is to be alive” was a recurrent insight, captured in different facets in all three consecutive themes: “The arduous path back to living” was the emotional facet, expressing the ups and downs during the suffering from a life-threatening illness to finally being grateful for the new life. “A pleasurable new phase of life” was the legitimization, reflecting the appreciation of gaining weight and returning to a healthy appearance after having overcome the illness. “I am allowed to look like this now” was the consoling facet of the suffering from a life-threatening illness to finally being grateful for the new life. I am allowed to look like this now was the emotional facet, expressing the ups and downs during the suffering from a life-threatening illness to finally being grateful for the new life. I am allowed to look like this now was the consoling facet, expressing the ups and downs during the suffering from a life-threatening illness to finally being grateful for the new life. I am allowed to look like this now was the consoling facet, expressing the ups and downs during the suffering from a life-threatening illness to finally being grateful for the new life.

Conclusion: Understanding the patients’ dynamic lived experiences, beliefs and motivations on post-LTx weight gain is crucial in providing tailored care. Interventions should be offered early because the comforting insight “I am allowed to look like this now” may hinder the patient’s motivation to further engage in weight loss interventions. Our suggestions on time and content of education and self-management support, based on the transteoretical model, may guide professionals’ clinical practice.
Development of a nurse led hepatology ambulatory review service

Victoria Wharton, Bryony Butler. John Radcliffe Hospital, Hepatology, Oxford, United Kingdom
Email: victoria.wharton@ouh.nhs.uk

Background and aims: The Liver Unit in Oxford was significantly impacted by COVID-19-highlighting a need for a nurse-led Hepatology ambulatory review service to help minimise inpatient admissions and assess patients with newly diagnosed decompensated liver disease. The Hepatology DCU were providing a nurse led abdominal paracentesis clinic and between appointments the team were able to accommodate clinical reviews. The aims for this service were to reduce Emergency Department (ED) and hospital admissions, facilitate safe and early discharges, expedite care for long term management plans and to allow a single point of access for patients and their families.

Method: Since its creation, the two founding Clinical Nurse Specialists (CNS) have collated key metrics pertaining to the patients treated by the service. These metrics included the route of referral, hospital details, date of referral, the reason for referral and whether they needed a hospital admission. Using this dataset, the effectiveness of the service has been critically assessed.

Results: Between April 2020–September 2021 the Hepatology DCU reviewed a total of 407 patients. 210 patients were seen from April 2021–September 2021; a monthly average increase of 118%, when compared to the previous year. Not included in these figures, were patients reviewed by the hepatology medical team in ED and medical/surgical ambulatory units. Of the 210 patients reviewed in DCU since April 2021, 76 patients were hepatology ward discharges reviewed by either CNS, hepatology specialist registrar or a consultant within 7–10 days of discharge. Furthermore, since starting the service just 3.9% of patients required admission from daycase. 224 (55%) of the patients seen in the ambulatory review service just 3.9% of patients required admission from daycase. 224 (55%) of the patients seen in the ambulatory review service since April 2020 were for ascites/oedema review ± diuretic management. The ambulatory reviews are in addition to the patients’ routine follow up appointments-aiding close management of their liver disease and expedition of the relevant investigations required for their long-term management, resulting in early interventions. Following completion of an Independent and Supplementary Prescribing module by the CNS, the ambulatory review service became nurse-led in September 2020.

Conclusion: Although the service is in its infancy, the number of patients reviewed has doubled since starting the hepatology ambulatory review service in April 2020. This has freed up outpatient clinic capacity and prevented delays to assessments. The Hepatology DCU currently provides a five-day service to help reduce ED attendances and reduce inpatient admissions; it is staffed by two full time band 7 CNS.

Conclusion: The number of patients requiring admission to hospital for a paracentesis has reduced by 65% since founding a nurse-led daycase paracentesis service. The nurse-led abdominal paracentesis clinic has reduced the number of patients attending ED for ascites management alone and has provided patients with a single point of contact for managing their ascites requiring paracentesis.

FRI240
Development of a nurse led daycase abdominal paracentesis service

Victoria Wharton, Bryony Butler. John Radcliffe Hospital, Hepatology, Oxford, United Kingdom
Email: victoria.wharton@ouh.nhs.uk

Background and aims: Patients living with advanced liver disease often require symptomatic management of ascites with abdominal paracentesis. At Oxford University Hospitals Trust, there was previously no routine care pathway to manage the accumulation of ascites. Instead, patients would frequently present to the emergency department (ED) or to their GP in discomfort and then require emergency admission to the hepatology ward for paracentesis. This resulted in delayed care and often a lengthy hospital admission. A need was identified to provide a nurse-led, daycase paracentesis service for these patients. The aim of this service was to improve patient experience, reduce ED attendances and inpatient admissions, standardise care across the trust and build effective relationships with patients and their families.

Method: The Hepatology Day Case Paracentesis service commenced in October 2018. Initially, clinics occurred once a week, a maximum of four patients were reviewed and paracentesis was performed by a ward-based doctor. However, due to inpatient ward pressures, patients would often experience lengthy delays, when waiting for the doctor to insert their drains. This led to the development of a fully nurse delivered service. To facilitate its creation, a training programme was developed for the Clinical Nurse Specialists, in addition to postgraduate study. A 5-year dataset on patients presenting to ED with ascites (provided by clinical coders) was used to critically assess the effectiveness of the nurse-led daycase paracentesis service.

Results: Since the introduction of a fully nurse-led daycase paracentesis service in January 2020, we have performed 399 ultrasound guided paracentesis in 61 patients up to and including October 2021. Between April 2016–March 2021 a total of 124 patients presented to ED with ascites; 104 of which required an inpatient admission and 65 had a paracentesis. Furthermore, the number of patients needing admission specifically for a paracentesis fell from 20 in 2016–2017 to 7 in 2020–2021. Whilst the number of patients attending ED and requiring admission does not appear to have reduced, the number of patients admitted for paracentesis has reduced significantly.
FRI241
Implementing a cirrhosis order set: a qualitative analysis of provider-identified barriers and facilitators
Ashley Hyde1, Emily Johnson1, Michelle Carbonneau2, Dawn Schroeder2, Thea Luigi1, Denise Campbell-Scherer1, Puneeta Tandon1. 1University of Alberta Faculty of Medicine and Dentistry, Edmonton, Canada; 2Alberta Health Services, Edmonton, Canada.

Background and aims: Resulting from vascular and hepatocellular injury, cirrhosis is a chronic condition that results in profound impairments in quality of life, and high rates of morbidity and mortality. Hospitalizations and readmissions become more commonplace as cirrhosis advances, with a 90-day readmission rate of 53% noted in a large North American cohort of over 1000 patients. Cirrhosis Care AB (CCAB) is a pragmatic trial which aims to address current gaps in cirrhosis care in Alberta through the implementation of a standardized order set across multiple acute care sites. Prior to implementation of such a large-scale quality improvement initiative, it is essential to understand the implementation contexts, including perceptions of the proposed intervention, and potential barriers and facilitators to implementation.

Method: We used a qualitative descriptive approach to (i) understand participant’s past experiences with implementation of standardized order sets, (ii) to identify potential barriers and facilitators to implementation of the cirrhosis order set, and (iii) to develop tailored implementation strategies for each study site. We used the Consolidated Framework for Implementation Research (CFIR) and the Normalisation Process Theory (NPT) to guide development of our interview guide and coding framework. We conducted focus groups using a semi-structured interview guide. Focus groups were recorded and transcribed verbatim. A deductive content analysis approach using the core constructs of CFIR and NPT was used.

Results: We conducted a total of 8 focus groups, that were attended by 54 healthcare providers. Of the attendees, 20% were prescribers (MDs & NPs), with the remainder comprised of nurses, social workers, pharmacists, and physiotherapists. Barriers to implementation of the cirrhosis order set included the significant investment of time and resources required, the “change fatigue” of providers, and poor communication across provider groups. Facilitators included a recognized advantage of the efficiencies offered by the cirrhosis order set, the strength of the evidence on which the order set was based, leadership support of the initiative, and recognition of the need to improve care for patients with cirrhosis.

Conclusion: The findings of this study suggest that healthcare provider’s perceptions of the cirrhosis order set were greatly influenced by their past experiences with the implementation of other quality improvement initiatives. Crucial to the success of the cirrhosis order set will be the use of tailored implementation strategies to promote uptake including: (i) the identification of site champions, (ii) use of implementation meetings to share learnings across study sites, and (iii) leveraging the facilitators including highlighting efficiencies in work processes that can be made possible by the cirrhosis order set.

FRI242
Quality of life in patients with advanced cirrhosis. Relationship with the development of complications
Ana Belen Rubio1,2,3,4, Adria Juañol1,2, Martina Perez1,2, Marta Caro1,2,3,4, Carla Riha1,4,5, Sara Martinez1,2,4, Marta Cervera1,2,3,4, Emma Avitabile1,2, Ann Ma1,2, Laura Napoleone1,2, Octavi Bassegoda1,2, Jordi Gratacós-Gines1,2, Elisa Pose1,2,3, Isabel Graupera1,2,3, Anna Soria1,2, Pere Gines1,2,3,4, Núria Fabrellas1,2,3,4, 1Hospital Clinic, Liver Unit, Barcelona, Spain; 2University of Barcelona, Faculty of Medicine and Health Sciences, Barcelona, Spain; 3Instituto de Investigaciones Biomédicas August Pi i Sunyer (IDIBAPS), Barcelona, Spain; 4Centro de Investigación Biomédica en Red de Enfermedades Hepáticas y Digestivas (CIBERehd), Madrid, Spain; 5Fundació Clinic per la Recerca Biomèdica (FCRB), Barcelona, Spain.

Background and aims: Liver cirrhosis causes an alteration in the Quality of Life (QoL) of patients that is more intense in patients in the decompensated phase. The alteration of QoL affects both the physical and mental dimensions of the patients. It is not known whether the alteration of QoL correlates with a higher risk of developing complications of the disease. To investigate whether the intensity of QoL alteration is associated with a higher risk of developing complications of cirrhosis.

Method: This study was conducted in the cohort of patients of the MACHT study (J Hepatol 2018; PMID: 30138685), a study investigating the effect of midodrine and albumin in patients with decompensated cirrhosis on the liver transplant waiting list. QoL was assessed using the Short Form Health Survey (SF-36) and the Chronic Liver Disease Questionnaire (CLDQ). The relationship between different QoL parameters and the development of complications during follow-up was investigated.

Results: Under baseline conditions the two groups of patients, placebo and treatment, were similar with respect to QoL parameters, and were therefore considered as a single cohort. Of the 159 patients included, 53 (33%) developed complications during follow-up (median 80 days). Patients who developed complications had more marked alterations in CLDQ and most parameters of the physical and mental domains of SF-36 as compared to patients who did not develop complications measured under baseline conditions. The more intense alteration of CLDQ and SF-36 was also associated with a higher risk of developing hepatic encephalopathy during follow-up. In a multivariate analysis, both the mental and physical components of the SF-36 were independent predictive factors of development of hepatic encephalopathy.

Conclusion: In patients with cirrhosis, the QoL parameters are not only useful to assess the degree of the patient’s impairment, but also indicate a higher risk of developing complications, especially hepatic encephalopathy. These parameters provide useful clinical information for clinical practice and should be taken into account in clinical studies evaluating the efficacy of new treatments for the disease.
Effects of the COVID-19 pandemic on the activity of an advanced practice nurse clinic on liver cirrhosis

Martina Perez1,2,3, Ann Ma1,3,4, Marta Cervera1,2,3,4, Marta Carol1,2,3,4, Ana Belen Rubio1,3,4, Sara Martinez1,3,4, Carlota Riba1,3,4, Laura Napoleone1,3,4, Jordi Gratacos-Gines1,3,4, Anna Soria1,3, Emma Avitabile1,3,4, Octavi Bassegoda1,3,4, Adria Juanola1,3,4, Elisa Pose1,3,4, Isabel Graupera1,3,4, Pere Gines1,2,3,4, Núria Fabrellas1,2,3,4, Hospital Clínico de Barcelona, Liver Unit, Barcelona, Spain; 2Facultat de Medicina-Universitat de Barcelona, Barcelona, Spain; 3Centro de Investigación Biomédica en Red de Enfermedades Hepáticas y Digestivas (CIBERehd), Barcelona, Spain; 4Institut d’Investigacions Biomèdiques August Pi i Sunyer (IDIBAPS), Barcelona, Spain.

Background and aims: Liver cirrhosis is associated with significant morbidity and mortality and is, in addition, responsible for a high number of hospitalizations, which represent a high burden for health systems. As the disease progresses, serious complications can occur, such as ascites, gastrointestinal bleeding, encephalopathy and jaundice, marking the transition to the decompensated phase. Due to the high progression rate of the disease, these complications tend to recur over time. The role of the nurse is increasingly recognized as instrumental in the management of patients with chronic liver disease, with positive impacts noted on patient education, patient independence and early detection of complications. Nevertheless, patient care was severely impacted in the year 2020 by the COVID-19 pandemic, profoundly changing the internal organisation of hospitals and the type of care we have been able to offer to patients. Therefore, the aim of this study was to evaluate the evolution of the activity of the advanced practice nurse clinic in liver cirrhosis, taking into account its recent implementation and the COVID-19 pandemic.

Method: We performed a retrospective observational descriptive study, analyzing the activity of the liver cirrhosis outpatient nurse clinic of the Hepatology Department of the Hospital Clinic in Barcelona. We included all patients visited by the specialized hepatology nurse over a period of 2.5 years, from 01/03/2019 to 31/08/2021. The data were analyzed considering five periods, each lasting 6 months. The first corresponds to the beginning of the pandemic, the fourth and fifth correspond to the consecutive months until August 2021. The second and third periods correspond to the consecutive months until December 2020. The fifth period is from January to August 2021. The second, third and fifth periods correspond to the months of the COVID-19 pandemic.

Results: A total of 2398 visits were completed, 1772 (73.8%) by telephone and 626 (26.1%) in person. During the third period (01/03/2020–31/08/2020), face-to-face visits decreased by 30% compared to previous periods, while telephone visits increased by 50%. There was an 8-fold increase in the total number of visits in the last period compared to the first. This increase is due to an increase in telephone visits, a trend that was probably precipitated by the the COVID-19 pandemic, but that has persisted since.

Conclusion: Despite the restrictions on face-to-face visits during the first months of the COVID-19 pandemic, visits in the advanced practice nurse clinic have continued to increase, and it has been possible to respond to patients’ care needs. The specialized nurse plays a key role in the management of patients with cirrhosis and has been fundamental in responding to their needs particularly in the context of the COVID-19 pandemic.

Stigmatization is common in patients with metabolic associated fatty liver disease and correlates with quality of life

Marta Carol1,2,3,4, Martina Perez1,3,4 Elsa Solà1,2,3,4, Marta Cervera1,2,3,4, Sara Martinez1,2,3,4, Adria Juanola1,2,3, Carlota Riba1,2,3, Ann Ma1,2,3,4, Emma Avitabile1,2,3, Laura Napoleone1,2,3, Elisa Pose1,2,3, Isabel Graupera1,2,3, Maria Honrubia4, Marko Korenjak5, Ferran Torres6,7, Pere Gines1,2,3,4, Núria Fabrellas1,2,3,4, Hospital Clinic de Barcelona, Liver Unit, Barcelona, Spain; 2Centro de Investigación Biomédica en Red de Enfermedades Hepáticas y Digestivas (CIBERehd), Barcelona, Spain; 4Institut d’Investigacions Biomèdiques August Pi i Sunyer (IDIBAPS), Barcelona, Spain.

Background and aims: Stigmatization is a well-documented problem of some diseases. Perceived stigma in alcohol-related liver disease and hepatitis C, but little information exists on stigma in patients with metabolic associated fatty liver disease (MAFLD). Aim of the study was to investigate frequency and characteristics of perceived stigma among patients with MAFLD.

Method: One-hundred and ninety-seven patients seen at the liver clinic were included: a study group of 144 patients with MAFLD, 50 with cirrhosis, and a control group of 53 patients with alcohol-related cirrhosis. Demographic, clinical, and laboratory data were collected.

Quality-of-life was assessed by chronic liver disease questionnaire (CLDQ). Perceived stigma was assessed using a specific questionnaire for patients with liver diseases categorized in 4 domains: stereotypes, discrimination, shame, and social isolation.

Results: Perceived stigma was common in patients with MAFLD (99 patients, 69%) and affected all 4 domains assessed. The frequency was slightly higher, yet not significant, in patients with MAFLD cirrhosis vs those without (72% vs 67%, respectively; p = 0.576). In patients without cirrhosis perceived stigma was unrelated to stage of disease, since frequency was similar in patients with no or mild fibrosis compared to those with moderate/severe fibrosis (66% vs 68%, respectively). Among patients with cirrhosis, stigmatization was more common in alcohol-related vs MAFLD-cirrhosis, yet differences were only significant in two domains. In patients with MAFLD, perceived stigma correlated with poor quality-of-life, but not with demographic or clinical variables.
Conclusion: Perceived stigmatization is common among patients with NAFLD, is associated with impaired quality-of-life, and may be responsible for stereotypes, discrimination, shame, and social isolation, which may affect human and social rights of affected patients.

FRI245
Effect of e-health-based interventions on weight loss in patients with NAFLD: a systematic review and meta-analysis of randomized controlled trials
Ferya Celik1, Merve Yuksel1, Hicran Bektas1
1Akdeniz University, Internal Medicine Nursing, Antalya, Turkey
Email: feryacelik@gmail.com

Background and aims: The only effective treatment is 7%–10% weight loss of non-alcoholic fatty liver disease (NAFLD). Lifestyle changes consisting of diet and physical activity are the cornerstone of weight loss. To synthesize the effect of e-health-based interventions on weight loss in patients with NAFLD.

Design: A systematic review and meta-analysis of randomized controlled trials following Cochrane methods.

Data resources: Systematic searches were conducted in Ovid, Science Direct, Web of Science, CINAHL Complete, PubMed, Cochrane Library, Scopus for studies published in English without year limitations up to January 2022.

Method: The risk of bias in eligible studies was evaluated by two researchers using the Cochrane Collaboration tool. Disagreements were resolved with the third researcher. The meta-analysis data were analyzed using the Comprehensive Meta-Analysis 3 program. PRISMA-2020 was used to report the findings.

Results: Four studies with 253 participants met the inclusion criteria. Lifestyle intervention enabled by e-health-based interventions was dietary and/or physical intervention in all studies. E-health-based interventions were applied by text messages, telephone/video calls, mobile applications. The overall effect of e-health-based interventions on weight loss was statistically significant. E-health-based interventions had a large effect on weight loss in patients with NAFLD (p = 0.03, Hedge’s g = −0.91, 95% confidence interval [CI]−1.75 to −0.07) (Figure 1).

Figure 1: The results of the meta-analysis of the effect of e-health-based interventions on weight loss.

Conclusion: E-health-based interventions had a large effect on weight loss in patients with NAFLD. E-health-based interventions can assist in lifestyle change and weight loss in patients with NAFLD. In this way, liver-related complications can be reduced. Nurses can use affordable, practical and accessible e-health-based interventions to assist with weight loss in patients with NAFLD.

Keywords: e-health-based interventions, liver disease, NAFLD, nursing care, weight loss.

Rare liver diseases (including paediatric and genetic)

FRI246
Role of mutant alpha-1-antitrypsin in determining liver cell fate during embryonic development and in HCC origin
Francesco Annunziata1. 1TIGEM, Translational UNIT, Pozzuoli, Italy
Email: f.annunziata@tigem.it

Background and aims: Alpha1-antitrypsin deficiency (AATD) is the most common genetic cause of liver disease in children. The toxic gain-of-function mutation of alpha-1-antitrypsin (ATZ) leads to its accumulation and retention in the endoplasmic reticulum (ER) of the hepatocytes resulting in liver injury and, later in life, in increased risk of hepatocellular carcinoma (HCC). Preliminary data suggest that ATZ starts to be expressed and accumulated as globules early during embryogenesis. However, it is not known whether ATZ may influence liver cell fate commitment and functionality during development. In addition, it has been speculated that globule-devoid (GD) hepatocytes may have a proliferative advantage over globule-containing (GC) hepatocytes and be responsible for HCC development and progression. However, it is not clear yet which cell has to be considered the cell of origin of HCC in AATD patients. Therefore, our aims are: i) study the effects of ATZ expression and accumulation in liver cells during development and differentiation to evaluate alterations in cellular identity that can be harmful during disease progression; ii) lineage trace liver cholangiocytes/progenitors (C/P) cells and mature hepatocytes to identify the cell of origin of HCC in AATD patients.

Method: To characterize the effects of ATZ expression on pathways demonstrated to be crucial for cell fate commitment, we performed RNA sequencing analysis at several stages over embryonic development on liver from the AATD mouse model (Piz) and wild type (WT) mice. Histological analyses have been performed to confirm alterations in cell fate commitment.

To investigate the cell of origin of the HCC in AATD, we are performing lineage tracing experiments by using C/P- and hepatocyte- specific Cre-recombinase and reporter mouse lines. In addition, to support our in vivo experiments, we are investigating the capacity of both C/P cells and hepatocytes to generate liver organoids.

Results: We observed that pathways involved in cell differentiation/proliferation (e.g., Wnt and Hippo pathways) were altered in Piz compared to WT livers. In addition, immunostainings for C/P- and hepatocyte- specific markers showed hybrid identity of liver cells in Piz at P0. These results suggest that at very early stages during development ATZ accumulation impairs cell differentiation resulting in immature hepatocytes that are not able to play their crucial role in cell metabolism and homeostasis. Interestingly, we observed that Piz derived hepatocytes from adult mice are not able to form cysts/organoids as the WT, while C/P form organoids faster than the WT. These results may suggest that C/P cells and not hepatocytes are involved in liver regeneration and are the cell of origin of HCC in Piz mice.

Conclusion: In summary, our study evaluated the effects of ATZ expression and accumulation in liver cells during embryogenesis and
Background and aims: Timely diagnosis is a critical challenge and crucial to improved survival of biliary atresia (BA) patients. We aim to evaluate accuracy of Matrix Metalloproteinase-7 (MMP-7) protein as a marker for screening BA at 3 days old.

Method: Using dried blood spot screening for neonatal cholestasis patients (DBS-SCReNC), this study had enrolled pediatric patients with definite diagnosis of BA and compared with non-BA children. Children were recruited from September 12, 2018, to May 14, 2021 and followed-up until at least 6-month-old. The study was conducted in a tertiary hospital, National Taiwan University Children Hospital hepatology clinic, general pediatric clinic and well-child clinic. Stored newborn screen dried blood spot (DBS) at 3 day old children enrolled in DBS-SCReNC study were retrieved from newborn screening (NBS) centers in Taiwan. There were 25 BA children and 107 non-BA children. MMP-7 on DBS was quantified in 2021 using a sensitive sandwich enzyme-linked immunosorbent assay.

Results: The age of the 25 children with BA (15 male, 10 female) was 3.3 ± 1.3 years, and age of 107 non-BA children (56 male, 51 female) was 2.2 ± 1.2 years old. Of the non-BA children, 3 children were diagnosed with choledochal cyst, 2 with liver hemangioma, 9 with cholestasis diseases and 93 children visited NTUH due to non-biliary hepatobiliary diseases or for well-child visits. The time of BA patients received Kasai operation was at 43 ± 20 days old. The DBS MMP-7 level of BA children was significantly higher than that of non-BA children (19.2 ± 10.4 vs 5.6 ± 2.7 ng/ml, p < 0.0001). The DBS MMP-7 level showed good diagnostic accuracy with AUC of 93.7% (95% CI, 87.7%–99.7%). MMP-7 cut-off at 7.8 ng/ml has sensitivity of 92.0% (95% CI, 74.0%–99.0%), specificity of 92.5% (95% CI, 85.8%–96.7%), positive predictive value of 71.9% (95% CI, 56.3%–87.5%), negative predictive value of 98.0% (95% CI, 95.3%–100.0%) (p < 0.001).

Conclusion: In this study, DBS MMP-7 is able to distinguish BA from other conditions. This test allows us to screen BA children as early as 3 days old.
Search for biomarkers and prognostic indicators of liver degeneration in glycogen storage disease type Ia

Robert Resaz1,2, Davide Cangelosi3, Daniela Segalerba1, Martina Morini1, Maria Carla Bosco1, Sabrina Paci1, Annalisa Sechi1, Daniela Melis1, Maja Di Rocco1, David Weinstein8, Alessandra Eva1.
1IRCCS Istituto Giannina Gaslini, Laboratory of Molecular Biology, Genoa, Italy, 2Università degli Studi di Pavia, Department of Molecular Medicine, 3IRCCS Istituto Giannina Gaslini, Bioinformatic Unit, Genova, Italy, 4Ospedale San Paolo, Clinical Department of Pediatrics, Milan, Italy, 5Presidio Ospedaliero Universitario di Udine, Regional Coordinating Center for Rare Diseases, 6Università degli Studi di Salerno, Department of Medicine, Surgery and Dentistry “Scuola Medica Salernitana”, Section of Pediatrics, 7IRCCS Istituto Giannina Gaslini, Department of Pediatrics, 8University of Connecticut School of Medicine, Department of Pediatrics, Farmington, United States
Email: roberta.resaz@hsanmartino.it

Background and aims: Glycogen storage disease type Ia (GSDIa) is an inherited metabolic disorder caused by mutations in the enzyme glucose-6-phosphatase-alpha (G6Pase-alpha). Affected individuals develop renal and liver complications, including the development of hepatocellular adenoma/carcinoma and kidney failure. The purpose of this study was to identify potential biomarkers of the evolution of the disease in GSDIa patients. To this end, we analyzed the expression of exosomal microRNAs (Exo-miRs) in the plasma exosomes of 45 patients aged 6 to 63 years. We found that the altered expression of several Exo-miRs correlates with the pathologic state of the patients and might help to monitor the progression of the disease and the development of late GSDIa-associated complications. In addition, the Exo-miRs expression profile obtained from the patients was correlated with the liver-specific Exo-miRs profile obtained from a patient with late GSDIa-associated complications. To this end, we analyzed the expression of exosomal microRNAs (Exo-miRs) in the plasma exosomes of 45 patients aged 6 to 63 years. We found that the altered expression of several Exo-miRs correlates with the pathologic state of the patients and might help to monitor the progression of the disease and the development of late GSDIa-associated complications. In addition, the Exo-miRs expression profile obtained from the patients was correlated with the liver-specific Exo-miRs profile obtained from a mouse model for GSDIa we have generated (LS-G6pc−/−), to derive a common signature that could be specific and prognostic of liver degeneration and connected with biological pathways associated with tumor development and progression.

Method: We analyzed the expression of exosomal microRNAs (Exo-miRs) in the plasma exosomes of 45 patients aged 6 to 63 years. Plasma from age-matched normal individuals were used as controls. microRNAs were purified with exoRNeasy Serum/Plasma Midi kit (Qiagen) from plasma exosomes. TaqMan Array Human microRNA A card (Thermo Fisher Scientific), enabling the quantification of 381 microRNAs each, were used to analyze exosomes-derived microRNA (ExomiR) expression.

Results: We found several deregulated Exo-miRs that correlate with the pathologic state of the liver patients. We identified microRNAs associated with liver disease and metabolic alterations of glucose and lipid pathways. We also found deregulation of microRNAs relevant in liver tumor development and, finally, several microRNAs whose altered expression has been associated with diabetic and chronic kidney diseases. Interestingly, we found that deregulated Exo-miR profiles correlate with the altered proteome profile and the altered Exo-miR profile identified in LS-G6pc−/−. Conclusion: The altered expression of several Exo-miRs correlated with various pathologic liver states associated with the progression of the disease. Thus, our results provide evidence that the Exo-miRs profiles identified may relate to the specific affected organ gene expression and that the long-term consequences of GSDIa can be monitored through Exo-miRs assessment. In conclusion, our results may evolve into protocols to counteract both the progression of liver degeneration leading to HCA and HCC onset as well as kidney disease and failure using circulating microRNAs as biomarkers.
Background and aims: Acute hepatic porphyria (AHP), a group of rare genetic diseases of haem biosynthesis, is characterised by neurovisceral pain attacks. This study evaluated the impact of AHP on patient-reported outcomes (PROs) and disease burden in AHP patients who experience sporadic or recurrent attacks.

Method: Adult patients having >1 AHP attack within the past 2 years or receiving intravenous hemin and/or glucose for attack prevention were recruited from the United States, Italy, Spain, Australia, Mexico, and Brazil and administered an online survey from January 19 to April 26, 2021. Patients taking givosiran were excluded. Descriptive and bivariate analyses were performed to evaluate differences between patients with sporadic attacks (annualised attack rate [AAR], <6 within past 2 years) and recurrent attacks (AAR, ≥6). Attacks included those leading to a hospitalisation, an emergency room visit, an outpatient doctor visit, or self-management. PROs were assessed with the Generalized Anxiety Disorder-7 (GAD-7) scale (0–21) and the Patient Health Questionnaire (PHQ-8) scale (0–24). Burden of chronic symptoms was also reported.

Results: Of the 92 AHP patients who completed the survey, 55 (60%; mean age, 40.3 years) reported sporadic attacks and 37 (40%; mean age, 42.3 years) reported recurrent attacks. Most patients were female (sporadic, 92.7%; recurrent, 86.5%), and the most frequent diagnosis was acute intermittent porphyria (sporadic, 83.6%; recurrent, 59.4%). A majority of patients in the sporadic (52.7%) and recurrent (67.6%) groups reported a PHQ-8 score ≥10, indicating moderate to severe depression; 43.6% and 56.8% of patients in the sporadic and recurrent groups, respectively, reported a GAD-7 score ≥10, indicating moderate to severe anxiety (Figure 1A). Pain was reported as one of the top 3 most burdensome chronic symptoms in the sporadic (50.9%) and recurrent (55.9%) groups (Figure 1B). Of patients reporting their daily activities being limited by severe chronic symptoms, 83.3% of those in the sporadic (Figure 1C) and 90.6% in the recurrent group (Figure 1D) reported muscle weakness as a top 3 symptom having a moderate to severe impact.

Conclusion: While disease burden appeared greater for AHP patients experiencing recurrent attacks, both sporadic and recurrent group patients experienced a substantial impact on physical, mental, and emotional quality of life.
Results: For 198 patients, serial POLCA scores were available. The study group consisted of young (54.8±11.3), mostly female (83%) patients with predominant ADPKD (63%). Median time of follow-up was 48 months. Liver volumetry was available for 96 patients, showing a median hLV of 1967 ml.

There was a significant correlation (Spearman’s rank) between POLCA severity of perceived illness (SPI) score and hLV (r = 0.48; 0.30–0.63). Patients who underwent LT had significantly higher scores on all POLCA subscales and hLV, compared to those not considered to be LT candidates (table 1). SPI score ≥16.5 predicted the need of LT with a sensitivity of 81.3% and a specificity of 88.9%

<table>
<thead>
<tr>
<th>Table: Comparison of POLCA subscales and hLV</th>
</tr>
</thead>
<tbody>
<tr>
<td>POLCA</td>
</tr>
<tr>
<td>-------</td>
</tr>
<tr>
<td>Severity of perceived illness POLCA</td>
</tr>
<tr>
<td>GERD complaints</td>
</tr>
<tr>
<td>Impact on food intake</td>
</tr>
<tr>
<td>Perception of enlarged liver</td>
</tr>
<tr>
<td>hLV (ml)</td>
</tr>
</tbody>
</table>

Longitudinal data showed a significant correlation between the change in SPI score and the change in hLV (r = 0.45; 0.26–0.61) and a significant reduction in hLV (−80 ml) by SA resulted in a decrease in SPI score (−6.0 vs +4.5).

Conclusion: This prospective study confirms the use of the POLCA score as a self-report instrument to assess the severity of PCLD-related symptoms. It is a clear reflection of both evolving symptom severity as well as objective changes in liver volume. Our findings highlight the potential of the POLCA score as a tool for longitudinal follow-up of PCLD patients and as a guide for clinicians when evaluating the need for medical or surgical intervention.

FRI254
Improvements in quality of life in odevixibat responders and nonresponders: an analysis of pooled data from the PEDFIC 1 and PEDFIC 2 studies
Cara L. Mack1, Chad Gwatney2, Quanhong Ni3, Qifeng Yu3, Velichka Valcheva2, Lise Kjems2, Patrick Horn3, Children’s Hospital Colorado, University of Colorado School of Medicine, Aurora, CO, United States; 2VUmc, Amsterdam, Netherlands; 3Albireo Pharma, Boston, MA, United States

Background and aims: Children with progressive familial intrahepatic cholestasis who received odevixibat in the 24-week PEDFIC 1 study had significant reductions vs placebo-treated patients in total serum bile acids (sBAs) and pruritus. Here, we evaluated changes in sBAs and pruritus in patients from PEDFIC 1 categorised by sBA response (R) and by failing in ursodeoxycholic acid (UDCA) use.

Method: Patients eligible for PEDFIC 1 had elevated sBAs and significant pruritus at screening. Concomitant UDCA was allowed provided the patient’s dose was stable. Three categories of patients among those randomised to odevixibat (n = 42) were analysed here: sBA Rs (ie, sBAs reduced ≥70% from baseline [BL] or levels ≤70 μmol/L), sBA partial Rs (PRs [ie, did not meet sBA R criteria but had sBAs reduced ≥30%), and sBA nonresponders (NRs [ie, did not meet either sBA R or PR criteria]). Parameters evaluated included sBA composition (ie, total, primary, and secondary BAs, with UDCA concentration included as secondary BA) as measured by liquid chromatography–tandem mass spectrometry and pruritus as rated by caregivers (range: 0–4; higher scores indicate worse symptoms, with pruritus R defined as a ≥1-point reduction from BL); pruritus outcomes were also compared by whether patients had concomitant UDCA use and/or sBA R.

Conclusion: Odevixibat Rs and, particularly, their families, experienced QoL improvements that were sustained over time; QoL for NRs and their families was largely unchanged with up to 72 weeks of treatment. Further analysis of specific domains within PEDS and Fi that were most highly impacted in Rs is ongoing.
Results: Mean BL total sBAs were higher with vs without UDCA treatment in all 3 sBA R categories (Figure, A), which could be primarily accounted for by UDCA concentrations (66, 116, and 42 μmol/L in sBA Rs, PRs, and NRs, respectively). During odevixibat treatment, sBA Rs (n = 17) had the largest decreases in total and primary sBAs, whereas sBA PRs (n = 7) had intermediate decreases, and sBA NRs (n = 18) had minimal changes. Among all odevixibat-treated patients, sBA Rs experienced greater mean reductions in monthly pruritus scores vs sBA PRs and sBA NRs (Figure, B). sBA PRs who used UDCA had smaller reductions in monthly pruritus score vs those who did not (Figure, B). Among pruritus Rs with UDCA use, the rate of sBA R, PR, and NR was 69%, 0%, and 31%, respectively; among pruritus Rs without UDCA use, these rates were 50%, 25%, and 25%.

Conclusion: UDCA treatment resulted in higher sBAs at BL, but this did not seem to affect sBA R to odevixibat. A sBA PR was not associated with a mean decrease in pruritus with concomitant UDCA use. All sBA R groups included patients for whom pruritus R did not correlate with sBA R.
Conclusion: In patients with PFIC treated with odevixibat assessed to date, growth improved, autotaxin levels decreased, and C4 levels increased over time; changes in hepatic and sleep parameters in some PFIC types were more variable (eg, PFIC3, PFIC6), but these conclusions may be limited by the small size of these subgroups, particularly at later timepoints. Odevixibat was generally well tolerated.

FR1256

Analysis of quality of life, hepatic biochemical markers, and sleep in patients with progressive familial intrahepatic cholestasis who had a pruritus response with odevixibat treatment

Girish Gupte1, Richard J. Thompson2, Lorenzo D’Antiga3, Tassos Grammatikopoulos2,4, Emmanuel González2, Florence Lacaille3, Alain Lachaux4, Bertrand Roquelaure5, Ulrich Baumann6, Elke Lainka7, Ekkehard Sturm8, Eyal Shteyer9, Patrick McKiernan17, Cara L. Mack18, Angelo Di Giorgio19, Qifeng Yu20, Giovanni XXIII, Bergamo, Italy; 4Paediatric Liver, GI and Nutrition Centre Toronto, ON, Canada; 6Paediatric Gastroenterology and Hepatology, 13Hacettepe University Faculty of Medicine, Ankara, Turkey; 11Akdeniz University, Antalya, Turkey; 12Department of Paediatric Gastroenterology, Center for Liver Disease and Transplantation, Columbia University Medical Center, New York, NY, United States; 16Emory University School of Medicine, Children’s Healthcare of Atlanta, Atlanta, GA, United States; 17Division of Gastroenterology/Hepatology/Nutrition, UPMC Children’s Hospital of Pittsburgh, Pittsburgh, PA, United States; 19Department of Paediatric Gastroenterology Hepatology and Transplantation, ASST Papa Giovanni XXIII, Bergamo, Italy; 20Albireo Pharma, Inc., Boston, MA, United States

Email: t.grammatikopoulos@nhs.net

Background and aims: Patients with progressive familial intrahepatic cholestasis (PFIC), a group of rare paediatric cholestatic liver diseases, have debilitating symptoms including severe pruritus that can impact sleep and quality of life (QoL). In the phase 3 PEDFIC 1 and PEDFIC 2 studies, the ileal bile acid transporter inhibitor odevixibat reduced serum bile acids (sBAs) and improved pruritus and sleep in children with PFIC. Using pooled data from these studies, we examined secondary and exploratory efficacy endpoints and safety outcomes in patients who met criteria for a pruritus response with odevixibat treatment.

Method: PEDFIC 1 was a 24-week, randomised, placebo-controlled study in children with PFIC1 or PFIC2. PEDFIC 2 is an ongoing 72-week extension study in patients of with any PFIC type. Pruritus was rated using the Albireo observer-reported outcome instrument (range: 0–4). This pooled analysis spans from patients’ first dose of odevixibat to a cut-off of 4 December 2020. We analysed sBAs, QoL (Pediatric QoL Inventory [PedsQL] and PedsQL family impact [FI] questionnaire; higher scores indicate improved QoL), alanine aminotransferase (ALT), total bilirubin, sleep parameters, and treatment-emergent adverse events (TEAEs) in patients with a pruritus response (ie, ≥1-point drop in pruritus score from baseline) following odevixibat treatment.

Results: Of 82 patients in the pooled population (of whom, 49% were female), 44 (54%) were pruritus responders. Of these 44 pruritus responders (mean age, 4.6 years), 24 (55%) were female; 23%, 68%, and 7% had PFIC 1, 2, and 3, respectively. Mean sBA levels were 247 μmol/L at baseline (n = 44) and decreased over time by 77% at weeks 70–72 in pruritus responders who reached this timepoint (n = 18). Mean PedsQL and FI total scores were 56 (n = 30) and 50 (n = 42) at baseline and increased by 11 (n = 8) and 24 (n = 14) at week 72, respectively, in pruritus responders. Mean ALT and total bilirubin levels decreased over time from 109 U/L and 40 μmol/L at baseline to 40 U/L and 18 μmol/L (n = 15) (Figure 1A, B), and sleep parameters improved over time in these patients (Figure 1C, D). There were no drug-related serious TEAEs.

Conclusion: Overall, patients with PFIC with a pruritus response following treatment with odevixibat experienced improvements in sBAs, QoL, hepatic biochemical markers, and sleep parameters that were sustained over time. Odevixibat was generally well tolerated.
Background and aims: Homozygous Pi*Z mutation in the SERPINA1 gene (Pi*ZZ genotype) confers a strong predisposition to lung and liver disease. Since the pace of liver disease progression and suitable prognostic factors remain unknown, we evaluated risk factors (i.e., demographics and lifestyle) and the predictive utility of non-invasive tests in the European Pi*ZZ liver cohort.

Method: 480 Pi*ZZ individuals without concomitant liver diseases or pathological alcohol consumption, decompensated liver disease, or hepatocellular carcinoma were evaluated by a standardized baseline clinical, laboratory, and elastographic assessment. 340 of them had a detailed follow-up interview at least 12 months after their baseline examination.

Results: During a median follow-up of 3.85 years, 23 Pi*ZZ individuals deceased. The main causes of mortality were lung and liver disease, each accounting for 8 deaths. 10/4 individuals received a lung/liver transplant, 3 additional Pi*ZZ individuals developed hepatic decompensation. Compared to the remaining Pi*ZZ participants, 15 individuals who developed a hepatic endpoint (liver transplant/death, or decompensated cirrhosis) presented with significantly higher body mass index (29.3 vs. 24.5 kg/m², p = 0.003), liver stiffness measurement (LSM, 14.0 vs. 5.2 kPa, p = 6.3 × 10⁻⁷), AST-to-platelet ratio index (APRI, 0.97 vs. 0.31 units, p = 9.4 × 10⁻⁹), fibrosis-4 index (FIB-4, 3.6 vs. 1.3, p = 6.0 × 10⁻⁸) and liver enzymes in their baseline examination. Multivariate Cox regression analysis revealed LSM ≥ 25 kPa (aHR 39.6, 95% CI 10.1–154.7, p = 1.2 × 10⁻⁷) as strong predictors of liver-related mortality.

Conclusion: LSM and APRI accurately stratify Pi*ZZ individuals according to their risk of liver-related events. Thus, these non-invasive tests may facilitate risk stratification in clinical practice as well as patient selection for clinical trials.

**Conclusion:** Post hoc analysis indicates that gender might have an influence on neurologic symptom regression and disease course in WD patients on trientine maintenance therapy. The trend of continuous improvement in neurological symptoms is mainly seen in female WD patients—even after long-term therapy. These findings warrant further prospective evaluation and have implications for future study designs.
Background and aims: Progressive familial intrahepatic cholestasis (PFIC) is a group of paediatric cholestatic liver diseases characterised by disruption of biliary production and transport, pruritus, and progressive liver disease. Here, using pooled data from two phase 3 studies in patients with PFIC (PEDFIC 1 and PEDFIC 2), we describe key long-term outcomes with odevixibat, an ileal bile acid transporter inhibitor, in the subgroup of patients treated with odevixibat for ≥72 weeks.

Method: PEDFIC 1 was a 24-week, placebo-controlled, double-blind study of odevixibat in children with PFIC1 or PFIC2. PEDFIC 2 is an ongoing, 72-week extension study in patients of any age with any type of PFIC. This pooled analysis spans from patients' first dose of odevixibat in PEDFIC 1 or PEDFIC 2 to a cut-off of December 4, 2020. The following outcomes are described over time in the subgroup of patients who had ≥72 weeks of exposure to odevixibat: serum bile acids (sBAs), caregiver-reported pruritus score (range, 0–4; higher scores indicate worse symptoms), laboratory parameters, growth, and safety.

Results: Of 84 patients in the pooled population, 27 were treated with odevixibat for ≥72 weeks (median range, 92 [76–128] weeks). Of these 27 patients (mean age, 3 years), 52% were male, 70% had PFIC2, and 30% had PFIC1. At baseline, 82% of these 27 patients were using ursodeoxycholic acid (UDCA), 56% were using rifampicin, and 89% were using UDCA and/or rifampicin. Mean (SE) sBA levels at baseline were 291 (76) μmol/L, which decreased by ~185 (28) at weeks 70–72 of odevixibat treatment (Figure). Mean (SE) pruritus score at baseline was 2.9 (0.1), which decreased by ~1.56 (0.2) at weeks 61–72 (Figure).

At week 72 of odevixibat treatment, decreases in alanine aminotransferase (~64.9 U/L), aspartate aminotransferase (~18.8 U/L), and total bilirubin (~5.4 μmol/L) were also observed; mean (SE) height and weight Z scores increased by 0.8 (0.1) and 0.5 (0.2), respectively. In this group of patients with ≥72 weeks of odevixibat treatment, 26 (96%) patients experienced any treatment-emergent adverse event (TEAE) and 52% experienced drug-related TEAEs. There were no TEAEs leading to discontinuation.

Conclusion: Odevixibat was well tolerated and demonstrated durable clinical treatment benefits for up to 72 weeks in improving sBA levels, pruritus scores, hepatic parameters, and growth in patients with PFIC who were treated for at least 72 weeks.

FRI260
In vitro rescue of the bile acid transport function of some ABCB11 variants by CFTR potentiators: a targeted pharmacotherapy in progressive familial intrahepatic cholestasis type 2

Eloïde Mareux1, Martine Lapalrus1, Marion Almes1,2, Pauline Adnot1, Mounia Lakli1, Amel Ben Saad1, Jean-Luc Decourt3, Thomas Falguieres1, Isabelle Callebat4, Emmanuel Gonzalez1,2, Emmanuel Jacquier1,2.

1Inserm, UMR_S1193 Physiopathogénése et traitement des maladies du foie, Université Paris-Saclay, Hepatinov, Orsay, France; 2Assistance Publique-Hôpitaux de Paris, Faculté de médecine Paris-Saclay, CHU Bicêtre, Paediatric Hepatology and Paediatric Liver Transplant Department, National Reference Center for Rare Paediatric Liver Diseases, FILFOIE, ERN RARE LIVER, Le Kremlin-Bicêtre, France; 3Assistance Publique-Hôpitaux de Paris, Faculté de médecine Paris-Saclay, CHU Bicêtre, Paediatric Hepatology and Paediatric Liver Transplant Department, National Reference Center for Rare Paediatric Liver Diseases, FILFOIE, ERN RARE LIVER, Le Kremlin-Bicêtre, France; 4CNRS, Département de pharmacochimie moléculaire, Université de Grenoble Alpes, Grenoble, France; 5CNRS, UMR 7590, Institut de Minéralogie, de Physique des Matériaux et de Cosmochimie, Sorbonne Université, Muséum National d'Histoire Naturelle, Paris, France

Email: eloide.mareux@universite-paris-saclay.fr

Background and aims: ABCB11 is expressed at the canicular membrane of hepatocytes and is responsible for biliary bile acid secretion. Variations in the ABCB11 gene cause a spectrum of rare liver diseases. The most severe form is progressive familial intrahepatic cholestasis type 2 (PFIC2). Current medical treatments of these conditions have limited efficacy. Hence, the identification of alternative therapies is a major challenge.

Method: Three ABCB11 disease-causing variations identified in PFIC2 patients (A257 V, T463I and G562D) were studied by 3D structure

of the transporter in ABCB11 mutants. This was evaluated in vitro by comparing the effects of ABCB11 on hormone-induced ATPbinding activity and on the rescue of bile acid transport function in ABCB11 mutants in the presence of CFTR potentiators.
modelling. The variations were reproduced in a plasmid encoding a rat Bsep—green fluorescent protein. After transfection, the expression and the localisation of the variants were studied in HepG2 and Can 10 cells. Tritiated taurocholate ([3H]TC) transport activity and the effect of Ivacaftor (VX-770, Kalydeco®), a clinically approved cystic fibrosis (CF) treatment, GLPG1837 in phase 2 CF clinical trials as well as SBC040 and SBC219, known as potentiators of CFTR were studied in Madin-Darby canine kidney (MDCK) clones co-expressing Abcb11 and the rat sodium taurocholate co-transporting polypeptide (Ntcp/ Slc10A1).

**Results:** As predicted by 3D structure modelling, the three variants were correctly expressed at the canalicular membrane of HepG2 and Can 10 cells but had a defective function when studied in MDCK cells with a [3H]TC transport activity ranging from 28 to 70 % of the one observed in MDCK cells expressing the wild type (wt) Abcb11 (Figure). Ivacaftor, GLPG1837, SBC040 and SBC219 increased the [3H]TC transport activity of A257 V, T463I and G562D by 1.3 to 1.9-fold, allowing the [3H]TC transport activity of the A257 V variant to reach the one of the wt Abcb11. Furthermore, an additive effect was observed for the T463I variant when ivacaftor was combined with SBC040 or SBC219.

**Conclusion:** Potentiator drugs could increase the pharmacopoeia available for patients with ABCB11 deficiency due to missense variations affecting the transport function and may delay or even suppress the need for liver transplantation in these patients.

---

**FRI261**

**Plasma-based proteomics profiling of patients with Wilson’s disease**

Rui Hua1, Jie Su1, HaiTao Qi2, Yonggeng Jiao2, Lishuang Qi2, Junqi Niu1.

1The First Affiliated Hospital of Jilin University, Hepatology, Changchun, China; 2Harbin Medical University, College of Bioinformatics Science and Technology, Harbin, China; 3Jilin Province P&AW General Hospital, Anesthesiology, Changchun, China

Email: huar@jlu.edu.cn

**Background and aims:** Wilson’s disease (WD) is an inherited disorder resulting from abnormal copper metabolism. Current diagnostic criteria is inadequacy since biochemical indexes related to copper are unreliable and genetic testing is expensive. The study aimed to reveal WD-related proteomic alterations, from which protein based molecular diagnostic model was developed.

**Method:** We performed a LTQ-Orbitrap (LC-ESI-MS/MS) comparative quantitative proteomics analysis to reveal the differentially expressed proteins (DEPs) between 20 WD subjects (10 liver type and 10 brain type) and 10 healthy controls. Then, functional enrichment analysis of Gene Ontology (GO) and coexpression protein-protein interaction (PPI) network based on STRING database were performed to reveal the dysregulated biological functions. Next, eXtreme Gradient Boosting (XGboost) was used to construct an optimal classifier to distinguish liver- and brain-type WDs from healthy controls. Finally, 16 independent serum samples were collected, and detected by ELISA method to validate the disease-associated DEPs and the diagnostic classifier.

**Results:** Of all the identified DEPs of liver-type WD and brain-type WD, there were 62 common DEPs between the two types including 18 were up-regulated and 44 were down regulated. GO enrichment analysis revealed that the common DEPs were mainly involved in inflammation, coagulation cascade, protein transport and activation. And the coexpression PPI network showed that several DEPs interacted with many DEPs implicated in WD, such as Heparin cofactor 2 (SERPIND1), Transthyretin (TTR) and Coagulation factor IX (F9). Hereby, we constructed a classifier consisting of two down-regulated proteins (F9 and C4b-binding protein beta chain (C4BPB) with 100% accuracy. ELISA test validated the differential down-regulations of F9 and C4BPB in 16 independent WD samples when compared with 26 healthy controls. In the independent samples, the area under the ROC curve (AUC) of the diagnostic classifier was 0.986, and its sensitivity and specificity was 93.8% and 96.2%, respectively.

**Conclusion:** Our study demonstrates for the first time that mass spectrometry proteomic combined with bioinformatics analysis of serum samples is a potential approach to identify candidate markers associated with WD. Further studies are warranted to evaluate the clinical utility of these biomarkers in patients with WD.
FR1262
Management of hepatic sarcoidosis-multicentric approach
Janina Sollors1, Andreas Teufel2, Christoph Antoni1, Matthias Ebert2, Svetlana Hetjens3, Yuxuan Qian1, Bernhard Schlevoigt4, Marcus-Alexander Woerns5, Peter Galle6, Cleo-Aron Weis6, Raoul Bergner2, Janina Sollors1, Andreas Teufel2, Christoph Antoni1, Matthias Ebert2, Svetlana Hetjens3, Yuxuan Qian1, Bernhard Schlevoigt4, Marcus-Alexander Woerns5, Peter Galle6, Cleo-Aron Weis6, Raoul Bergner2, 1University Medical Center Mannheim, Department of Internal Medicine II, Mannheim, Germany; 2University Medical Center Mannheim, Medical Faculty Mannheim, Heidelberg University, Department of Internal Medicine II, Mannheim, Germany; 3Medical Faculty University Heidelberg, University Hospital Mannheim, Internal Medicine II, Germany; 4University Medical Center Muenster, Department of Medicine B, Muenster, Germany; 5University Medical Center Mannheim, Medical Faculty Mannheim, Heidelberg University, Department of Pathology, Mannheim, Germany; 6Ludwigshafen Medical Center, Division of Rheumatology, Department of Medicine A, Ludwigshafen, Germany
Email: jsollors@web.de

Background and aims: Sarcoidosis is systemic granulomatous disorder of unknown cause, characterized by activation of T-lymphocytes and macrophages involving multiple organs. Main manifestations are bilateral lymphadenopathy, pulmonary densification but also skin, joint and eye involvement. However, liver involvement may occur in up to 60% of all patients. As many patients experience only minor symptoms, a high number of undiagnosed cases must be assumed.

In order to successfully identify patients with hepatic sarcoidosis, a thorough characterization of these patients and their course of disease is necessary. However, the currently available evidence was mostly collected several decades ago.

Method: We collected 40 patients from four German centers to evaluate current treatment standards and course of disease. All of our patients underwent liver biopsy with histologically proven granulomatous hepatitis.

Results: Detailed characterization of these patients showed an overall benign course of disease. Treatment of these patients was very diverse with glucocorticoids for 1 year in 55% (22/40), 5–10 years in 18% (7/40), and permanently in 18% (7/40).

Other treatments included Disease-Modifying Anti-Rheumatic Drugs (DMARDs) of the conventional e.g. non-biological type (methotrexate (MTX), azathioprine (AZA), hydroxychloroquine (HCQ), sulfasalazine (SSZ), leflunomid (LEF)) in 53 %, of these, AZA 81%, MTX 46%, HCQ 10%, furthermore mycophenolatmofetil (MMF) in 10% and cyclophosphamide in 10% and biologicals in 8% of all patients in whom detailed documentation was available.

Conclusion: Despite these very diverse treatments, patients generally showed only slow progression of the disease. Only one patient died due to spontaneous bacterial peritonitis. None of our patients received liver transplantation. Based on our experience, we proposed a diagnostic work up and surveillance strategy as a basis for future, prospective register studies.

FR1263
Plasma proteomics identifies hepatic steatosis and sex differences in 2, 147 children and adolescents
Lili Niu1,2, Sara Stinson3, Louise Holm3,4, Morten Lund3,5, Citius Fonvig3,4, Helene Baek Juel1, Simon Rasmussen1, Jens-Christian Holm1,4,5, Torben Hansen1, Matthias Mann1,2, 1University of Copenhagen, Novo Nordisk Foundation Center for Protein Research, Copenhagen, Denmark; 2Max Planck Institute of Biochemistry, Department of Proteomics and Signal Transduction, Martinsried, Germany; 3University of Copenhagen, Novo Nordisk Foundation Center for Basic Metabolic Research, Copenhagen, Denmark; 4Copenhagen University Hospital Holbæk, The Children's Obesity Clinic, Department of Pediatrics, Holbæk, Denmark; 5University of Copenhagen, The Faculty of Health and Medical Sciences, Copenhagen, Denmark
Email: mmann@biochem.mpg.de

Background and aims: Childhood obesity constitutes a serious health challenge predisposing children and adolescents to cardio-metabolic- and liver diseases. In particular, the prevalence of pediatric non-alcoholic fatty liver disease (NAFLD) is estimated to be 36% in the context of obesity. Percutaneous liver biopsies are considered the gold standard for diagnosing NAFLD, but due to its invasive nature, its clinical application is limited in children. This study aims to use mass spectrometry-based proteomics to identify non-invasive biomarkers for early detection of hepatic steatosis in children and adolescents, taking into account sex-specific changes in plasma proteins during puberty.

Method: We included 2, 147 children and adolescents, aged 5 through 20, from an obesity clinic cohort and a population-based cohort in Denmark, in a cross-sectional study design. We acquired plasma proteomics data using the Evesope One liquid chromatography system coupled online to an Orbitrap Exploris 480 mass spectrometer. We performed adjusted correlation analysis to identify age-associated proteins. We then used unsupervised hierarchical clustering to identify clusters of protein trajectories changing with age. Liver fat percentage, as quantified by proton magnetic resonance spectroscopy, was available for 764 children (80% of whom were from the obesity clinic). Among these, 13.5% exhibited hepatic steatosis, defined as a liver fat percentage above 5%. We performed student’s t-test (two-sided) to identify differentially abundant proteins between children and adolescents with and without hepatic steatosis. Receiver operator characteristics area under the curve (ROC-AUC) was used to identify potential biomarkers. We used the liver damage marker, alanine aminotransferase (ALT) (plasma concentrations) as a benchmark.

Results: On average, 394 proteins were quantified per sample. Among these, 70 proteins significantly correlated with age. Hierarchical clustering identified puberty-related clusters of protein trajectories, which exhibited sex-dependent differences, such as sex hormone-binding globulin. Student’s t-test identified 84 significantly differentially abundant proteins, including 44 upregulated and 40 downregulated in the group with hepatic steatosis. The top 20 best-performing proteins which predicted hepatic steatosis, exhibited ROC-AUCs between 0.63 and 0.81. Combining the top two and top eight proteins resulted in an ROC-AUC of 0.82 and 0.87, respectively, which was superior to ALT.
Conclusion: Temporal plasma proteome trajectories reflect sex differences during puberty. A panel of eight proteins shows promising potential as a non-invasive diagnostic marker for hepatic steatosis in children and adolescents. This would need to be externally validated.

FR1264
Pregnancy outcomes in women with Budd Chiari syndrome: a single center experience
Sagnik Biswas1, Sabreena Sheikh1, Manas Vaishnav1, Anshuman Elhence1, Naba Farooqui2, Abhinav Anand1, Shivandan Gamanagatti1, Shalimar1.1 All India Institute of Medical Sciences, New Delhi, Gastroenterology and Human Nutrition, New Delhi, India; 2Mayo Clinic, Rochester, Rochester, United States; 3All India Institute of Medical Sciences, New Delhi, Radiodiagnosis, New Delhi, India

Email: drshalimar@yahoo.com

Background and aims: Budd Chiari Syndrome (BCS) is associated with primary infertility and adverse pregnancy outcomes in affected females. Scant literature is available on the effect of an endovascular intervention on fertility and the outcome of future pregnancies in these patients.

Method: In this retrospective analysis, 121 female patients with BCS attending our liver clinic from 2017 to 2020 were included. Patients were categorized into three groups- no prior conception (group 1), any conception before disease onset but before completion of the family (group 2), and disease onset post completion of the family (group 3). Pregnancy outcomes (live birth, stillbirth, or abortions), mode of delivery, teratogenicity in the fetus, bleeding risk in the mother, decompensation of liver disease, or occlusion of the stent during pregnancy were assessed.

Results: BCS was diagnosed before any conception in 58 women (Group 1; median age: 22 years), during or after pregnancy but before completion of family in 39 (Group 2; median age: 27 years) and after completion of family in 24 women (Group 3; median age: 34 years). Median CTP and MELD scores of the whole cohort were 7, and 12 respectively. The primary infertility rate was 19.8% (24/121). In Group 1: 15 women with primary infertility underwent endovascular intervention with 5/15 (33%) women conceiving subsequently, resulting in 4 live births and 7 abortions. In Group 2: 5 women had developed BCS during pregnancy, and 11 in the postpartum period; 11/39 patients had a history of one or more abortions. Overall, 8/34 (23.5%) patients who underwent endovascular intervention could conceive, resulting in 4/8 (50%) live births. However, no patient developing BCS during pregnancy was able to conceive subsequently despite endovascular intervention. Group 3: No patient had any major complications during past pregnancies. Only one patient developed a TIPSS block in the postpartum period. The mode of delivery was vaginal in 88% of cases. No congenital anomaly/major bleeding episodes/decompensation/maternal mortality occurred.

Conclusion: Infertility is common in patients with BCS. Pregnancy is well tolerated in those with compensated liver disease. Normal vaginal delivery is a safe method of childbirth in these patients. No fetal malformations or major bleeding episodes were noted despite the use of oral anticoagulants.

FR1265
New cases of Budd-Chiari syndrome and splanchnic vein thrombosis after COVID-19 vaccination-a vascular liver disease group (VALDIG) initiative
1Erasmus University Medical Centre, Department of Gastroenterology and Hepatology, Rotterdam, Netherlands; 2Reaujon Hospital, Department of Hepatology, Paris, France; 3University College London, Institute of Liver and Digestive Health, London, United Kingdom; 4Royal Free London NHS Foundation Trust, Hepatology and Liver Transplantation, London, United Kingdom; 5Hospital Clinic, Institut de Investigacions Biomèdiques August Pi i Sunyer (IDIBAPS), University of Barcelona, Barcelona, Barcelona Hepatic Hemodynamic Laboratory, Liver Unit, Barcelona, Spain; 6CHU Grenoble Alpes, 38043 Grenoble Cedex, Service d’Hépato-Gastroentérologie, Grenoble, France; 7Radboud University Medical Center, Department of Gastroenterology and Hepatology, Nijmegen, Netherlands; 8AP-HP Hôpital Pâul-Brousse, INSERM, Université Paris-Saclay, UMR-S 1139, Université Paris-Saclay, INSERM, FHI Hepatinaon, 94800, Centre Hépato-Biliaire, Physiopathogénèse et traitement des maladies du Foie, Villejuif, France; 9University Hospital of Toulouse and Toulouse III Paul Sabatier University, Toulouse, France; 10CHU Rennes Univ Rennes, F-35000, Liver Disease Department, Rennes, France; 11CHU Reims, Department of Hepato-Gastroentérologie, Reims, France; 12University Hospital, Côte de Nacre, Department of Hepatology and Gastroenterology, Caen, France; 13Department of Hepatology and Gastroenterology, Orleans, France, Orleans, France; 14Centro Hospitalar Universitario do Porto, EpiUnit, Instituto de Saúde Pública da Universidade do Porto, Porto, Portugal; 15Erasmus University Medical Centre Rotterdam, Department of Hematology, Rotterdam, Netherlands
Email: r.maan@erasmusmc.nl

Background and aims: Since the world-wide COVID19 vaccination efforts, several studies have reported on a rare side effect of ChAdOx1 nCoV-19 (AstraZeneca) with vaccine-induced immune thrombocytopenia and thrombosis (VITT). We aimed to collect consecutive new cases of splanchic vein thrombosis (SVT) or Budd-Chiari Syndrome (BCS) following SARC0V2 vaccination within the Vascular Liver Disease Group (VALDIG) network.

Method: This prospective international cohort study started on 01.05.2021 to include all incident cases of definite VITT (5/5 criteria: onset of symptoms 4–42 days post COVID vaccination, new thrombosis, platelets <150 × 109/L, positive anti-PF4/HIT ELISA and D-dimer >4000 FEU) or otherwise vaccine-related (<5/5 criteria) SVT or BCS. Diagnosis was radiologically confirmed, and onset of symptoms was within 6 weeks after 1st or 2nd SARC0V2 vaccination. Patients with malignancy or cirrhosis were excluded. Statistics were descriptive with frequency (%) and median (range) values. We are presenting our data until 01.11.2021.

Results: In total, 22 patients were included from 13 centers with median age 47 (21–66) and 46 % females. Median time from vaccination (AstraZeneca N = 11, Pfizer N = 9, Moderna N = 1, Johnson N = 1) to symptoms was 10 (2–32) and to diagnosis was 16 days (3–56). Patients presented with abdominal pain (86%), ascites (41%), fever (32%), elevated AST (35 U/L, 22–20100), ALT (45 U/L, 17–9528), INR (1.18; 0.88–5.1), D-dimer (6, 570 FEU; 530–63,000), white blood cell count (10, 7 × 109/L; 4, 2–26) and decreased platelets
Hepatology, Maastricht, Netherlands; 3Maastricht UMC, Department of Gastroenterology and Polycystic liver disease is related to abdominal wall hernia. We found a clear predominance of umbilical hernias (25.8%, n = 125) while multiple hernias were present in 6.2% (n = 30). Using multivariate analysis, male sex (OR 2.727 p < 0.001), abdominal surgery (OR 2.575, p < 0.001) and disease severity according to the Gigot classification (Type 3 OR 2.853, p < 0.001) were identified as risk factors. Total liver volume was an independent PLD specific risk factor in the subgroup of patients with known total liver volume (OR 1.203, p = 0.001). Patients with multiple hernias were older (62.1 vs 55.1, p = 0.001) and more frequently male (22.0 vs 50.0%, p = 0.001).

**Table:**

<table>
<thead>
<tr>
<th>Abdominal wall hernia</th>
<th>N (%)</th>
<th>Median diameter in mm (IQR)*</th>
</tr>
</thead>
<tbody>
<tr>
<td>Overall</td>
<td>194 (100.0)</td>
<td>12 (7) (n = 180)</td>
</tr>
<tr>
<td>Epigastric</td>
<td>8 (4.1)</td>
<td>18 (6) (n = 7)</td>
</tr>
<tr>
<td>Umbilical</td>
<td>125 (64.4)</td>
<td>11 (6) (n = 109)</td>
</tr>
<tr>
<td>Cricialical</td>
<td>3 (1.5)</td>
<td>26 (58) (n = 3)</td>
</tr>
<tr>
<td>Inguinal</td>
<td>67 (34.5)</td>
<td>13 (8) (n = 53)</td>
</tr>
<tr>
<td>Other hernia</td>
<td>4 (2.1)</td>
<td>10 (1) (n = 2)</td>
</tr>
<tr>
<td>Multiple hernias</td>
<td>30 (15.3)</td>
<td>13 (7) (n = 30)</td>
</tr>
</tbody>
</table>

Complex hernia*^*

| Yes                   | 50 (25.8)  | 13 (6) (n = 43)             |
| No                    | 131 (67.5) | 12 (7) (n = 109)            |
| Unknown               | 13 (6.7)   | Unknwon                     |

IQR = interquartile range. * N represents the number of hernias in which the diameter could be measured in two different directions (lateralateral and craniocaudal). ** Complex hernia according to Slater criteria; 13 cases were unknown because hernia repair was performed before the imaging.

**Conclusion:** Abdominal wall hernias occur frequently in polycystic liver disease with a predominance of umbilical hernias. Hepatomegaly is a clear disease-specific risk factor.

**FRI267**

**MR-derived metrics have utility in identifying paediatric patients with stable autoimmune hepatitis**

Piotr Pawliszak1, Elizabeth Shumbayawonda2, Jędrzej Sarnecki3, Paulina Opyrcha1, Kamil Janowski3, Piotr Socha1, Małgorzata Woźniak1, Elżbieta Jurkiewicz3, 1Children’s Memorial Health Institute, Radiology, Warsaw, Poland; 2Oxford, Oxford, United Kingdom; 3Children’s Memorial Health Institute, Gastroenterology, Warsaw, Poland Email: pedro_pawliszak@yahoo.es

**Background and aims:** Paediatrics with autoimmune hepatitis (AIH) are monitored using liver biochemistry and histology, however, liver biopsy is invasive, expensive and carries the risk of pain and bleeding. Non-invasive imaging techniques (NITs) such as elastography and multiparametric MRI are showing increasing utility in supporting patient management and disease stratification, but have never been compared head-to-head in children. The aim of this study was to investigate the utility of imaging markers to stratify those with stable from those with active disease and thus identify those who may not
require a biopsy or in whom a it may be delayed leading to improvement in cost-effectiveness of AIH patient management.

**Method:** N = 36 with biopsy-confirmed AIH (14 ± 3 years) and N = 16 healthy controls [HC; 14 ± 2 years] underwent non-invasive imaging to obtain liver stiffness (LS; magnetic resonance elastography), spleen stiffness (SS) and corrected T1 (cT1). All AIH patients also underwent a liver biopsy. Kruskal-Wallis test was used to compare imaging markers between HC and AIH patients, as well as those with active vs stable disease. Correlations between NITs and histological scores were performed using Spearman’s rank tests. Stable disease was defined as having both lobular and portal inflammation ≤1 and Ishak fibrosis ≤2. Discrimination between active and stable disease using NITs was investigated using area under the receiver operator characteristic curve (AUC).

**Results:** Compared to HC, AIH patients had higher cT1 (827 ms vs 756 ms; p < 0.001) and LS (3 kPa vs 2.6 kPa; p = 0.031) but not SS (4.9 kPa vs 5.6 kPa, p = 0.068). N = 18 had stable disease and lower mean cT1 (p = 0.011) and SS (p = 0.017) and LS (p = 0.048) compared to those with active disease. cT1 correlated with fibrosis (r = 0.37; p = 0.049), lobular (r = 0.42, p = 0.025) and portal inflammation (r = 0.5, p = 0.005), LS (r = 0.42, p = 0.007) and SS (r = 0.43, p = 0.028). LS correlated with fibrosis (r = 0.47, p = 0.005), SS (r = 0.5, p = 0.004) and portal inflammation (r = 0.37, p = 0.029). For predicting disease activity, cT1 had AUC:0.77 (0.6–0.94), SS had AUC:0.75 (0.54–0.96) and LS had AUC:0.74 (0.57–0.9).

**Conclusion:** Those with active AIH have higher fibroinflammation, liver and spleen stiffness compared to those with stable AIH. NITs have utility in identifying paediatric patients with stable disease who may not benefit from invasive liver biopsy. Further work exploring the utility of these NITs in the AIH clinical pathway is warranted.

**FRI268 Development and validation of a novel ICP-MS method to quantify different copper species in human plasma from patients with Wilson disease**

Tao Liang, Haijing Zhang, Linwen Zhang, Scott Moseley, Ping Guo, Meng Chen, Tracey Hall, Ming Li, Eugene Swenson, Wei-Jian Pan, Brian Meltzer, Ryan Pelto, Mark Ma, Aexion, AstraZeneca Rare Disease, Boston, United States; Frontage Laboratories Inc., Exton, United States

**Email:** mark.ma@aexion.com

**Background and aims:** Wilson disease (WD) is a rare autosomal recessive genetic disorder. Functional mutation of ATP7B causes inadequate loading of copper (Cu) into ceruloplasmin (CP) and defective Cu excretion into bile, resulting in Cu accumulation in liver and other organs. Currently, WD treatment monitoring lacks reliable and fully validated bioanalytical methods. The calculated non-CP Cu (NCC) method assumes a CP-Cu:NCC ratio of 6:1 and can yield negative NCC values, which are biologically implausible. A direct assay is needed to monitor NCC, especially for patients treated with an investigational Cu-binding agent, ALXN1840 (bis-choline tetrathiomolydate), which mobilizes tissue Cu, contributing to a non-bioavailable pool of circulating Cu.

**Method:** A novel method utilizing immunocapture of CP, followed by chelation and filtration to isolate different Cu fractions subject to ICP-MS analysis (Figure) was developed to fractionate and directly quantify multiple Cu species from human plasma. It permits measurement of CP-protein via LC-MS method and Cu species including CP bound Cu (CP-Cu), direct NCC, and labile bound Cu (LBC) via one workflow. Methods were validated for precision, accuracy, selectivity and stability following the FDA guidance for Bioanalytical Method Validation. A monoclonal anti-Cu antibody was screened and selected for long-term assay use. Samples from healthy volunteers and from patients with WD were assessed for the Cu concentration in the CP fraction and the CP-Cu:Cp ratio.

**Results:** Full validations were successfully performed for each Cu fraction as well as CP-protein and showed a linear range from 5 to 1000 ng/ml (0.08–15.75 μM) for CP-Cu, direct NCC, LBC, and 5.00–800 μg/ml (0.03–59.7 μM) for CP-protein. The mean [95% confidence interval] for the CP-Cu:CP ratio was 4.68 [4.35, 5.00] in healthy volunteers and 4.09 [3.36, 4.82] in patients with WD, both being below the assumed ratio of 6.

**Conclusion:** Conventional calculated NCC is inaccurate and cannot be used for therapeutic guidance for WD. A novel method was developed that utilizes an immunocapture step and subsequent quantification of various fractions, including CP-Cu, direct NCC, LBC, and CP-protein. Validation data met defined acceptance criteria in terms of precision, accuracy, selectivity and stability. The assay is precise and reproducible and is valuable for accurate quantification of CP-Cu:CP-protein ratio, direct NCC and LBC, which may benefit WD therapy development.

**FRI269 Quantitative magnetic resonance cholangiopancreatography identifies features of ductal disease change in primary sclerosing cholangitis: a prospective observational cohort study**

Palak Trivedi, Katherine Arndtz, Nadir Abbas, Alison Telford, Liam Young, Rajarshi Banerjee, Peter Eddowes, Kartik Jhaveri, Gideon Hirschfield, National Institute of Health Research (NIHR) Birmingham Biomedical Research Centre (BRC), Centre for Liver and Gastrointestinal Research, University of Birmingham, Birmingham, United Kingdom; Institute of Immunology and Immunotherapy, University of Birmingham, Birmingham, United Kingdom; Institute of Applied Health Research, University of Birmingham, Birmingham, United Kingdom; Liver Unit, University Hospitals Birmingham, Birmingham, United Kingdom; Perspectum Ltd, Oxford, United Kingdom; NIHR Nottingham BRC, University of Nottingham, Nottingham, United Kingdom; Nottingham University Hospitals NHS Trust, Nottingham, United Kingdom; Joint Department of Medical Imaging, University Health Network, University of Toronto, Toronto, Canada; Toronto Centre for Liver Disease, University Health Network, Toronto, Canada; Department of Medicine, University of Toronto, Toronto, Canada

**Email:** liam.young@perspectum.com

**Background and aims:** Primary sclerosing cholangitis (PSC) is a chronic, progressive liver disease, characterised by multi-focal strictureing throughout the biliary tree. Biomarkers of parenchymal fibrosis are widely used for risk stratification. However there is a need to better characterise the extent of ductal disease involvement, its evolution over time, and the utility of quantitative biliary metrics for monitoring disease progression longitudinally. This study aimed to evaluate the utility of quantitative MRCP (MRCP+) in characterising...
the extent of ductal disease involvement and monitor changes over 1 year in patients with stable biochemical and liver fibrosis readings.

**Method:** Patients (pts) with PSC were prospectively recruited for standardized heavily T2-weighted MRCP imaging on a Siemens Verio 3 T system at baseline and 1-year thereafter. Scans were processed with MRCP+ to enhance and quantify tubular structures using multiscale Hessian analysis, gradient vector flow analysis, an intelligent path search algorithm and novel duct modelling algorithms. The 92 metrics generated by MRCP+ were reduced to 24 metrics expected to have clinical significance by an expert hepatopancreatobiliary radiologist. Changes in selected metrics over time were analyzed using linear mixed-effects models assuming patients as random effects.

**Results:** Non-cirrhotic pts with PSC were enrolled (n = 27; median age 45 yr, 70% male) with a baseline PVC Mayo Risk Score –0.93 (IQR –1.2–0.3), ALP 142 iU/L (IQR 84–281), ALT 51 iU/L (IQR 26–91), and transient elastography score of 7.7 kPa (IQR 6.2–11.5). Intra- and extra-ductal involvement was seen in 92% and 36% pts with median modified Amsterdam cholangiographic score (MAS) of 2 (IQR 2–2) and 0 (IQR 0–2), respectively. Over a median 371-day follow-up (IQR 365–442), 67% pts manifested features of ductal disease change, evidenced by an increase in the total number of strictures (n = 15, p = 0.036), the total length of strictures (n = 17, p = 0.030), the total stricture burden (n = 17; p = 0.012), or a combination of metrics, which showed a significant dependence on time (Figure 1). Serum ALP (p = 0.51), ALT (p = 0.40), bilirubin (p = 0.39), liver stiffness values (transient elastography, p = 0.07) and biliary strictures assessed using MAS (p = 0.80) did not change significantly over time.

**Conclusion:** When quantitative imaging is reviewed one year apart, ductal disease change is apparent in the majority of pts with PSC, in the absence of significant variation in liver biochemistry or fibrosis values. Larger scale validation, alongside robust clinical outcome data, is essential to develop quantitative MRCP+ as a radiological toolkit for future PSC clinical trials.

**FRI270**

**Development of Hepatoblastoma organoids as a patient-derived ex-vivo system**

Laura Zanatto1, Paula Cantallops Vilà1, Silvia Ariño Mons1, Beatriz Aguilar-Bravo1, Juan Carrillo2, Laura Roys3, Joan Pallares1, Montserrat Domingo-Sabat4, Alvaro del Rio5, Juanjo Lozano6, Francisco Hernandez Oliveros7, Laura Guerra8, Barbara Torres Guerola9, Constantino Sábado10, Gabriella Guíllen10, Marta Garrido10, José Antonio Salinas11, Moira Garraus11, María Esther Llinares12, Silvia Affo1, Carolina Armengol2, Pau Sancho-Brú1.  

1Institut d’Investigacions Biomèdiques August Pi i Sunyer (IDIBAPS), Liver Cell Plasticity and Tissue Repair, Barcelona, Spain; 2Health Sciences Research Institute Germans Trias i Pujol (IGTP), Childhood Liver Oncology Group. 3Catedra de Investigación Biomédica en Red de Enfermedades Hepáticas y Digestivas, Barcelona, Spain; 4University Hospital La Paz, Pediatric Surgery Department, Madrid, Spain; 5University Hospital La Paz, Pathology Department, Madrid, Spain; 6University Hospital La Fe, Medical Oncology Department, Pediatric Oncology Department, Valencia, Spain; 7Hospital Vall d'Hebron, Pediatric Oncology Department, Barcelona, Spain; 8Hospital Vall d'Hebron, Pediatric Surgery Department, Barcelona, Spain; 9Hospital Vall d'Hebron, Pathology Department, Barcelona, Spain; 10Hospital Universitari Son Espases, Division of Hematology-Oncology, Department of Pediatrics, Palma de Mallorca, Spain; 11Hospital Sant Joan de Déu, Pediatric Cancer Center Barcelona, Barcelona, Spain; 12Instituto Murciano de Investigación Biosanitaria (IMIB), Pediatric Oncology Service, Clinic University Hospital Virgen de la Arrixaca, Murcia, Spain.

Email: LZANATTO@clinic.cat

**Background and aims:** Hepatoblastoma (HB), the main pediatric liver tumor, is a rare disease with few therapeutic options and increasing incidence. With chemotherapy being the only effective treatment, survivors are doomed to suffer serious side effects and new therapeutic options are urgently needed. The lack of suitable models has strongly compromised the investigation of this pediatric tumor. Here we hypothesize that patient-derived organoids may represent a novel tool to explore the mechanisms involved in HB development and to design new therapeutic options.

**Method:** Parental tumor (T) and non-tumor (NT) tissues collected from different Spanish hospitals were used to generate a collection of...
patient-derived organoids. Organoids and primary tissues were characterized through: (i) RT-qPCR to analyze the mutation status; (ii) immunofluorescence analysis to evaluate the expression of HB biomarkers; (iii) transcriptomic studies by performing total- and small-RNA sequencing.

Results: Fourteen stable organoid lines have been successfully generated from T and NT tissues using a specific isolation protocol and have been grown in expansion media enriched in growth factors. T- and NT-organoids present differences in morphology and doubling time, with T organoids growing slower and in darker small structures compared to the NT organoids. Moreover, the T-organoids present the same mutations of the primary tissues. Additionally, T- and NT- organoids show different gene and protein expression of markers associated with hepatocyte- (HNF4) and progenitor-phenotype (KRT19, EpCAM), as well as HB-related genes, such as DLK1; and cytoplasmic localization of both GS and β-catenin. Interestingly, principal component analysis of total RNA and small RNA transcriptome revealed that HB organoids maintain general features of the tumor of origin. Finally, functional analysis has revealed conserved pathways between T- and NT-primary tissues and T- and NT-organoids, among them epigenetic regulation, proliferation, Wnt activation and altered metabolism, indicating the maintenance of tumor features by organoids.

Conclusion: In conclusion, we have developed a new patient-derived ex vivo 3D system mimicking HB features, including specific gene and protein expression. Specifically, these data suggest that HB-derived organoids are a reliable model to investigate this poorly understood pediatric tumor towards the development of personalized treatments.

FRI272 High rates of histological findings compatible with porto-sinusoidal vascular disease in patients with constantly elevated gamma-glutamyl transferase levels undergoing a liver biopsy Nicola Pugliese1, Luca Di Tommaso1, Roberto Ceriani1, Ludovico Alfaroné1, Elisabetta Mastorocco1, Maria Terrin1, Virginia Solitano1, Francesca Colapietra1, Chiara Masseti1, Ana Lleo1, Luigi Terracciano1, Alessio Aghemo1, Humanitas Research Hospital, Cascina Perseghetto, Italy Email: alessio.aghemo@humimed.eu

Background and aims: Isolated elevations in gamma-glutamyl transferase (GGT) levels are commonly found in patients referred to liver specialists, however their clinical impact is unknown. Data on the histological findings in these patients are scarce.

Method: All consecutive patients who underwent a liver biopsy between March 1st, 2015 and December 1st, 2020, in our Liver Unit for isolated and persistent (at least 2-fold ULN for three tests within 12 months) elevation of GGT value were retrospectively analyzed for clinical and histological features. Excluded were patients with concomitant AILD or AST elevation, intake of Hepato-toxic drugs or over the counter medications, alcohol intake > 20 g/day and metabolic associated fatty liver disease (MAFLD). Data about age, gender, body mass index (BMI), comorbidities (including findings compatible with portal hypertension), smoking habit and disease severity (APRI and FIB-4), were collected. All liver biopsies were blindly reviewed by 2 experts in liver pathology.

Results: During the study period a total of 640 patients performed a liver biopsy. 29 patients (4.5%) met the inclusion criteria and were enrolled. Most of the patients were males (19/29, 65.5%) and their mean age was 49.7 ± 11.4 years (28-73). The mean BMI was 24.5 ± 2.97 (18.8-30) and only two patients presented FIB-4 suggestive of advanced liver disease. The histological findings were compatible with porto-sinusoidal vascular liver disease (PSVD) in 13/29 (45%) patients, hepatic sarcoidosis in 3/29, non-alcoholic steatohepatitis (NASH) in 3 and congenital hepatic fibrosis (CHF) in 3. Histology did not allow a definite diagnosis in 6/29 (21%) patients. Patients with PSVD were male in 10/12 (%); with a mean age of 47 ± 10.9 years (28–57), without any clinical signs of portal hypertension, in only one patient FIB-4 score was compatible with advanced liver disease. When comparing patients with PSVD to patients with any other liver etiology, we found no difference in gender, age, BMI, smoking habit, FIB-4, GGT, albumin and bilirubin values.

Conclusion: Liver histology in patients with isolated elevated GGT levels is useful as it allows to diagnose chronic liver conditions associated with a significant impact on survival. The high rate of patients with histological findings compatible with PSVD in the absence of signs of portal hypertension, requires careful assessment on how to manage these patients in the long term.

FRI273 Plasma metabolomics and machine learning characterizes metabolite signature capable of segregating patients with poor outcome in pediatric cirrhosis Babu Mathew1, Gaurav Tripathi1, Vipul Gautam2, Akhilesh Saini1, Manisha Yadav1, Nupur Sharma3, Vasundhra Bindal3, Bikrant Bihari Lal2, Vikrant Sood2, Rajeev Khanna1, Jaswinder Maras1, Seema Alam2, 1Institute of Liver and Biliary Sciences, Molecular and Cellular Medicine, New Delhi, India; 2Institute of Liver and Biliary Science, Pediatric Hepatology, New Delhi, India Email: jassi2param@gmail.com

Background and aims: Pediatric cirrhosis is a life-threatening illness with high mortality up to 40%. Primary causes of cirrhosis in children are biliary atresia, genetic-metabolic diseases, autoimmune hepatitis, Wilson's disease and others. Development of cirrhosis in children's predisposes them to early development of sepsis and/or poor outcome. Early diagnosis of cirrhosis, sepsis and/or poor outcome in such patients may increase survival rate; therefore, development of new diagnostic methods is crucial. We investigated whether metabolomics and machine learning (ML) approaches could segregate patients with poor outcome (sepsis/mortality) in pediatric cirrhosis at baseline.

Method: Plasma metabolomics was studied using ultra-high-performance liquid chromatography and high-resolution mass-spectrometry to identify patients with poor outcome (sepsis/mortality) in pediatric cirrhosis at baseline. Altogether, 154 pediatric patients were analysed of them, 54 in derivative [40 Cirrhotics (C) and 14 Non-cirrhotics (NC)] and 100 in validation cohort [75 C, 25 NC]. Differentially expressed metabolites (DEM) with highest AUC and lowest mean decrease in accuracy were identified in cirrhotics, sepsis and were correlated with the severity (PELD score) and outcome (mortality) in pediatric patients.

Results: Of the 762 annotated features (metabolomic/biochemical/spectral databases), at baseline 120 plasma metabolites (Up-109, Down-regulated-11) discriminated Cirrhotics from Non-Cirrhotics in pediatric patients (FC > 1.5, p < 0.05). Cirrhotics documented significant increase in Tryptophan metabolism, steroid hormone biosynthesis, purine metabolism and others (p < 0.05). Most importantly high L-Formylkynurenine (546 Folds), 3-Hydroxy-1H-quinolin-4-one (20 Folds), Cortisone (18 Fold), 12-Hydroxydodecanoic acid (12 Folds), L-Isoleucine (11 Folds), Hypoglycine-A (5 folds), Aminopropylcadaverine (5 Folds), 2, 3, 4, 5-Tetrahydrodipicolinate (3 Folds) and others segregated Cirrhosis from Non-Cirrhosis (p < 0.05). Additionally, plasma L-Formylkynurenine, 3-Hydroxy-1H-quinolin-4-one, 12-Hydroxydodecanoic acid, L-Isoleucine and Cortisone segregated sepsis and non-survivors (FC > 2, p < 0.05, AUC > 0.8). In validation cohort, baseline plasma L-Formylkynurenine; hazard-ratio (HR) of 3.5 (1.2-5.6), and Cortisone; HR:3 (1.5-5.2) showed high reliability [AUC > 0.95 (0.91-0.97)] for predicting non-survivors and correlated with PELD score (r2 > 0.5, p < 0.05). L-Formylkynurenine (9.5 FC), and Cortisone (9 FC) cut-off reliably segregated non-survivors (log-rank p < 0.01) and showed >86% accuracy, >95% sensitivity and >95% specificity using Random Forest-based Machine-Learning model.
Conclusion: Plasma metabolite L-Formylkynurenine (>9.5 FC), and Cortisone (>9 FC) can reliably predict cirrhosis, sepsis and poor outcome in pediatric patients.

FRI274
Experience of cholestatic pruritus emphasized by patients with PBC: results from the PBC Foundation app survey
Chris Mitchell¹, James Neuberger², Terri Kim³, Andrew Yeoman⁴, Robert Mitchell-Thain¹. ¹PBC Foundation, Edinburgh, United Kingdom; ²Birmingham Community Healthcare NHS Foundation Trust, United Kingdom; ³Escient Pharmaceuticals, San Diego, United States; ⁴Royal Gwent Hospital: Opthalmology, United Kingdom
Email: chris@pbcfoundation.org.uk

Background and aims: Pruritus is a common symptom of cholestatic liver disease and treatment has limited efficacy. Patients with pruritus often suffer from intense itch, associated stress, and a negative effect on overall quality of life, including mental health issues.

Using PBC Foundation’s App, we collected insights from Primary Biliary Cholangitis patients with pruritus, focussing on what may affect patient’s daily experience of itch.

Method: An ongoing itch survey, live for over 6 months, was cross referenced with a previous survey exploring demographics and treatments. Due to cross-referencing, the number of respondents varies between questions. The main survey has 455 respondents. We defined mild, moderate and severe itch as at least 1, 4 and 7 respectively, on a numerical scale of 0 (no itch) to 10 (worse itch).

Results: Overall, similar to other studies 73% respondents suffer from itch. Over half of those itch daily and 3 in 4 patients have moderate to severe itch on their worst day.

In those aged <50 itch occurred more likely than in those >50 yr (77% vs 64%) and was more likely to be present daily (53% vs 44%). Itch occurred in the highest frequency in those within the first 5 yr of diagnosis (76%) with the lowest occurring in those >20 yr (45%).

Looking at disease modifying treatments: itch, daily itch, normal day severity and worst day severity for those on obeticholic acid were no worse than other therapies.

Information was only available for those taking cholestyramine, antihistamines or emollients and shows that itch is not present daily while on these therapies suggesting potential benefit. However itch on the worst day was almost exclusively severe and only partially ameliorated by therapy.

Conclusion: This study has a number of limitations, e.g. cross referencing different surveys taken at different times, and the risk of only itch-affected patients engaging. These surveys show that whilst some of the treatments may decrease the incidence of pruritus on a daily basis, severity of pruritus on a normal day is only slightly improved compared to the severity on the worst day. Pruritus can affect anyone within the PBC patient population and does so often and with profound effect.

Table: (abstract: FRI274).

<table>
<thead>
<tr>
<th>PBC management medication</th>
<th>N</th>
<th>Respondents who itch (%)</th>
<th>Itch daily (%)</th>
<th>Moderate to severe itch on normal day (%)</th>
<th>Modest to severe itch on worse day (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ursodiol</td>
<td>307</td>
<td>69</td>
<td>50</td>
<td>60</td>
<td>85</td>
</tr>
<tr>
<td>Obeticholic acid</td>
<td>118</td>
<td>67</td>
<td>52</td>
<td>64</td>
<td>86</td>
</tr>
<tr>
<td>Bezafibrate</td>
<td>153</td>
<td>70</td>
<td>49</td>
<td>54</td>
<td>75</td>
</tr>
<tr>
<td>Fenofibrate</td>
<td>16</td>
<td>44</td>
<td>30</td>
<td>0</td>
<td>100</td>
</tr>
<tr>
<td>Itch remedy</td>
<td>312</td>
<td>87</td>
<td>52</td>
<td>90</td>
<td>99</td>
</tr>
<tr>
<td>Cholestyramine</td>
<td>390</td>
<td>90</td>
<td>50</td>
<td>76</td>
<td>92</td>
</tr>
<tr>
<td>Antihistamines</td>
<td>411</td>
<td>91</td>
<td>49</td>
<td>66</td>
<td>88</td>
</tr>
<tr>
<td>Topical emollients</td>
<td>42</td>
<td>71</td>
<td>59</td>
<td>62</td>
<td>75</td>
</tr>
<tr>
<td>Prednisone</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Age in years</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>21–30</td>
<td>1</td>
<td>100</td>
<td>100</td>
<td>100</td>
<td>100</td>
</tr>
<tr>
<td>31–40</td>
<td>8</td>
<td>75</td>
<td>67</td>
<td>67</td>
<td>100</td>
</tr>
<tr>
<td>41–50</td>
<td>21</td>
<td>76</td>
<td>47</td>
<td>61</td>
<td>83</td>
</tr>
<tr>
<td>51–60</td>
<td>44</td>
<td>63</td>
<td>55</td>
<td>71</td>
<td>88</td>
</tr>
<tr>
<td>61–70</td>
<td>35</td>
<td>63</td>
<td>31</td>
<td>44</td>
<td>74</td>
</tr>
<tr>
<td>&gt;70</td>
<td>9</td>
<td>78</td>
<td>43</td>
<td>71</td>
<td>100</td>
</tr>
<tr>
<td>Years diagnosed</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>&lt;1</td>
<td>22</td>
<td>68</td>
<td>44</td>
<td>63</td>
<td>78</td>
</tr>
<tr>
<td>1–2</td>
<td>17</td>
<td>59</td>
<td>36</td>
<td>37</td>
<td>67</td>
</tr>
<tr>
<td>3–5</td>
<td>19</td>
<td>100</td>
<td>37</td>
<td>53</td>
<td>83</td>
</tr>
<tr>
<td>6–10</td>
<td>21</td>
<td>67</td>
<td>57</td>
<td>67</td>
<td>86</td>
</tr>
<tr>
<td>11–15</td>
<td>14</td>
<td>71</td>
<td>70</td>
<td>70</td>
<td>100</td>
</tr>
<tr>
<td>16–20</td>
<td>14</td>
<td>57</td>
<td>55</td>
<td>50</td>
<td>78</td>
</tr>
<tr>
<td>21–25</td>
<td>10</td>
<td>40</td>
<td>30</td>
<td>40</td>
<td>40</td>
</tr>
<tr>
<td>&gt;25</td>
<td>1</td>
<td>100</td>
<td>0</td>
<td>100</td>
<td>100</td>
</tr>
<tr>
<td>Sex</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Female</td>
<td>315</td>
<td>72</td>
<td>52</td>
<td>60</td>
<td>80</td>
</tr>
<tr>
<td>Male</td>
<td>11</td>
<td>55</td>
<td>45</td>
<td>33</td>
<td>55</td>
</tr>
</tbody>
</table>
**Background and aims:** The acute hepatic porphyrias (AHP) are associated with a high risk of hepatocellular carcinoma (HCC). Patients with AHP-associated liver cancer typically do not have a well-defined underlying liver diseases or cirrhosis. Although the carcinogenic mechanisms are unknown, a strong association between HCC and biochemical AHP-activity with elevated porphyrin precursors 5-aminolevulinic acid (ALA) and porphobilinogen (PBG) has been established. The cancerogenic potential of ALA and findings of increased cancer risks in small cohort studies have led to an assumption that AHP is a risk factor for cancer in general. Risk estimates are however uncertain, and little is known about how biochemical activity affects the risk. Our aim was to assess the risks of non-hepatic cancers in correlation to biochemical activity in the largest AHP cohort assembled to date.

**Method:** All patients in the Swedish porphyria registry with verified AHP were included and matched 1:10 to reference individuals from the general population by age, sex and municipality. Data on incident cancers were collected from the national cancer and cause-of-death registries. Overall cancer incidence and incidence of a predetermined set of specific cancers were compared by incidence rate ratio. Data on biochemical disease activity based on maximal urinary PBG were used to assess the correlation between biochemical AHP activity and cancer risk.

**Results:** We identified 1, 245 patients with AHP between 1987 and 2015 with a median follow-up of 19 years. Health registries identified 180 AHP-subjects (12.2%) with non-hepatic cancer, similar to 1607 non-AHP subjects (12.3%) in the matched reference population (n = 12, 367). Preliminary results indicate that AHP patients have a higher risk of kidney cancer 0.8% (n = 10) vs. 0.2% (n = 27) in the matched reference population (p < 0.001, confirming findings in previous smaller cohorts. The risks of other common forms of cancer are however not significantly different in patients with AHP compared to the reference population. More detailed risk estimates regarding each cancer type, combined with subgroup analysis based on biochemical AHP-activity will be presented at the conference.

**Conclusion:** In addition to the increased risk of hepatocellular carcinoma, patients with AHP have an increased risk of kidney cancer. Preliminary results have not identified increased risks for other non-hepatic cancers.

**FRI276**

**Innovative approach using clinical metagenomics for the diagnosis of non-elucidated liver disease**

Anna Sessa1,2, Christophe Rodriguez3, Julien Calderaro1, Slim Fournat1, Giulianna Amandeo4, Jean-Michel Pawlotsky1, Vincent Leroy3, 1APHP, Hopital Henri Mondor, Hepatology, Créteil, France; 2Henri Mondor Hospital, Hepatology, Créteil, France; 3APHP, Hopital Henri Mondor, Hepatology, Créteil, France; 4APHP, Hopital Henri Mondor, Hepatology, Créteil, France

Email: asessa1990@gmail.com

**Background and aims:** Diagnostic of acute and chronic liver diseases (CLD) may be challenging when main etiologies are absent. Liver histology usually provides hints but often fails to accurately identify the etiologic factor that can be toxic, genetic, auto-immune or infectious. Clinical metagenomics (CMg) is a new technique based on sequencing of nucleic acids allowing the identification of microorganisms in an exhaustive manner. Our aim was to evaluate the performance of CMg for the diagnosis of non-elucidated liver diseases.

**Method:** All patients seen between 2019 and 2021 in a single tertiary centre for a non-elucidated liver disease were included. Inclusion criteria were elevated biochemical liver tests with no definite diagnosis after a comprehensive work-up including a liver biopsy. Patients with known CLD could be included if their features were not consistent with the etiology. The cut-off of 6 months discriminated acute and chronic profiles. Shotgun metagenomics was performed on each liver biopsy specimen with the aim to detect unexpected microorganisms.

**Results:** 48 patients (median age: 49, male: 58%) were included. Their current presentations consisted of acute cytology with or without jaundice (n = 9, 19 %, median ALT: 284 IU/L), acute cholestasis or mixed pattern (n = 19, 40 %, median ALP: 225 IU/L), chronic cytology (n = 8, 16.7 %, median ALT 166 IU/L) and chronic cholestasis (n = 12, 25%, median ALP: 146 IU/L). 20 patients (42%) had immunosuppression due to solid organ transplantation (n = 9, 19%), HIV infection (n = 6, 13%) and hematopoietic cancer (n = 5, 10%). Results of CMg were negative in 36 (75%), false positive due to contamination in 3 (6%), and positive in 9 (19%) patients. In 7 patients, CMg results allowed an etiologic diagnosis that changed the clinical management. Pathogens identified were adenovirus in one patient presenting with acute hepatitis, HCV in one seronegative liver-transplant recipient with recently acquired infection, HBV in one patient with unexplained cytology and low HBV DNA, HDV in 2 seronegative HBsAg (+) patients, Mycobacterium spp in an HIV-infected patient with unexplained granulomatosis, and Shigobium spp in a cirrhotic patient presenting with uncommon ACLE. Additionally, 2 patients had positive results that were considered as putative cofactors. Pathogens were EBV in one HIV-infected patient with tuberculosis, and TTv in one patient on immunotherapy for hematopoietic cancer. Taking the whole population, a definitive diagnosis was eventually made after a comprehensive work-up combined to follow-up in 35 patients including 7 infectious diseases diagnosed by CMg (20%), and 13 patients remained with no definite diagnosis.

**Conclusion:** CMg performed on liver tissue is technically feasible and may bring etiologic diagnosis in patients with non-elucidated acute or chronic liver disease.

**FRI277**

**Accumulation of molybdenum in major organs following chronic oral administration of bis-choline tetrathiomolybdate in Sprague Dawley rats**

Khrmen Billimoria1, Timothy Morley2, Maria Estela del Castillo3, Stanislav Stekoptov3, Heidi Goenaga-Infante1, John Foster3, 1LGC, National Measurement Laboratory, Teddington, United Kingdom; 2Advotox, Harrogate, United Kingdom; 3LGC, National Screening Laboratory, Teddington, United Kingdom; 4ToxPath Sciences Ltd, Congleton

Email: khrmen.billimoria@LGCGroup.com

**Background and aims:** Molybdenum (Mo) is an essential dietary element, functioning as a cofactor to activate essential enzymes including sulphite, aldehyde and xanthine oxidases. Bis-choline tetrathiomolybdate (BC-TTM) is under development as a therapeutic copper chelating agent for Wilson Disease with doses administered ranging from 15 to 60 mg/day (equivalent to 0.2 to 0.9 mg/kg/day in a 70 kg man.). In a rat preclinical model (average bodyweight of 250 g), this would equate to a range of 0.8 to 3.6 mg/kg. The aim of this study was to determine if chronic administration of BC-TTM is associated with accumulation of molybdenum in major organs of a non-WD animal model and if tissue deposits of this metal are associated with haematological and biochemical abnormalities.
**Method:** Sprague Dawley (SD) rats were randomised to 3 groups of 12 [control, 15 mg/kg (low), 60 mg/kg (high)] and the BC-TTM was dosed by single oral gavage each day at volume of 5 ml/kg for 3 months. This drug exposure was equivalent to 3.75 to 15 mg/day in humans for nine years. Blood samples for clinical monitoring were taken at baseline, monthly and prior to euthanasia. Laser ablation inductively coupled plasma time-of-flight mass spectrometry (LA-ICP-ToF-MS) is an imaging technique used to confirm and spatially resolve the elemental distribution within a tissue. Tissue samples from major organs were prepared for conventional histopathology and LA-ICP-ToF-MS, to produce maps of Mo accumulation, quantified using a novel calibration strategy.

**Results:** Animals tolerated medication and no adverse clinical observations were made during the study. Dose dependent changes included increasing pigmentation of phagocytic and epithelial cells within each organ using conventional histopathological techniques were observed. However, data from LA-ICP-ToF-MS (Figure shown is from liver and brain) shows scaled spatial distribution of molybdenum deposits by concentration, increasing from blue to red. This accumulation was not associated with either biochemical or haematological abnormalities.

**Conclusion:** LA-ICP-ToF-MS demonstrated dose dependent Mo accumulation in major organs and our findings show the limitations of conventional histopathology to characterise these deposits. SD rats exposed to BC-TTM for 3 months did not exhibit blood or biochemical abnormalities; this may provide false reassurance of molybdenum accumulation following chronic exposure.

**FRI279**

Liver fibrosis and fat by transient elastography in patients with Alpha-1 antitrypsin deficiency

Hassaan Yousuf1, 2, Tobias Maharaj1, 2, Daniel Fraughen2, 3, Noel G. McElvaney1, 3, John Ryan1, 2, Beaumont Hospital, Hepatology, Dublin, Ireland; 2 Royal College of Surgeons in Ireland, Ireland; 3 Beaumont Hospital, Respiratory Medicine, Dublin, Ireland

Email: Hassaanmyousuf@hotmail.com

**Background and aims:** Alpha-1 Antitrypsin Deficiency (AATD) is a common, inherited disorder which can lead to significant morbidity and mortality. The most severe form is seen in individuals with the homozygous PiZZ variant, with almost no circulating levels of AAT, while heterozygous (PiMZ, PiSZ) variants are associated with milder disease. While AATD effects on the lungs have been extensively studied, its effects on the liver are poorly understood. Transient Elastography is widely used to stage liver disease by liver stiffness measurement (LSM), and provides a measure of hepatic steatosis, the Controlled Attenuation Parameter (CAP).

**Method:** Clinical data along with TE measurement was obtained on adult patients attending a dedicated AATD at our centre over a 4-month period (July – October 2021). LSM cutoffs used were >7.1 kPa for fibrosis, and >10 kPa for advanced fibrosis/cirrhosis

**Results:** 80 patients were recruited; TE failed on 4 patients; 48 (60%) were female. 39/80 (48%) were homozygous PiZZ, 24/80 PiMZ (30%), 12 PiSZ and 4 were PiSS. 29/76 (38%) had LSM >7.1 KPa; of these 12 (16%) had LSM >10 KPa. Of the patients with advanced fibrosis, 8 were PiZZ, 2 were PiMZ and 1 each of PiSZ and PiMS. 16/39 (41%) PiZZ had evidence of fibrosis; 9 PiMZ (37.5%) had evidence of fibrosis, but only 2 had advanced fibrosis.

For PiZZ homozygotes, the median LSM was 6.3 kPa, and 6.25 kPa for heterozygotes (PiMZ/PiSZ); there was no significant difference in LSM between heterozygotes and homozygotes (Mann-Whitney U test, p = 0.84).

The median CAP for homozygotes PiZZ was 252 dB/m, and for heterozygotes (PiMZ/PiSZ) was 282.5 dB/m; there was no statistical significance between the 2 groups (Mann-Whitney U test p = 0.128). 6/12 (50%) individuals with advanced fibrosis were obese (BMI >30 kg/m²). In total 17 out of 29 (59%) patients with evidence of fibrosis were either overweight or obese. Of the 29 individuals found to have liver fibrosis by TE, only 6 were known to have chronic liver disease, the rest (79%) were all new diagnoses.

Among the patients with PFTs available, fibrosis was evident on TE in 3/14 (21.4%) patients with GOLD stage IV COPD, 4/14 (28.5%) with GOLD stage II/III COPD, and 10/34 (29.4%) with GOLD stage 0.

**Conclusion:** In this study, a high rate of undiagnosed advanced liver fibrosis in AATD individuals was evident on routine screening using transient elastography. No association between lung and liver disease severity was noted, nor were there significant differences in liver stiffness or steatosis between AATD genotypes. Of note, a high prevalence of overweight/obesity was seen in those with liver fibrosis.
This study highlights the importance of screening AATD patients for liver fibrosis, and the potential clinical utility of transient elastography for these patients.

**FRI280**

**Novel imaging feature in patients with porto-sinusoidal vascular disorder (PSVD)-radiological evaluation guiding diagnosis**

Georg Semmler1,2, Katharina Lampichler1, Katharina Wörnan4, Benedikt Simbrunner1,2, Mathias Jachs3,2, Lukas Hartl1,2, David J. M. Bauer1,2, Lorenz Balcar1,2, Matthias Pinter1,2, Michael Trauner1, Mattias Mandofer1,2, Dietmar Tamandl3, Judith Stift4, Ahmed Ba-Ssalamah1, Thomas Reiberger1,2, Georg Semmler1,2, Katharina Lampichler3, Katharina Wöran4, Benedikt Simbrunner1,2, Mathias Jachs3,2, Lukas Hartl1,2, David J. M. Bauer1,2, Lorenz Balcar1,2, Matthias Pinter1,2, Michael Trauner1, Mattias Mandofer1,2, Dietmar Tamandl3, Judith Stift4, Ahmed Ba-Ssalamah1, Thomas Reiberger1,2, Martina Scharitzer3, Bernhard Scheiner3,4, 1Medical University of Vienna, Division of Gastroenterology and Hepatology, Department of Internal Medicine III, Vienna, Austria; 2Medical University of Vienna, Vienna Hepatic Hemodynamic Lab, Division of Gastroenterology and Hepatology, Department of Internal Medicine III, Vienna, Austria; 3Medical University of Vienna, Department of Biomedical Imaging and Image-Guided Therapy, Vienna, Austria; 4Medical University of Vienna, Clinical Institute of Pathology, Vienna, Austria

**Background and aims:** Porto-sinusoidal vascular disorder (PSVD) is a recently defined vascular liver disease often complicated by pre-sinusoidal portal hypertension (PH). Diagnosis is challenging and requires liver biopsy, and thus, PSVD is often misdiagnosed as cirrhosis. We investigated radiological features that are distinct between PSVD and cirrhosis.

**Method:** Demographic, clinical and laboratory parameters of patients with histologically-confirmed PSVD vs. cirrhosis vs. non-cirrhotic liver disease and available CT/MRI scans were retrospectively evaluated. The following imaging features were analyzed: Portosystemic collaterals, ascites, splanchic vein thrombosis, spleen size, portal tract abnormalities, perfusion disorders, FNH-like lesions, changes in liver morphology and liver surface nodularity.

**Results:** 54 PSVD, 156 cirrhosis, and 41 non-cirrhotic patients were included. PSVD patients were younger (45.6 ± 16.3 vs. 56.4 ± 12.8, p < 0.001) and had lower HVPG (8 [IQR: 5–12] mmHg vs. 15 [IQR: 10–21] mmHg, p < 0.001), liver stiffness (8.4 [IQR: 6.8–12.2] kPa vs. 29.2 [IQR: 16.0–65.1] kPa, p < 0.001), and MELD (9 ± 3 vs. 13 ± 6 points, p < 0.001). Specific clinical signs of PH according to PSVD-definition were similarly common in both groups. Intrahepatic portal tract abnormalities (52% vs. 15%; p < 0.001), splanchic vein thrombosis (24% vs. 12%; p = 0.025) and FNH-like lesions (33% vs. 1%; p < 0.001) were significantly more common in PSVD patients. Hypertrophy of segment I (43% vs. 69%; p < 0.001), atrophy of segment IV (24% vs. 46%; p = 0.004) and nodular liver surface (19% vs. 87%; p < 0.001) were more common in patients with cirrhosis. In patients with adequate gadoxetic acid-enhanced MRI (PSVD: n = 25, cirrhosis: n = 95, non-cirrhotic controls: n = 41), we identified the imaging feature of ‘periportal hyperintensity’ in the hepatobiliary phase (HBP) as very specific for patients with PSVD: 52% in patients with PSVD vs. 1% in cirrhosis vs. 0% in non-cirrhotic controls; p < 0.001).

**Conclusion:** Diagnosis of PSVD must be considered in younger patients presenting with clinical features of PH, portal tract abnormalities, splanchic vein thrombosis, and FNH-like lesions on CT/MRI. ‘Periportal hyperintensity’ on HBP-MRI was identified as a very specific radiological feature of PSVD patients.

**FRI281**

**Liver involvement in systemic light chain amyloidosis: is the heart guilty?**

Margaux Charles1, Amira Zarouri2, Sebastien Mulé2, Françoise Roudot Thoraval3, Christophe Duvoux1, Danny Thibaud2, Edouard Rezine3, Vincent Leroy4, 1Hôpital Henri Mondor, Hepatology, Créteil, France; 2Hôpital Henri Mondor, Cardiology, Créteil, France; 3Hôpital Henri Mondor, Radiology, Créteil, France; 4Hôpital Henri Mondor, Hepatology, Créteil, France

**Background and aims:** Systemic light-chain (AL) amyloidosis is a systemic disease caused by the deposition in organs of unstable monoclonal light chains secreted by clonal plasma cells. Prognosis is mainly related to the degree of cardiac involvement. Elevated liver enzymes and/or hepatomegaly are frequently observed and may be related to deposition of amyloid fibrils in the liver, congestive hepatopathy or confounding factors such as DILI. Diagnostic approach for hepatologists can be extremely challenging, with certain reluctance to perform liver biopsies. The aim of our study was to describe in a large cohort of patients with cardiac AL amyloidosis the characteristics of liver abnormalities, their relationships with cardiac status and their potential prognostic value.

**Method:** All patients seen from 2008 and 2021 in a single national reference centre for new diagnosis of histologically proven AL amyloidosis with cardiac involvement and available longitudinal liver features were included. Clinical, biological and echocardiographic data were collected. Liver imaging mainly consisted of MRI, or when not available CT-scan. All images were read by a single expert radiologist with specific attention to liver morphometry and signs of congestion.

**Results:** 200 patients (median age: 66 years, male: 61%) were included. The majority of them had severe heart failure (stage III of Mayo Clinic). Chemotherapy was given in 90% of patients. At baseline, 98 (49%) patients had elevated liver enzymes greater than 1.5 fold the upper limit of normal. Liver abnormalities were associated to higher Pro-BNP and Troponin serum levels. Enzyme patterns were cholestatics, cytolsis and mixed in 81%, 4% and 15%, respectively. Liver abnormalities were significantly associated with higher concentrations of troponin and Pro-BNP. Liver imaging showed hepatomegaly.
in 31% of cases, sinusoidal dilation in 43% and hepatic vein dilatation in 26%. Compared to patients with normal liver tests, the cholestatic pattern group had more often hepatic vein dilatation (40% vs 12%, p < 0.006) and sinusoidal dilatation (57% vs 30%, p < 0.04), these features being significantly associated with lower cardiac flow and echocardiographic features of right ventricular dysfunction. There was no association between liver abnormalities and left ventricular ejection fraction. A liver biopsy was performed in 11 patients and showed amyloid deposits in 9 and features of congestion in 5 patients. During the follow-up, a significant increase of liver tests was observed after 3 months. A cytolysis pattern was associated with a peak of Pro-BNP and short-term mortality.

**Conclusion:** Liver involvement is frequent in patients with cardiac AL amyloidosis and seems mainly related to right cardiac dysfunction. The potential role of hepatic amyloid deposits is under investigation by scintigraphy and final results will be presented.

**FRI282**

**The role of the mechanistic target of rapamycin (mTOR) in Alpha-1 Antitrypsin Deficiency**

Lisa Bewersdorf1, Pavel Strnad1, Anniha Gross1, Yizhao Luo1, Thorsten Cramer2, 1University Hospital RWTH Aachen, Medical Clinic III, Aachen, Germany; 2University Hospital RWTH Aachen, Clinic for General, Visceral and Transplant Surgery, Aachen, Germany

**Background and aims:** Alpha1-antitrypsin (AAT) mutations lead to the retention of the otherwise secreted hepatocellular protein in the endoplasmic reticulum (ER) thereby giving rise to AAT’s deficiency (AATD). Liver disease arising due to the proteotoxic stress is the second leading cause of mortality in AATD. mTOR signalling acts as the central proteostatic regulator. Our aim was to study the importance of mTOR signalling in AATD.

**Method:** Animals overexpressing the characteristic AAT mutation (PiZ mice) were crossed-bred with rodents harboring a hepatocyte-specific-ablation of the interaction partners RAPTOR/RICTOR corresponding to mTOR complexes 1/2 (mTORC1/2) or with mice lacking hepatocellular mTOR.

**Results:** At two month of age, PiZ-mTORΔhep and PiZ-RICTORΔhep mice showed elevated liver enzyme levels, signs of increased liver injury and apoptosis despite diminished AAT accumulation. While PiZ-RICTORΔhep animals displayed increased levels of the pro-apoptotic protein CHOP, CHOP ablation did not rescue the phenotype. As a potential underlying mechanism, we observed reduced levels of several chaperones, i.e., Hsp90 or Grp94.

**Conclusion:** mTORC1 but not mTORC2 plays an important role in PiZ induced liver injury.

**FRI283**

**Cerebrotendinous xanthomatosis: long-term course in 5 patients and first description of a successful pregnancy management during therapy with chenodesoxycholic acid (CDCA)**

Jan Köhler1, David Schoeler1, Petra May1, Linus Mrzek1, Renate Kimmerle2, Tom Lüdde1, Stephan vom Dahl1, 1University Hospital Düsseldorf, Heinrich-Heine-University, Department of Gastroenterology, Hepatology and Infectious Diseases, Düsseldorf, Germany; 2Endokrinologische Schwerpunktpraxis, Düsseldorf, Germany

**Background and aims:** Cerebrotendinous xanthomatosis (OMIM #231700) is a rare autosomal-recessive bile acid synthesis defect due to defective mitochondrial sterol 27-hydroxylase CYP27A1, leading to tendon xanthomas, bilateral cataracts, diarrhea and progressive neurologic manifestations. Patients are usually diagnosed during adulthood. Oral therapy with CDCA, a bile acid, reverses the potentially debilitating symptoms and prolongs life span. To our knowledge, this is the first description of a successful pregnancy with CTX.

**Method:** After biochemical diagnosis, CTX patients were monitored in 6-month intervals with abdominal ultrasound, cMR imaging, ophthalmologic examinations and determination of cholestanol blood levels. Therapy with CDCA (10–15 mg/kg body wt.) was initiated along with lipid-lowering combination therapy and in one female patient, after positive pregnancy testing in 2019, CDCA was continued and monitoring intervals were shortened.

**Results:** Three siblings, their mother and aunt from a consanguinous family were diagnosed with CTX at ages of 38, 27, 18, 14, and 9 respectively. The aunt was diagnosed in 1997, the mother in 2003 and the siblings in 2005. Mean follow-up in this cohort was 18 ± 2 years. At baseline, tendon xanthomas were present in 4/5, diarrhea and ataxia in 1/5, hypercholesterolemia and hypertriglyceridemia in all patients. 3/5 patients suffered from cataracts and required surgical therapy. Slight cognitive impairment occurred in 4/5 patients. Ataxia and diarrhea subsided. Total cholesterol (TC), LDL-C, and HDL-C at baseline were 217 ± 16 mg/dl, 108 ± 15 mg/dl and 77 ± 5 mg/dl and were reduced to 195 ± 7 mg/dl, 115 ± 12 mg/dl and 53 mg/dl ± 6 mg/dl at last visit. Peri- and postpartum cholestanol levels and 7α-hydroxycholesterol were 3.1 ± 0.2 mg/dl (ref. range 0.21 to 0.67 mg/dl) and 3857 ± 802 ng/ml (ref. range <0.5 ng/ml) decreased to 0.3 ± 0.02 mg/dl and 76 ± 10 ng/dl. In a pregnant patient, blood cholesterol and cholestanol levels were stable, and after an uncomplicated pregnancy, she gave birth to a healthy baby boy in term on 08/2020, who was age appropriate and reached normal developmental milestones up to now.

**Conclusion:** Oral CDCA therapy can help stabilize/reverts the control clinical symptoms of CTX and can successfully be continued during pregnancy. CTX is underdiagnosed and should be suspected in any adult dyslipidemic patients with heterogeneous neurologic manifestations and cataracts.

**FRI284**

**A rare genetic variant in the manganese transporter SLC30A10 and elevated liver enzymes in the general population**

Anne-Sofie Seidelin1, Borge Nordestgaard2, Anne Tybjerg Hansen1, Hanieh Yaghootkar3, Stefan Stender1, 1Rigshospitalet, Clinical Biochemistry, København, Denmark; 2Herlev Hospital, Clinical Biochemistry, Herlev, Denmark; 3University of Exeter, United Kingdom

**Background and aim:** A rare genetic variant in the manganese transporter SLC30A10 (rs188273166) was associated with increased plasma alanine transaminase (ALT) in a recent genome-wide association study in the UK Biobank (UKB). The aims of the present study were to validate the association of rs188273166 with ALT in an independent cohort, and to begin to test the clinical, hepatic and biochemical phenotypes associated with the variant.

**Method:** We included n = 334,886 white participants from UKB, including 14,462 with hepatic magnetic resonance imaging (MRI), and n = 113,612 individuals from two Danish general population cohorts, the Copenhagen City Heart Study and the Copenhagen General Population Study combined.

**Results:** Genotyping SLC30A10 pThr95Ile identified 816 heterozygotes in the UKB and 111 heterozygotes in the Copenhagen cohort. Compared to non-carriers, heterozygotes had 4 U/L and 5 U/L higher levels of plasma ALT in the UKB and Copenhagen cohort, respectively, and 3 U/L higher plasma aspartate transaminase and gamma glutamyl-transferase in the UKB. Heterozygotes also had an eight-fold increased risk of biliary tract cancer in UKB (p = 5 × 10−7), but no change in MRI-quantified steatosis (p = 0.57). SLC30A10 pThr95Ile heterozygotes had an eight-fold increased risk of biliary tract cancer in UKB (p = 5 × 10−7), but this association was not replicated in the Copenhagen cohort.

**Conclusion:**
Conclusion: SLC30A10 p.Thr95Ile was associated with elevated liver enzymes in two large general population cohorts, and with MRI-quantified hepatic inflammation. We hypothesize that Thr95Ile heterozygosity associates with a mild form of hepatic manganese accumulation leading to liver damage.

FRI285
A small molecule chaperone for alpha-1 antitrypsin deficiency-associated liver disease reduces liver polymer burden in the PiZ mouse model
Britta Handyside1, Lening Zhang1, Katina Ngo1, Ryan Murphy1, Joseph Chen1, Nicole Galicia1, Olivia Gorostiza1, Glenn Pacheco1, Lin Xie1, Donald Mackenzie1, Heidi Jones1, Brian Heglar1, Bing Wang1, Shripad Bhagwat1, David Lomas1, James Irving2, Riccardo Ronzoni2, Sherry Bullens1, Sylvia Fong1, Stuart Bunting1, 2BioMarin Pharmaceutical Inc., Novato, United States; 2University College London, S534 Journal of Hepatology

 backgrounds and aims: Alpha-1 antitrypsin deficiency (AATD) is caused by mutations in the SERPINA1 gene encoding alpha-1 antitrypsin (AAT). AAT is primarily produced by hepatocytes and is secreted into the blood stream where it functions as a neutrophil elastase inhibitor.
The most clinically severe form of AATD is caused by the Z mutation (Glu342Lys) resulting in expression of the mutant protein Z-AAT. Pathogenic Z-AAT protein can misfold, polymerize and accumulate in the endoplasmic reticulum (ER) of hepatocytes leading to progressive liver fibrosis and low levels of circulating AAT. There is currently no effective treatment for AATD-associated liver disease. Here we tested BMN 349, a molecular chaperone, for its ability to prevent Z-AAT polymerization in hepatocytes while increasing circulating Z-AAT in the PiZ mouse, a model for AATD-associated liver disease. Method: Young (5 week) and adult (12 week) female heterozygous PiZ mice expressing human Z-AAT were treated twice daily for 30 days with 50 or 100 mg/kg of BMN 349 via oral gavage (10–13 mice per group). Plasma and liver Z-AAT levels were analyzed by ELISA, Z-AAT polymer globules in hepatocytes were evaluated using periodic Acid-Schiff with Diastase (PAS-D) stains. Liver and plasma pharmacodynamic biomarkers were assessed using mass spectrometry-based proteomics.
Results: Treatment with BMN 349 increased levels of circulating Z-AAT and reduced liver polymer levels in both age groups. In adult mice a dose-response was observed with a liver polymer reduction of 33% with 50 mg/kg (p = 0.00098) and 49% with 100 mg/kg (p < 0.0001) of BMN 349 compared to vehicle as determined by ELISA. Histological analysis using the PAS-D stain confirmed a significant reduction in liver Z-AAT polymer globules by 25% (p = 0.0008) and by 34% (p = 0.0232) with 50 or 100 mg/kg of BMN 349, respectively. In young mice, a greater than 80% reduction in liver polymers was detected by ELISA (p < 0.0001) and a >85% reduction of Z-AAT polymer globules (p < 0.0001) was observed with either dose of BMN 349 compared to vehicle. Together, the data from both age groups showed that a greater effect on liver polymer burden was achieved when treatment was initiated early. Proteomics analysis revealed an increase in ER stress markers including GRP78 in PiZ mouse liver and plasma and reduced levels of circulating liver-derived clotting factor VII in PiZ mouse plasma compared to wildtype mice, suggesting impaired liver function. Treatment with BMN 349 resulted in a significant decrease of GRP78 and increase of FVII towards wildtype levels, demonstrating BMN 349 helped reduce cellular stress and restore normal biosynthetic function of the liver in PiZ mice in addition to reducing liver polymer burden.
Conclusion: Taken together, these data indicate that BMN 349 is effective in reducing Z-AAT polymer burden, reversing liver damage, and restoring liver function in the PiZ mouse model.

FRI286 A ‘melting pot’ of genetic variability in Wilson’s disease-real world study from London, UK
James Liu Yin1, Aftab Ala1, ‘King’s College Hospital, Institute of Liver Studies, London, United Kingdom
Email: aftab.alal@nhs.net

Background and aims: Wilson’s disease (WD) has been shown to have more than 600 different variants causing abnormal function of the ATP7B peptide. There is wide global diversity in these variants with different variants appearing to be more prominent in certain geographical areas and populations than others. London, UK is one of the largest, ethnically diverse cities in Western Europe with a growing population of over 9 million. It receives over 100,000 international migrants a year, with the largest proportions from the European Union and Indian Subcontinent. We aimed to review the genetic results from King’s College Hospital, London from patients with abnormal WD genetics and compare this to known global distribution.
Method: We retrospectively collected data on all WD genetic testing done at KCH since becoming one of the national testing centres (2015-present). We further extracted information on specific cDNA, protein change and zygosity status. We subsequently used WilsonGen, (Comprehensive genomic variant resource) which has compiled the largest database of variants, (2267 entries currently) to compare whether our variants were unique or previously documented.
Results: We identified 207 WD patients, 30 homozygous, 91 compound heterozygotes and 86 heterozygotes (Mean 28.5 years, range 4–70). Within this, there were 113 different variants identified. The most common was His1069Gln (11%), followed by Cys271Ter (3.6%), Met769Val (3.6%) and Ser1365fs (3.2%). On comparison with the WilsonGen database we found that 44 variants were not listed on their records (38.9%). We had ethnicity data accessible for 137 patients, 49% were documented as unspecified and the remaining were: Caucasian (35%), Indian Subcontinent (7%), Middle Eastern (4%), Black/Caribbean (3%), Chinese (1%) and other (<1%).
Conclusion: Our results demonstrate significant genetic variation in London with the most common mutation only accounting for 11% of the overall total. As genetic testing becomes a more utilized tool in forthcoming diagnostic pathways we need to understand that this variation may have significance. A recently suggested ATP7B-mutation specific diagnostic test would be less effective in a population like London and other Metropolitan cities. This needs to be taken into account in further studies to ensure that genetic variation will not delay or prevent diagnosis of new cases.

The importance of ATP7B genetic variation is yet to be fully understood and characterised with respect to the pathogenesis of WD. Within our cohort, the presence of novel variants was 39% which is a significant portion and higher than previously reported UK data (27% Coffey et al). Considering the wide spread of variation including novel variants, specific mutations have not been shown to confer benefit thus far and therefore further understanding of its significance is needed.

S534 Journal of Hepatology 2022 vol. 77(S1) S569–S564
The alpha-1 antitrypsin Pi*Z allele is an independent risk factor for liver transplantation/death in patients with advanced chronic liver disease

Background and aims: Alpha-1 antitrypsin (AAT) deficiency causes/predisposes for advanced chronic liver disease (ACLD). However, the role of the SERPINA1 Pi*Z allele in patients who have already progressed to ACLD is unclear. Thus, we aimed to evaluate the impact of the Pi*Z allele on the requirement of liver transplantation/liver-related death in ACLD, while adjusting for the severity of liver disease at inclusion.

Method: 1118 ACLD patients who underwent HVPG-measurement and genotyping for the Pi*Z/Pi*S allele at the Vienna Hepatic Hemodynamic Lab were included in this retrospective analysis. Requirement of liver transplantation/liver-related death was the outcome of interest, while non-liver-related death and removal of the primary etiological factor were considered as competing risks.

Results: Viral hepatitis was the most common etiology (44%), followed by alcoholic (31%) and non-alcoholic fatty liver disease (11%). Forty-two (4%) and forty-six (4%) patients harboured the Pi*Z and Pi*S variants, respectively. Pi*Z carriers had more severe portal hypertension (HVPG: 19 ± 6 vs. 15 ± 7 mmHg; p < 0.001) and hepatic dysfunction (Child-Turcotte-Pugh: 7.1 ± 1.9 vs. 6.5 ± 1.9 points; p = 0.050) at inclusion, as compared to non-carriers. Contrarily, the Pi*S allele was unrelated to liver disease severity.

In competing risk regression analysis, harbouring the Pi*Z allele was significantly associated with an increased probability of liver transplantation/liver-related death (Figure), even after adjusting for liver disease severity at inclusion. The detrimental impact of the common Pi*MZ genotype (vs. Pi*MM) was confirmed in a fully adjusted subgroup analysis. In contrast, Pi*S carriers had no increased risk for events.

Conclusion: Genotyping for the Pi*Z allele identifies ACLD patients at increased risk for adverse liver-related outcomes, thereby improving prognostication. Therapies targeting accumulated abnormal AAT should be evaluated as disease-modifying treatments in Pi*Z allele carriers with ACLD.
are needed in pediatric biliary cirrhosis to delay liver transplantation, our aim was to investigate the presence of premature senescence in biliary atresia (BA) and to test the senolytic properties of Medicinal Signaling Cells in a preclinical model of biliary cirrhosis.

Method: Senescence was investigated through senescence-associated β-galactosidase activity assay (SA-beta-gal) as well as p16 and p21 gene/protein expression in BA livers at the time of hepatoporate-toxotomy (n = 5) or liver transplantation (n = 30) as compared to control livers (n = 10). Co-localized expression of senescence (gammaH2AX or p21) with CK19, HNF4alpha, alphaSMa and Ki67 was also assessed. Bile duct ligature (BDL) was performed on 2-months old rats and senescence was characterized in the model through above-mentioned techniques. Human allogeneic liver-derived progenitor cells (HALPC) were injected in BDL rats 48 hours after the surgery at high (12.5 × 10^6 cells/kg; n = 6) versus low dose (1.25 × 10^6 cells/kg; n = 6) and compared to the vehicle (n = 6).

Results: Senescence was similarly increased in both BA stages as compared to control livers (SA-beta-gal: 5.9 ± 1.4 and 5.4 ± 1 vs 0.6 ± 0.1 stained area/total, p < 0.01) and was also confirmed in BDL livers one and two weeks after the surgery (SA-beta-gal: 1.6 ± 0.6 and 6.6 ± 2.4 vs 0.2 ± 0.1 stained area/total, p < 0.05). The pattern of senescence in BA and BDL was similar as senescence first appeared in cholangiocytes of the ductular reaction and subsequently developed in hepatocytes. HALPC transplantation at both doses decreased senescence in BDL rats (p21 gene expression: 0.4 ± 0.04 and 0.5 ± 0.1 vs 1 ± 0.2 fold change; p < 0.05).

Conclusion: Premature senescence occurs in BA livers and HALPC display senolytic properties in a preclinical model of biliary cirrhosis.

FRI290
PNPLA3 rs738409 G allele increases the risk of liver cirrhosis in SERPINA1 MZ heterozygotes
Sona Frankova 1, Zuzana Rabekova 2, Magdalena Neroldova 3, Ondrej Fabian 4, Martin Kveton 5, Jaroslav A. Hubahcek 6, Julius Spicak 7, Vera Adamkova 8, Milan Jirsa 9, Jan Spertl 10
1 Institute for Clinical and Experimental Medicine, Department of Hepatogastroenterology, Prague, Czech Republic; 2 Institute for Clinical and Experimental Medicine, Department of Hepatogastroenterology, Prague, Czech Republic; 3 Institute for Clinical and Experimental Medicine, Laboratory of Experimental Hepatology, Prague, Czech Republic; 4 Institute for Clinical and Experimental Medicine, Department of Clinical and Transplant Pathology, Prague; 5 Institute for Clinical and Experimental Medicine, Atherosclerosis Research Laboratory, Prague; 6 Institute for Clinical and Experimental Medicine, Preventive Cardiology Centre, Prague, Czech Republic

Background and aims: Homozygous carriage of mutated Z allele in rs28929474 locus of SERPINA1 encoding alpha-1-antitrypsin (A1AT) leads to lung emphysema and liver cirrhosis. Recent data show that the SERPINA1 MZ genotype increases the risk of liver cirrhosis in patients with various liver diseases. The mechanism behind this finding has not been elucidated so far. Our study aimed to demonstrate the synergy between the SERPINA1 Z allele and unfavourable alleles in other liver disease-modifying genes.

Method: The study group consisted of 1079 liver transplant candidates with liver cirrhosis of various aetiology (642 males, 437 females, average age of 54 years). The aetiology of cirrhosis was as follows: 352 alcoholic, 309 cholestatic, 217 viral, 142 NASH, 59 metabolic. Patients with A1AT deficiency were excluded. The control group consisted of 3329 healthy individuals from the MONICA study group. Genomic DNA was isolated from peripheral blood by Qiagen QIAamp DNA Blood Kit (Qiagen, Hilden, Germany). SERPINA1 rs28929474, PNPLA3 rs738409, TM6SF9 rs58542926 and GCKR rs1260326 loci were genotyped by TaqMan RT-PCR SNP assays (Thermo Fisher Scientific, Waltham, MA). Aggregates of A1AT in hepatocytes in liver explants were stained by PAS-D and immunostained with an anti-A1AT polyclonal rabbit antibody (Cell Marque, Inc., Rocklin, CA, USA).

Results: The frequency of SERPINA1 MZ heterozygotes was significantly higher in the group with liver cirrhosis in comparison with the control group, 56/1079 (5.2%) vs. 89/3329 (2.7%), p < 0.0001, MZ heterozygotes thus have an increased risk of liver cirrhosis (OR 2.0, CI 95% 1.4–2.8).

Re-evaluation of 1009 histopathological reports of the explanted liver specimens revealed that PAS-D positive aggregates were detected in 52/56 (93%) MZ heterozygotes and 18/953 (1.9%) MM homozygotes (p < 0.0001). Forty-six out of 56 available specimens of MZ heterozygotes were assessed by immunohistochemistry; A1AT aggregates were confirmed in all cases. PNPLA3 rs738409 genotype frequencies were 21 CC (37.5%), 24 CG (42.9%), and 11 GG (19.6%) in 56 SERPINA1 MZ heterozygotes with cirrhosis and 59 CC (66.3%), 26 CG (29.2%) and 4 GG (4.5%) in 59 MZ heterozygotes in the control group. The frequency of the unfavourable PNPLA3 G allele was significantly higher in SERPINA1 MZ carriers with cirrhosis than in healthy heterozygotes, and the carriage of the PNPLA3 G allele increased the risk of liver cirrhosis (p = 0.001; OR = 3.278, CI 95% 1.633–6.581). Contrarily, the frequencies of the TM6SF2 and GCKR genotypes in SERPINA1 MZ heterozygotes did not differ significantly between the patients with cirrhosis and controls.

Conclusion: Our results suggest that the risk genotypes of PNPLA3 accelerate the progression of fibrosis in SERPINA1 MZ heterozygotes with chronic liver disease.

FRI291
Patient experience of their Primary Biliary Cholangitis (PBC) management compared to clinical practice guidelines
Chris Mitchell 1, Angela Eddy 2, James Neuberger 3
1 PBC Foundation, Edinburgh, United Kingdom; 2 PBC Foundation, Edinburgh, United Kingdom; 3 NHS, Birmingham Queen Elizabeth Medical Centre, Birmingham, United Kingdom
Email: chris@pbcfoundation.org.uk

Background and aims: Primary Biliary Cholangitis (PBC) is a chronic, cholestatic, autoimmune liver disease, which can have a profound impact on patients’ quality of life and a significant demand for healthcare services. PBC management guidelines were published in 2017 by European Association for the Study of the Liver (EASL), which include recommendations for daily dosage (13–15 mg/kg) of licensed first-line therapy (ursodeoxycholic acid (UDCA)) and referrals for alternative treatment if UDCA response is inadequate, of which obeticholic acid (OCA) is the only licensed treatment alongside other re-purposed agents.

This study explored the efficacy of patient– clinician collaborations to manage PBC in accordance with EASL guidelines from a patient perspective.

Method: A closed question questionnaire was designed focussing on the application of treatments and the inclusion of patients in the management of their PBC. The questionnaire was piloted with PBC Foundation service users during a focus group testing its reliability and face validity. A convenience sample was used and participants recruited via the PBC Foundation’s app during March 2022. Intercept Pharmaceuticals provided financial support and input into the questionnaire, however the PBC Foundation has retained editorial discretion over survey outputs.

Results: 172 patients completed the survey. 154 respondents (90%) take UDCA and 132 respondents (77%) received a timely UDCA prescription (0–3 months after diagnosis). 91% of UDCA patients believe they are taking the recommended dosage however only 54% of UDCA patients report taking dosage within guidelines.

Of those patients who are unresponsive or intolerant to UDCA, 68% were offered alternative treatment and 57% were included in discussions about the most suitable option.
22% of all patients take 2nd line treatment (5% OCA and 17% unlicensed). 8% of all patients take no treatment for PBC management.

54% of patients had no access to face-to-face clinical appointments and 39% had appointments delayed or cancelled during the COVID pandemic. Patient comfort in raising PBC related queries ranges from 86% in face-to-face meetings, 46% on the telephone and 31% on screen-calls.

Latest blood test results were discussed with 73% of patients. 50% of patients believe they understand their test results and 40% say their test results help them manage their PBC.

**Conclusion:** Unmet PBC patient needs are evident in numerous stages of the life-long clinical journey. Data indicates substantial disparity between published PBC treatment guidelines and actual care delivered to patients, particularly relating to optimal application of PBC management therapies and patient inclusion in important discussions (test results and further treatment referrals). Unmet needs have been exacerbated during the COVID pandemic when timely appointments in patients’ preferred formats were adversely affected.

**FRI292**
**Evaluation of the clinical impact of the Ceruloplasmin variant p.Thr551Ile in liver cirrhosis**

Marlene Panzer1,2, Benedikt Schaefer1, André Viveiros1, Herbert Tilg1, Heinz Zoller1,3, 1Medical University of Innsbruck, Department of Medicine I, Innsbruck, Austria; 2VASCage Research Center of Vascular Ageing and Stroke, Innsbruck, Austria; 3Christian Doppler Laboratory on Iron and Phosphate Biology, Innsbruck, Austria

**Background and aims:** Ceruloplasmin is a multicopper oxidase and is involved in cellular iron efflux. Aceruloplasminemia (ACP) is a recessive disease, caused by pathogenic variants in the gene encoding ceruloplasmin (CP). The disease is characterized by iron accumulation in liver, pancreas and brain. Patients typically present in their 5th decade of life with the triad of retinal degeneration, diabetes mellitus and neurodegeneration. Early biochemical signs of ACP include hyperferritinemia and low transferrin saturation. Recent reports suggest that heterozygous variants in CP can also cause hyperferritinemia and hepatic siderosis in patients with non-alcoholic fatty liver. The aim of the present study was to investigate the allele frequency and the clinical impact of the common ceruloplasmin variant p.Thr551Ile in an unselected cohort of patients with liver cirrhosis.

**Method:** A cohort of patients referred to the Hepatology Laboratory at the Medical University of Innsbruck for PNPLA3 genotyping was retrospectively assessed. Patients diagnosed with liver cirrhosis and available serum CP concentrations were included in this study (n = 568). Demographic, biochemical and clinical parameters were collected by review of patient records. Genotyping for the CP variant p.Thr551Ile (rs61733458) was performed by allelic discrimination PCR.

**Results:** Genotyping results revealed 2 homozygous and 27 heterozygous patients for p.Thr551Ile. This corresponds to an allele frequency of 2.73% (31 of 1136) in the liver cirrhosis cohort which is not different from the general population as reported in gnomAD (7795 of 282414; 2.76%). Biochemical surrogates of liver disease severity and serum iron parameters did not show significant differences when patients were stratified according to CP genotype. Reduced CP concentrations (≤20 mg/dL) were detected in 17.2% of patients carrying the variant p.Thr551Ile and in 11.7% in the normal group, which is not significantly different. Median CP concentrations were also numerically lower in patients heterozygous or homozygous for p.Thr551Ile, but this difference did not reach statistical significance (27.7 mg/dL vs 27.8 mg/dL; p = 0.368). Median time of transplant-free survival was significantly reduced in the group with decreased CP concentration (p = 0.004), but no significant difference in survival probability was observed when patients were stratified according to CP genotype. Cox regression analysis including age and NaMELD showed that CP serum concentration but not p.Thr551Ile genotype was an independent predictor of transplant-free survival.

**Conclusion:** Reduced serum ceruloplasmin is common in patients with liver cirrhosis and is independently associated with reduced transplant-free survival in unselected patients with cirrhosis. The CP variant p.Thr551Ile shows no association with serum iron parameters or transplant-free survival.

**FRI293**
**Circulating miR-21 parallels the incidence of IBD in PSC patients**

André A. Santos1,1, Joana Torres2, Susana Saraiva2, Catarina Ferreira Gouveia2, Catarina Bravo2, Marília Cravo2, Cecília M. P. Rodrigues1, 1Research Institute for Medicines (iMed. ULisboa), Faculty of Pharmacy, Universidade de Lisboa, Lisbon, Portugal; 2Hospital Beatriz, Angelo, Loures, Portugal

**Background and aims:** Primary sclerosing cholangitis (PSC) is a chronic and progressive cholestatic liver disease. The major risk factor for developing PSC is having a concomitant diagnosis of inflammatory bowel disease (IBD). Around 71% of PSC patients have IBD. Conversely, PSC is present in only 3–8% of patients with established IBD. Although both diseases run distinct courses, patients with PSC-IBD present a characteristic phenotype, contributing to a high risk of colitis-associated neoplasia. Recently, small non-coding RNAs such as microRNAs (miRNAs) have been correlated with disease onset and progression. miR-21, one of the most studied oncogenic miRNAs, is known to be overexpressed in IBD. Here we aim to further explore miR-21 in patients in a systematic manner and determine its contribution to the typical PSC-IBD phenotype.

**Method:** In this case-control study we included 12 patients in the PSC–IBD group, 30 patients in the IBD-alone group, and 19 patients in the control group. Serum samples were collected for fasting serum miR-21 expression. Stool samples were used for calprotectin analysis and miR-21 expression. Gut microbiome was investigated using next generation sequencing analysis. During colonoscopy, two biopsies in the right and left colon were performed and expression analysis of miR-21 and inflammation, tight junction and oncogene analysed. In statistical data analysis, outliers were removed (ROUT Q = 1%) and Kruskal-Wallis test or ANOVA Tukey’s multiple comparisons test were performed on non-parametric or parametric data, respectively.
Hepatocellular carcinoma in Fontan associated liver disease: uncharted territory—are we doing enough?

Michael Christmas1, Anthony Bergin 1, Wei Lian Tan 1, Myat Khaing 1, Lei Lin1, Yuming Ding1, Tony Rahman1, Ryan Maxwell2, Vishva Wijesekera2. 1The Prince Charles Hospital, Gastroenterology, Chermside, Australia; 2The Prince Charles Hospital, Cardiology, Chermside, Australia
Email: michael.christmas@health.qld.gov.au

Background and aims: Fontan associated liver disease (FALD) is a well-recognised consequence of the congestion and hypoxia created from the Fontan palliative procedure. Improved clinical management has led to significantly improved life expectancy and thus the paradigm of increased risk of developing FALD and HCC. There are no FALD specific surveillance guidelines for HCC. AASLD and EASL suggest biannual monitoring of serum alpha fetoprotein and ultrasound imaging as the gold standard for HCC screening in the cirrhotic population. This clinical audit seeks identify and audit compliance to the gold standard being offered in our Hepatology clinics.

Method: Retrospective analysis of Fontan patients and clinical, biochemical, radiological and endoscopic databases correlation was undertaken at the Hepatology clinic serving the quaternary regional referral centre for adult congenital heart diseases in Queensland (The Prince Charles Hospital, TPCH). Cirrhosis was identified in patients who had features identified on their liver ultrasound. The current conventional HCC screening requirements were then applied to identified patients. For each OGD, procedure indication, endoscopic findings and therapeutic interventions were noted.

Results: Seventy-two post-Fontan patients were identified from our database. Of which 49% (n = 35) were female with a mean age of 30.3 years. Only 44% (n = 32) had an OGD, the indications included variceal surveillance, iron deficiency and dyspepsia. Among the cirrhotic FALD patients (n = 32), only 43.7% (n = 14) had an OGD. Of this subgroup 22.8% (n = 7) had grade I oesophageal varices, none of which required treatment. None were taking primary prophylaxis.

Conclusion: FALD patients with cirrhosis should at least have one screening OGD. While 25% of our screened cirrhotic patients had varices, concerning only 43.7% had underwent an OGD. Future multi-centre collaborative research is needed to facilitate the development of guidelines on variceal surveillance for this growing cohort of FALD patients. The majority of cirrhotic patients in this cohort are linked in with a liver clinic. The young age of this cohort should not disguise or detract from the risk of cirrhosis and life threatening variceal bleeding. This study has identified an opportunity for education to improve the awareness and importance of variceal screening and this unique evolving population, for staff, patients and carers.
Method: We retrospectively analyze a monocentric cohort of WD patients with liver damage from a referral center for rare diseases. Patients of the cohort were regularly assessed with a maximal interval of 6 months. Patients with a history of cirrhosis had a bimonth ultrasound examination. Occurrence, treatment and outcome of primary liver tumors were analyzed.

Results: We analyzed 149 WD patients of the cohort, with a mean follow up of 15 years. The mean age at diagnosis of WD was 20.1 years. Sixteen patients were diagnosed with a primary liver tumor during follow up. The mean age at onset of a liver tumor was 52.5 years, with a mean interval between diagnosis of WD and occurrence of tumor of 19.2 years. We diagnosed a hepatocellular carcinoma (HCC) for 10 patients and a cholangiocarcinoma (CCK) for 6 patients. Histological proof could be obtained for 7/10 patients with HCC and for all patients (6/6) with CCK. For the 3 other patients, diagnosis of HCC was based on the morphological aspect (hyper vascular tumor with washout) and elevated AFP markers. All patients who developed a liver tumor had evidence of cirrhosis at the diagnosis of WD. At the diagnostic of tumor, there was no cirrhosis on the pathological examination of the non-tumoral liver for 6 patients (2/10 patients with histological proof of HCC and 4/6 patients with CCK). For all patients with primary liver tumor, a treatment could be proposed. Resection was possible for 8 patients and liver transplantation for 5 patients. During follow up, six patients died from complications of tumor extension (3 from HCC and 3 from CCK).

Conclusion: WD patients with history of cirrhosis are at risk of developing primary liver tumor and require morphological screening, even if there is a regression of fibrosis. The proportion of CCK (37.5%) among these tumors suggests an interest of the biopsy for diagnosis of liver cancer in WD patients.

FRI297 Defining the boundaries for “stability” in Wilson disease patients on maintenance chelation therapy: lessons from the CHELATE trial
C. Omar Kamlin1, Michael Schilsky2, Peter Ott3, Karl Heinz Weiss4, Massimo Giovanni Zuin5, Aurelia Poujois6, Aftab Al7, Koenraad D’Hollander8, 1Orphalan SA France, Medical Affairs, London, United Kingdom; 2Yale University, Division of Internal Medicine and Liver Unit, United States; 3Aarhus University Hospital, Aarhus, Denmark; 4Salem Medical Center, Heidelberg, Germany; 5University of Milan, Milan, Italy; 6Fondation Hospital Rothschild, Department of Neurology, Paris; 7Kings College University Hospital, London, United Kingdom; 8International Drug Development Institute (IDDI), Belgium
Email: omarkamlin@doctors.org.uk

Background and aims: “Clinical stability” of patients with Wilson disease (WD) is a treatment goal for long-term maintenance therapy and a desired entry point for intervention trials. The present study aimed to define biochemical stability in Wilson disease patients on maintenance chelation therapy.

Method: We performed a secondary analysis of published guidance and practice opportunities for biochemical screen failures to re-enter trial were made to improve trial feasibility. We reviewed day 1 data for all screened patients.

Results: Twenty-five of 76 (33%) screened patients had NCC-Sp <50 mcg/L at first sampling, majority (20/25) between 25 and 50 mcg/L. The mean (SD) age was 40.4 (14.3) years; 13 were female. Serum NCC-Sp, UCE, ALT and dose of DPA in mg/kg are shown in the Table. For comparison, graphs of NCC-Sp and NCC-Ex versus UCE at screening are shown in the figure. Though a wide range of UCE was observed, UCE and NCC had a positive correlation. Two subjects with ALT >ULN of 54 (73 and 61) U/L, had corresponding NCC-Sp of 41 and 44.8 mcg/L respectively. UCE ranged widely, however mean UCE was within 200–500. Dose of DPA was 13.2 ± 3.5 mg/kg (7.4–19), within the recommended guidance of 10–15. Sixteen (64%) with NCC -Sp <50, including 3/4 who underwent re-screening, were randomized.

FRI298 Precision-cut liver slices as an ex vivo model to assess impaired hepatic glucose production
Kishore Alagere Krishnamurthy1, Ligia Akemi Kiyuna1, Miriam Langelaar1, Albert Gerding1, Trijnie Bos1, Dorenda Oosterhuis2, Peter Olinga2, Karen Van Eunen1, Barbara Bakker1, Maaike Oosterveer1, 1University Medical Center Groningen, Groningen, Netherlands; 2University of Groningen, Groningen, Netherlands
Email: a.k.kishore@umcg.nl

Background and aims: Disturbed glucose metabolism is a common feature of metabolic diseases. For example, fasting hypoglycemia is a severe symptom of various inborn errors of metabolism, among which glycogen storage disease type 1 (GSD I). Due to the liver’s central role in endogenous glucose production, the availability of a liver-specific ex vivo model will enable unravelling the mechanisms underlying perturbed glucose homeostasis. Given the limitations of in vitro hepatocyte cultures (e.g. reduced Glucose-6-phosphatase activity, proliferative nature), this study aims to optimize and characterize precision-cut liver slices (PCLS), both from the human and murine liver, as a model to study hepatic glucose production ex vivo.

Table: Patients with Serum NCC-Sp <50 mcg/L at trial screening

<table>
<thead>
<tr>
<th>NCC-Sp (mcg/L)</th>
<th>Mean</th>
<th>Max</th>
<th>Min</th>
<th>SD</th>
</tr>
</thead>
<tbody>
<tr>
<td>32.4</td>
<td>46.9</td>
<td>170</td>
<td>8.9</td>
<td></td>
</tr>
<tr>
<td>NCC-Ex</td>
<td>36.5</td>
<td>48.8</td>
<td>13.1</td>
<td>8.5</td>
</tr>
<tr>
<td>UCE (mg/24 hr)</td>
<td>475</td>
<td>798</td>
<td>47</td>
<td>221</td>
</tr>
<tr>
<td>ALT (U/L)</td>
<td>26</td>
<td>73</td>
<td>6</td>
<td>16.3</td>
</tr>
<tr>
<td>DPA dose (mg/kg)</td>
<td>13.2</td>
<td>19.0</td>
<td>7.4</td>
<td>3.5</td>
</tr>
</tbody>
</table>

Conclusion: Re-screening of patients in clinical trials of rare disease facilitates recruitment. Single and multiple biochemical parameter analyses are helpful in defining the boundaries for “stability” of WD patients and lower values of NCC are common with the optimal lower limit requiring further study. Dosing in patients with very low NCC (<25 mcg/L) should be re-evaluated to avoid overtreatment. NCC may be a useful parameter for response guided dosing of therapy for chelation in WD.
Method: PCLS were prepared from fed and 12h-fasted male C57BL/6 mice and incubated in Williams E glucose-free medium supplemented with gluconeogenic precursors: (1) 10 mM glycerol, (2) 20 mM lactate plus 2 mM pyruvate, or (3) 10 mM dihydroxyacetone (DHA). Net cumulative glucose production was assessed at different time intervals (2 h–24 h). The amino acids in the medium and slice glycogen content were quantified at different time points to assess the source of glucose. Additionally, the efficacy of glucose production in response to fatty acid supplementation (500 μM palmitate), hormonal (0.1–1 μM glucagon or insulin), and pharmacological (10–20 μM forskolin or 50–100 μM dibutyryl-cAMP) stimulation were evaluated. Finally, to study GSD type 1 ex vivo, we used either PCLS derived from GSD Ia/Ib mouse models (L-G6PC−/− and L-SLC37A4−/−) or subjected wildtype PCLS to pharmacological inhibition of G6P exchanger SLC37A4 (S4048).

Results: PCLS derived from fed and fasted mice produced glucose, both in the presence and absence of gluconeogenic precursors. The glycogen content in the PCLS was substantially and equally reduced in all conditions after 5 h in culture. No substantial changes were observed in the amino acid concentrations in any condition. Both forskolin and dibutyryl-cAMP increased net cumulative glucose production, while palmitate, glucagon or insulin did not alter glucose production. Lastly, PCLS from both pharmacological and genetic models of GSD type 1 showed markedly reduced glucose production and elevated lactate production, in line with the clinical disease phenotype.

Conclusion: PCLS can be used to study glucose production ex vivo up to 24 h in culture and DHA seems to result in the higher net glucose production. In ongoing follow-up experiments, 13C-labelled DHA and/or glycerol are used to test their role as a gluconeogenic precursor or a gluconeogenic regulator. Finally, PCLS offer the possibility to use patient liver biopsy, murine genetic models and pharmacological intervention. Hence, they are an excellent and promising ex vivo platform to study endogenous glucose production in GSD type 1 and other inborn errors of metabolism.

FRI299
Interim 52-week analysis of immunogenicity to the vector capsid and transgene-expressed human FVIII in GENER8-1, a phase 3 clinical study of valoctocogene roxaparvovec, an AAV5-mediated gene therapy for hemophilia A

Brian Long1, Sylvia Fong1, Britta Handside1, Tara Robinson1, Jonathan Day1, Hua Yu1, Kelly Lau1, Kathryn Patton1, Greg de Hart1, Josh Henshaw1, Suresh Agarwal1, Christian Vettermann1, Soumi Gupta1, 2BioMarin Pharmaceutical Inc. San Rafael, CA. USA 94901

Email: brian.long@bmrn.com

Background and aims: Valoctocogene roxaparvovec is an AAV5-mediated gene therapy under investigation for the treatment of hemophilia A and encodes a codon-optimized B-domain deleted human FVIII protein (hFVIII-SQ) under control of a liver-selective promoter. This report describes clinical immunogenicity monitoring data from up to 1 year of follow-up from GENER8-1, an ongoing, fully enrolled, Phase 3, single-arm, open-label study in 134 male patients with severe hemophilia A.

Method: Participants were required to test negative for anti-AAV5 total antibody (AAV5 TAb) utilizing a bridging electrochemiluminescent (ECLA) screening assay being developed as a companion diagnostic by ARUP Laboratories (Salt Lake City, USA). Additionally, all participants were required to be on FVIII prophylaxis and have had at least 150 exposure days to FVIII replacement products without previously clinically detectable FVIII inhibitor development. Following dose administration, plasma was analyzed for AAV5 TAb, and a cell-based AAV5 transduction inhibition (TI) assay was used to further characterize the capsid-neutralizing potential of the anti-AAV5 antibodies. Development of FVIII inhibitors was monitored using the Nijmegen-modified Bethesda assay, and FVIII-specific TAB were assessed by bridging ECLA. Additionally, peripheral blood mononuclear cells were collected for analysis in a validated IFN-γ ELISPOT assay for detection of capsid-specific and hFVIII-SQ-specific cellular immune responses.

Results: All participants developed a humoral antibody response to valoctocogene roxaparvovec following dose administration. Transient, low level AAV5 capsid-specific cellular immune responses were detected in the majority of subjects where incidence peaked at Week 2 following dose administration and often declined or reverted to negative over the first 52 weeks. Similarly, sporadic positive FVIII cellular immune responses were detected in a limited number of subjects. No subjects developed FVIII inhibitors following administration of BMN 270.

Conclusion: Immune responses to valoctocogene roxaparvovec were predominantly directed toward the AAV5 capsid, characterized by the production of anti-AAV5 binding and neutralizing antibodies as well as transient AAV5 capsid-specific cellular immune responses. Capsid-specific cellular immune responses showed a moderately positive correlation with plasma levels of the liver enzyme ALT suggesting these responses may be a contributing factor to transient elevations in ALT in some participants. There was no clinical evidence of inhibitor formation in subjects dosed with valoctocogene roxaparvovec.
**Friday 24 June**

**Viral hepatitis C: Clinical aspects except therapy**

**FRI301**

**Sex effect on key intrahepatic gene networks in hepatitis C virus infection**

Emanuele Marchi¹, Paul Klenerman¹, Narayan Ramamurthy¹, Azim Ansari², Eleanor Barnes¹, Caroline Harrer¹. ¹University of Oxford, NDM-Nuffield Department of Medicine, Oxford, United Kingdom

Email: emanuele.marchi@ndm.ox.ac.uk

**Background and aims:** Spontaneous HCV clearance and successful antiviral therapy rates are largely in favour of women and/or in subjects with a specific IFNL4 genotype. The unfavourable IFNL4 genotype leads to an exaggerated interferon response eventually detrimental for the patient. However, women tend to have a more robust and prompt interferon activity. Beyond this, the causes of sex differences in infections are insufficiently understood. The transcriptional response in the liver during hepatitis C virus (HCV) infection is critical for determining clinical outcomes. This issue remains relatively unexplored as tissue access to address this at scale is usually limited. We aimed to profile the transcriptomics of HCV infected livers to describe the expression networks involved and assess the effect on them of major predictors of clinical outcome such as IFNL4 host genotype and sex.

**Method:** We took advantage of a large clinical study of hepatitis C therapy accompanied by baseline liver biopsy to examine the drivers of transcription in tissue samples in 195 patients also genotyped genome-wide for host and viral SNPs. We addressed the role of host factors (disease status, sex, genotype, age) and viral factors (load, mutation) on transcriptional responses.

**Results:** We observe key modules of transcription which can be impacted differentially by host and viral factors. Underlying cirrhotic state had the most substantial impact, even in a stable, compensated population. Notably, sex had a major impact on antiviral responses in concert with IL28B (interferon lambda) genotype, with stronger interferon and humoral responses in females. Males tended towards a dominant cellular immune response. In both sexes there was a strong influence of the underlying host disease status and of specific viral mutations, and sex-specific eQTLs were also observed.

**Conclusion:** These features help define the major influences on tissue responses in HCV infection, impacting on the response to treatment and with broader implications for responses in other sex-biased infections.

**FRI302**

**Active case management to connect hepatitis C notifications to care and treatment in Australia (CONNECT study), a randomised controlled trial**

Tafireyi Marukutira¹,², Karen Moore³, Margaret Hellard¹, Jacqui Richmond¹, Kate Turner¹, Alisa Pedrana¹, Shannon M. Melody³, Louise Owen³, Wijnand Van Den Boom², Nick Scott¹, Alexander Thompson³, David Iser⁴, Tim Spelman¹, Mark Veitch⁵, Mark Stoove¹, Joseph Doyle¹. ¹Burnet Institute, Melbourne, Australia; ²Monash University, Melbourne, Australia; ³Tasmanian Department of Health, South Launceston, Australia; ⁴St. Vincent’s Hospital Melbourne, Fitzroy, Australia

Email: tafireyi.marukutira@burnet.edu.au

**Background and aims:** Despite the simplicity, tolerability and subsidised access of directly acting antivirals (DAAs), hepatitis C (HCV) treatment uptake in Australia is declining. Initiatives are needed to actively engage people living with HCV to link them to care and treatment. In this study, we measured the impact of using...
POSTER PRESENTATIONS

hepatitis C notifications systems to engage diagnosing general practitioners (GPs) and improve patient access to treatment.

Method: The CONNECT study was a randomised controlled trial that compared enhanced case management delivered to clinicians notifying new/repeat HCV diagnoses to standard of care in Tasmania, Australia over 12 months in 2020–2021. GPs were randomised based on their first HCV notification during the study period. The intervention involved a health department nurse specialist contacting notifying GPs directly and providing stepwise support by telephone, and direct patient contact if required. The primary outcome was the proportion of individuals with HCV who initiated DAAs within 12 weeks of HCV antibody notification. Secondary outcomes compared proportion completing pre-treatment HCV RNA testing and blood work-up.

Results: A total of 171 GPs were enrolled and randomised to the intervention (n = 85) or the standard of care (n = 86) arms. Over the observation period, GPs in the intervention notified 111 HCV antibody positive cases compared to 115 in standard of care. A higher proportion of HCV notifications in the intervention compared to standard of care completed HCV RNA testing (96% vs. 86%; p = 0.03) and 33% compared to 30% were HCV RNA+ve (p = 0.19) respectively. Pre-treatment workup among those eligible for treatment (RNA+ve) was similar between intervention and standard of care arms (62% vs. 65%; p = 0.82). The proportion of all HCV notifications that initiated treatment was similar between intervention and standard of care arms (20% vs. 14%; p = 0.24). The proportion of treatment eligible cases initiating treatment within 12 weeks of notification was also similar between study arms (38% vs 32%; p = 0.63) (Figure 1). Most cases who did not initiate were lost to follow up or were referred to a specialist.

Conclusion: This is the first prospectively randomised study that explored the utilisation of HCV surveillance data to enhance linkage to HCV treatment. While there was no difference in treatment initiation, the intervention encouraged more GPs to complete RNA testing as the initial stage of assessing DAA eligibility. Health Department follow up could potentially augment HCV antibody testing to ensure DAA eligibility is assessed early.

FRI303
Find out HCV patients: systematic study of 2013–2020 HCV files of a MDT viral hepatitis expert unit on the future of patients has made it possible to find out the lost ones and put them into treatment
André-Jean Remy1, Sonia Djazouli1, Hakim Bouchkira1, Jeremy Hervet1, Berengere Roy1. 1Perpignan Hospital, Mobile Hepatitis Team, Perpignan, France
Email: andre.remy@ch-perpignan.fr

Background and aims: Access to direct antiviral agents (DAA) has been progressively needed since 2013. But what happened to the patients, treated or not, seen since that date? Several studies have been conducted to find patients seen in consultation or hospitalization but without assessing the fate of the entire active queue. Our objectives were to evaluate follow-up of patients spent in multidisciplinary team meeting (MDT) within our hospital viral hepatitis expert unit, even when it was no longer mandatory for an DAA, treatment decision in the absence of current healing, to offer them DAA treatment.

Method: All MDT sheets from September 2013 to December 2020 have been reviewed. We contacted GP, patient or private hepatologist by email or telephone for an estimated 5 hours of work per week. Follow-up data were collected via our hospital’s computerized file. In the absence of direct contact; national death database was consulted.

Results: As of 31th August 2021, 1158 MDT files were initially studied corresponding to 1032 different patients; there were 683 men and 349 women of average age 37 years and 41% of F3F4 fibrosis; 97 patients were known to have died (69% of non-hepatic cause), 413 cured without liver complications; 153 followed for their cirrhosis and 41 for hepatocellular carcinoma; 328 were lost of sight of 68 previously followed by our team and 146 by liberal hepatologists. As of 31th October 2021, the contact information for 54patients was missing or incorrect; no information had yet been obtained for 126 patients followed in liberal; 37 additional patients were found within one month of which 8 were already cured and 15 died; 14 were eligible for immediate treatment due to an available positive viral load; 11 patients accepted an appointment for a referral of which 9 had already started the treatment and 2 patients refused the care; there were 90 patients followed by our team to contact or relaunch, which should be achieved within 3 months.

Conclusion: Maintaining MDT transition of all patients with chronic hepatitis C allows for an efficient database and to find untreated and/or untreated patients and offer them treatment. Number of refusals to care remains low, less than 10%. Our study, initially planned as a cohort retrospective analysis, found patients with chronic hepatitis C with RNA positive and untreated and immediately treated. This work shows that there are still patients who know they are infected with HCV but have not yet been treated. The research and treatment of these patients is essential to the elimination of hepatitis C.

FRI304
Effectiveness of a central monitoring system for the continuum of care of hepatitis C in Brazil during COVID-19 pandemic
Paulo Bittencourt1, Liana Codes1, Maria Lucia Ferraz1. 1Brazilian Liver Institute
Email: plbbr@uol.com.br

Background and aims: Several healthcare facilities dedicated to hepatitis C testing and linkage and retention to care were closed in Brazil due to the COVID-19 pandemic, leading to a 40%-50% reduction in the distribution of HCV rapid tests as well as new treatments for HCV in 2020. To mitigate the adverse impact of the pandemic on the hepatitis C elimination plan, the Brazilian Liver Institute (Ibrafig) sponsored a remote patient support program (PSP) to monitor all aspects of the HCV care continuum (HCV CC) in the public health system. The aims of the present study were to assess the results of this strategy in different steps of the HCV CC in Brazil.
Method: After mapping of the active healthcare facilities offering HCV rapid tests to the general population as well as diagnosis and treatment for HCV, Ibrafig launched a remote PSP to follow-up subjects in all steps of HCV CC from testing of hepatitis C until HCV cure. The remote PSP was comprised by trained healthcare personnel and contacts were made through phone calls, SMS, email or whatsapp according to users preferences. Awareness campaigns concerning hepatitis C elimination were coupled with nationwide advertising of the remote CMS on social media, TV and radio.

Results: From August 2020 to July 2021, 11,049 interactions were recorded between users and CMS, most of them by Whatsapp (91%). Most of them became aware of the PSP by radio and/or TV (41%) and social media (31%). After informed consent, 601 subjects were registered in the PSP including 74 patients already diagnosed with HCV who were lost in the public healthcare system due to the COVID-19 pandemic. Overall, 501 subjects were referred for HCV testing. Fifteen (5%) out of the 115 subjects who reported their test results were positive for HCV. Up to now, 53 (60%) out of 89 HCV positive patients have scheduled their 1st consultation, 12 (13%) are enrolled in care and 14 (16%) are under antiviral treatment. Seven (8%) who achieved end of treatment response are waiting HCV sustained virological response.

Conclusion: Our preliminary data showed that a remote PSP was an effective strategy to monitor the HCV CC. It was capable to refer at risk subjects for HCV testing and to provide linkage and retention to care of those HCV positive subjects in the Brazilian public health system during the COVID-19 pandemic.

FRI305
Retrieval of HCV patients lost to follow-up as a strategy for hepatitis C microelimination: results of a brazilian multicentric study
Paulo Bittencourt1, Maria Lucia Ferraz1, Gustavo Henrique Santos Pereira2, Liana Codes1, Antonio Andrade2, Carlos Brandão-Mello2, 1Brazilian Liver Institute; 2Brazilian Society of Hepatology
Email: plbbr@uol.com.br

Background and aims: Several HCV positive patients in Brazil were lost to follow-up in the last two decades before achievement of sustained virological response (SVR) due to either non-response to interferon-based therapy or lack of treatment due to comorbidity or mild fibrosis. The purpose of the present study was to identify and retrieve those lost patients to offer treatment with the current highly effective direct acting antivirals (DAAs).

Method: All medical charts from three major reference centers for treatment of hepatitis C were retrospectively reviewed by trained healthcare personnel to identify all HCV positive subjects, their treatment status and, in those HCV RNA positive patients, the main reasons for non-achievement of SVR or lack of treatment. After review of a local senior hepatologist, all patients who were not treated or cured were contacted in order to offer therapy with DAAs.

Results: 7,498 medical charts were reviewed, 5,549 (74%) from HCV positive patients (50, 1% males, mean age 51±12 years). Advanced fibrosis or cirrhosis and hepatocellular carcinoma were observed in 1929 and 95 subjects, respectively. Only 3272 (59%) were submitted to treatment. SVR, non-response to IFN-based and IFN-free regimens was observed in 2348 (72%), 658 (20%) and 266 (8%) subjects, respectively. Lack of treatment due to loss of FU (29%) or other reasons (12%) such as comorbidity, mild fibrosis or treatment refusal were reported in the remaining patients. Until October 2021, 2745 patients were considered eligible to be retrieved by local investigators and 1953 phone calls were made with a callback success rate of 15%. 43 (2%) patients were retrieved for treatment. Most of the remaining patients have been treated elsewhere (n = 61) or have died or underwent liver transplantation (n = 69).

Conclusion: Our preliminary data showed that identification and retrieval for treatment of HCV patients lost to FU is an effective microelimination strategy despite the low callback success rate.

FRI306
Reorganizing and simplifying HCV diagnosis and treatment in special populations during COVID pandemic and beyond
Paolo Scivetti1, Elisa Perfetti1, Lorenzo Somaini2, Sarah Vecchio2, Antonio Panero1, Paola Zaldera3, 1ASLBI Ospedale degli Infermi, SOC Internal Medicine-Hepatology Centre, Ponderano, Italy; 2ASlbi, Addiction Treatment Centre, Biella, Italy; 3ASlbi, Casa Circondariale-Health Section, Biella, Italy
Email: paolo.scivetti@aslbi.piemonte.it

Background and aims: Hepatitis C infection has a high prevalence among prisoners and in people who use drugs (PWUDs) and his identification and treatment are a pivotal factor to achieve HCV elimination by 2030. However, PWUDs and prisoners often face multiple barriers during the treatment cascade. In our Local Health Unit of Biella we have already developed a shared model of care between Addiction Treatment Centre (SerD), prison and hospital hepatology centre, to gather clinical evaluations within a single visit in order to ameliorate the HCV treatment rate. Subsequently, the treatment journey has been complicated by Covid pandemic. The aim of this study is to describe the new model of care we have developed to overcome old and new barriers to HCV treatment in these special populations.

Method: Since march 2020 a new model of care has been developed and centered on three crucial elements: a collaboration between SerD, prison and hospital hepatology centre; the introduction by AIFA (Italian Agency of Drugs) of the “criterion 12” that allows treatment after ruling out liver fibrosis by APRI and FIB-4 without elastography; the evidence that these scores allow us to exclude severe fibrosis, the risk of a hepatocarcinoma and the need of an ultrasound test. Patients attending SerD performed HCV viral load by mean of on-site fingerstick assay and inmates by mean of salivary test for antiHCV. HCVrna positive patient’s data were recorded into a database shared between the three services. After ruling out severe fibrosis by APRI and FIB-4, hepatologist prescribed the DAAs (direct-acting antiviral agent) with virtual “computer-generated” evaluation of the patients. DAAs were delivered by the SerD’s or prison’s health professionals. The patients were directly visited by the hepatologist only in the case of severe fibrosis at the scores.

Results: HCVrna was detected in out of 33/250 SerD patients’ and in out of 4/44 inmates, respectively. Linkage to care was possible for a total of 34 patients (30 SerD and 4 Prison). The patients were mostly male, and heroin addicted. Sixteen of them had only a virtual evaluation, conversely 18 patients underwent to direct examination. Overall, 34 patients completed the treatment, and all of them achieved Sustained Virologic Response.

Conclusion: Our new model of care highlights the feasibility of the on-site HCV testing and the efficacy of this simplified virtual “computer-generated” procedure for the treatment of HCV in special populations. This new model of care has allowed us to continue the diagnosis, the linkage to care and the treatment of patients even during COVID-19 pandemic and hopefully beyond.
Background and aims: The ACTG MINMON trial demonstrated that HCV treatment with no planned in-person monitoring is safe and efficacious. We report resource utilization and cost in the MINMON trial.

Method: ACTG A5360 (MINMON) was a 5-country, single arm study providing 12 weeks of sofosbuvir/velpatasvir to people with HCV infection with no planned visits prior to SVR evaluation (Week 24). Trial records included planned/unplanned lab tests and visits. Participants completed a 4-week recall questionnaire at weeks 0, 24, and 48 reporting hospital nights, emergency department visits, and ambulatory visits. To cost MINMON, we tabulated consumption and multiplied units of consumption by country-specific cost. We report cost of MINMON per SVR attained (2020 US$) from the program perspective (includes costs of medications and monitoring from study entry to Week 24), and the health sector perspective (includes costs of medications and monitoring outside the study prior to cure, plus the additional (or reduced) healthcare utilization observed after HCV treatment).

Sensitivity analyses explored potential cost savings of MINMON compared to the standard of care (SoC). We consulted in-country experts to develop country-specific SoC treatment protocols and compared to the standard of care (SoC). We consulted in-country experts to develop country-specific SoC treatment protocols and compared to the standard of care (SoC). We consulted in-country experts to develop country-specific SoC treatment protocols and compared to the standard of care (SoC). We consulted in-country experts to develop country-specific SoC treatment protocols and compared to the standard of care (SoC).

Results: MINMON cost/SVR (healthcare sector perspective) varied by country from $5, 256/SVR in Brazil, to $149, 257/SVR in the U.S. The cost of pharmaceuticals was the largest component of treatment cost, ranging between 76%–96% of cost from the program perspective. MINMON had a lower cost/SVR (program perspective) than the SoC across broad assumptions about cure rates. Outside of the U.S., the cost/SVR of MINMON was lower than that of the SoC even when the SoC achieved higher cure than MINMON. In the U.S., the MINMON cost/SVR was lower than the SoC unless the SoC would be expected to achieve at least a 4-percentage point higher cure rate.

Conclusion: MINMON is likely a cost saving strategy compared to the SoC for HCV treatment.
Background and aims: The WHO has declared the elimination of HCV until 2030 a global public health goal. We present the interim results of this ELIMINATE project including data/results from eight centers.

Method: First, we identified patients with a "last-positive" HCV-RNA PCR result from 2010 and 2020 in laboratories of Eastern Austria (Burgenland, Lower Austria, Vienna) and (ii) described their demographic characteristics. Subsequently, (ii) a systematic recall of these patients to the respective HCV treatment centers was performed, and (iii) HCV-DAA was initiated and SVR was monitored. Here we report the interim results of this ELIMINATE project including data/results from eight centers.

Results: Overall, 22692 patients underwent HCV-RNA PCR testing, 11216 (49.4%) ever showed a positive HCV-RNA result, and in 6223 (27.4%) patients the last available HCV-RNA result was positive (suggesting persisting HCV-viremia). For this interim report, 1795/6223 HCV-RNA PCR (+) patients were evaluated: 305 (17.0%) were linked to HCV-care. 82 (4.6%) underwent liver disease evaluation and in 64 (3.6%) DAA treatment was initiated. In 10 (0.6%) sustained virologic response was documented. Main reasons for the suboptimal cascade of care included invalid contact data (663; 36.9%) or patients’ unavailability at the time of recall (172; 9.6%) and death (289; 16.1%). Successful DAA therapy at other centers had already been conducted in 366 patients (20.4%).

Conclusion: This lab record-based ELIMINATE project identified a considerable number of 6223 HCV patients with potential persisting viremia. Invalid contact data (36.9%) and pre-treatment death (16.1%) represent major problems/barriers. Importantly, at this interim stage 305 (17.0%) patients were successfully linked to care and 64 (3.6%) patients started DAA therapy.

The Korean hepatitis C virus care cascade in a tertiary institution: current status and changes in testing, link to care, and treatment initiation

Background and aims: The care cascade for hepatitis C virus (HCV) infection is impeded by multiple barriers, including suboptimal HCV Ab testing, link to care, and diagnosis. We explored the changes in the care cascade of HCV for the past 20 years and its current status in a large cohort from a tertiary referral center.

Method: We analyzed 1,144,468 patients who had HCV Ab testing between January 2001 and June 2020. Metrics related to the care cascade of HCV infection and the long-term prognosis of patients were explored.

Results: The seroprevalence of HCV Ab was 1.8%, with a recent decreasing trend. In all, 69.9% of HCV Ab-positive patients performed HCV RNA testing, with a 65.7% positivity. Patients who did not have HCV RNA testing were older and more likely to have a non-hepatocellular carcinoma (HCC) malignancy, normal ALT level, and good liver function. Linkage times for HCV RNA testing from the HCV Ab positivity and for antiviral treatment from HCV diagnosis decreased, notably after 2015, when highly efficacious oral antiviral treatment was introduced to Korea. The average treatment uptake rate was 35.4%, which increased to 38.9% after 2015. Of the 5,302 patients analyzed regarding long-term prognosis, the annual incidences of HCC were 1.02 and 2.14 per 100 person-years in patients with and without a sustained virological response, respectively.
**Conclusion:** The care cascade of HCV infection has been suboptimal for the past 20 years, despite the recent changes. More effort should be made to increase HCV RNA testing and treatment uptake.

**FRI311**

**Macroeconomic assessment of overall and per-patient healthcare costs of Hepatitis C-infected patients in an integrated health system in the era of direct-acting antiviral therapy**

David Kaplan1,2, Claire Durkin 1, Marina Serper 1.

**Background and aims:** Treatment of acute and chronic hepatitis C infection on a national or system-wide scale requires significant investment to acquire, dispense and monitor antiviral therapy with the intent to reduce downstream costs related to reduced liver-related complications. The US Veterans Administration (VA) initiated universal access to HCV direct acting antiviral (DAA) therapy in 2015. The Aim of this study was to quantify the total healthcare costs expended on prior and current hepatitis C-infected individuals before, during after the universal introduction of DAA therapy.

**Method:** All patients in the VA healthcare system with a positive HCV RNA by a qualitative or quantitative PCR tests at any time between 1999 and 2020 were identified. Exposure to antiviral therapy was identified by prescription fills for interferons and DAA medications. Treatment completion was assigned as 28 days after the final release of a specific regimen and the first date for possible assessment of SVR12 assigned to 84 days after treatment completion. Each course of therapy was characterized based on post-SVR12 date PCR results as cured, relapsed or untested if no PCR test was available. Health Economics Research Center (HERC) average cost estimates and Fee-Basis costs were utilized for outpatient and inpatient care within the VA and external costs, respectively. Cost of outpatient pharmacy were obtained from Managerial Cost Accounting data. For this analysis, total, outpatient, inpatient and pharmacy were aggregated by fiscal year (years 2010–2020) and presented as aggregate or per-patient costs. All costs were inflation-adjusted to year 2021 dollars using the consumer price index and post-treatment costs were discounted by 3% per year.

**Results:** During fiscal year 2010, 214,531 unique infected individuals expended on prior and current hepatitis C-infected individuals during fiscal year 2010–2020 were identified. Exposure to antiviral therapy was characterized based on post-SVR12 date PCR results as cured, relapsed or untested if no PCR test was available. Health Economics Research Center (HERC) average cost estimates and Fee-Basis costs were utilized for outpatient and inpatient care within the VA and external costs, respectively. Cost of outpatient pharmacy were obtained from Managerial Cost Accounting data. For this analysis, total, outpatient, inpatient and pharmacy were aggregated by fiscal year (years 2010–2020) and presented as aggregate or per-patient costs. All costs were inflation-adjusted to year 2021 dollars using the consumer price index and post-treatment costs were discounted by 3% per year.

**Results:** During fiscal year 2010, 214,531 unique infected individuals were under care. By 2020, only 68,086 HCV-infected patients did not have documentation of SVR12 (Figure 1A). Total cost expenditures prior to DAA availability ranged between $5.3–5.8B then peaked at $9.0B in FY2015 due to massive increases in pharmacy-related costs (Figure 1B) then declined to pre-DAA levels by FY2020. Modest increases of outpatient and inpatient costs were observed from FY2010 to FY2018 at which point a significant decline occurred. However, the cost per-patient under care never declined to pre-DAA levels and only a modest decline in outpatient and inpatient expenditures was observed FY2019–2020 (Figure 1C).

**Conclusion:** These data suggest that reductions in overall healthcare costs for a hepatitis C-infected population cannot be observed within the first several years after implementation of universal treatment. Reductions in total cost to pre-DAA levels appear more related to patient attrition than to reduction of average patient treatment costs.

**FRI312**

**Awareness of chronic hepatitis B and C among men who have sex with men (MSM): epidemiological survey and on-site screening**

Marie Coessens1,2,3, Tom Holvoet4, Jeffrey Schouten2,5.

**Background and aims:** In order to eradicate Hepatitis B (HBV) and Hepatitis C (HCV) by 2030, the WHO focuses on screening in targeted high-risk populations, including men who have sex with men (MSM). The objectives of this study are to assess awareness and knowledge (1) and prevalence (2) of HBV and HCV infections in the MSM population in Flanders and Brussels.

**Method:** An online questionnaire in Dutch of 5 to 10 minutes was used, as well as face-to-face questionnaire using a tablet at the Belgian and Antwerp Pride (1). In 2018–2020 we joined Senseo (a Flemish expertise center for sexual health) during outreach projects and tested visitors voluntarily at 14 gay bars, parties and saunas in Flanders by means of an oral quick test for HCV (e.g. Orasure Intercept 2). In addition, HCV test results collected by Ex Aequo (an MSM organization in Brussels that provides sexually transmitted diseases (STD) screening at offices and during on-site actions) in 2019 were analyzed (2).

**Results:** 300 MSM participated in the online Dutch questionnaire with a median age of 36 years old. HIV status was known to be positive in 7.7%. Knowledge of HBV and HCV infections was poor. Of all participants, 40.5% and 47, 6% thought HBV and HCV patients would always have symptoms; 52.9% thought there was an HCV vaccine; 37.1% thought there was no medication against HCV and of those who knew there was medication, 75% thought that treatment was long and hard. Only 15% and 1%, respectively, knew which sexual practices were with or without risk for HBV and HCV infection. The knowledge of HBV was significantly correlated to the knowledge of HCV (p < 0.0001, r = 0.324) and the degree of education (p < 0.001, r = 0.209). The knowledge of HCV was significantly correlated to the number of sexual partners in the last six months (p = 0.024, r = 0.131), the number of risky sexual practices (p < 0.0001, r = 0.205).
In Sensoa’s HCV prevalence study, only 1 of 260 test results was positive (0.38%) and this was an HIV co-infected patient. The Ex Aequo’s HCV prevalence study yielded no positive test results. The HIV prevalences were 1.15% (Sensoa) and 1.3% (Ex Aequo) and the syphilis prevalence was 2.5% (Ex Aequo).

**Conclusion:** There is a big knowledge gap of HBV and HCV infections in the MSM community in Flanders. More awareness campaigns that focus on transmission, disease process, treatment and vaccination need to be created that also target people with a low educational level.

The prevalence of hepatitis C infection and other STD’s was low in the MSM population studied of 500 participants. Presumably a young MSM population that voluntarily has themselves tested represents a rather low risk profile for HCV infection. HCV prevalence may be higher in an older population and/or in an illegal environment where more risk factors for HCV infection co-exist and that is more difficult to reach. However, given the high workload and low case finding, an on-site screening approach cannot be recommended.

**FRI313**

**Predictive factors for lost to follow-up pre and post-hepatitis C treatment: Data from the British Columbia hepatitis C virus network**

Alnoor Ramji1, Edward Tam2, Julia MacIsaac3, Jean-Philippe Wallach3, Jeanette Feizi2, Hin Hin Ko1. 1University of British Columbia, Gastroenterology, Vancouver, Canada; 2Pacific Gastroenterology Associates, Vancouver, Canada; 3University of British Columbia, Vancouver, Canada

Email: ramji_a@hotmail.com

**Background and aims:** In British Columbia (BC) 60% of identified HCV RNA (+) individuals remain untreated. A major challenge is the durable linkage to care of persons who are HCV RNA (+), many are lost to follow-up (LFU) prior to therapy (pre-LFU), or post therapy (post-LFU). Understanding patient profiles will inform resources for HCV elimination. Our aim was to determine predictive factors of HCV patients who are LFU pre- and post-treatment.

**Method:** Retrospective review of HCV RNA (+) persons in the BC HCV Network to determine the predictive factors of pre-LFU and post-LFU compared to treated persons with SVR12. Chi-square and multivariable regression analysis were performed.

**Results:** A total of 4057 patients were included, 2823 (70%) completed HCV therapy, 1123 (27.5%) were pre-LFU. See table. Pre-LFU patients were more likely to be male (70%), have psychiatric disorder (30%), history of injection drug-use (IDU) (37%), and heavy alcohol use (38%) compared to treated patients (64%, 18%, 26%, and 27% respectively, p < 0.001). Fewer persons with advanced fibrosis (FIB4 > 3.25 or LSM > 12.5 kPa) were in the pre-LFU group (22%) compared to treated group (30%), p < 0.001.

2823 patients completed HCV therapy, 2410 (85.5%) had SVR12 and/or treatment response. 413 (14.5%) did not achieve treatment response. Male gender (69%), history of psychiatric disorder, IDU (36%), and heavy alcohol use (27.5%) were pre-LFU. As of September 30, 2021 results are shown in this figure:

**Conclusion:** Male gender, history of psychiatric disorder, IDU, or and heavy alcohol use are predictive of LFU both pre- and post-HCV therapy. Successful HCV elimination strategies will need to incorporate interventions to improve durable engagement of these populations.

**FRI314**

**HCV screening in a tertiary french hospital: just do it !**

Si Nafa Si Ahmed1, Souad Benali1, Magalie Madau1, Rania Kibeche1, Romain Albénois2, Michaël Ghez2, Ines Belasri1, Christine Hernandez1, Paola Ramirez1, Julien Negre1, Laurence Lecomte1, Floriane Sellier1, Olivia Pietri1, Paul Castellani1, Xavier Adhoute1, Marc Bourliere1, 1Hôpital Saint Joseph, Hepatology Unit, Marseille, France; 2Hôpital Saint Joseph, Laboratory Unit, Marseille, France; 3Hôpital Saint Joseph, DIM, Marseille, France

Email: ssiahmed@hopital-saint-joseph.fr

**Background and aims:** Universal screening appears to be the most cost-effective strategy to reach the HCV elimination planned by WHO for 2030. All HCV patients have currently access to treatment. In France HCV screening is based on identification of Risk Factor. The aim of the present study was to test universal screening strategy in all hospitalized patients.

**Method:** From November 2019 to November 2021, we conduct a prospective, longitudinal monocentric study screening all consent patients for HCV regardless identification of Risk Factor. All HCV Ab positive was followed by HCV RNA screening. All replicating patients were proposed to be treated according to the other pathologies for which the patients were hospitalized. The study was authorized by CPP Toulouse.

Because of occurrence COVID 19 pandemics, conducting this study we identify several limitations leading to the prolongation of inclusion time and to develop adaptive measures such as oral consent.

**Results:** As of September 30, 2021 results are shown in this figure:

**Conclusion:** Male gender, history of psychiatric disorder, IDU, or and heavy alcohol use are predictive of LFU both pre- and post-HCV therapy. Successful HCV elimination strategies will need to incorporate interventions to improve durable engagement of these populations.
Conclusion: HCV Ab prevalence recorded is significantly higher than that observed in the general population in France. However only 15.8% of hospitalized patients have been included. Motivation of all health care workers is essential. Final results of the study will be present at the meeting

FRI315
Hepatitis C screening rates by age cohort 1945–1965 in a large community health system before, during and after the COVID pandemic

David Bernstein, Nitzan Roth, Ben Da, Sanjaya Satapathy, Henry Bodenheimer, Christian Kuntzen, Tai Ping Lee. Donald and Barbara Zucker School of Medicine at Hofstra/Northwell, Hempstead, United States

Email: dav31475@gmail.com

Background and aims: In the outpatient primary care setting, New York State mandates the offering of hepatitis C (HCV) testing for persons born between 1945 and 1965. Despite this mandate, <50% of HCV screening candidates are offered screening and among those found to be HCV Ab positive, not all patients undergo HCV RNA testing and even fewer are referred for treatment.

Method: We implemented a system where nurse educators personally visited 60 outpatient primary care offices to educate regarding HCV screening. Visits occurred for the first 2 years of the project and then were stopped due to the COVID pandemic. We evaluated our results by birth year, dividing patients into 4 groups, those born between 1945 and 1950, between 1951 and 1955, between 1956 and 1960 and between 1961 and 1965.

Results: From April 1, 2018–August 31, 2021, 50, 047 previously unscreened patients born between 1945 and 1965 were screened with an HCV Ab with reflex testing to HCV RNA in all positive HCV ABS. 10819 were born between 1945 and 1950, 11573 were born between 1951 and 1955, 13586 were born between 1956 and 1960 and 14069 between 1961 and 1965.

Background and aims: The Cepheid, GeneXpert provides hepatitis C virus (HCV) PCR results <90 minutes. A major limitation is the need to load finger prick samples <15 minutes, as patients must be co-located with the machine. Venous blood collected into EDTA tubes can be stored for up to 72 hours at 2–8°C prior to processing. In this project finger-prick blood collected into EDTA capillary tubes and processed >15 minutes after collection was compared with venepuncture (gold standard) and dried-blood spot testing (DBST) to facilitate testing remote from the machine (e.g. prison clinics on different wings remote from a centrally located machine) but still delivering rapid turn-around times with testing in close proximity to the point of need.

Method: Capillary tubes (MiniCollect® Tube 0.25/0.5 ml K3E K3EDTA-450530) were spiked with venepuncture blood from 25 adult patients undergoing HCV testing, processed on the Cepheid and the results compared. HCV positive patients in the community undergoing testing (venepuncture or DBST) were then approached to provide an additional EDTA capillary tube finger-prick sample. Samples were left for >15 minutes <72 hours prior to processing and results compared. As the lower limit of quantification on the Cepheid is 40 IU/ml, results below this level were analysed separately.

Results: From the first 36/50 patients are reported here. The time between sample collection and testing ranged from 44 minutes to 94 hours 34 minutes. Samples with longest delays tested positive (no suggestion of the results being affected). Two venepuncture results were detected, viral load <12 IU/ml. Corresponding Cepheid results were negative as expected (results are not included below). One sample registered as “error” (Cepheid) and was not detected by DBST. In one sample the Cepheid result was not detected and the DBST result detected in the “unreliable zone” – 10 IU/ml. The LLD of DBST is 1000 IU/ml and this likely is a false positive DBST result. Of the remaining HCV positive samples (n = 32, log viral loads 0.19–2.05 IU/ml). The Cepheid successfully detected HCV in 30 (93.75%) (Figure 1). In the remaining two samples the Cepheid result was “invalid.” This could be due to internal quality standards, probe check failures, system computer failures or PCR process inhibition.

FR316
Maximizing the potential of Cepheid, GeneXpert PCR rapid testing for hepatitis C through use of finger prick blood samples collected into EDTA capillary tubes

Anam Choudhry, Louise Davies, Nicki Palmer, Jade Davies, Bazga Ali, Rhys Oakley, James Plant, Louise Evans, Chinlye Chng, Helen Thompson-Jones, Lorraine Wall, Sarah Nicholas, Brendan Healy, Cardiff University School of Medicine, Cardiff, United Kingdom; 2Public Health Wales Cardiff, Cardiff, United Kingdom; 3Public Health Wales Swansea, Swansea, United Kingdom; 4University Hospital Wales, Cardiff, United Kingdom; 5Cardiff and Vale Pharmacy, United Kingdom; 6Swansea Bay UHB BBV Team, Swansea, United Kingdom; 7Cardiff and Vale UHB BBV Team, Cardiff, United Kingdom; 8Public Health Wales, United Kingdom

Email: choudhrya4@cardiff.ac.uk

Background and aims: The Cepheid, GeneXpert provides hepatitis C virus (HCV) PCR results <90 minutes. A major limitation is the need to load finger prick samples <15 minutes, as patients must be co-located with the machine. Venous blood collected into EDTA tubes can be stored for up to 72 hours at 2–8°C prior to processing. In this project finger-prick blood collected into EDTA capillary tubes and processed >15 minutes after collection was compared with venepuncture (gold standard) and dried-blood spot testing (DBST) to facilitate testing remote from the machine (e.g. prison clinics on different wings remote from a centrally located machine) but still delivering rapid turn-around times with testing in close proximity to the point of need.

Method: Capillary tubes (MiniCollect® Tube 0.25/0.5 ml K3E K3EDTA-450530) were spiked with venepuncture blood from 25 adult patients undergoing HCV testing, processed on the Cepheid and the results compared. HCV positive patients in the community undergoing testing (venepuncture or DBST) were then approached to provide an additional EDTA capillary tube finger-prick sample. Samples were left for >15 minutes <72 hours prior to processing and results compared. As the lower limit of quantification on the Cepheid is 40 IU/ml, results below this level were analysed separately.

Results: From the first 36/50 patients are reported here. The time between sample collection and testing ranged from 44 minutes to 94 hours 34 minutes. Samples with longest delays tested positive (no suggestion of the results being affected). Two venepuncture results were detected, viral load <12 IU/ml. Corresponding Cepheid results were negative as expected (results are not included below). One sample registered as “error” (Cepheid) and was not detected by DBST. In one sample the Cepheid result was not detected and the DBST result detected in the “unreliable zone” – 10 IU/ml. The LLD of DBST is 1000 IU/ml and this likely is a false positive DBST result. Of the remaining HCV positive samples (n = 32, log viral loads 0.19–2.05 IU/ml). The Cepheid successfully detected HCV in 30 (93.75%) (Figure 1). In the remaining two samples the Cepheid result was “invalid.” This could be due to internal quality standards, probe check failures, system computer failures or PCR process inhibition.
Conclusion: The Cepheid successfully detected 93.75% of the HCV positive samples detected by venepuncture or DBST. The two samples that were not positive returned invalid results which would have prompted retesting. The one discordant result with a very low level DBST result is likely due to a false positive result on DBST. As such, none of the results from finger prick samples collected into EDTA capillary tubes and processed on the Cepheid returned false negative results. This method of sampling is now going to be adopted in Wales with ongoing monitoring of results over the next 12 months.

FRI317 Healthcare resource utilization in treatment-naïve patients with compensated cirrhosis receiving 8-weeks' glecaprevir/ pibrentasvir stratified by drug use and socioeconomic status: a retrospective chart review

Jian Isidro Uriz Otano1,2, Armand Abergel3, Alessio Aghemo4,5, Adriana Ahumada6, Massimo Andreoni1, Tarik Asselah6, Abhi Bhagat7, Isabel Butrymowicz8, Brian Conway9, Antonio Gasbarrini1, Francisco Jorquera1,2, Pietro Lampertico14, Maria Luisa Manzano Alonso15, Lindsy Myles10, Marcello Persico17, Alnoor Ramji18, Dimitri Semizarov9, Yanna Song9, Erica Villa19, Qingqing Xu9, Navarra Institute for Health Research (IdISNA), Pamplona, Spain; 2Department of Gastroenterology, Liver Unit, Complejo Hospitalario de Navarra, Pamplona, Spain; 3CHU Estaing, UMR 6602 CNRS Université d’Auvergne, Clermont Ferrand, France; 4Department of Biomedical Sciences, Humanitas University, Rozzano, Italy; 5Department of Gastroenterology, Humanitas Research Hospital IRCCS, Rozzano, Italy; 6Hospital General Universitario Gregorio Marañón, Liver Unit, Madrid, Spain; 7University of Tor Vergata, Rome, Italy; 8Service d’Hépatologie, Hôpital Beaujon, INSERM UMR 1149, Université de Paris, Clichy, France; 9AbbiVie Inc., North Chicago, United States; 10Vancouver Infectious Diseases Center and Simon Fraser University, Vancouver, Canada; 11Internal Medicine and Gastroenterology, Fondazione Policlinico Universitario A. Gemelli IRCCS, Rome, Italy; 12Digestive System Service, Complejo Asistencial Universitario de León, IBIOMED and CIBERehd, León, Spain; 13Foundation IRCCS Ca’ Granda, Ospedale Maggiore Policlinico, Policlinico-Division of Gastroenterology and Hepatology-CRC ‘AM and A Migliavacca’ Centre for Liver Disease, Milan, Italy; 14University of Milan, Milan, Italy; 15Liver Unit, Hospital Universitario 12 De Octubre, Madrid, Spain; 16Barrie GI Associates, Barrie, Ontario, Canada; 17Dipartimento di Medicina Clinica Medica, Epatologia e Lungodegenza, AOU OO. RR. San Giovanni di Dio Ruggi e D’Aragona, Salerno, Italy; 18University of British Columbia, Vancouver, BC, Canada; 19UC Gastroenterology, Dipartimento di SpecialitàMediche, Azienda Ospedaliera Universitaria di Modena, Modena, Italy

Email: ji.uriz.otano@navarra.es

Background and aims: Identifying factors that may influence healthcare resource utilization (HCRU) among patients with hepatitis C virus (HCV) infection is important to support the development of initiatives that reduce healthcare resource burden and allow for more patients to be treated. This study describes HCRU among treatment-naïve, compensated cirrhotic patients treated with 8-weeks’ glecaprevir/pibrentasvir (G/P), according to their history of drug use (DU) and socioeconomic status.

Method: Here we present an interim subanalysis of the ongoing, noninterventional, multicenter CREST study which includes chart review data from France, Canada, Italy, and Spain. Demographic and baseline characteristics were reported overall and for patients with history of DU. HCRU was described by history of DU and occupational status. In the group of patients with DU, HCRU was described according to active vs former drug use, and route of drug administration.

Results: This analysis included 206 patients who received ≥1 dose of G/P; 139 (67.5%) were male, the median (range) age was 57 (31–88) years (assessed in 203 patients), 185 (89.8%) had stable housing, and 52 (25.2%) were employed full-time. Among 75 (36.4%) patients with history of DU, 52 (69.3%) were intravenous drug users (IVDUs), and 23 (30.7%) were active drug users. Other characteristics included: aged >50 years (n = 51; 68.0%), stable housing (n = 63; 84.0%), and employed full-time (n = 16; 21.3%). Full-time employed patients, compared with those not in full-time employment, had fewer visits to general physicians (0.9 vs 2.0), but more visits to hospitalists (2.0 vs 1.4) and gastroenterologists (0.2 vs 0.1), and a greater number of noninvasive procedures (1.9 vs 0.9). Patients with history of DU, especially IVDUs, had more general physician and nurse visits and fewer hospitalist and gastroenterologist visits than those with no history of DU. Additionally, active drug users had higher on-treatment laboratory test (3.7 vs 2.1) and noninvasive diagnostic procedures (1.7 vs 1.3) compared with former drug users. HCRU in IVDUs was mostly similar to those administering drugs through other routes (Figure).

Conclusion: This analysis focused on identifying factors that may influence healthcare resource utilizations among patients with hepatitis C virus infection. The study demonstrated differences in healthcare resource utilization among treatment-naive patients with compensated cirrhosis receiving glecaprevir/pibrentasvir stratified by drug use and socioeconomic status. These findings can help guide healthcare resource allocation and patient management in the real-world setting.
POSTER PRESENTATIONS

FR1318
Progress towards hepatitis C elimination: the feasibility and success of a nurse and harm reduction practitioner led model of care utilising rapid point of care HCV RNA testing at a medically supervised injecting room in Melbourne, Australia
Michael MacIsaac1,2, Bradley Whitten1, Jenine Anderson3, Matthew Penn1, Anthony Weeks3, Shelley Coggan1, Kasey Elmore1, David Pemberton3, Tim Papaluca1,2, Margaret Hellard4,5,6, Mark Stove4,6, David Wilson5, Alisa Pedrana4,6, Joseph Doyle1,5, Nico Clark3,7, Jacinta Holmes1,2, Alexander Thompson1,2.

Monash University, School of Public Health and Preventive Medicine, Melbourne, Australia; 2The Royal Melbourne Hospital, Addiction Medicine, Parkville, Australia; 3University of Melbourne, Faculty of Medicine, Parkville, Australia; 4Burnet Institute, Disease Elimination Program, Melbourne, Australia; 5Alfred Hospital, Infectious Diseases, Melbourne, Australia; 6Monash University, School of Public Health and Preventive Medicine, Melbourne, Australia; 7The Royal Melbourne Hospital, Addiction Medicine, Parkville, Australia

Email: michael.macisaac@svha.org.au

Background and aims: To achieve HCV elimination targets, efforts must focus on models of care engaging people who inject drugs (PWID). The XpertÒ HCV viral load fingerstick point of care (POC) test provides an HCV RNA level within 1 hour, allowing rapid diagnosis and treatment. We previously reported a successful nine-week pilot study incorporating HCV RNA POC testing at a medically supervised injecting room (MSIR) in Melbourne, Australia. We now present the 12-month outcomes of this program.

Method: Prospective cohort study recruiting PWID attending a high-volume MSIR in Melbourne, Australia between 9/11/20 to 9/11/21. Clients were offered HCV screening using the XpertÒ HCV RNA POC test. Venepuncture for HBV/HIV screening and fibrosis assessment (APRI/FibroScan) were also offered to clients, regardless of HCV RNA status. HCV RNA results were returned same day if clients were still present, or via phone or at next MSIR visit if they had already departed. POC testing/treatment was led by a full-time hepatology fellow during the initial nine-week pilot program, and a nurse or harm reduction practitioner (HRP) for the remainder of the study period. DAA treatment was prescribed immediately upon return of a positive HCV test if the hepatology fellow was on-site, or by a GP/hepatologist after remote consultation for nurse/HRP assessment. Clients were invited to be followed 4-weekly during treatment and at SVR12. Primary endpoints were number of clients screened for HCV and number commencing DAs. Testing rates were compared to a historical control period (9/11/18–9/11/19) of standard of care HCV venepuncture testing at the MSIR.

Results: 573 PWID consented to HCV RNA POC testing. By comparison, 180 clients underwent HCV testing during the control period, representing a 218% increase with POC testing. Median age was 42 yrs (IQR 37–49) and 75% male. 161 (28%) were HCV RNA+. An APRI score was calculated for 337 clients and 154 (45/32, 50% with APRI ≥1) had a FibroScan performed. Cirrhosis was uncommon (6% HCV RNA+, 5% overall), as was HBV (n = 3, 2%) and HIV co-infection (n = 0). 50% (n = 145/161) of HCV RNA+ clients were prescribed DAA therapy. Median time to treatment start was 8 days (IQR 2–22); 13 clients (9%) initiated treatment same day as diagnosis. There was no difference in the number of clients linked to treatment with hepatology fellow led on-site prescribing compared to remote prescribing following nurse or HRP assessment (94% vs 88%, p = 0.204). Among those with complete follow up data (n = 43), SVR was 74%. Causes of non-SVR were re-infection (n = 3), relapse (n = 4), and non-response from medication non-adherence (n = 4).

Conclusion: Rapid HCV POC testing in a MSIR rapidly upscales testing and was associated with high rates of treatment initiation. Nurse or HRP led POC testing/treatment with remote prescribing is highly feasible, with similar rates of treatment initiation achieved.


FR1319
Screening for hepatitis C in Denmark-the effect of a mobile outreach intervention
Sandra Droeos1,2,3, Lone Wulff Madsen1,2, Gustav Bang Harvald1, Søren Grinderslev1, Karen Kofod1, Lone Kræmer1, Anne Øvrehus1,2, Peer Christensen1,2,3, Odense University Hospital, Department of Infectious Diseases, Odense, Denmark; 2University of Southern Denmark, Clinical Institute, Odense, Denmark; 3Odense University Hospital, Open Patient Data Explorative Network, Odense, Denmark

Email: peer.christensen@dadmiket.dk

Background and aims: The prevalence of hepatitis C (HCV) in Denmark is low (0.21% of the adult population), 24% of HCV infected are undiagnosed (corresponding to 700 HCV patients in the Region of Southern Denmark (RSD)) and among diagnosed less than half have been cured. As part of the “C-Free-South” program we launched an outreach test and treat center on wheels in the Region of Southern Denmark in June 2020, targeting people with drug or alcohol use and/ or psychiatric illnesses as well as festivals and open markets. The aim of this study is to describe the results of the intervention after the first 17 months.

Method: Low threshold non governmental organizations were approached by a mobile unit with medical personnel from the infectious disease department at Odense University Hospital. We used an HCV point of care rapid test for antiHCV, dried blood spot test for HCVRNA and a FibroScan® devise for diagnosis of liver fibrosis. Infected patients were offered treatment either by referral to the nearest clinic or in the mobile unit, as deemed feasible.

Results: 584 persons were tested in 37 different locations of whom 148 were in shelters or other residential institutions. Overall 7% (43) had a positive antiHCV by POC test and 2% (12) had current infection of whom at least 5 (42%) were reinfections after HCV cure. Men constituted 55% of all tested, and 70% of all antiHCV positives (p < 0.05). Median age at test was 50 years (IQR 48–60) with no relation to HCV status. Overall 95% of the 43 antiHCV positives had been tested before, 81% recalled being antiHCV positive at last test, 5% recalled being negative, (suggesting resent infection) and a total of 71% reported to have been cured for HCV (universal treatment for HCV became available Denmark in 2018). The prevalence of antiHCV was 165 (26/162) in facilities open to all (who accepted drug users) and 0% (0/187) in facilities restricted to psychiatric patients or alcohol users. Correspondingly, 91% of the 43 antiHCV positives had injected drugs compared to 8% of antiHCV negatives. We found no infections (0/71) when testing the general population (i.e. at markeds).

Conclusion: Our study suggests that most hepatitis C infected in Denmark have been identified and cured, and we found a very low proportion of undiagnosed (5%) compared to the previous national estimate of 24%. However our study is a selected sample of the population at risk for HCV and may not be representative for our region or Denmark. The low absolute number of current infection (2% of tested) suggest that our outreach campaign in its current form is unlikely to diagnose and treat the remaining patients with HCV in our region. An improved case finding strategy is needed to reach the WHO target of 90% diagnosed and 80% cured by 2030. This could be monetary incentives to be tested, and increased use of peer based testing (“snowballing”). A full update of treatment results and new screening methods will be presented at the meeting.
Screening for HCV infection combined with SARS-CoV-2 vaccination in the Campania region
Pietro Torre1, Mario Masarone1, Roberta Sciorio1, Monica Annunziata1, Roberta Coppola1, Laura Staiano2, Carmine Coppola2, Marcello Persico1, 1University of Salerno, Internal Medicine and Hepatology Unit, Department of Medicine, Surgery and Dentistry, “Scuola Medica Salernitana”; 2OORR Area Stabiese, Plesso Nuovo Cagnano, Naples, Italy, Department of Internal Medicine-Unit of Hepatology and Interventional Ultrasonography

Email: mpersico@unisa.it

Background and aims: The health emergency caused by the SARS-CoV-2 pandemic has negatively impacted the management of HCV infection, potentially jeopardizing the achievement of the goal of eliminate hepatitis C by 2030. To take advantage of the current sanitary situation, associated screening for HCV and SARS-CoV-2 infection have been carried out. We decided to propose HCV screening also to people who undergone SARS-CoV-2 vaccination.

Method: Screening for hepatitis C was carried out by finger-prick test for HCV antibodies. It took place in the minutes following the SARS-CoV-2 vaccination, in two different vaccination centers of the Campania region, and in two different time frames. In the period 1 May–20 July 2021, screening for hepatitis C was offered to the general population who got the vaccine at the Fisciano (province of Salerno) vaccination center. In the period 20 September–11 October 2021, screening for hepatitis C was offered to the general population who underwent vaccination at the San Leonardo Hospital (Castellammare di Stabia, metropolitan city of Naples). In both sites, Pfizer-BioNTech, Moderna, or Oxford-AstraZeneca vaccines were used.

Results: Out of 5095 people who underwent vaccination at the Fisciano vaccination center, 1952 (38.8%, average age 41.6 years) performed screening for hepatitis C. 5 of these (0.25%, average age 54.2 years) resulted HCV-Ab positive; all 5 were aware of their condition; 4 had previous treatment; 1 (0.05%) was found to have active HCV infection. Out of 2202 people vaccinated at the San Leonardo Hospital, 1207 (54.8%, average age 43, 1 years) underwent screening for hepatitis C. Among these, 9 (0.7%, average age 54, 3) resulted positive. 5/9 tested negative on the confirmatory test; 2/9 were aware of their condition and had previous treatment; 1 subject (0.08%) was found to have active HCV infection; 1 subject is awaiting the results at time of writing.

In both sites a consistent percentage of people refused the HCV-Ab test. Moreover, the prevalence of HCV-Ab positivity and HCV active infection was found to be lower than the national data. Frequent reasons for refusing the test were lack of knowledge of the disease, fear of a positive result, and distrust in the test’s effectiveness. Someone refused the test because vaccination was considered a particularly stressful event. The low prevalence of HCV infection found in these projects could be at least partly attributable to the under-participation of the elderly, as at the time the screenings were carried out most of them had probably already received the expected doses of SARS-CoV-2 vaccine.

Conclusion: In conclusion, we believe that SARS-CoV-2 vaccination could be an opportunity to screen for HCV infection, but to maximize the benefits of this screening, the characteristics of the subjects to be tested should be reconsidered, by focusing particularly on the elderly population.

Treating children with HCV close to home through a virtual national multidisciplinary network
Deirdre Kelly1,2, Carla Lloyd3, Maxine Brown1, Kinza Ahmed1, Ivana Carey1, Sarah Tizzard1, Joanne Crook3, Penny North-Lewis4, Palaniswamy Karthikeyan4, Sanjay Bansal1, Graham Foster5, 1Birmingham Children’s Hospital, United Kingdom; 2University of Birmingham, United Kingdom; 3King’s College Hospital, United Kingdom; 4Leeds General Infirmary, United Kingdom; 5Barts and The London School of Medicine and Dentistry, United Kingdom
Email: carla.lloyd1@nhs.net

Background and aims: Hepatitis C virus (HCV) infection is a major global health problem in adults & children. The recent efficacy of Direct Acting Anti-viral therapy (DAA) has cure rates of 99% in adults and adolescents. These drugs were also developed for children 3–12 yrs during the recent coronavirus pandemic. To ensure equitable access, safe & convenient supply during lockdown, we established a virtual national treatment pathway for children with HCV in England & evaluated its feasibility, efficacy & treatment outcomes.

Method: A paediatric Multidisciplinary Team Operational Delivery Network (pMDT ODN), supported by NHS England (NHSE), was established with relevant paediatric specialists to provide a single point of contact for referrals & information. Referral & treatment protocols were agreed for HCV therapy approved by MHRA & EMA. On referral the pMDT ODN agreed the most appropriate DAA therapy based on clinical presentation & patient preferences, including ability to swallow tablets. Treatment was prescribed in association with the local paediatrician & pharmacist, without the need for children & families to travel to national centres. All children were eligible for NHS funded therapy; referral centres were approved by the pMDT ODN to dispense medication; funding was reimbursed via a national NHSE agreement. Demographic & clinical data, treatment outcomes & SVR 12 were collected. Feedback on feasibility & satisfaction on the pathway was sought from referrers.

Results: In the first 6 months, 34 children were referred; 30- England; 4-Wales; median [range] age 10 (3.9–14.5) yrs; 15M; 19F; Most were under 18 yrs, 14.5 yrs; 15M; 19F: Most were able to swallow tablets; 4/7 are awaiting release of granules. 11/27 Epclusa (11); Maviret (2). 27/34 could swallow tablets; 3/7 received DAA therapy with the MDT & many found it educational. There were difficulties in providing the medication through the local pharmacy. However there are manufacturing delays in providing granule formulations because suppliers focused on delays in providing granule formulations because suppliers focused on treatment for COVID, leading to delays in referring and treating children unable to swallow tablets.

Conclusion: The National HCV pMDT ODN delivers high quality treatment & equity of access for children & young people, 3–18 yrs with HCV in England, ensuring they receive care close to home with 100% cure rates.
Background and aims: While HCV treatment with direct-acting antivirals is highly efficacious in clinical trials, medication receipt and adherence is challenged by both policy and patient-specific barriers in real-world settings. Previous research suggests that sustained antivirals is highly efficacious in clinical trials, medication receipt and adherence are lower in real-world settings. Previous research suggests that sustained virologic response can be achieved with imperfect adherence, but current data is unclear on how the amount and timing of nonadherence impacts sustained virologic response (SVR).

Method: Data was pooled from two real-world investigations of HCV treatment using direct-acting antivirals from 2015 to 2020, ASCEND and ANCHOR. The analysis was limited to individuals with an anticipated duration of 12 weeks, who were dispensed at least one month of medication, on whom SVR was assessed. Measures of adherence were assessed in three ways: (1) medication receipt (MR), defined as the actual number of 28-pill bottles dispensed; (2) medication gap (MG), defined as the difference in days between expected medication receipt and actual medication receipt; and (3) on treatment detectable viral load (DVL), defined as viral load >1000 IU/ml at week 4 or >100 IU/ml at week 12.

Results: Of 628 individuals, 472 were treated with LDV/SOF (75%), 93 with SOF/VEL (15%), and 63 with ELB/GZV (10%). Overall, the cohort was median age 59, majority (60%) male, with 94% Black race, 28% with current heroin use, 16% with current cocaine use, and 27% unstably housed. Fifteen patients (2.3%) received 1 bottle, 43 (6.8%) received 2 bottles, and 570 (90.8%) received 3 bottles, and MR was significantly associated with SVR (p < 0.0001), but was not associated with gender, race, or substance use. Of the 570 who received all 3 bottles, 211 (37%) had a MG of at least 1 day (range 1–197, median 7), MG of 14 days or more was inversely associated with SVR (p = 0.037), however MG of 7 days or more was not associated with SVR. Of the 211 with MG, 89 individuals had a gap between months 1 and 2, 79 between months 2 and 3, and 43 between both. There was no association with timing of MG and SVR. Of 567 patients who received 3 bottles and who had on treatment VL assessment, 22 (3.9%) had DVL, which was >1000 IU/ml at week 4 or >100 IU/ml at week 12.

Conclusion: In this analysis of 628 individuals treated with DAA, 10% did not complete treatment, and more than a third had medication gaps, which were inversely associated with SVR. Despite this, patients with imperfect adherence still achieved rates of SVR greater than 75%. These data suggest that while nonadherence to DAA is common, patients should be continued on treatment regardless of imperfect adherence. Finally, these data suggest removal of polices which can delay medication receipt, such as mandatory on-treatment phone calls, visits, or lab checks.
Conclusion: The ATA haplotype, which is related to lower IL-10 production, associated with liver cirrhosis in patients chronically infected with HCV. Also, phase angle, a nutritional marker that reflects the integrity of cell membranes, was inversely associated with cirrhosis in patients with chronic hepatitis C.

FRI324
Use of Glecaprevir/Pibrentasvir (G/P) for the treatment of HCV infection among fentanyl users: an interim analysis of the GRAND PLAN study
Brian Conway1,2, David Truong1, Leo Yamamoto1, Rossitta Yung1, Shawn Sharma1, 1Vancouver Infectious Diseases Centre, Vancouver, Canada; 2Simon Fraser University, Burnaby, Canada
Email: bconway5538@gmail.com

Background and aims: To achieve the World Health Organization mandate of eliminating Hepatitis C Virus (HCV) infection as a public health concern by the end of the decade, we must design and implement plans of intervention for all affected populations, including the most vulnerable and difficult to reach. We describe a community-based program targeting HCV-infected inner-city residents with active fentanyl use.

Method: Through weekly events held at single room occupancy dwellings in the inner city of Vancouver, Canada, we identified subjects with HCV infection and a history of ongoing fentanyl use. We engaged them in a multidisciplinary program of care to meet medical, psychological, social and addiction-related needs and provided HCV treatment with Glecaprevir/Pibrentasvir (G/P) within this context. HCV medications were administered in a way to maximize the likelihood of adherence and follow-up to the sustained virologic response (SVR) 12 time point. This included daily dispensing with opiate agonist therapy or weekly delivery of medications to the place of residence. If a subject was unavailable for weekly check-ins, interventions were immediately implemented to re-integrate into care. This analysis presents the rate of documented cure (achievement of SVR12) in the target population.

Results: We identified 118 eligible HCV-infected fentanyl users who were enrolled in the program. Key demographic characteristics include: 91 (77%) male, median age 47 (26–75) years, 102 (86%) on opiate agonist therapy, F0/1 (86, 73%), ≥F2 (32, 77%), known fentanyl use (74, 63%), other drug use (92, 78%). Of 107 who initiated treatment, 88 completed treatment to date and 82 achieved cure at the SVR12 and/or SVR24 time point. Those lost to follow-up included 2 overdose-related deaths prior to SVR12 time point and 4 disengaged from care. There were no cases of documented virologic failure.

Conclusion: To treat HCV infection among the most vulnerable inner-city populations, specific programs for integration and maintenance in care must be designed and evaluated. We have shown that this can be accomplished even among active fentanyl users who are precariously housed. This may provide the basis for successful interventions among similar populations in different settings.

FRI325
Indigenous methodologies in practice through community engagement and telehealth outreach increase hepatitis C access to care in Alberta, Canada
Kate Dunn1, Samuel Lee2, 1Indigenous Wellness Core, Calgary, Canada; 2University of Calgary Cumming School of Medicine, Medicine, Calgary, Canada
Email: samlee@ucalgary.ca

Background and aims: Hepatitis C virus (HCV) is a major public health burden in Canada, with prevalence in Indigenous (First Nation, Metis and Inuit) communities 4–6 times higher than non-Indigenous population. Conventional care models have created barriers to curative DAA therapy in remote Indigenous communities. Innovative approaches are required to improve access to HCV services.

Method: The ECHO+ telehealth program in Alberta aims to increase access to HCV treatment through a hub-and-spoke model led by a hepatologist (hub) working with Indigenous communities (spokes) designing a model of care tailored to local needs. We incorporated Indigenous ways of knowing (see figure), including building a predominantly Indigenous team, and embedding the 5 R’s of Indigenous Research Methodology (Respect, Relationship, Relevance, Reciprocity, and Responsibility). ECHO+ builds relationships with Indigenous community healthcare teams while using a novel co-design approach to remove barriers while increasing awareness, screening for HCV, and providing telehealth access to specialist care.

Results: Collaborative methods included developing information resources translated into local languages; building infrastructure and supporting community-directed implementation to include other health topics. Due to the COVID-19 pandemic, virtual awareness presentations (HCV awareness topics, community interaction and knowledge sharing, opportunity to follow up with mailed resources packages, and sharing lived experience stories from Indigenous youth and Elders) have been shared with every Indigenous community in Alberta. Practitioners were interviewed to identify barriers to care. Biweekly Zoom meetings with community healthcare teams have expanded during the pandemic to include pandemic topics, and other liver diseases. Collaboration between ECHO+ and Indigenous community leadership and healthcare teams has improved HCV screening, de-stigmatization, increased treatment access, and supported local community healthcare providers to effectively access DAA therapy. Thus, currently 92% of the 53 Indigenous communities in Alberta have engaged with ECHO+, compared to 23% before this approach. This reflects success of the 5R method.

Conclusion: A culturally-sensitive framework combines Indigenous with western approaches to improve access to HCV awareness and care in remote Indigenous communities. This approach has increased community communication and involvement, facilitated engagement with every Indigenous community, and provided practical support throughout the pandemic.
**Background and aims:** Hepatitis C (HCV) is a global health problem since it affects about 3% of the world’s population. The major complications during the disease are related to the progression of liver fibrosis. Therefore, it is of great importance to study the sociodemographic factors that increase or decrease the risk of developing fibrosis. The aim of this work was to evaluate the involvement of Metabolic associated fatty liver disease (MAFLD) and sex of patients in the risk of developing liver fibrosis during hepatitis C infection.

**Method:** Cross-section study of Hepatitis C (HCV) newly diagnosed patients, information of age, sex, BMI, comorbidities, and laboratory results were obtained in the first medical consultation with a certified hepatologist, HCV was diagnosed by qualitative RT-PCR test COBAS AMPLICOR and MAFLD was diagnosed according to the international expert consensus statement Eslam (2020). Liver fibrosis was quantified using The Fibrosis-4 (FIB-4) Index. Four groups were formed: 1.- Men+NonMAFLD, 2.- Men+MAFLD, 3.- Women+NonMAFLD and 4. Women+MAFLD. Level of FIB-4 was obtained of each group and global statistical significance (SSI) of the distribution of FIB-4 among groups was evaluated with the Kruskal Wallis test. Post Hoc analysis was performed using the Kruskal Wallis test, alpha was adjusted with the Bonferroni method to obtain the SSI of the FIB-4 distribution within the groups.

**Results:** A total of 84 patients (26.2% Male) were studied. The median age of the patients were 62 years (IQR 53–71), Distribution in the age and FIB-4 between men and women was not SSI. The prevalence of MAFLD was 73.75%. The difference of MAFLD between sexes was not SSI. The global difference among FIB-4 levels between the four groups was very close to SSI (p = 0.07). The Post Hoc analysis (Figure 1) found differences in the levels of FIB-4 between the groups Men+NonMAFLD vs Men+MAFLD (2.25 [IQR 1.68–2.67] vs 4.98 [IQR 2.99–8.35], p = 0.01) and Men+NonMAFLD vs Women+NonMAFLD (2.25 [IQR 1.68–2.67] vs 5.56 [IQR 2.98–6.89], p = 0.01). No SSI differences in FIB-4 levels were found between women with and without MAFLD.

**Conclusion:** In the studied population MAFLD is a risk factor for developing fibrosis in men. Men without MAFLD had lower risk of developing fibrosis than women without MAFLD. Although the literature mentions a lower risk in women of developing fibrosis in hepatitis C, our results could be explained by the age range of our patients in which most of the women were postmenopausal.
Background and aims: An epidemic of acute hepatitis C virus (HCV) infections (AHC)-observed predominantly among men who have sex with men (MSM)—may now decline due to wide availability of direct-acting antivirals (DAAs). This study aimed to investigate changes in the epidemiology of AHC in a Viennese referral center over a 13-year period.

Method: Patients presenting with AHC between 01/2007–12/2020 at the Vienna General Hospital were retrospectively enrolled and compared to the pre-DAA-era prior to 09/17. The introduction of unrestricted DAA-access after 09/17 defined the DAA-era compared to the pre-DAA-era prior to 09/17.

Results: We identified 134 AHC cases in 119 patients with a mean age of 39 ± 9 years at inclusion. The majority of patients were male (92%), HIV-positive (88%), and MSM (85%). In the DAA-era, a history of prior chronic HCV infection at inclusion was found in 24% (11/46) compared to 7% (5/73) in the pre-DAA-era (p = 0.012). The annual rate of AHC cases increased in the DAA-era (17.11 per-year) compared to the pre-DAA-era (7.76 per-year). The DAA-era included an AHC-genotype-2 cluster and more HIV-negative AHC cases (0% vs. 7% (5/73) in the pre-DAA-era (p = 0.012). The annual incidence of re-infections per 100-patient-years was 9.66 (95%CI: 3.57–9.66).

Conclusion: We observed a high incidence of AHC in Vienna in the DAA-era—primarily among HIV-positive MSM, but increasingly also in HIV-negative MSM. Sufficient screening and prevention strategies combined with fast treatment initiation are needed to confine further spread of HCV.
Conclusion: Collaborations between health, social and non-profit organizations is key for Hepatitis C elimination. In this sense, enabling HCV detection assays to be performed outside the hospital enhances the chances of identifying positive patients. Moreover, the short-cut for setting up the appointment allows faster access to treatment (presential or remote antiviral dispensation) at hepatology unit. At the same time, the possibility of doing phone visits and remote antiviral dispensation in patients refusing to be attended at the hospital increases treatment success rate. Coordinating these actions together can lead to a Hepatitis C-free city.

Acknowledgement: AEEH and Gilead Science for research grant and SAPD and Abbvie for providing Oralquick® and DBS®.

FRI330
Success of a peer-led community based model of hepatitis C treatment support for marginalised populations
Binta Sultan1, 2, John Gibbons1, Indrajit Ghosh3, Julian Surey1, 2, Mark Leonard4, 1University College London Hospital, Find&treat, United Kingdom; 2University College London; 3Mortimer Market Centre, United Kingdom; 4Groundswell, United Kingdom
Email: b.sultan@ucl.ac.uk

Background and aims: Community-based models of HCV care have been developed and shown to be an effective way of supporting marginalised people. Many outreach models of HCV care were scaled down during the pandemic. The Find&treat team established a peer-led HCV outreach treatment service for vulnerable people in North London during the pandemic, to ensure continued access to care for these patients. We present a description and evaluation of this model of care, which was a multi-component intervention delivered by a highly trained peer.

Method: The model of care was peer-led with clinician support as needed and began in June 2020. Patients with confirmed current HCV infection were referred by drug services, Find&treat service outreach HCV testing team and local clinics. All patients had a degree of social complexity, which included drug use and or experience of homelessness. The peer and clinician reviewed all patients who were referred. The whole HCV assessment and treatment cascade was managed in the community.

Interventions: Confirmatory bloods and liver fibroscan assessment was undertaken by the peer and a treatment referral was made to the local treatment approval centre. The peer took HCV medication to the patient at their place of residence, provided in monthly or weekly dosset boxes. The peer engaged the patient with appropriate treatment support which included daily text reminders, telephone calls, home visits, video supported care, blood tests for monitoring side effects and treatment response with capillary bloods, and support for hospital appointments. The clinician reviewed patients who had co-morbidities e.g. cirrhosis or other acute health needs and made referrals to secondary care as necessary. The peer supported people with engagement with drug and alcohol services and GP engagement. Routine clinical data was collected in electronic medical records. Data was captured about all interventions and healthcare interactions. This model of care is being evaluated using the integrated HCV candidacy framework developed by Iheji and colleagues (2019).

Results: As of October 2021, 72 patients were referred to the service, all with confirmed HCV infection. 2/72 had HIV co-infection, 2/72 had HBV co-infection, 57 were male, 42/72 had unstable housing, 72/72 had problematic drug or alcohol use. 72/72 had treatment approved, 68/72 have started treatment, 66/72 currently in or completed treatment, 48/72 completed treatment, 25/72 have SVR 12, 1/72 failed treatment.

Conclusion: A peer-led community-based HCV treatment model is effective at supporting people with social complexity to complete treatment. The components of the peer-led intervention addressed multiple domains in the candidacy framework for engagement of vulnerable populations. This model of care is essential to achieving HCV elimination targets and improved health outcomes, especially for vulnerable populations.

FRI331
Impact of hepatitis C virus point-of-care (Poc) viral load assay compared to laboratory-based assays on uptake of testing and treatment, and turnaround times: a systematic review and meta-analysis
Philippa Easterbrook1, Adam Trickey2, Emmanuel Fajardo3, Daniel Alemu1, Adelina Artenie2, 1World Health Organization, Global Hepatitis Programme, Geneva, Switzerland; 2University of Bristol, Bristol, United Kingdom; 3World Health Organization, Geneva, Switzerland
Email: easterbrookp@who.int

Background and aims: The requirement for a confirmatory hepatitis C virus (HCV) viral load (VL) test for diagnosis of chronic HCV infection leads to significant loss to follow-up in the care cascade. Point of care (Poc) HCV VL assays are now being used as an alternate to laboratory-based HCV RNA NAT assays. We undertook a systematic review and meta-analysis to evaluate the impact of using PoC HCV VL compared to laboratory-based standard-of-care approaches on uptake of HCV RNA testing and treatment, and turnaround times (TAT) from HCV antibody (HCVAb) testing to treatment initiation.

Method: We searched PubMed, Embase, and Web of Science on 23/09/2020 for studies in English that used HCV PoC RNA assays and had data on key outcomes. We also searched relevant conference abstracts from 2016 to 2020 not picked up by the main search. We categorised study arms according to whether the PoC HCV VL assay was based on-site at the clinic (Model 1), in a mobile unit (Model 2), or in a laboratory (Model 3) versus a HCV lab-based high-throughput viral load assay (Model 4). For each model, studies were further stratified by whether testing and treatment were delivered at the same or different sites, and on the same day. For TATs we calculated the weighted median of medians. We analysed RNA testing and treatment uptake using random effects meta-analysis. Risk of bias was assessed using a tool adapted from Hoy et al and the ROBINS-I tool.

Results: We included 45 studies with 64 within-study arms: 28 studies among people who inject drugs (PWID)/homeless, 4 among prisoners, 9 among general populations, and 4 among persons with HIV. All were observational studies. The pooled median TAT between HCVAb test and treatment was shorter with PoC RNA assays on site (18.5 days [95% CI: 14–53]) than with use of either lab-based PoC RNA assays (64 [64–64]), or lab-based high-throughput RNA assays (67 [50–67]). Treatment uptake was higher with onsite PoC RNA assays
77% (95% CI: 72%-83%), and PoC assays in a mobile unit 81% (60%-97%) compared to lab-based high-throughput assays 53% (31%-75%). p value = 0.03 (models 1/2 vs 4). The effects were greatest among PWID. 4 studies had direct within-study comparisons between a PoC assay arm and a lab-based assay arm. The pooled relative risk for testing uptake was 1.11 (95% CI: 0.89–1.38) and 1.32 (1.06–1.64) for treatment uptake. Risk of bias was high for 36% of studies and moderate for 40%.

**Conclusion:** Access to PoC HCV VL was associated with reduced time to treatment initiation and increased treatment uptake, especially among PWID. It is now recommended by WHO guidelines as an additional strategy to promote access to VL testing, especially in marginalised populations with high rates of loss to follow-up.

FRI332
**Diagnostic accuracy of point-of-care HCV viral load assays for HCV diagnosis: a systematic review and meta-analysis**

Weiming Tang1, Yusha Tao1, Emmanuel Fajardo2, Elena Ivanova2, Roger Chou3, Jo Tucker1, Philippa Easterbrook2.

1UNC Project-China; 2Oregon Health & Science University

**Background and aims:** Despite the widespread availability of short-course curative HCV treatment, a significant proportion of HCV patients remain undiagnosed and untreated. The requirement for a confirmatory HCV viral load (HCV VL) test can result in substantial care cascade attrition. New point-of-care HCV RNA assays may enhance access to testing by decentralizing HCV RNA testing outside of laboratory settings. We undertook a systematic review and meta-analysis to compare the diagnostic performance of PoC HCV viral load assays to laboratory-based nucleic acid testing.

**Method:** We searched three databases, used Cochrane methods, and registered the protocol Studies were eligible if they utilized a laboratory reference standard to evaluate PoC HCV RNA assays and if they reported or had raw data that could be extracted to calculate sensitivity, specificity, the limit of detection, and bias. Data were extracted by geographic region, collection year, risk group, and specimen type. Random effects bivariate models were used to summarize estimates and describe the variability in test performance across studies. We used the GRADE approach to assess the certainty of the evidence.

**Results:** A total of 25 studies including data from 8, 791 people were summarized. XX studies in high-income countries and XX in low and middle-income countries. Assays included the Xpert HCV Viral Load assay (Cepheid, USA) Xpert HCV VL Fingerprick (Cepheid, USA) Genedrive HCV ID Kit, Truenat HCV assay, and SAMBA II. Across all assays, the pooled sensitivity and specificity were 99% (95% CI: 98–99%) and 99% (95% CI: 99–100%), respectively, compared to a lab-based reference standard. High sensitivity and specificity were also observed across different study settings (including LMICs and HICs) and populations, using different assays. The evidence was moderate-high certainty. Specificity showed no difference among different specimen types.

**Conclusion:** PoC HCV viral load assays have excellent sensitivity and specificity compared to gold standard laboratory-based nucleic acid testing methods across diverse settings and populations. WHO now recommends the use of PoC HCV viral load assays as an additional strategy to promote access to treatment. The adoption of PoC viral load assays will be facilitated through increasing availability of integrated molecular multiplex technologies that utilize the same technology for several assays and/or across diseases.

**Disclosure:** No significant relationships.
Background and aims: Case detection remains a major challenge for hepatitis C virus (HCV) elimination. We have previously published results from a pilot of an emergency department (ED) semi-automated screening program, SEARCH; Screening Emergency Admissions at Risk of Chronic HCV. In this pilot, 5000 consecutive patients were screened including 4778 overseas born (targeted) from 14,093 ED presentations. HCVAb was positive in 181 patients (3.6%); 51 (1.0%) were HCV RNA positive. This cost analysis aimed to accurately describe the overall costs of this pilot service. It also aimed to report on costs per patient tested, per HCV Ab positive patient detected and per RNA positive patient treated. We modelled the effect of proposed service refinements (SEARCH 2.0).

Method: All direct costs of HCV testing until direct acting anti-viral (DAA) therapy initiation were calculated. Cost was assessed in 2018 Australian Dollars. A cost analysis of the initial program and refinements are presented. Sensitivity analysis to understand impact of variation in staff time, laboratory test cost, changes in Australian Dollars. A cost analysis of the initial program and refinements are presented. Sensitivity analysis to understand impact of variation in staff time, laboratory test cost, changes in

Results: The total SEARCH pilot, testing 5000 patients was estimated to cost $110,549.52 (range $92,109.79 – $129,581.24) comprising of $68,278.67 for HCV Ab testing, $21,568.99 for follow up and linkage to care of positive patients and $20,701.86 to prepare HCV RNA positive patients for treatment. Refinements resulted in a 32% cost reduction overall and reduced the cost of HCV antibody screening from $13.66 to $8.46 per test and the total cost per positive HCV Ab, positive HCV RNA and treated patient to $611.77, $2,168.64 and $3,566.11 respectively. Our sensitivity analysis indicates costs are modest so long as HCV Ab prevalence was 1% or greater.

Conclusion: ED screening is an affordable strategy for HCV case detection and elimination.
Conclusion: Preliminary results of this study demonstrate that HCV self-testing increases HCV screening rates in a peri-urban/rural setting consistent of a mostly illiterate population in a low-middle income country like Pakistan.

FRI336
HCV-viral load fingerstick assay to simplify screening and linkage to care of people who use drugs attending Italian addiction treatment centres

Sarah Vecchio1, Lorenzo Somaini2, Luigi Bartoletti3, Daniela Musi3, Roberta Gaudenzi4, Eugenia Vernole5, Claudio Leonardi6. 1ASL Biella, Addiction Treatment Center, Biella, Italy; 2ASL Biella, Addiction Treatment Center, Biella, Italy; 3ASL Alessandria, Addiction Treatment Center, Alessandria, Italy; 4ASL Umbria 1, Addiction Treatment Center, Perugia, Italy; 5ASL Bari, Addiction Treatment Center, Bari, Italy; 6ASL Roma 2, Addiction Treatment Center, Roma, Italy

Background and aims: People who use drugs (PWUDs) are the major drivers of HCV transmission in the world, representing the target population for HCV screening and treatment. In Italy, the estimate prevalence of HCV infection in drug users exceeds the 80%, with 205,000 PWUDs not yet treated. Simplified strategies are required for the screening and diagnosis of hepatitis C infection among PWUDs, and HCV-RNA viral load fingerstick assay can help in overcoming existing challenges and barriers to HCV diagnosis and care. The aims of this prospective study were to evaluate the feasibility and the acceptability of HCV-RNA viral load fingerstick assay use to improve HCV screening and treatment among Italian PWUDs attending different Italian Addiction Treatment Centres (Ser.D) in an outpatient setting.

Method: Between October 2020 and December 2021, the HCV screening was offered to 1258 consecutive PWUDs from 5 Addiction Treatment Centres of 4 Regions of Northern, Central and Southern Italy. HCV analysis was carried out by means of a fingerstick capillary whole blood RNA test. Results were given in 60 minutes.

Results: 1221/1258 (97%) consecutive PWUDs were enrolled. Patients were mostly male (973/1221, 80%), with a mean age of 42.9 years ± 10.7 and a mean addiction treatment duration of 10.1 years ± 8.5. The main HCV risk factors identified were heroin addiction (935/1221, 76%), a history of injecting drug use (700/1221, 57%) and tattooing (794/1221, 65%). HCV RNA was identified in 240/1221 patients (20%) participants. The most common HCV genotypes, among available data, were 3 (40/240, 17%) and 1a (38/240, 16%). Among patients with detectable HCV RNA, 89% (214/240) were referred to specialists for HCV treatment and, at the time of writing, 53% (127/240) completed the treatment. All the treated patients achieved SVR (Sustained Virologic Response).

Conclusion: This is one of the largest HCV-RNA screening projects, highlighting the feasibility and the acceptability of onsite testing performed with HCV-RNA viral load fingerstick assay in PWUDs attending Ser.Ds. At present, HCV screening and linkage to care remain worldwide far from comprehensive. The described easy to use approach favours PWUDs engagement and increases HCV treatment and elimination, as evidenced by the high rate of completed treatments.

FRI337
From extensive to intensive screening, co-operations model of hepatitis C elimination in out-patients and people who inject drug population in southwest of China

Qing Lin1, Youzhi He2, Long Chen3, Jingchun He4, Xiaojuan Yuan5, Zhenglin Wang1, Guohui Wu4, 1The People’s Hospital of Jiulongpo District, Chongqing, China; 2Methadone Maintenance Therapy Clinic of Jiulongpo District, Chongqing, China; 2Chongqing Public Health Medical Center, Chongqing, China; 3Jiulongpo District Center for Disease Control and Prevention, Chongqing, China; 4Jiulongpo District, Chongqing, China; 5Chongqing Center for Disease Control and Prevention, Chongqing, China

Background and aims: The Southwest China has a relatively higher HCV prevalence rate among the whole country for large proportion of people who inject drugs (PWID) reside here. We established a co-operation model combined with intensive and extensive HCV screening, and this study aimed to determine its efficacy on the HCV elimination in PWIDs and general out-patients (GOP).

Method: The co-operation network consists of local Centers for Disease Control and Prevention (CDC) and the medical association including 39 community health centers, 15 district hospitals and 1 methadone clinic. The CDC was responsible for educational training, funding and patient-network management. The medical association was responsible for HCV antibody screening and linkage to care with the cascade referral system. Patients with positive HCV antibody were referred to the designated hospital for HCV RNA testing, in which positive patients will receive anti-HCV treatment of sofosbuvir/velpatasvir (SOF/VEL) for 12 weeks with or without RBV. The call-back system in methadone clinic requested the HCV RNA-positive PWID patients to return for further therapy. The patient-education and management were carried out in the district hospitals monthly. Reimbursement and free RNA testing were provided to enhance treatment affordability. The effect and safety of SOF/VEL were evaluated.

Results: From March 2021 to March 2022, 102873 residents and 1,199 PWID were screened. The seropositive rate of anti-HCV and HCV RNA were 0.58% (595/101674), 22.01% (131/595) in GOPs and 87.49% (1199/1319) in PWID, respectively. 85.49% (112/131) GOPs patients and 41.52% (71/171) PWID initiated anti-HCV treatment, while only 8% before the model establishment. The genotype distribution is as follows: GT3a 22.13% (29/131), GT3b 20.61% (27/131), GT1b 18.32% (24/131) in GOPs, while GT3a 47.37% (81/171), GT3b 42.69% (73/171) and GT1b 9.94% (17/171) in PWID.

The percentage of liver fibrosis, cirrhosis and hepatocellular carcinoma was 9.1% (12/131), 9.1% (12/131) and 0.7% (1/131) in GOPs, while 26.31% (45/171), 13.45% (23/171) and 1.75% (3/171) in PWID.

Conclusions: From extensive to intensive screening, co-operations model of hepatitis C elimination in PWID show an effective and safe strategy.
Conclusion: The co-operation model was effective in HCV elimination in both groups. The HCV prevalence of PWIDs was significantly higher than GOPs in the district scale. Although PWIDs had lower treatment adherence, the treatment rate in PWIDs were improved significantly by intensive follow-up. Both groups achieved high SVR with good safety profile by SOF/VEL treatment. The co-operations model with intensive and extensive screening was an optimal option for GOP and PWID to eliminate HCV.

FRI338
Using time to positivity of hepatitis rapid detection test results to determine active viremia
Saeed Sadiq Hamid 1, Sultan Salahuddin 2, Aliya Hasnain 3, Muraduddin Gulab 2, Taj Muhammad 2, Sabiha Khan 2. 1Aga Khan University, Karachi, Pakistan; 2Aga Khan University, Medicine, Karachi, Pakistan
Email: saeed.hamid@aku.edu

Background and aims: The recommended time taken to run the Rapid Diagnostic tests (RDTs) for HCV screening is 20 mins, which is followed by reflex PCR testing for confirmation of chronic HCV infection. Confirmatory viral load testing is a barrier in the HCV cascade of care as it is a cost and time-intensive step. This study hypothesises the correlation between shorter read time and active viremia in HCV infected patients, which can reduce the need for reflex RNA tests and help implement rapid-test-and-treat models for HCV.

Method: The findings from this study were obtained from a community-based micro-elimination study which targets a high burden HCV endemic area in Karachi, Pakistan. Door-to-door visits were performed to conduct rapid screening of individuals with unknown HCV status, using the finger-stick Abbott SD Bioline HCV diagnostic kits. The time taken for the RDT to display a positive result was measured using a stopwatch to record the duration from the point the blood sample was placed in the test kit till the point the test line appeared. Blood samples of individuals with a positive screening test were collected for Hepatitis C core antigen testing, on Abbott Architect i2000SR, to determine viremia.

Results: A total of 1327 participants, median age (IQR) 47 years (39–56), with 70% females, who screened positive on HCV RDT and had HCV core antigen testing done, were included. Overall, 730/1327 (55%) patients were viremic and in all cases, the HCV RDT test was positive within 5 minutes. 50% (366/730) of all viremic cases had a positive screening result within 20–30 seconds. No. of cases with active viremia decreased as the time taken for a positive result to appear on rapid screening increased \( r = -0.63 \). Less than 1% of cases with active viremia were found amongst those who had a positive screening result from 120 seconds to 300 seconds.

Conclusion: The time to read SD Bioline HCV RDT can be reduced to 5 mins to identify patients with HCV infection. In patients displaying a positive result between 20 and 30 seconds HCV treatment using DAAs can be initiated using rapid test-and-treat models reducing loss to follow up and need for HCV RNA testing in resource limited settings.

FRI339
Liver-related mortality among people with hepatitis B and C: a validation study using linked healthcare administrative datasets
Syed Hassan Bin Usman Shah 1, Maryam Alavi 2, Behzad Hajarizadeh 2, Gail Matthews 3, Marianne Martinello 3, Mark Danta 3, Janaki Amin 3, Matthew Law 3, Jacob George 3, Hamish Innes 3, Gregory Dore 2. 1The Kirby Institute, Viral Hepatitis Clinical Research Program, UNSW, Kensington, Australia; 2The Kirby Institute, Viral Hepatitis Clinical Research Program, UNSW, Kensington, Australia; 3St Vincent’s Hospital Sydney, Darlinghurst, Australia; 4Macquarie University, Macquarie Park, Australia; 5The Kirby Institute, Kensington, Australia; 6Westmead Hospital, Westmead, Australia; 7Glasgow Caledonian University, United Kingdom
Email: hbinusman@kirby.unsw.edu.au

Background and aims: Routinely collected and linked healthcare administrative datasets could be used to monitor mortality among people with hepatitis B and C virus (HBV and HCV). This study aimed to validate a definition for liver-related mortality among people with an HBV or HCV notification, including any death (i.e. all-cause) following hospitalization for end-stage liver disease (ESLD), which included a first-time hospital admission due to decompensated cirrhosis (DC) or hepatocellular carcinoma (HCC).

Method: In New South Wales, Australia, HBV and HCV notifications (1993–2017) were linked to hospital admissions (2001–2018), all-cause mortality (1993–2018), and cause-specific mortality (1993–2016) databases. Hospitalization-defined ESLD-related mortality was validated in comparison with two death certificate-based definitions of liver deaths coded among primary and secondary cause-specific mortality data, including ESLD-related (deaths due to DC and HCC) and all-liver deaths (ESLD-related and other liver-related causes).

Results: Of 63, 292 and 107, 430 individuals with an HBV and HCV notification, there were 4, 478 (2.6%) post-ESLD hospitalization deaths, 5, 572 (3.3%) death certificate liver disease deaths, and 2, 910 (1.7%) death certificate ESLD deaths. Between 2001 and 2016, 63% (562/891) of HBV post-ESLD hospitalization deaths had death certificate ESLD deaths recorded, including 58% (390/676) of DC and 85% (431/510) of HCC deaths. Further, 83% (741/891) of HBV post-ESLD hospitalization deaths had death certificate ESLD deaths recorded, including 58% (2, 082/3, 587) of HBV post-ESLD hospitalization deaths had death certificate ESLD deaths recorded, including 56% (1, 817/3, 236) of DC and 82% (1, 007/1, 224) of HCC deaths. Further, 87% (3, 135/3, 587) of HCV post-ESLD hospitalization deaths had death certificate liver disease deaths, including 87% (2, 812/3, 236) of DC and 96% (1, 171/1, 224) of HCC deaths.

Conclusion: Our findings support the use of healthcare administrative datasets as an efficient method and a reliable information source to represent liver-related mortality rates accurately; however, concordance between post-hospitalization and death certificate-based cause of death is clearly higher for HCC than DC.

FRI340
Identifying risk factors associated with hepatitis C virus infection in participants in the national health and nutrition examination survey using Super Learner
Laura Telep 1,2, Rachael Phillips 3, Anan Chokkalingam 1,2. 1Gilead Sciences, Inc., Foster City, United States; 2University of California, Berkeley, Epidemiology, Berkeley, United States; 3University of California, Berkeley, Biostatistics, Berkeley, United States
Email: laura.telep@gilead.com

Background and aims: Under-diagnosis is a key impediment to eliminating hepatitis C virus (HCV) infection in the United States (US).
Machine learning methods offer an opportunity to support expanded HCV screening in a resource-optimized way by identifying the characteristics that are most influential in predicting HCV.

**Method:** The ensemble machine-learning method Super Learner (SL) was used with National Health and Nutrition Examination Survey (NHANES) data collected from 2013 to 2018 to build an HCV infection risk prediction algorithm. Because only 1% of survey participants tested positive for HCV RNA, case-control sampling was used to address class imbalance, with five HCV-uninfected individuals randomly selected for each HCV-infected individual (n = 1,008). The SL was fit to the case-control data, its performance was evaluated with the area under the precision-recall curve (AUC-PR), and then it was used to predict HCV infection in the full NHANES dataset (n = 15,237). We also identified the features that had the greatest impact on AUC-PR, and thus were most predictive of HCV infection.

**Results:** The SL's AUC-PR on the full NHANES dataset was 52%, a 47-fold improvement over baseline. At the probability threshold that optimized the F1 score, the SL achieved 55.4% precision and 61.3% recall; that is, if the goal was to identify at least 60% of those infected with HCV, then for every 100 individuals classified as HCV-infected, more than 50% would be true positives. Features that were most predictive of HCV infection included alanine aminotransferase (ALT), aspartate aminotransferase (AST), injection drug use, age, albumin, globulin, and HBV infection status. Additional influential predictors included smoking-related features, risk factors for heart disease or stroke (triglycerides, total cholesterol, recommendations by a doctor to take low dose aspirin), and features related to oral health.

**Conclusion:** As outreach continues to identify the undiagnosed HCV-infected population in the US, knowledge of the characteristics most predictive of HCV infection should be utilized to guide screening and prevention efforts. Next steps include identifying HCV infection predictors from widely available data such as features collected in a single routine medical care visit and exploring variation in highly predictive features by age category. Algorithms such as the one demonstrated here can be useful tools to support these activities.

---

**Viral Hepatitis C: Post SVR and long term follow up**

**FRI343**

**Hepatocellular carcinoma incidence after hepatitis C cure among patients with advanced fibrosis or cirrhosis: a meta-analysis**

Ian Lockart1,2, Malcolm Guan Hin Yeo2, Behzad Hajarizadeh3, Gregory Dore1,3, Mark Danta1,2. 1St Vincent's Hospital, Sydney, Australia; 2St Vincent's Clinical School, UNSW Sydney, Australia; 3The Kirby Institute, UNSW Sydney, Australia

**Email:** m.danta@unsw.edu.au

**Background and aims:** Hepatitis C virus (HCV) cure reduces but does not eliminate the risk of hepatocellular carcinoma (HCC). HCC surveillance is recommended in populations where the incidence exceeds 1.5% per year. In cirrhosis, HCC surveillance should continue after HCV cure, although it is uncertain if this should be indefinite. For patients with advanced fibrosis (F3), guidelines are inconsistent in their recommendations. This systematic review evaluated the incidence of HCC after HCV cure among patients with F3 fibrosis or cirrhosis.

**Method:** We searched bibliographic databases and conference abstracts for studies assessing the incidence of HCC after HCV cure among patients with F3 fibrosis or cirrhosis. Meta-analyses were used to cumulate HCC rates and meta-regression was used to explore heterogeneity across studies.

**Results:** Forty-four studies were included (36,183 patients; 109,385 person-years of follow up). The incidence of HCC was 2.2 per 100 person-years (95% CI 1.9–2.4) among patients with cirrhosis, and 0.5 per 100 person-years (95% CI 0.3–0.7) among patients with F3 fibrosis. In meta-regression analysis among patients with cirrhosis, older age (adjusted rate ratio [aRR] per 10-year increase in mean/median age: 1.34; 95% CI 1.04–1.74) and prior decompensation (aRR per 10% increase in the proportion of patients with prior decompensation: 1.05; 95% CI 1.00–1.11) were associated with an increased incidence of HCC. Longer follow-up after HCV cure was associated with a decreased incidence of HCC (aRR per year increase in mean/median follow-up: 0.87; 95% CI 0.80–0.96).
Background and aims: Patients with chronic hepatitis C virus (HCV) infection have a genuine risk of developing liver fibrosis and cirrhosis, potentially resulting in hepatocellular carcinoma (HCC), a risk that remains even after sustained viral response (SVR). It is of utmost importance to closely monitor these patients during and after antiviral treatment, which today consists of direct-acting antiviral drugs (DAAs). Glycomics-based biomarkers are an attractive tool to answer this medical need, as alterations in the abundance of N-glycans reflect an altered state of the liver. Progression of liver fibrosis has been linked to changes in serum glycosylation patterns before. Accordingly, our previously developed GlycoFibroTest measures the ratio of NGA2FB to NA3. The aim of this study was to assess the GlycoFibroTest for the evaluation of fibrosis regression during and after treatment of HCV with DAAs.

Method: N-glycosylation patterns were analyzed in sera from 36 HCV-infected patients, collected between January 2015 and June 2016. Patients showed liver biopsy-proven advanced fibrosis (F3, n = 12) or established cirrhosis (F4, n = 24) before therapy initiation, all patients achieved SVR after treatment and none of them showed liver regrowth. GlycoFibroTest was measured on serum samples at three timepoints: at the start (week 0), the end (week 12) and during follow up (week 24), by the use of an optimized glycomic technology on a DNA sequencer (DSA-FACE, Applied Biosystems).

Results: All patients achieved SVR after treatment and none of them developed HCC. Figure 1 demonstrates the significant decrease of the GlycoFibroTest (p < 0.0001) in all patients (F3 + F4) [12]. More specifically, this decrease was seen from week 0 to weeks 12 and 24, but no significant decline could be retained between weeks 12 and 24. Statistical analysis was performed using IBM SPSS Statistics version 28.0. Since measurements were repeated on the same subject and values were not normally distributed, the non-parametric Friedman’s test was used. Statistical significance was set at the alpha level of 0.05.

Conclusion: Among patients with cirrhosis, the incidence of HCC decreases over time after HCV cure and is lowest in patients with younger age and compensated cirrhosis. The substantially lower incidence in F3 fibrosis is below the recommended threshold for cost-effective screening.

FRI344 Glycomics-based serum marker as reliable tool for assessment of viral response after treatment with direct-acting antiviral drugs in hepatitis C virus infection

Nicky Somers1, Elisabeth Vandekerckhove1, Anja Geerts1, Helena Degroote1, Sander Lefere1, Lindsey Devisscher2, Leander Meuris3,4, Nico Callewaert3,4, Hans Van Vlierberghe1, Xavier Verhelst1. 1Ghent University, Ghent University Hospital, Hepatology Research Unit, Department Internal Medicine and Paediatrics, Liver Research Center Ghent, Ghent University, Ghent University Hospital, Ghent, Belgium, Belgium; 2Ghent University, Gut-Liver Immunopharmacology Unit, Department of Basic and Applied Medical Sciences; Liver Research Center Ghent, Ghent University, Ghent, Belgium, Belgium; 3Vlaams Instituut voor Biotechnologie, Center for Medical Biotechnology, VIB, Ghent, Belgium, Belgium; 4Ghent University, Department of Biochemistry and Microbiology, Ghent University, Ghent, Belgium

Email: nicky.somers@ugent.be

Background and aims: While direct acting antivirals (DAA) can cure chronic hepatitis C virus (HCV) infection in almost all patients, some patients remain at risk of liver disease despite HCV cure. We aimed at identifying predictors for liver-related morbidity and death after viral cure.

Method: The DHC-R (German Hepatitis C-Registry) is a national multicenter real-world registry. Patients are followed for up to 7 years after DAA therapy. Normal alanine transaminase (ALT; at 37°C) was
Results: 97.4% of patients achieved sustained virological response (SVR). In patients achieving SVR, elevated ALT at SVR24 was documented in 657/6982 (9.4%), elevated ALT (AASLD) in 2609/6982 (37.4%) and elevated GGT in 1777/6982 (25.5%). At SVR24, elevated ALT was associated with categorized higher body mass index (BMI; p < 0.05), liver cirrhosis (OR 2.29, p < 0.001), alcohol consumption (≥30/40 g/day) (OR 2.93, p < 0.001), elevated ALT at baseline (OR 4.46, p < 0.001) and no SVR (OR 43.49, p < 0.0001). The same variables were identified using AASLD criteria plus female sex (OR 2.39, p < 0.001). Increased GGT at SVR24 was associated with male sex (OR 2.12, p < 0.001), higher BMI (OR1.04, p < 0.05), age >50 years (OR 1.60, p < 0.01), liver cirrhosis (OR 3.97, p < 0.0001), alcohol consumption (OR 2.99, p < 0.001), diabetes mellitus (OR 1.63, p < 0.001), non-SVR (OR 8.00, p < 0.0001) and elevated GGT at baseline (OR 17.12, p < 0.001). More importantly, we identified elevated GGT at SVR24 as the best predictor of overall survival, hepatic decompensation or HCC development over elevated ALT or ALT (AASLD; Figure). Combining ALT and GGT did not improve sensitivity substantially.

Conclusion: We here define risk factors for developing clinical complications after cure form HCV infection. In this context, elevated GGT may highlight the relevance of non-alcoholic fatty liver disease (NAFLD), diabetes mellitus, and alcohol consumption.

FRI346
The impact of liver function improvement after direct-acting antiviral therapy on the outcome in hepatitis C virus patients with decompensated cirrhosis

Yuki Tahata1, Hayato Hikita1, Satoshi Mochida2, Nobuyuki Enomoto3, Norifumi Kawada4, Masayuki Kurosaki5, Akio Ido6, Hitoshi Yoshiji7, Daiki Miki8, Yusufiro Takikawa9, Ryotaro Sakamori10, Yoichi Hisa10, Hiroshi Yatsushashi11, Kazuhiko Nakao12, Naoya Kato13, Yoshiyuki Uno14, Yoshiro Itoh15, Ryosuke Tateishi16, Goki Suda17, Taro Takami18, Kentaro Matsuura19, Taro Yamashita12, Norio Akuta20, Tatsuya Kanto21, Yasunori Nakamoto22, Yusufi Asahina24, Shuji Ierai25, Masahito Shimizu26, Ryoko Yamada1, Takahiro Kodama1, Tomohide Tatsunami1, Tomomi Yamada2, Tetsuo Takehar1. Osaka University Graduate School of Medicine, Department of Gastroenterology and Hepatology; 2Satama Medical University, Department of Gastroenterology and Hepatology; 3University of Yamanashi, First Department of Internal Medicine, Faculty of Medicine; 4Graduate School of Medicine, Osaka City University, Department of Hepatology; 5Musashino Red Cross Hospital, Department of Gastroenterology and Hepatology; 6Kagoshima University Graduate School of Medicine and Dental Sciences, Digestive and Lifestyle Diseases, Department of Human and Environmental Sciences; 7Nara Medical University, Department of Gastroenterology; 8Gifu University Graduate School of Medicine, Department of Biomedical and Health Sciences, Hiroshima University, Department of Gastroenterology and Metabolism; 9Keio University, Division of Hepatology, Department of Internal Medicine; 10Ehime University Graduate School of Medicine, Department of Gastroenterology and Metabolism; 11National Hospital Organization Nagasaki Medical Center, Clinical Research Center; 12Nagasaki University Graduate School of Biomedical Sciences, Department of Gastroenterology and Hepatology; 13Graduate School of Medicine, Chiba University, Department of Gastroenterology; 14Faculty of Medicine, Yamagata University, Department of Gastroenterology; 15Graduate School of Medical Science, Kyoto Prefectural University of Medicine, Department of Molecular Gastroenterology and Hepatology; 16Graduate School of Medicine, The University of Tokyo, Department of Gastroenterology; 17Graduate School of Medicine, Hokkaido University, Department of Gastroenterology and Hepatology; 18Yamaguchi University Graduate School of Medicine, Department of Gastroenterology and Hepatology; 19Nagoya City University Graduate School of Medical Sciences, Department of Gastroenterology and Metabolism; 20Kanazawa University Hospital, Department of General Medicine; 21Toranomon Hospital, Department of Hepatology; 22National Center for Global Health and Medicine, The Research Center for Hepatitis and Immunology; 23Faculty of Medical Sciences, University of Fukui, Second Department of Internal Medicine; 24Tokyo Medical and Dental University, Department of Gastroenterology and Hepatology, Department of Liver Disease Control; 25Graduate School of Medicine and Dental Sciences, Niigata University, Division of Gastroenterology and Hepatology; 26Gifu University Graduate School of Medicine, Department of Gastroenterology/Internal Medicine; 27Osaka University Hospital, Department of Medical Innovation

Email: yuki.tahata@g.med.osaka-u.ac.jp

Background and aims: Direct-acting antiviral (DAA) therapy can improve liver function in the short term even in patients with hepatitis C virus (HCV)-related decompensated cirrhosis. However, the impact of DAA therapy on long-term outcome among patients with decompensated cirrhosis is unclear.

Method: This study enrolled 396 patients with HCV-related compensated or decompensated cirrhosis who started DAA therapy between February 2019 and December 2020 at 33 Japanese hospitals. Patients were excluded when sustained virologic response (SVR) could not be determined or died before SVR confirmation. SVR was defined as undetectable serum HCV-RNA for at least 12 weeks after the end of treatment (EOT). Our endpoints are the incidence of decompensated cirrhosis events with hospitalization and overall survival. Decompensated cirrhosis events were defined as aggravation of ascites or encephalopathy, rupture of varices, and the onset of spontaneous bacterial peritonitis, sepsis or acute kidney injury. We evaluated the impact of delta MELD score between at baseline and at 12 weeks after the EOT on these endpoints. Delta MELD score was classified into three groups: the MELD score decreased 2 points or more (MELD improved), the MELD score increased 2 points or more (MELD deterioration) and others (MELD stable).

Results: The median age was 70 years. The SVR rates of patients with CP class A, B and C were 100% (224/224), 96% (142/148) and 96% (22/23), respectively. Among 396 patients, delta MELD score were evaluated in 347 patients. The number of patients with MELD improved, MELD stable and MELD deterioration were 41, 275 and 31, respectively. During the median observation period of 20 months, 34 patients experienced decompensated cirrhosis events (the most
frequent event was ascites), 10 patients died, and two patients underwent liver transplantation. In patients with CP class A, five patients experienced decompensated cirrhosis events and two patients died. MELD changes at 12 weeks after the EOT were not associated with the incidence of decompensated cirrhosis events and overall survival. In patients with CP class B or C, the cumulative incidence rate of decompensated cirrhosis event at 2 years with MELD improved, MELD stable, MELD deterioration were 7%, 22% and 58%, respectively. Overall survival rates of patients at 2 years with MELD improved, MELD stable and MELD deterioration were 100%, 97% and 69%, respectively. Patients with MELD deterioration had a higher incidence of decompensated cirrhosis events and poorer overall survival than the other two groups.

**Conclusion:** In patients with decompensated cirrhosis who were treated with DAA, MELD score deterioration at 12 weeks after the EOT indicated an unfavorable outcome.

**FRI347**

**De novo occurrence of portal vein thrombosis in patients with HCV-related cirrhosis after sustained virological response: medium to long term observations from the ongoing PITER cohort**

Loreta Kondili1, Maria Giovanna Quaranta1, Luigina Ferrigno1, Carmine Coppola2, Monica Monti2, Roberto Filomia3, Giuseppina Brancaccio4, Maurizia Brunetto5, Elisa Bilotti6, Donatella Ieluzzi7, Andrea Iannone8, Salvatore Madonia9,10, Xhimi Tata1, Luisa Cavalletto11, Valentina Cossiga12, Simona Amodeo13, Vincenza Calvaruso14, Elena Rosselli Del Turco15, Maria Grazia Rumi16, Maurizio Pompili17, Alessia Ciancio18, Nicola Cesario19, Leonardo Giuseppi Ieluzzi8, Andrea Iannone9, Simona Amodeo13, Vincenza Calvaruso14, Elena Rosselli Del Turco15, Maria Grazia Rumi16, Maurizio Pompili17, Alessia Ciancio18, Nicola Cesario19, Leonardo Giuseppi Ieluzzi8, Andrea Iannone9, Simona Amodeo13, Vincenza Calvaruso14, Elena Rosselli Del Turco15, Maria Grazia Rumi16, Maurizio Pompili17, Alessia Ciancio18, Nicola Cesario19, Leonardo Giuseppi Ieluzzi8, Andrea Iannone9, Simona Amodeo13, Vincenza Calvaruso14, Elena Rosselli Del Turco15, Maria Grazia Rumi16, Maurizio Pompili17, Alessia Ciancio18, Nicola Cesario19, Leonardo Giuseppi Ieluzzi8, Andrea Iannone9.

**Results:** Of 1632 patients evaluated, 40 (2.5%) developed de-novo PVT. Kaplan-Meier analysis and log rank test evaluated the PVT rates by DAA achievement following the DAA treatment. The two year PVT free survival was 99% for patients who achieved the SVR and 93% for those who didn’t (p = 0.002). Of 1555 patients who achieved the SVR (median age 65 years, 55% males, 85% Child A and 15% Child B), 34 (2.2%) experienced de-novo PVT (median follow-up 36 months after EOT; IQR 24–44.7). Of them, 18 reported HCC development previous or after achieving the SVR; in 6 of whom (17.6%) PVT was of neoplastic nature. The PVT occurrence in patients who achieved the SVR, not related to HCC development, was 1.8% (28 patients); the median time to de-novo PVT occurrence was 33.8 months (IQR 17–45 months) after EOT. At pretreatment evaluation, patients who experienced de-novo non-neoplastic PVT were more likely Child B (39.3% vs. 14.2%, p < 0.001) and by Cox regression analysis, pre-treatment variables independently associated with de-novo PVT development were: platelet count ≤120.000/μL (HR: 3.56, CI 95%: 1.03–12.33), albumin level <3.5 g/dL (HR: 2.66, CI 95%: 1.15–6.15) and bilirubin level >1.1 mg/dL (HR: 2.70, CI 95%:1.10–6.65). Patients with de-novo, non-neoplastic PVT had higher risks of hepatic decompensation (39.3% vs. 4.5%; p < 0.001) and liver-related death (13% vs. 2%, p < 0.001) regardless the SVR achievement following the DAA treatment.

**Conclusion:** The risk of de-novo non-neoplastic PVT in patients with cirrhosis who achieved the SVR is low and mainly related to the severity of liver disease. Development of de-novo, non-neoplastic PVT following the SVR may identify patients with higher risks of hepatic decompensation and mortality despite viral eradication by DAA treatment.

**FRI348**

**Suboptimal follow-up, high re-infection, and drug-related death, among HCV-treated people who inject drugs in Tayside, Scotland**

Christopher Byrne1,2, Lewis Beer2, Sarah Inglis3, Emma Robinson1, Andrew Radley3, Sharon Hutchinson4,5, David Goldberg4,5, Matthew Hickman6, John Dillon1,2, University of Dundee, Molecular and Clinical Medicine, Dundee, United Kingdom; University of Dundee, Tayside Clinical Trials Unit, Dundee, United Kingdom; NHS Tayside, Public Health, Dundee, United Kingdom; Glasgow Caledonian University, School of Health and Life Sciences, Glasgow, United Kingdom; Health Protection Scotland, Glasgow, United Kingdom; University of Bristol, Population Health Sciences, Bristol, United Kingdom; NHS Tayside, Gastroenterology, Dundee, United Kingdom

**Background and aims:** In 2017, Tayside, in East Scotland, rapidly scaled-up Hepatitis C Virus (HCV) treatment among People Who Inject Drugs (PWID) using new care pathways. This study aimed to quantify HCV re-infection and routes of re-treatment; mortality; and efficacy of re-infection follow up.

**Method:** Annual follow-up RNA testing is offered. Re-infection follow-up was measured by calculating the proportion of cases with follow-up tests received in line with local policy. We estimated re-infection incidence, overall and by pathway, per 100 person-years (PY), assuming a Poisson distribution. Mortality was similarly calculated; time-at-risk was from primary HCV treatment to censor date or death.

**Results:** There were 713 treatments and 577 SVRs. 236 cases among 231 people were followed-up for re-infection. Of cured cases, 39% had ≥1 follow-up test. 87 (15%) cases had repeat testing in the first 12 months, in line with policy. Within 2 years, 110 (19%) had a follow-up test. Of those, 20 (18%) were continued follow-up. Within 3 or 4 years, 19 were tested. Re-infection occurred 39 times over 256.57 PY, yielding a rate of 15.20 per 100 PY (95% CI 10.81–20.78). For recent injectors, there were 26 re-infections over 175.43 PY, yielding a rate of 14.82 per 100 PY (95% CI 9.68–21.72). Re-infection incidence was highest among needle exchanges (table 1), as was subsequent re-treatment.
Table 1: Clinical pathways of re-infected PWID, Tayside 2017–20.

<table>
<thead>
<tr>
<th>Clinical pathway</th>
<th>n (%)</th>
<th>PY Incidence per 100PY</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pathway prior to re-infection (n = 39)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Community pharmacy</td>
<td>12 (30.8)</td>
<td>92.25 (13.01 (6.72–22.73)</td>
</tr>
<tr>
<td>Needle exchange</td>
<td>19 (48.7)</td>
<td>64.08 (29.65 (17.85–46.30)</td>
</tr>
<tr>
<td>Other</td>
<td>8 (20.5)</td>
<td>77.31 (10.35 (4.47–20.39)</td>
</tr>
<tr>
<td>Pathway post re-infection (n = 25)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Drug treatment centre</td>
<td>4 (16.0)</td>
<td></td>
</tr>
<tr>
<td>Needle exchange</td>
<td>15 (60.0)</td>
<td></td>
</tr>
<tr>
<td>Nurse-led community clinic</td>
<td>4 (16.0)</td>
<td></td>
</tr>
<tr>
<td>Prison</td>
<td>2 (8.0)</td>
<td></td>
</tr>
</tbody>
</table>

Abbreviations: HCV, hepatitis c virus; PWID, people who inject drugs; PY, person-years.

Conclusion: Re-infection and drug-related mortality were high in this cohort of HCV-treated PWID, and follow-up was subsequential. Harm reduction services in Tayside need strengthening alongside comprehensive follow-up RNA testing.

FR1349

Hepatitis C virus reinfection following direct acting antiviral treatment in the prison setting: the SToP-C study

Joanne Carson1, Gregory Dore1, Andrew Lloyd1, Jason Grebely1, Marianne Byrne1, Evan B Cunningham1, Janaki Amin2, Peter Vickerman3, Natasha Martin4, Carla Treloar5, Gill Matthews1, Behzad Hajarizadeh1, The Kirby Institute, UNSW Sydney, Sydney, Australia; 2Macquarie University, Sydney, Australia, Faculty of Medicine and Health Sciences, Sydney, Australia; 3University of Bristol, Population Health Sciences, Bristol, United Kingdom; 4University of California San Diego, Division of Infectious Diseases & Global Public Health, San Diego, United States; 5Centre for Social Research in Health, UNSW Sydney, Sydney, Australia

Email: jcarson@kirby.unsw.edu.au

Background and aims: Ongoing injecting drug use risk behaviours following successful treatment for hepatitis C virus (HCV) may lead to reinfection, reversing benefits of cure, particularly if harm reduction measures are not optimal. This study assessed HCV reinfection risk following direct-acting antiviral therapy in Australian prisons, where opioid agonist therapy is available, but not needle-syringe programs.

Method: The Surveillance and Treatment of Prisoners with hepatitis C (SToP-C) study enrolled people incarcerated in four prisons in Australia between 2014 and 2019. Participants successfully treated for HCV were followed every 3–6 months to assess for reinfection (identified by HCV sequencing). The incidence of HCV reinfection and associated factors were evaluated.

Results: Among 388 participants receiving treatment, 161 had available post-treatment follow up (92% male; median age 33 years; 67% injecting drug use in prison; median follow-up 9 months). During 145 person-years (py) of follow up, 18 cases of reinfection were identified. Reinfection incidence was 12.5 per 100 py (95%CI: 7.9–19.8) overall and 11.6 per 100 py (95%CI 6.6–20.4) among those continuously incarcerated. Incidence was highest among those injecting in the past month and sharing needles/syringes (28.7 per 100 py; 95%CI 16.3–50.6). In adjusted analysis, injecting drug use with sharing needles/syringes was associated with increased reinfection risk (adjusted hazard ratio 14.62; 95%CI 1.84–116.28; p = 0.011).

Conclusion: A high rate of HCV reinfection was observed within a four-prison network. Post-treatment surveillance and retreatment are essential to limit the impact of reinfection. Enhanced access to harm reduction services, including needle and syringe programs, should be considered within prisons.

FR1350

Five-years follow-up of cured HCV patients with or without cirrhosis under real-world interferon-free therapy

Robert Flišiak1, Dorota Żarebska-Michalak2, Ewa Janczewska2, Magdalena Kołalska1, Ewa Karpińska4, Tomasz Mikula2, Beata Bolewsk2a, Jolanta Białkowska2, Katarzyna Fleischer-Stepniewska3, Krzysztof Tomasiwicz3, Kornelia Karwowska2, Monika Pazgan-Simon11, Piekarska Anna12, Hanna Berak13, Tronina Olga14, Aleksander Garlicki15, Jerzy Jaroszewicz16, Medical University of Białystok, Department of Infectious Diseases and Hepatology, Poland; 2Jan Kochanowski University, Department of Infectious Diseases; 3Medical University of Silesia, Bytom, Department of Basic Medical Sciences, Faculty of Health Sciences in Bytom; 4Pomeranian Medical University, Department of Infectious Diseases, Hepatology and Liver Transplantation, Szczecin; 5Medical University of Warsaw, Department of Infectious and Tropical Disease and Hepatology, Warsaw; 6Poznan University of Medical Sciences, Poznan, Department of Infectious Diseases; 7Medical University of Lodz, Department of Infectious and Liver Diseases; 8Wrocław Medical University, Department of Infectious Diseases, Liver Diseases and Immune Deficiencies; 9Medical University of Lublin, Department of Infectious Diseases and Hepatology; 10Collegium Medicum, Nicolaus Copernicus University, Department of Infectious Diseases and Hepatology, Bydgoszcz; 11Wrocław Medical University, Department of Infectious Diseases and Hepatology; 12Medical University of Lodz, Department of Infectious Diseases and Hepatology; 13Hospital of Infectious Diseases in Warsaw, Daily Unit; 14Medical University of Warsaw, Department of Transplantation Medicine, Nephrology and Internal Medicine; 15Jagiellonian University Medical College, Department of Infectious and Tropical Diseases; 16Medical University of Silesia, Department of Infectious Diseases and Hepatology, Katowice

Email: robert.flišiak1@gmail.com

Background and aims: Treatment of hepatitis C virus (HCV) infections with direct-acting antivirals (DAA) has demonstrated high efficacy even in patients with liver cirrhosis. The three-year stability of a sustained virological response (SVR) and an improvement in liver function with a persistent risk of hepatocellular carcinoma (HCC) has so far been confirmed in the literature. The purpose of the current study is to evaluate the virologic response, changes in liver function, stiffness and risk of HCC five years following the treatment.
Method: A total of 192 patients originally infected with HCV genotype 1 or 4 were analyzed five years after treatment with ombitasvir/paritaprevir/ritonavir with or without dasabuvir and with or without ribavirin. Most of the patients were diagnosed with cirrhosis before treatment (57%) and did not respond to previous treatment attempts (68%).

Results: We confirmed that HCV clearance after DAA treatment is stable regardless of baseline advancement of the disease. We found that SVR is associated with a gradual but significant reduction in liver stiffness over 5 years. Liver function improved during the first 2 years of follow-up and remained stable thereafter. The risk of death due to HCC or any reason persists through 5 years after successful DAA treatment. However, in non-cirrhotic patients, it appears to clear up 3 years after treatment.

Conclusion: Despite the successful treatment of HCV infection 5 years after its completion, patients with cirrhosis are still at risk of developing liver cancer. This justifies screening for HCV, allowing therapy before the development of liver cirrhosis.

FRI351
Clearance of hepatitis C virus infection did not ameliorate the response to hepatitis B vaccine

Ebada Said, Tamer Al Eraki, Dalia Abdelhassеб, Shaimaa Ragab, Mona El Awady, Benha University, Egypt; Email: ebada.abdelhamid@fmed.bu.edu.eg

Background and aims: In Egypt, citizens older than 30 years did not get the compulsory vaccination against hepatitis B virus (HBV) infection during infancy. Patients with chronic hepatitis C (CHC) are advised to get vaccinated against HBV. The aim was to assess the response to HBV vaccine in CHC patients treated with direct acting antivirals (DDAs) in comparison to treatment-naïve patients and healthy subjects and to identify predictors of weak response.

Method: This prospective study was carried out on 360 adult subjects subdivided into 3 groups. Group I (GI) included 150 consecutive CHC patients who initiated vaccination after getting sustained virologic response (SVR) following treatment with DDAs. Group II comprised 110 consecutive CHC treatment- naïve patients while the control group (GII) comprised 100 healthy subjects. The mean age of the 3 groups was 50, 45 and 39 year, respectively. Demographic and laboratory variables including HCV-viral load, FIB4 score, Schistosomal antibody (Ab) titre, and Fibroscan® values were assessed. All the studied groups had received 3 intradeltoid, 20 μg, doses of HBV-vaccine (Euvax B, LG Life Sciences, Korea) given at 0, 1 & 6 months. Hepatitis B surface antibody (HBsAb) titres were tested 6–8 weeks after the 3rd dose.

Results: Patients of groups I & II showed a mean FIB4 score of 1.4 & 1.8 while a mean fibroscan value of 8.2 & 9.8 KPa, respectively.

CHC patients either treated (GI) or treatment-naïve (GII) had highly significant lower mean HBsAb titre than controls (p < 0.001). Twelve patients (8%) in GI had negative response to the HBV-vaccine (HBsAb titres of <10 mIU/ml) compared to 5 patients (4.5%) in GII and only one subject (1%) in the control group. Those who got HBsAb titres of >100 mIU/ml were 125/150 (83.3%), 89/110 (80.9%) and 98/100 (98%) in group I, II and III respectively.

Regarding patients with SVR, univariate regression analysis showed that HBsAb titre was negatively associated with higher age (p < 0.001), FIB4 score (p < 0.001), fibrosis stage (p = 0.001) and ALT levels (p = 0.03) while positively associated with platelet count (p < 0.001). Higher fibroscan values (Kpa) were the most significant predictors of weak response to HBV vaccine. In treatment naïve CHC patients, HBsAb titre was negatively associated with ALT (p = 0.001), AST (p = 0.03), FIB4 score (p = 0.01) and schistosomal Ab titre (p < 0.001) and positively associated with platelet count (p = 0.001). Vaccination response showed no association with gender, body mass index, viral load or other variables.

Conclusion: Patients with CHC demonstrate a significantly weak response to HBV-vaccine, particularly those with older age, fibrosis advancement and schistosomiasis. Treatment and SVR achievement did not ameliorate this response.

FRI352
Reverse Inflamaging: biological age is accelerated in chronic HCV patients and decelerates after HCV cure

Carlos Oltmanns, Zhaoli Liu, Jasmin Mischke, Jan Tauwaldt, Yonatan Mekonnen, Heiner Wedemeyer, Anke Kraft, Cheng-Jian Xu, Markus Cornberg, TWINCORE a joint venture of Helmholtz Centre for Infection Research and Hannover Medical School, Hannover, Germany; 2Hannover Medical School, Department of Gastroenterology, Hepatology and Endocrinology, Hannover, Germany; 3German Center for Infection Research, Partner-Site Hannover-Braunschweig, Hannover, Germany; 4Centre for Individualised Infection Medicine (CiIM), Hannover, Germany; Email: oltmanns.carlos@mh-hannover.de

Background and aims: Recently, HIV and HBV infections have been shown to cause significant biological age acceleration. Accelerated epigenetic or biological age may be a predictor of all-cause and cancer mortality. Thus, we analyzed if HCV is associated with biological age acceleration and if this is reversible after HCV cure.

Method: We included well-characterized 54 patients (mean age 56 years) with chronic hepatitis C at three time points (baseline, end of treatment and follow-up 24–240 (mean 96 weeks) weeks after the end of treatment). Genome-wide DNA methylation data were generated using the illuminaEpigenome array on PBMC and were used to calculate the epigenetic age acceleration (Horvath clock).

Results: Our results show that chronic HCV infection leads to a significant acceleration of epigenetic age (p = 3.577e-05). While chronic HCV patients without evidence of cirrhosis have a lower age acceleration, patients with cirrhosis have a higher biological age. Treatment of HCV patients with DAA results in reversal of age acceleration, but this effect is only detectable at long-term follow-up (p = 0.02). Epigenetic acceleration does not correlate with estimated blood cell counts.

Interestingly, patients who developed HCC after SVR (n = 8) have the highest age acceleration and show no evidence of complete reversion after treatment.

Conclusion: Hepatitis C patients with cirrhosis show biological age acceleration that may be reversible after HCV cure. Lack of reversibility appears to be associated with HCC risk. Our findings underline the need for more individualized infectious disease medicine based on biological rather than chronologic age in the future.
Overall mortality in patients with chronic hepatitis C: major effects of social vulnerability, tobacco smoking, and history of unhealthy alcohol use (ANRS CO22 HEPATHER cohort)

Lauren Perieres, Fabrice Carrat, Marta Lotto, Celine Dorival, Clémence Ramier, Fabienne Marcellin, Carole Cagnot, Elizabeth Delarocque-Astagneau, Patrizia Carriéri, Stanislas Pol, Helene Fontaine, Camelia Protopopescu, Aix Marseille Univ, INSERM, IRD, SESSTIM, Sciences Economiques & Sociales de la Santé & Traitement de l'Information Médicale, ISSNAM, Marseille, France; Institut National de la Santé et de la Recherche Médicale (INSERM), Institut Pierre Louis d'Épidémiologie et de Santé Publique, Sorbonne Université, Hôpital Saint-Antoine, Unité de Santé Publique, Assistance Publique-Hôpitaux de Paris (AP-HP), Paris, France; Institut National de la Santé et de la Recherche Médicale (INSERM), Institut Pierre Louis d'Épidémiologie et de Santé Publique, Sorbonne Université, Paris, France; ANRS/EMerging Infectious Diseases, Paris, France; Université Paris-Saclay, UVSQ, Inserm, CESR Team Anti- Infective Evasion and Pharmacoepidemiology, Montigny, France; Université de Paris, AP-HP, Hôpital Cochin, Département d'Hépatologie/Addictologie, Paris, France

Email: fabienne.marcellin@inserm.fr

Background and aims: The advent of direct acting antivirals has paved the way for a hepatitis C-free world. However, patients with hepatitis C virus (HCV) infection remain at high risk of morbidity and mortality, even after cure. We identify socio-behavioural factors associated with overall (i.e., all-cause) mortality in chronic HCV-infected patients.

Method: We used data collected from August 2012 to June 2018 in the French, multicentre, prospective cohort ANRS CO22 HEPATHER. The study sample comprised chronic HCV-infected patients who attended at least one annual follow-up visit. Analyses focused on the first five years of follow-up. Socio-behavioural data were collected at cohort enrolment (questionnaire administered by a physician). Living in poverty was defined as a standard of living below 1015€ (French poverty threshold in 2015), low educational level as level <high school diploma, unhealthy alcohol use as drinking >2 and >3 alcohol units/day for women and men, respectively, and elevated coffee intake as drinking ≥3 cups of coffee/day. Factors associated with overall mortality were identified using a Cox proportional hazards model. Adjusted population attributable fractions (PAF) were estimated for the modifiable factors of the multivariable analysis.

Results: Of the 10,366 patients in the study sample, 697 died during follow-up. After multivariable adjustment (for sex, age, educational level, HCV genotype, HCV transmission category, and HCV cure), living in poverty (adjusted hazard ratio [aHR]: 1.34 [95% confidence interval, 1.13–1.60]), tobacco smoking (1.70 [1.35–2.14]), and a history of unhealthy alcohol use (1.48 [1.18–1.86]) were independently associated with increased overall mortality. By contrast, elevated coffee intake was associated with lower overall mortality (0.63 [0.52–0.77]). The risk factors accounting for the greatest mortality burden were tobacco smoking, low educational level, living in poverty, and a history of unhealthy alcohol use (PAF: 16.6%, 14.9%, 9.8%, and 7.4%, respectively), whilst HCV cure and elevated coffee intake averted a high proportion of deaths (86.0% and 13.4%, respectively).

Conclusion: In the era of HCV cure, tobacco cessation must be further encouraged in patients with chronic HCV infection, as a modifiable risk factor of mortality. Specific interventions should be developed to target socially vulnerable patients and those with a history of unhealthy alcohol use, who are at higher risk of mortality.

Is routine Ribavirin mandatory for genotype 3 hepatitis C compensated cirrhosis patients receiving Sofosbuvir/Velpatasvir? A meta-analysis

Jing Hong Loo, Flora Xu, Gerald Low, Wei Xuan Tay, Le Shaun Ang, Steve Yew-Chong Tan, Prem Harichander Thuraiarajah, Rahul Kumar, Yu Jun Wong, Yong Loo Lin School of Medicine, National University of Singapore; Education Resource Centre, Medical Board, Singapore General Hospital; National University Hospital, Division of Gastroenterology & Hepatology, Singapore, Singapore; Changi General Hospital, Department of Gastroenterology & Hepatology, Changi General Hospital, Singapore

Email: loojinghong@gmail.com

Background and aims: Simplified treatment regimen is crucial for rapid treatment upscale to achieve hepatitis C virus (HCV) elimination. Addition of ribavirin (RBV) to Sofosbuvir/Velpatasvir (SOF/VEL) has been shown improved sustained virological response at 12 weeks (SVR12) in genotype 3 (GT3) decompensated cirrhosis patients. However, the benefits of RBV in GT3 compensated cirrhosis patients receiving SOF/VEL, remains unclear. We aim to systematically review the efficacy and safety of SOF/VEL, with or without RBV in GT3 compensated cirrhosis patients.

Method: With help of medical librarian, we systematically searched four electronic databases (PubMed/MEDLINE, EMBASE, Cochrane Library and Web of Science) from inception up to June 2021 using both free text and MeSH terms. There was no restriction on language, geography, publication dates and publication status. All GT3 compensated cirrhosis patients treated with 12 weeks of SOF/VEL, with or without RBV, were included, regardless of age, gender or prior treatment experience. The primary outcome was the SVR12. The secondary outcome was treatment-related adverse events, as defined by symptomatic anaemia requiring transfusion or a drop in haemoglobin beyond 2 g/dL. The pooled relative risk (RR), 95% confidence interval (CI) and heterogeneity (I²) were estimated using Review Manager Version 5.3.

Results: From 1,752 citations, a total of 7 studies (2 RCTs, 5 cohort studies) with 1,088 subjects were identified. The SVR12 was similar in GT3 compensated cirrhosis patients, regardless of the use of RBV, for both the intention-to-treat (RR: 1.03, 95% CI: 0.99–1.07; P = 0%) and the per-protocol analysis (RR: 1.03, 95% CI: 0.99–1.07; I² = 48%). The overall pooled rate of treatment-related adverse events was 7.2%. Addition of RBV was associated with 4-fold higher risk of treatment-related adverse events in GT3 compensated cirrhosis patients. However, addition of RBV did not significantly increase the SVR12 among treatment-experienced GT3 compensated cirrhosis patients.

Conclusion: Ribavirin did not significantly increase the SVR12 in GT3 compensated cirrhosis patients receiving SOF/VEL. Our findings suggest limited role for RBV as routine add-on therapy to SOF/VEL in GT3 compensated cirrhosis patients.
Europe. Health services are working towards achieving the WHO target of HCV elimination by 2030. Reinfection following treatment is an important consideration for HCV elimination programmes because this has the potential to hamper elimination efforts. The aim of this work was to assess the rate of HCV reinfection in our region, where IDU is the predominant risk factor (>90%).

**Method:** All patients who completed treatment with direct acting antiviral (DAA) treatment for HCV in Tyne and Wear, North East England between Jan 2016 and May 2021 were included. Sustained virological response (SVR12) was defined as negative HCV RNA 12 weeks post treatment. Data was collected from our HCV database (HepCare), which automatically gathers laboratory data in real time from our hospital laboratory database. HCV reinfection was defined as a positive HCV RNA after achieving SVR12 or where a genotype has changed after completing DAA treatment when the SVR12 was not documented.

**Results:** 788 of the 840 patients (76% males; mean age 45.7 ± 11.4 years; 47% G1; 39% G3; 12% Cirrhosis) completing treatment achieved virological response (SVR12) which automatically gathers laboratory data in real time. The median time to reinfection was 1.37 years (range 0.1–5.2 years). 56 reinfections (7.1% of all SVRs and 12.2% of those SVRs who had follow up blood testing) were diagnosed. The median time to reinfection was 1.37 years (range 0.1–5.2 years) and the rate of reinfection was 0.1 per person years. 45 of the 56 (80%) reinfections developed chronic infection, 17 of which were retreated and achieved SVR, while 28 remain viraemic. 5 patients developed a second reinfection. Individuals with reinfection were significantly younger than those maintaining SVR (38.9 ± 7.9 vs 46.2 ± 11.9 years, p < 0.001). Reinfection was more common in those with primary G3 infection compared with other genotypes (9.8% vs 5.7% p = 0.049). Reinfections were similar between males and females (4.4% females vs 7.4% males p = 0.15).

**Conclusion:** HCV reinfection is common in our cohort and may slow our HCV elimination efforts. In order to address our high reinfection rates we need to improve harm reduction and increase treatment of active IDUs. We aim to implement ‘HCV track and trace’ for recent infections and reinfections to try to reduce onward HCV transmission.
treatment, to facilitate enhanced declines in advanced liver disease complications in the DAA era.

FRI357
Direct acting antiviral agents improve survival in patients with hepatitis C virus related hepatocellular carcinoma
Hyun Young Woo1, Won Lim2, Jeong Heo1, Young Joo Park1, 1Pusan National University Hospital, Internal Medicine, Busan, Korea, Rep. of South; 2Good Samsun Hospital, Internal Medicine, Busan, Korea, Rep. of South
Email: who54@hanmail.net

Background and aims: Survival data in patients with hepatitis C virus (HCV) associated hepatocellular carcinoma (HCC) treated with direct acting antivirals (DAAs) are limited. Survival rates were compared between patients with HCV-related HCC who were untreated for HCV and who treated with DAA.

Method: From 2010 to 2019, a total of 469 patients who were monoinfected with HCV-related HCC was categorized into patients untreated for HCV and patients treated with DAA. Multivariable Cox regression with HCV treatment status as a time-varying covariate was used to determine mortality risk.

Results: There were 95 untreated group and 94 DAA group. Of DAA group, 42 was active HCC state (patients without viable HCC). Baseline characteristics between untreated group and DAA with active HCC were balanced except genotype. Sustained virologic response rate was 88.2% by per protocol analysis in DAA treated patients. After time-varying adjustment for DAA treatment initiation compared with untreated patients, patients with DAA had significantly higher 5-year overall survival (76.7% vs. 22.4%, p < 0.001). Multivariate Cox regression showed that survival was significantly improved in patients with DAA treatment (p < 0.001), patients who were treated with curative treatment (0.034) and with history of interferon exposure (p = 0.045).

Conclusion: In this study, patients in HCV related HCC who treated DAA achieved 88.2% of SVR and showed significant improvement of survival compared with patients untreated with DAA.

FRI358
Lack of Alpha-fetoprotein reduction after successful Hepatitis C treatment in patients with cirrhosis predicts the development of hepatocellular carcinoma during surveillance—a single unit real-world experience
Aoife Alvain1, Jack Lee1, Eileen Shannon1, Mary Kavanagh1, Mary Bohan-Keane1, Margaret Scarry1, John Lee1,2, 1University Hospital Galway, Hepatology unit, Galway, Ireland; 2National University of Ireland, Galway, Galway, Ireland
Email: alvainae@tcd.ie

Background and aims: The value and limitation of alpha-fetoprotein (AFP) in hepatocellular carcinoma (HCC) screening is well established. In patients with chronic hepatitis C virus (HCV) infection and cirrhosis, AFP is often elevated in the absence of HCC. The aim of this study was to measure the impact of DAA treatment on AFP levels and cirrhotic patients remains high. Overall, AFP levels improve with DAA treatment. Failure to see an improvement in AFP after treatment predicts the development of HCC. This should be considered in stratifying individual patient HCC risk during real-world follow-up surveillance protocols.

Conclusion: The risk of HCC after successful HCV treatment in cirrhotic patients remains high. Overall, AFP levels improve with DAA treatment. Failure to see an improvement in AFP after treatment predicts the development of HCC. This should be considered in stratifying individual patient HCC risk during real-world follow-up surveillance protocols.
outcome among patients who were eligible for a liver transplant at treatment initiation.

Method: Retrospective cohort study including HCV patients with a history of current decompensated cirrhosis treated with DAAs in Europe and Canada. MELD purgatory was defined as presence of ascites or hepatic encephalopathy with sustained MELD-Na ≥15 after treatment initiation. The cumulative probability and factors associated with a poor outcome (sustained MELD purgatory, HCC or death) after treatment initiation were analyzed using Kaplan-Meier plots and multivariable (MV) Cox regression. The risk of death/HCC vs transplantation post-treatment was compared in those who were transplant ineligible at baseline.

Results: Among 877 patients: mean age 55 ± 9 years, 68% male, 86% Caucasian, median BMI 27 [24–30] kg/m², 24% diabetes and 44% history of alcohol abuse. At baseline, median INR was 1.3 (1.2–1.5), ALT was 54 (37–84) U/L, platelets were 77 (55–105) × 10^9/L, total bilirubin was 1.9 (1.2–2.8) mg/dL and mean albumin was 32 ± 5.8 g/L. Mean MELD-Na was 15 ± 5.5. The majority had MELD-Na ≥15 (62%), and 51% were decompensated at baseline. A total of 665 (80%) achieved SVR12. During a median follow-up of 35 (8–51) weeks and 51% were decompensated at baseline. A total of 665 (80%) achieved SVR12. During a median follow-up of 35 (8–90) weeks after treatment initiation, 194 (22%) entered sustained MELD purgatory, 114 (13.0%) developed HCC, and 106 died (12.1%). Cumulative probabilities of a poor outcome at 36, 72, and 108 weeks were 15%, 24%, and 32%, respectively (Figure). On MV Cox regression, older age (aHR 1.02, p = 0.037), lower sodium (aHR 0.95, p = 0.014), and lower albumin (aHR 0.97, p = 0.032) at baseline were associated with higher rates of a poor outcome. Of those who met the definition of MELD-purgatory before treatment initiation (n = 195), cumulative probabilities of death/HCC were 5.1%, 8.1% and 9.0% at 36, 72, 108 weeks post-treatment start, whereas rates of liver transplant were 4.2%, 9.0% and 12.3% at the same time points.

Conclusion: Patients with chronic HCV and decompensated cirrhosis are at risk for MELD purgatory, HCC or death, even when SVR is achieved. Caution should be taken when treating these patients, especially transplant-eligible patients who may be better off with liver transplantation prior to HCV treatment. Decompensated patients who are not transplant-eligible at treatment start have a similar probability of HCC/death as of receiving a transplant post-treatment, making treatment decisions particularly challenging and highlighting the need for careful post-treatment follow-up.

FR1360
The long-term effect of Hepatitis C eradication by direct-acting antivirals on patient’s mood and quality of life as determined by the Beck’s Depression Inventory and EQ5D Quality of Life questionnaires— a single unit study
Aoife Alvain1, Sarah Lanigan1, Mary Bohan-Keane1, Margaret Scarry1, Lynda Jordan1, Cynthia Garvey1, Priyanka Jose1, John Lee1,2, 4University Hospital Galway, Hepatology Unit, Galway, Ireland; 4National University of Ireland, Galway, Galway, Ireland
Email: alvain@tcd.ie

Background and aims: Direct-acting antiviral (DAA) treatments are established to be well tolerated and achieve Hepatitis C virus (HCV) eradication in the quasi-totality of patients. This prevents progression to liver cirrhosis, reduces the risk of hepatocellular carcinoma, and improves overall prognosis. The aim of this study was to investigate the long-term effects of HCV eradication by DAA on patient’s mood and quality of life.

Method: HCV patients completed a baseline Beck’s Depression Inventory and Quality of Life Questionnaire (EQ5D) prior to DAA treatment and were prospectively evaluated. After anti-viral therapy, the questionnaires were repeated with a minimum of 12 months follow-up. A Beck’s score of <10 is considered to be within the normal range of mood variation. An EQ5D of 5 represents optimal quality of life.

Results: A total of 54 patients with a mean age of 49.5 years were included (51.8% male). All patients had a sustained virological response to DAA treatment; the median follow-up was 41.1 years. Prior to treatment, 9 (16.7%) had established cirrhosis, and 14 (25.9%) had at least one psychiatric co-morbidity. The mean Beck’s score pre-treatment (Mean 7.88 ± SD 7.88) and at long-term follow-up (7.31 ± 6.22) was not significantly different (p = 0.29). Median Beck’s score pre-treatment (7) and at follow-up (6) were comparable, as were the number of patients with a Beck’s score <10 pre-treatment (n = 37, 68.5%) and at follow-up (n = 37, 68.5%). In the sub-group analysis, no significant difference was found with sub-groups defined by patient’s background psychiatric history, pre-treatment cirrhosis status or HCV mode of transmission (pre-treatment and follow-up median scores were comparable and so were the number of patients with a Beck’s score <10). There was no significant difference in the EQ5D pre-treatment (6.88 ± 2.30) and at follow-up (6.74 ± 2.45) (p = 0.39). Median score pre-treatment (6) and at follow-up (6) were comparable (6), as were the number of patients with EQ5D = 5 pre-treatment (n = 16) and at follow-up (n = 18).

Conclusion: In this prospective study of patients successfully treated for HCV with DAA treatment, the reported mood and quality of life at long-term follow-up did not significantly change from their pre-treatment baseline. It is expected that quality of life and mood would deteriorate in un-treated patients as they develop complications of chronic HCV and as such this study demonstrate the benefit of DAA treatment on mood and quality of life.

FR361
Assessing sustained virological response and reinfection from dried blood spots within an on-site hepatitis C diagnosis and treatment model of care in a harm reduction centre
Anna Noi1, Verónica Saludes1,2, Anna Miralpeix3,4, Mont Gálvez1,4, Antoni E. Bordoy1, Sara González-Gómez1, Noemí González2, Juliana Reyes-Ureña2, Xavier Major7, Joan Colom1, Xavier Forns3,4,8, Sabela Lens3,4,8, Elisa Martíró1,2, 1Hospital Universitari Germans Trias i Pujol, Institut d’Investigació Germans Trias i Pujol (IGTP), Microbiology Department, Badalona, Spain; 2Consorcio de Investigación Biomédica en Red de Epidemiología y Salud Pública (CIBERESP), Madrid, Spain; 3Hospital Clinico, Liver Unit, Barcelona, Spain; 4IDIBAPS, Barcelona, Spain; 5REDAN La Mina, Parc de Salut Mar, Sant Adrià del Besós (Barcelona), Spain; 6Center for Epidemiological Studies on HIV/AIDS and STIs of Catalonia (CEEISCAT), ASPCAT, Barcelona, Spain; 7Program for the Prevention, Control and Care of HIV, Sexually Transmitted Infections and Viral Hepatitis, ASPCAT, Barcelona, Spain; 8Consorcio de Investigación Biomédica en Red de Enfermedades Hepáticas y Digestivas (CIBEREHD), Madrid, Spain

Background and aims: Dried blood spot (DBS) samples are a reliable tool to diagnose viremic HCV infection. However, there is scarce data on the usefulness of DBS to assess cure and reinfection after antiviral
therapy. Here, we aimed to evaluate the use of DBS for the assessment of sustained virological response (SVR) and reinfection 12 weeks after on-site treatment with direct-acting antivirals at a harm reduction service (HRS) in Catalonia.

**Method:** This evaluation was performed within the context of an ongoing micro-elimination study targeting people who inject drugs (PWID) in the largest HRS in Barcelona. At the time of SVR assessment (FU12), HCV-RNA was detected from DBS with an in-house real-time RT-PCR assay (lower limit of detection -LoD-, 451 IU/ml of blood) in comparison with the reference method (viral load in fingerstick capillary blood by GeneXpert®; LoD, 40 IU/ml). Additionally, DBS samples (baseline vs. FU12) were used to assess reinfection vs. treatment failure by an in-house method based on NS5B nested-PCR amplification followed by Sanger sequencing and phylogenetic analysis. When mixed or no signal was obtained, samples were genotyped by a commercial real-time PCR genotyping assay (Abbott).

**Results:** Among treated patients, 105 DBS samples corresponding to FU12 were tested [55 negative and 50 positive]. The DBS-based HCV-RNA assay showed 100% specificity (55/55). Nine cases were not amplified, with viral loads between 116 and 4660 IU/ml; sensitivity RNA assay showed 100% specificity (55/55). Nine cases were not analyzed. When mixed or no signal was obtained, samples were amplified, one was indeterminate, and in seven cases the same genotype/subtype was detected at FU12 and baseline samples, with any of the two methods: three with low viral loads could not be classified by the presence of reinfection in 29 cases and of treatment failure in seven cases with high viral loads. The rest of cases could not be classified by any of the two methods: three with low viral loads could not be amplified, one was indeterminate, and in seven cases the same genotype/subtype was detected at FU12 and baseline samples, with phylogenetic classification not assessable from the commercial genotyping assay.

<table>
<thead>
<tr>
<th>HCV viral load threshold by Xpert HCV</th>
<th>Proportion</th>
<th>%</th>
</tr>
</thead>
<tbody>
<tr>
<td>Detectable</td>
<td>41/50</td>
<td>82.0</td>
</tr>
<tr>
<td>Quantifiable ≥100 IU/ml</td>
<td>41/49</td>
<td>83.7</td>
</tr>
<tr>
<td>(EASL Guidelines)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Quantifiable ≥1000 IU/ml</td>
<td>41/46</td>
<td>89.1</td>
</tr>
<tr>
<td>(WHO Testing Guidelines)</td>
<td>38/40</td>
<td>95.0</td>
</tr>
</tbody>
</table>

**Conclusion:** This study shows the usefulness of DBS samples for assessing cure and differentiating reinfection from relapse after HCV antiviral treatment in the real world, facilitating treatment decentralization in PWID attending HRS. However, some patients presented with low viral loads at FU12, limiting detection and genotyping. While the latter cases might reflect acute infections that may be spontaneously cleared, repeat testing over time would be required to identify all viricom cases.

**FR1363**

**Hepatitis C virus (HCV)-specific T cell confer resistance to HCV re-infection after sustained virologic response in a non-cytotoxic fashion among people who inject drugs: results from ANCHOR study**

Arshi Khanam¹, Alip Ghosh², Sarah Kattakuzhy³, Shyamansundar Kotttill³, Elana Rosenthal¹. ¹Institute of Human Virology University of Maryland School of Medicine, Division of Clinical Care and Research, Baltimore, United States; ²Institute of Human Virology, University of Maryland School of Medicine, Baltimore, United States

Email: akhanam@ihv.umaryland.edu

**Background and aims:** People who inject drugs (PWID) remain a major reservoir of chronic hepatitis C virus (HCV) infection. Ongoing injecting drug use is associated with re-infection, however the role of HCV specific immune response in PWID is not understood. In this study, we evaluated the immune correlates that are associated with re-infection of HCV in PWID after achieving sustained virologic response (SVR).

**Method:** ANCHOR is a study of 198 people with opioid use disorder, ongoing opioid misuse and chronic HCV. All participants received DAA, 157 achieved SVR, and 17 were reinfected. We studied 27 patients who achieved SVR without reinfection (Non-RI) and 13 patients who were reinfected (RI). Changes in the phenotypic profile of T cells were determined in the peripheral blood mononuclear cells (PBMCs) by flow cytometry. HCV specific T cell functions were investigated by stimulating the PBMCs with a pool of 21 overlapping peptides from envelope, core and NS5-NS5 regions of HCV. Immune profiles were evaluated at baseline (prior to HCV treatment) and after SVR (prior to reinfection) and compared between the two groups.

**Results:** At baseline, RI group displayed higher expression of inhibitory receptors including programmed death-1 (PD-1) (CD4 P = 0.002, CD8 P = 0.02) and 2B4 (CD4 P = ns, CD8 P = 0.01), and lower expression of activation markers CD38 (CD4 P = 0.02, CD8 P = ns) and HLA-DR (CD4 & CD8 T cells P = 0.02) on T cells than Non-RI group and continuously maintained exhaustive phenotype even after achieving SVR, suggesting persistent exhaustion of T cells in RI. At baseline, RI group constituted lower frequencies of naïve (14% vs. 29%) and terminally differentiated effector memory cells (3% vs. 10%) in CD4 T cell population that did not change upon SVR, while a marked reduction in effector memory cells were observed (48% vs. 31%) at SVR. Moreover, CD8 T cell population exhibited decreased percentage of naïve (17% vs. 35%) and central memory cells (3% vs. 8%) in RI group and similar profile was maintained upon SVR. However, the expression of the transcription factors Tbet and Eomes (CD4: 2% and 5%, CD8: 7% and 20%) was similar between both groups. Further, T cells from RI group persistently produced lower amounts of antiviral cytokines such as IFN-γ and TNF-α at baseline and after achieving SVR compared to the Non-RI (CD4 IFN-γ & TNF-α P = 0.04, P = 0.01) (CD8 IFN-γ & TNF-α P = 0.01, P = ns). In fact, polyfunctional T cell response determined by IFN-γ and TNF-α co-producing cells was also impaired in the RI compared to the Non-RI group (CD4 P = 0.03 and CD8 P = 0.04). However, cytotoxic potential of T cells evaluated by CD107a and perforin expression were maintained between both groups.

**Conclusion:** Peripheral T cells from PWID who were reinfected with HCV after achieving SVR displayed an exhaustive phenotype and had depressed anti-HCV response after SVR, suggesting a role for protection from re-infection by T cells in a non-cytotoxic fashion.

**FR1363**

**Lack of fibrosis remodelling in chronic hepatitis C post SVR, as demonstrated by YKL-40, is predictive of hepatocellular carcinoma occurrence**

Maria Guerra Veloz1, James Lok1, Chiara Mazzarelli2, Mary D Cannon1, Ivana Carey1, Kosh Agarwal1. 1King's College Hospital, Institute of Liver Studies, United Kingdom; 2ASST Grande Ospedale Metropolitano Niguarda-Milano

Email: maria.guerraveloz@nhs.net

**Background and aims:** The introduction of new direct-acting antivirals agents (DAA) have revolutionized the natural history of the chronic hepatitis C virus (HCV). However, the course of progressive liver damage, as well as the risk of developing HCC after achieving sustained virological response (SVR), is still uncertain. Our group’s preliminary data showed that YKL-40 (acting as a growth factor for fibroblasts and being involved in matrix remodeling) and Hyaluronic acid (HA, acting as promoter of hepatic fibrogenesis) decreased in patients who achieved SVR. The aim of our study was to determine whether YKL-40 and/or HA could be a predictor of HCC occurrence in patients with cirrhosis who achieved SVR.

**Method:** In this retrospective study, we included patients with hepatitis C related cirrhosis, who achieved SVR after DAA therapy, in whom YKL-40 and HA were measured prior to treatment and at 36
weeks post SVR. Cirrhosis was defined based on FibroScan® > 14.5 kPa and/or a combination of endoscopy and imaging criteria. Only those treated with DAA therapy between January 2015 and December 2016 were included. Patients were followed-up with until November 2021 or until HCC occurred.

**Results:** Our study included 71 patients of whom 64.8% were males with a mean age of 61 (±8) years. Of our total cohort, 62% had genotype 1, 55% were Child Pugh A (CPA), 24% were CPA with a previous decompensation, and 21% were CP B/C. During a median follow up of 60 months (IQR 41–70), 25.4% (18) of patients had developed HCC. Patients who developed HCC had more advanced liver disease (CP B/C 53.3% vs 20.5% CPA vs 11.8% CPA previous decompensation; p = 0.031), a lower baseline albumin (34.7 vs 38.4; p = 0.004) and an elevated YKL-40 at 36 weeks after SVR (4789 vs 3333; p = 0.036) compared to those who had not developed HCC (table 1). Between start of treatment and 36 weeks post SVR, the mean decrease in YKL-40 was significantly greater in those who did not develop HCC (from 5098 to 3333, p < 0.001; vs 4752 to 4789 p = 0.987). There was no difference in the dynamics of HA between the two groups. In the multivariate analysis, YKL-40 at 36 weeks post SVR (HR 1; CI 95% 1–1) was an independent factor associated with HCC. Child Pugh status A (HR 0.36; IC 95% 0.14–0.937) was an independent factor associated with lower HCC.

**Conclusion:** HCC occurrence was higher in patients with CP B/C and those who did not decrease YKL-40 after achieving SVR. YKL-40 could be a predictive factor of HCC occurrence however further studies with a larger sample are needed to confirm these results.


### FRI364

**HCV reinfection associated with IDU and cocaine use in a cohort of people with OUD: 4 Year follow-up data from the ANCHOR cohort**

Elana Rosenthal1, Junfeng Sun2, Britt Gayle1, Amelia Cover1, Ashley Davis1, Shivakumar Narayanan1, Catherine Gannon1, Grace Garrett2, Vivian Wang2, Meghan Derenoncourt2, Henry Makeu2, Shyamkumar Kotttil1, Sarah Kattakuzhy1, Division of Clinical Care and Research, Institute of Human Virology, University of Maryland School of Medicine, United States; 2National Institutes of Health/Critical Care Medicine Department, Bethesda, United States.

**Email:** erosenthal@ihv.umaryland.edu

**Background and aims:** People with HCV and opioid use disorder (OUD) who achieve sustained virologic response (SVR) may remain at risk of reinfection. Identification and treatment of reinfected individuals is critical to HCV elimination. We sought to evaluate the rate of reinfection and factors associated with reinfection in a cohort of high-risk patients over a 4 year follow-up period.

**Method:** ANCHOR is a 96 week, prospective cohort study of people with OUD, opioid misuse within a year and chronic HCV. All participants received HCV treatment. Those who achieved SVR were followed for reinfection for 18 months, and subsequently had the option to enroll in LOOP, a 2 year long-term follow-up study. Reinfection was defined as a genotype switch or detectable viral load after SVR. Patients were administered surveys at each visit to assess for ongoing risk behaviors and medication for OUD (MOUD) status. A logistic regression model with GEE was created using covariates with p < 0.10 to model the probability of reinfection.

**Results:** 157 individuals achieved SVR and were followed for 273.2 person-years, median 86.2 weeks (range 12–210 weeks). Subjects were predominantly male (66%), black (84%), middle-aged (median 57 years), and 50.3% unstably housed. Seventeen individuals (10.8%) were reinfected a median of 76.1 weeks (range 21–175 weeks) after HCV treatment, a rate of 6.2/100 person-years. Reinfection was associated with past month IDU (p = 0.006), and cocaine positive UDS (p = 0.03), however was not associated with age, race, gender, education, or visit specific opioid positive UDS, housing stability, MOUD engagement, or HIV risk score (all p > 0.05). Of the 17 reinfected individuals, 12 (71%) initiated HCV re-treatment, with 10 achieving SVR and 2 deaths.

**Conclusion:** In this cohort of high-risk people with OUD, we found high rates of HCV reinfection which were associated with past-month IDU and cocaine positive UDS at the time of detection. Given the rate and timing of reinfection, these data reinforce the importance of long-term engagement, ongoing HCV testing, and low-barrier treatment of HCV reinfection. Further, in the era of rising stimulant use, these data highlight the importance of assessing for and reducing harms associated with polysubstance use and injection drug use in people with opioid use disorder.

**FRI365**

**Noninvasive prediction of hepatocellular carcinoma development after oral antiviral therapy in patients with chronic hepatitis C: a multicenter study**

Yu Rim Lee1, Jung Gil Park2, Min Kyu Kang1, Jung Eun Song2, Byoung Kuk Jang4, Young Oh Kweon1, Won Young Tak1, Se Young Jang1, Changhyeong Lee1, Byung Seok Kim3, Jae-Seok Hwang4, Woo Jin Chung4, Soo Young Park1, Nae-Yun Heo3, Jeong Heo5, Hyun Young Woo1, Yong Hoon Baek1, Jun Sik Yoon6, Jooho Jeong1, Jae Young Jang1, Kyungpook National University, Kyungpook National University Hospital; 2Yeungnam University College of Medicine; 3Daegu Catholic University School of Medicine; 4Keimyung University School of Medicine; 5Inje University Haeundae Paik Hospital, Inje University College of Medicine; 6University of Ulsan College of Medicine, Ulsan University Hospital

**Email:** psyoung0419@gmail.com

**Background and aims:** Hepatocellular carcinoma (HCC) can still occur after achieving a sustained virologic response (SVR) to direct-acting antiviral (DAA) therapy in patients with hepatitis C. We aimed to identify non-invasive parameters that predict the HCC development for patient with chronic hepatitis C after SVR.

**Method:** A total of 3,489 HCV patients who treated with DAAs and had achieved SVR from nine hospitals in South Korea were included. Predictors of HCC occurrence and HCC risk scores were assessed.

**Results:** During a median follow-up of 2.3 years, HCC occurred in 158 patients (4.5%). LSM gradually decreased from baseline to SVR and 1 year after treatment (p < 0.001). Multivariate analysis using the Cox regression test identified that age (HR 1.055, 95% CI 1.036–1.074, P < 0.001), sex,
Background and aims: Injection drug use (IDU) and sharing of injection equipment and paraphernalia is the main mode of transmission of Hepatitis C Virus (HCV) in most Western societies. People who inject drugs (PWID) therefore need to be diagnosed, treated and cured in order to curb transmission and achieve the WHO goal of eliminating HCV infection as a public health threat by 2030. Starting in 2016, the Treatment as Prevention for Hepatitis C (TraP HepC) program in Iceland has offered direct acting antiviral agents (DAA) to all HCV-infected patients with permanent residence in the country without restrictions. It has from its inception focused on PWID, with special emphasis on active IDU. Vogur addiction hospital screens all patients who report IDU activity upon admission for HCV viremia in this key population.

Results: Prior to Trap HepC, 2010–2015 the prevalence of HCV viremia among admitted patients who gave history of ever injecting drugs was stable at 39.5–40.6%. Among those who were currently injecting at the time of admission (injecting within 6 months) the prevalence was stable at 53.2–57.7% during the same period. The prevalence of HCV viremia in the former group dropped to 32.9%, 12.0% and 8.6% during 2016, 2017 and 2018, respectively (p < 0.001) and subsequently has remained stable at 12.9% and 13.3% in 2019 and 2020.

Conclusion: In the absence of an effective vaccine, treatment with DAA remains the most efficient way to lower the prevalence of HCV. Efficacy among PWID is excellent and treatment has resulted in a sustained drop in HCV viremia in this population but continued monitoring of these patients is needed. Further studies and longer follow-up is needed to evaluate whether this drop eventually translates into a lower nationwide incidence of HCV in Iceland.
matched for sex and age in a 1:3 fashion. HCC infiltrative pattern, portal vein thrombosis (PVT), metastases, Milan criteria, Barcelona Clinic Liver Cancer (BCLC) staging, tumor-node-metastasis (TNM) staging, Cancer of the Liver Italian Program (CLIP), as well as the recurrence and overall survival rate at 18 months of follow-up, were compared in the 2 groups. This research was carried out in the Institute of Gastroenterology Iasi, Romania, between January 16, 2017 and December 31, 2019.

Results: The study included 124 patients that were divided into two groups according to DAAs status: 31 DAAs-treated HCC patients and 93 non-DAAs HCC patients. Overall, 65% were males, and the mean age was 58.9±6.8 years. The mean values of APRI and Fib-4 scores were significantly higher in the DAAs-treated group than in naïve patients (p<0.001). The frequency of the infiltrative HCC pattern, PVT, and metastasis was higher in the non-DAAs group (p=0.002). Furthermore, HCC recurrence rate was higher in naïve patients than in those DAAs-treated (16.2% versus 8.6%, p=0.002). The 18-months overall survival rate was 73.3% in the DAAs-treated group and 43.7% in non-DAAs group (p=0.008).

Conclusion: Our study indicates a better recurrence-free overall survival rate in patients with HCV-related hepatocellular carcinoma with SVR to DAAs compared with naïve patients, demonstrating the beneficial impact on the outcome of these patients.

FRI369
Long-term outcomes associated with task-shifting of HCV treatment by non-specialist providers: five year follow-up from the ASCEND cohort.
Sarah Mollenkopf1, Elana Rosenthal2, Gebeleyehu Tefere1, Rachel Silk2, Nivya George2, Henry Masur4, Shyamasundaran Kottipillil2, Sarah Kattakuzhy2, 1University of Maryland School of Medicine, Baltimore, United States; 2Institute of Human Virology, Division of Clinical Care and Research, Baltimore; 3Unity Health Care, Washington, United States; 4NIH, Critical Care Medicine Department, Bethesda, United States
Email: skattakuzhy@ihv.umaryland.edu

Background and aims: Since 2015, an increasing body of evidence has supported task-shifting of Hepatitis C (HCV) treatment with direct-acting antivirals (DAAs) to non-specialist providers, however, there are limited data on longitudinal outcomes associated with this treatment paradigm. We sought to assess outcomes of patients in the 5 years after initial DAA treatment by specialist and non-specialist providers, to evaluate the longitudinal evidence for task-shifting in the ASCEND cohort.

Method: This analysis included 525 patients treated for HCV with ledipasvir-sofosbuvir in the ASCEND investigation who had long term follow up data available. Chart review and abstraction of variables of interest from date of sustained virologic response (SVR) to June 2020 was completed. Baseline demographic and clinical characteristics were compared using t-tests, while change in outcomes was assessed using McNemar’s or chi-squared tests. All analysis was conducted in R, version 4.1.0.

Results: Amongst 525 patients at ASCEND baseline, the mean age was 59.5 years, with majority male (69%), Black race (95%), and genotype 1a (71%), with 20% with HIV, 20% with cirrhosis and 18% IFN-treatment experienced. In addition to 458 (87.2%) of patients with SVR at the end of the original investigation, 16 patients who were lost to follow up were found to have achieved SVR. Furthermore, of 32 patients with known NSVR, 23 were re-treated, 17 of whom achieved SVR. Therefore, 491 (93.5%) of ASCEND participants ultimately achieved HCV cure during the five-year follow up period.

Of the 458 patients who achieved SVR, 97% returned to clinic, of whom 70% were screened for HCV re-infection. Of 336 patients screened, only two (0.6%) were found to be reinfected. Twenty-five patients died during the follow up period. There was a significant difference in morality rates based on SVR status, with 4.1% mortality in those with SVR, compared to 35.7% with NSVR (p<0.05).

Conclusion: This five-year longitudinal follow-up of the ASCEND cohort identifies an even higher rate of SVR of 93.5% in an urban cohort, with limited reinfection. These data emphasize that task-shifting of HCV therapy to non-specialist providers results in both high rates of HCV cure, as well as favourable long-term outcomes. These data emphasize that restrictions on the basis of treating provider type stand as unnecessary hurdles in the HCV care continuum.

FRI370
Risk stratification of hepatocellular carcinoma in cirrhotic patients after hepatitis C virus eradication: Russian single-center experience.
Ekaterina Nabatchikova1, Daria Zasorina1, Teona Rozina1,2, Elena Nikulkina1, Elena Tanashchuk1, Dzhamal Abdurakhmanov2, Sergey Moiseev1,2, 1IM. Sechenov First Moscow State Medical University (Sechenov University), Russian Federation; 2M.V. Lomonosov Moscow State University, Russian Federation
Email: e.nabat4ikova@gmail.com

Background and aims: The risk of hepatocellular carcinoma (HCC) in cirrhotic patients after HCV eradication with direct-acting antivirals (DAAs) is reduced, but not completely eliminated. The aim of our study was to assess incidence, risk factors of HCC and develop a scoring system to predict in patients with HCV-related cirrhosis treated by DAAs.

Method: The prospective single-center cohort study included patients with HCV-related cirrhosis treated by DAAs between July 2015 and May 2020. Exclusion criteria was previous and present HCC. Patients who achieved sustained virological response underwent clinical, laboratory and imaging assessment every 3–6 months after the end of therapy.

Results: A total of 232 cirrhotic patients were enrolled. The median age was 54 (47; 60) years, 49.3% were males, diabetes was present in 19.8%, obesity-in 20.2%, HCV genotype 3-in 25.4% and 29.7% were treatment-experienced. Child-Pugh class B/C were found in 29.3%. Baseline median MELD score was 11 (9; 13), liver stiffness (n = 133)-23 (17.4; 30.6) kPa, platelet count ≤100 × 10³/ml were in 54% of patients, albumin ≤35 g/l-35.3%, bilirubin ≥34 μmol/l-19.4%, prothrombin time ≤60–19.4%, aspartate aminotransferase-platelet ratio index ≥2–56%, fibrosis-4 score (FIB-4) ≥3.25–67.7%. Esohedral varices 2/3 were in 60.3%, ascites-25.4%. The median follow-up time after EOT was 36 (24; 48) months. De novo HCC occurred in 19 (8.2%) patients. Median alpha-fetoprotein was 6.3 (2.8; 31) IU/ml. Sixteen patients (89%) were within the Milan criteria. The
The median time from EOT to HCC diagnosis was 18 (12; 42) months. At the multivariate analysis, baseline bilirubin level ≥34 μmol/l (HR 4.19; p = 0.002), baseline ascites (HR 6.6; p < 0.001), MELD ≥15 (HR 3.82; p = 0.007) and FIB-4 >3.25 (HR 6.4; p = 0.015) at the SVR time were independent risk factors for HCC. We determined the weight of each factor equal to HR, and then converted it into an integer: baseline bilirubin level ≥34 μmol/l-1 point, baseline ascites-2 points, MELD ≥15 at the SVR time-1 point, FIB-4 >3.25 at the SVR time-2 points. The resulting scale allows to set from 0 to 6 points. Patients with HCC had a large sum of points compared to patients without HCC (4 (3; 6) points vs. 1 (0; 2) points, p < 0.001). The AUROC of the model was 0.82 (0.71 – 0.93, p < 0.001). The sum of points equal to ≥3 has the maximum values of sensitivity (73%) and specificity (78%) and can be used as a threshold value for determining the HCC risk (figure a). The cumulative risk of developing HCC in patients with ≥3 points is significantly higher (HR 12.03, log-rank p < 0.001) (figure b).

Conclusion: We developed a predictive score using four risk factors, which can help to customize HCC surveillance strategies in cirrhotic patients after HCV eradication.

FRI371
Distinct hepatocellular carcinoma risks in treated chronic hepatitis C patients with different definitions of advanced chronic liver disease
Yen-Chun Liu1,2, Cheng Er Hsu1,2, Ya-Ting Cheng1,2, Chung-Wei Su1,2, Chia-Hung Tai1,2, Yi-Cheng Chen1,2, Yi-Chung Hsieh1,2, Rachel Wen-Juei Jeng1,2, Chun-yen Lin1,2, Rong-Nan Chien1,2, Tai Dar-In1,2, I-Shyan Sheen1,2.
1Chang Gung Memorial Hospital, Linkou Branch, Taiwan; 2College of Medicine, Chang Gung University, Taiwan
Email: rachel.jeng@gmail.com

Background and aims: To identify target population for hepatocellular carcinoma (HCC) is an important issue in chronic hepatitis C (CHC) patients after antiviral treatment. Advanced chronic liver disease (ACLD) patients have been suggested by the guideline as the target surveillance group for their remnant HCC risk after sustained virological response (SVR). However, the definition of ACLD composed of different diagnostic tools including liver stiffness measurement (LSM), FIB-4 or both or by ultrasonography image. This study aims to compare the predictability of HCC among CHC patients with SVR who meet ACLD criteria by different diagnostic measurements.

Method: CHC achieved SVR by interferon-free direct acting anti-viral agents (DAA), whose LSM by transient elastography (TE, Fibroscan) and FIB-4 index were both available before DAA therapy were enrolled. The ACLD was defined as LSM >10 kPa and/or FIB-4 >3.25 and/or ultrasonography signs of cirrhosis. Predictabilities for HCC and 3-year cumulative HCC incidences were compared among four groups of ACLD patients diagnosed by different non-invasive assessments (group A: FIB-4 > 3.25 but LSM ≤ 10; group B: FIB-4 ≤ 3.25 but LSM > 10; group C: FIB-4 > 3.25 + LSM > 10; group D: FIB-4 ≤ 3.25 and LSM ≤ 10 but ultrasonography showed cirrhosis.).

Results: Among 1600 enrolled patients, 922 (58%) patients met criteria of ACLD (group A, N = 128; group B, N = 369; group C, N = 406; group D, N = 19). The mean age was 62 years old, 41% was male and 63% was genotype 1. The annual incidence and 3-year cumulative HCC incidences showed 0.3% and 0.8%, 2.2% and 4.6%, 3.8% and 9.1% and 3.9% and 10.5% in patients with group A, group B, group C and group D (Log-rank p < 0.01), respectively (Figure). The negative predictive values (NPVs) for HCC were all the above 95% among these four groups with different ACLD definitions, while the sensitivity was much higher in group C of 62.5% compared to group A (1.4%), B (27.8%) and D (2.8%).
Conclusion: LSM >10 kPa ± FIB-4 >3.25 are more appropriate criteria for ACLD than FIB-4 >3.25 alone which PPV is only 0.8% and its 3-year HCC cumulative incidence be approximate to that of the non-ACLD (0.4%). Those with echo appeared cirrhotic features but not fit the criteria of ACLD due to LSM<10 kPA and FIB-4 < 3.25 were still at high risk of HCC and also shall be under HCC surveillance program.

FRI372
Hepatocellular carcinoma risks of liver fibrosis changes after viral eradication in chronic hepatitis C patients
Yen-Chun Liu1,2, Cheng Er Hsu 1,2, Ya-Ting Cheng1,2, Chung-Wei Su1,2, Chia-Hung Tai1,2, Yi-Cheng Chen1,2, Wei Teng1,2, Rachel Wen-Juei Jeng1,2, Chun-yen Lin1,2, Rong-Nan Chien1,2, Tai Dar-In1,2, I-Shyan Sheen1,2. 1Chang Gung Memorial Hospital, Linkou

Figure: (abstract: FRI372)
Background and aims: Hepatocellular carcinoma surveillance is suggested for chronic hepatitis C (CHC) patients with advanced chronic liver disease (ACLD) by the guideline. It is reported liver fibrosis in patients with advanced fibrosis or cirrhosis can be reversed after viral eradication by direct acting antivirals (DAA). The study aims to investigate the HCC risks among CHC sustained virological response (SVR) patients with fibrosis regression, stationary or progression after SVR, and predictors for ACLD regression.

Method: CHC achieved SVR by interferon-free DAA, whose LSM by transient elastography (TE, Fibroscan) and FIB-4 index were both available before DAA therapy and after SVR were enrolled. The ACLD was defined as LSM >10 kPa and/or FIB-4 >3.25 and/or ultrasound signs of cirrhosis. The 3-year cumulative HCC incidences were compared among four groups of dynamic fibrotic changes (group A: both pre-DAA and post-SVR timepoints: non-ACLD; group B: pre-DAA non-ACLD progressed to post-SVR ACLD; group C: pre-DAA ACLD regressed to post-SVR non-ACLD; group D: both pre-DAA and post-SVR: ACLD). Logistic regression was applied to find predictors for ACLD regression.

Results: There were 906 patients (group A: 378 (42%), group B: 18 (2%), group C: 153 (17%), group D: 357 (39%)) enrolling into the study with mean age of 62 years old, 38% of male and 92% of genotype 1. The 3-year cumulative HCC incidences showed 0.5%, 0%, 2.6% and 10.4% in patients with group A, group B, group C and group D (Log-rank p < 0.01), respectively (Figure). Logistic model showed that higher baseline ALT [adjusted OR (aOR): 1.006 (95% CI: 1.002–1.010), p = 0.007] was a predictor for ACLD regression, while higher baseline LSM [aOR:0.870 (0.825–0.917), p < 0.001] and FIB-4 [aOR:0.655 (0.496–0.864), p = 0.003] were unfavorable factors for post-SVR ACLD regression.

Conclusion: Patients with persistent ACLD after SVR posed the highest HCC risks, followed by those with ACLD regression. Those progressed from pre-therapy non-ACLD to post SVR ACLD occurred in 2% of all population with minimal HCC risk as that in the persistent non-ACLD group.

FRI373
Change in fibrosis and clinical progression three years after sustained virological response induced by direct antiviral agents in HIV/CHC subjects
Maria Carnevali Friaš, Lourdes Dominguz2, David Rial Crestelo1, Otilia Bishal1, Rafael Rubio Garcia1, Federico Pulido Ortega1. 1Hospital 12 de Octubre, Medicina Interna, Madrid, Spain; 2King's College Hospital, HIV/Sexual Health, London, United Kingdom
Email: macarfin@gmail.com

Background and aims: Sustained virological response (SVR) achieved after treatment of HCV infection with direct-antiviral agents (DAA) is associated with long-term clinical benefits. We evaluate changes in the estimated fibrosis on SVR confirmation and 3 years after SVR, and if changes on SVR confirmation are related to a decrease in the risk of liver events in people living with HIV (PLWH).

Method: A prospective observational cohort of PLWH with HCV infection and SVR after DAA therapy (January 2015–August 2016) was followed up until December 2020. Liver fibrosis was estimated by non-invasive methods: liver stiffness (LS), APRI and FIB4. Measures were done prior to treatment (baseline), 12 weeks post treatment (SVR12) and 3 years after SVR12 (3 y). Cut-off values for cirrhosis were ≥14.6 kPa (LS), ≥1 point (APRI), ≥2.25 points (FIB4). Cirrhosis regression or non-progression from non-cirrhosis was considered as fibrosis improvement. Clinical outcomes considered were liver-related complications occurred after SVR: death, portal hypertension decompensation (PHD), hepatocarcinoma (HCC) and a composite endpoint of these three.

Results: 393 people were followed-up for a median of 3.8 years (3.5–4.0). There was a significant improvement in LS, APRI and FIB4 from baseline to 3y [−3.0 kPa (−7.6 to 1.2); −0.4 points (−0.9 to 0.2); −0.5 points (−1.3 to −0.1)] and major changes were observed from baseline to SVR12. Before the HCV treatment 30.0%, 35.1% and 26.5% subjects were considered as having cirrhosis according to LSM, APRI or FIB4. More than half of them (58.8%, 87.2% and 70.7% respectively) did not remain in that category at the end of the study. Four HCC were detected [3y risk: 0.8% (0.3–2.4)]. At least one episode of PHD was reported in 13 patients [3y risk: 2.6% (1.4–4.8)]. 23 patients died [3 y overall mortality: 3.9% (2.4–6.4)] but only 3 of them due to liver-related causes [3 y related mortality: 0.3% (0.0–1.8)]. 15 patients developed the composite endpoint [3 y risk of any of the covered outcomes: 3.1% (1.8–5.4)]. Estimated liver fibrosis improvement from baseline to SVR12 was associated to lower risk of presenting any of these clinical outcomes, both in the global cohort and in the subgroup of patients with cirrhosis or advanced fibrosis.

Conclusion: There is a clinically relevant improvement in non-invasive liver fibrosis markers after 3 years of DAA-induced SVR in PLWH with HCV infection. Estimated fibrosis regression from baseline to SVR12 is associated with a reduction in liver-related complications.

FRI374
FOCUS Project: preliminary results toward hepatitis C Virus screening and elimination in Almeria, Spain
Anny Camelo Castillo1, Marta Casado1, Teresa Cabezas Fernandez1, Pedro Amado Villanueva1, Alba Carrodeguas2, Diogo Medina1, José Luis Vega Saénz1, Manuel Rodriguez Maresca1. 1Torrecárdenas University Hospital, Almeria, Spain; 2CILEAD SCIENCES INC, Madrid, Spain
Email: anjo134@gmail.com

Background and aims: Hepatitis C Virus (HCV) elimination is a global challenge, and Spain may be one of the first countries to achieve the World Health Organization’s goal of eliminating viral hepatitis by 2030. A 2017–2018 Ministry of Health serosurvey estimated 0.22% active HCV infection among the general Spanish population, 29.4% without prior infection records. Increasing HCV screening is key, particularly among vulnerable populations with high prevalence. Emergency departments (ED) often act as safety nets due to health equity issues for key populations affected by viral hepatitis, as they often lack optimal links with their primary care providers. Therefore, we aimed to evaluate HCV screening efficacy in the ED of Torrecárdenas University Hospital, in Almería, Andalucia, Spain.

Method: We implemented opportunistic HCV screening in the ED, using existing infrastructure and staff, aided by electronic health record system modifications to identify eligibility for the test and request serologies automatically. Patients were eligible for testing upon verbal consent if they were between 18 and 69, and had no known diagnosis or test performed in the previous year, and required blood tests in the current visit to the ED.
We used the LIAISON®X- Diasorin assay for HCV antibodies (anti-HCV) and the Roche Cobas® 6800 for viral RNA (HCV RNA) in the same specimen (i.e., reflex or single-step testing). Appropriate follow-up or discharge was given, regardless of test results. We contacted positive patients to ensure and monitor linkage to specialist medical care.

**Results:** We screened 1,131 patients for HCV from August to October 2021, finding 28 (2.47%) anti-HCV positive patients (with an average age of 55, 71% males), and 5 (0.44%) HCV RNA positive patients (80% males), 80% of whom had no prior records or knowledge of their infection.

**Conclusion:** Undocumented HCV infection among our ED population is higher than estimated in the general population, with twice the active infection rate and nearly two times undiagnosed infection. Thus, opportunistic HCV screening in EDs is feasible, non-disruptive, and effective in increasing diagnosis.
longitudinal data of log AFP and time-to-event endpoint (HCC) were applied for analysis, combining the linear mixed effects model and the Weibull model for survival.

**Results:** 870 SVR patients, median age 65 (IQR 55–73, 58% males), 92% Child-Pugh A were enrolled. During a median 34 (IQR 14–43) months of post SVR follow-up, 71 patients developed HCC, corresponding to a cumulative incidence at 1, 2 and 3 years of 3.3% (95% CI 2.3–4.8), 5.4% (95% CI 4.0–7.4), 8.3% (95% CI 6.4–10.7), respectively. The joint model considering log AFP values in a time dependent way achieved the best performance to predict the risk of developing HCC, HR 2.44 (95% CI 2.10–2.82, p < 0.001). The log-AFP value progressively increased in patients who developed HCC as compared to those who did not (p < 0.001). A log AFP increase was associated to increased risk of developing HCC with HR 21.9 (95% CI 9.5–49.6) compared to those who did not (p < 0.001). The joint model considering log AFP values in a time dependent way achieved the best performance to predict the risk of developing HCC, HR 2.44 (95% CI 2.10–2.82, p < 0.001). The log-AFP value progressively increased in patients who developed HCC as compared to those who did not (p < 0.001). A log AFP increase was associated to increased risk of developing HCC with HR 21.9 (95% CI 9.5–49.6) compared to those who did not (p < 0.001).

**Conclusion:** In cured HCV cirrhotic patients the AFP value over time is associated to HCC development and may help to refine the HCC surveillance strategies. The increase of AFP levels above 21 ng/ml at any time after SVR is associated with a specificity of 99% for the prediction of HCC development, albeit with low sensitivity.

**FR1377**
A 4 year multi-centre study of persons who inject drugs in Luxembourg, looking at hepatitis C virus seroprevalence, treatment uptake and reinfection rates
Madiha Sharaf1, Vic Arendt2, Thérése Staub3, Carole Devaux4, Emily Montosa Nunes5, Centre Hospitalier Luxembourg, Emergency Department, Luxembourg, Luxembourg; 2Centre Hospitalier Luxembourg, National Service of Infectious Diseases, Luxembourg, Luxembourg; 3Centre Hospitalier National Service of Infectious Diseases, Luxembourg, Luxembourg; 4Luxembourg Institute of Health, Department of Infection and Immunity, Esch-sur-Alzette, Luxembourg
Email: madiha.sharaf@gmail.com

**Background and aims:** The global figure of persons who inject drugs (PWID) stands at 15.6 million persons. 50% of PWID have been estimated to be exposed to the Hepatitis C virus (HCV), and 39% are said to suffer from chronic HCV, in comparison to 1% of the general population. Chronic HCV can result in liver cirrhosis, hepatocellular carcinoma and premature death over 20 to 40 years. The “Hepatitis C among Drug Users”-“HCV-UD” study is the largest multi-centre study in Luxembourg looking at patterns of HCV prevalence amongst PWID, including uptake of treatment and reinfection.

**Method:** 480 participants were recruited at harm reduction sites throughout the country from November 2015 to December 2019. Participants were offered HCV screening, direct acting anti-viral (DAA) treatment and follow-up with an infectious disease specialist, without cost.

**Results:** 356 participants (74%) were exposed to HCV versus 124 participants (26%) who had no evidence of exposure. 51% were cured of which 25% were cured through treatment, as evaluated with a sustained viral response at 12 weeks or more. Of these, 27% were reinfected again with HCV. 75% were cured during the course of the study, attributed to previous unrecorded treatment or spontaneous cure. 47% of participants continued to have ongoing infection, of which 7% had undergone treatment, and 93% had not taken any treatment. There was missing data for 6 participants. The results are summarised in the figure below.

**Conclusion:** The outreach set up of the study enabled insights into the treatment and HCV status of PWID, which the authors feel is a closer representation of reality. HCV prevalence was comparable to other study estimates in the literature. Treatment uptake was low, despite the free DAA treatment offered, however within this subset only 27% went on to be reinfected. What is worrying, however, is that 47% of participants continued to be infected with HCV. This begs the question as to which barriers to care within a psychosocial framework need to be addressed to enable the World Health Organisation’s (WHO) target of eradicating HCV as a public health risk by 2030.

**Viral hepatitis C: Therapy and resistance**

**FR1381**
Benefits associated with HCV cure in people with mental disorders
Benjamin Rolland1, Elias Benabadj2, Olivier Lada2, Pascaline Rabiega3, Fayssol Fouda3, Nabil Hallouche4, Stanislas Pol5

1Université de Lyon-Sud and Service d’Addictologie de Lyon (HCL/CH Vinatier), Lyon, France; 2Gilead Sciences, Boulogne-Billancourt, France; 3IQVIA, France; 4GHU Paris Psychiatrie et Neurosciences, Paris; 5Université de Paris et Hépatologie de Cochin (AP-HP), Paris, France
Email: stanislas.pol@aphp.fr

**Background and aims:** Retrospective and prospective studies have reported hepatic and extra-hepatic benefits after direct-acting antivirals (DAAs) treatment of hepatitis C virus (HCV) chronic infection. However, the ability of virologic cure to improve the neuro-cognitive troubles is still questioned: HCV cure could improve neuro-cognitive troubles as the neurotropism of HCV has been suggested (in glial cells and astrocytes). Our main objective was to evaluate, in the subpopulation of patients with psychiatric disorders, the impact of DAAs (assimilated to HCV cure) on hospitalizations, both in general medicine and in psychiatric ward.

**Method:** All adult patients identified in the French administrative health care databases (SNDs) with DAAs treatment initiation between 2015 and 2018, and with at least one psychiatric disorder, were included. Individuals were assigned into one or several psychiatric disorder sub-groups based on algorithms: “addictive disorders,” “neurotic and mood disorders,” “psychotic disorders” and “other psychiatric disorders.” A longitudinal approach was then used to compare the frequency and the duration of hospitalizations one
year before and one year after HCV treatment, both in general medicine (all-cause) and in psychiatric ward.

**Results:** Between 2015 and 2018, a total of 17,203 HCV patients with at least one psychiatric disorder initiated a treatment in France. 57.4% of the subjects were hospitalized at least once the year before DAAs initiation, while only 41.6% were during the year following treatment ($p < 0.0001$). Put differently, the number of patients with at least one hospitalization decreased by 28% after HCV cure (9,874 versus 7,153 patients hospitalized respectively).

The mean number of hospitalizations per patient per year in general medicine department was 1.2 during the pre-DAAs year and decreased to 0.8 the post-treatment year ($p < 0.0001$). Similarly, this number decreased from 1.4 to 1.2 in psychiatric ward. Among the patients hospitalized at least once in general medicine ($n = 2,515$), both the year before and the year after treatment, the duration of hospital stay decreased significantly from 20.5 days to 16.7 days after HCV treatment ($p < 0.0001$). In psychiatric wards ($n = 589$) a decreasing trend was also observed from 73 days to 68.9 days but was not significant ($p = 0.2132$).

Interestingly, similar results were also observed in all four sub-groups and were statistically significant.

**Conclusion:** DAAs treatment in patients with psychiatric disorders results in a significant reduction in the frequency and the duration of hospitalizations the year following treatment, and even for the patients with severe psychiatric conditions. These results point out both the individual benefit—a better global and psychiatric prognosis—and the collective benefit—fewer resource utilization—of HCV cure in patients with psychiatric disorders.

**FRI382**  
Dismal prognosis for cirrhotic HCV patients after initial DAA treatment failure, rescue therapy may be life-saving  
Johan Westin$^{1}$, Rune Wejstål$^{1}$, Christian Kampmann$^{2}$, Magdalena Ydireborg$^{1}$, Ola Weiland$^{3}$, $^{1}$University of Gothenburg and Sahlgrenska University Hospital, Department of Infectious diseases; $^{2}$Skåne University Hospital, Department of Infectious Diseases, Lund, Sweden; $^{3}$Karolinska Institute and Karolinska University Hospital, Dept of Medicine, Division of Infectious Diseases, Stockholm, Sweden  
Email: johan.westin@gu.se

**Background and aims:** Effective direct-acting antiviral (DAA) treatment against hepatitis C virus (HCV) infection is universally available. A small portion of HCV patients does not respond, irrespective of treatment regimen. The aim was to study the long-term prognosis after initial DAA treatment failure in HCV infected patients, in a real-life setting.

**Method:** Data from all adult patients registered in the national Swedish HCV treatment register who did not achieve sustained virological response (SVR) after their initial DAA treatment course, were retrieved from 2014 through 2018.

**Results:** In total, 288 patients with primary DAA failure were included, of whom 236 underwent a second treatment course as rescue therapy after a median delay of 353 (IQR: 215–650) days. 15 patients received a third treatment course as second rescue treatment after a further median delay of 193 (IQR: 160–378) days. One-hundred-eleven out of 124 (90%) non-cirrhotic and 62/79 (78%) cirrhotic patients achieved SVR following the first rescue treatment. SVR was achieved by 108/112 (96%) patients after a triple DAA regimen. In total 69 (24%) patients were lost to follow-up or died waiting for rescue treatment. Baseline cirrhosis was associated with poor long-term survival. Overall survival 3 years after initial treatment failure was 70% for patients compared with over 90% for patients without baseline cirrhosis (Figure 1).

**Conclusion:** Our study indicates that rescue therapy in most patients with primary DAA failure have an excellent outcome, in particular when a triple DAA regimen was given. A significant number of patients were lost to follow-up or died waiting for rescue therapy, and the overall long-term prognosis for patients with baseline cirrhosis was poor. This indicates that patients with primary DAA failure should be offered rescue therapy, using a triple DAA regimen, without delay.

**FRI383**  
Requests for drug-drug interaction data on direct-acting antivirals and enzyme inducing anti-epileptic agents: an overview of the HEP Interaction checker database of the University of Liverpool  
David Burger$^{1}$, David Back$^{2}$, Jasmine Martin$^{2}$, Daryl Hodge$^{2}$, Minou Van Seyen$^{3}$, Justin Chiong$^{2}$, Alison Boyle$^{2}$, Fiona Marra$^{2}$, $^{1}$University of Liverpool, Liverpool, United Kingdom; $^{2}$Jeroen Bosch Ziekenhuis, ’s-Hertogenbosch, Netherlands; $^{3}$University of Liverpool, Liverpool, United Kingdom  
Email: david.burger@radboudumc.nl

**Background and aims:** Drug-drug interactions (DDIs) between direct-acting antivirals (DAAs) for hepatitis C virus (HCV) infection and enzyme inducing anti-epileptic agents (eiAEs) are among the most difficult to manage, and form a potential barrier towards elimination of HCV. When patients are not able to switch the eiAE to a non-eiAE, DAA treatment is often deferred. With new data published recently on successful combined treatment of eiAEs and DAAs (Buti et al J Hepatol 2021; Natali et al J Pharm Practice 2021) we wondered how often people are looking for eiAE-DAAs interactions at the University of Liverpool’s HEP Interaction Checker (www.hepdruginteractions.org) to gauge some information about how widespread this problem may be.

**Method:** We extracted DDI queries submitted to the HEP Interaction Checker between July 1, 2017 and September 30, 2021. We removed queries on DAAs that are no longer in use (e.g. boceprevir, telaprevir). We only looked at eiAEs (including: carbamazepine, phenytoin, phenobarbital, primidone, oxcarbazepine and eslicarbazepine) as non-eiAEs (e.g. gabapentin, pregabalin) are less of interest from a DDI perspective, and are more often used for other indications such as...
neuropathic pain, mood stabilization, etc. Queries to the database are anonymous, the key information that is recorded is the country of origin.

**Results:** During 51 months of follow-up, a total of 94,695 queries from 98 countries were recorded by website users to check DDIs between eiAEs and DAAs. The most frequently requested DDIs were glecaprevir/pibrentasvir (GP; 23.3%) and sofosbuvir/velpatasvir (22.3%). Among the eiAEs, carbamazepine was the most frequently requested eiAE (37.9%) followed by phenytoin (19.9%) and oxcarbazepine (18.7%). Until recently, all of these combinations were contraindicated (red flag). On an individual level, the most frequently requested DDI between an eiAE and a DAA was carbamazepine & GP (n = 7,773 queries).

**Conclusion:** During our observation period, we received an average number of 1,857 requests per month for a potential DDI between an eiAE and a DAA, demonstrating a huge demand globally for advice on concomitant use of these drugs. Our recommendations have recently been updated to reflect recent real-life data. Given the high number of DDI requests involving an eiAE and DAAs, we believe physicians should be informed that treatment options have now been improved, and HCV treatment should no longer be deferred when an eiAE is on board.

FRI384
Changing HCV patient profiles: insights from a large multinational real-world sofosbuvir/velpatasvir (SOF/VEL) dataset
Alessandra Mangia1, Stefano Fagioli2, Vito Di Marco3, Stephen Shafro6, Mandana Khalili4, Scott Milligan5, George Papatheodoridis2, Denis Ouzan6, Silvia Rosati9, Amaoor Ramji2, Elisabetta Testi11, Montserrat Garcia-Retortillo12, Francisco Andrés Pérez Hernández13, Alexander Wong14, Chris Fraser15, Sergio Rodríguez-Tajes16, Elena Jiménez Mutilló17, Luis Enrique Morano Amado18, Joss O’Loan19, Francesca Campanale20, Guilherme Macedo21, Michele Millella22, Christian Brixko23, Maria Buti24, María Guerra Veloz25, Roberto Ranieri26, Sergio Borgia27, AnnaLisa Bascia1, Conrado Manuel Fernandez Rodriguez28, Brian Conway29, Victor de Lédinghen30, Mary Fenech31, Pablo Ryan32, Ivana Maid33, Alexandra Martins34, Stacey Scherbakovs35, Joanna Ntalla36, Candido Hernández37, Kim Vanstaelen38, Juan Turnes39, IRCCT-Ospedale Casa Sollievo Della Sofferenza, San Giovanni Rotondo, Italy; 1IRCCS-Università degli Studi di Bari, Italy; 2Asst Papa Giovanni XXIII-Lombardia HCV Network, Italy; 3University of Bari, Italy; 4Clinical and Biochemical Sciences, University of Sassari, Italy; 5Liver Unit, Hospital Doctors, Porto, Portugal; 6Clinical and Health Services Research, Hospital Doctor Porto, Porto, Portugal; 7Liver Unit, Hospital Clinic Barcelona, IDIBAPS, CIBERehd, Spain; 8Liver Unit, Hospital Universitario Policlinico La Paz, Madrid, Spain; 9The profile of HCV patients (pts) being started on direct-acting antivirals (DAAs) has shifted towards more vulnerable populations. This large real-world analysis describes the diverse profile of these populations according to age and sex.

**Method:** Adult HCV pts (aged 18+ years) from 37 clinical cohorts across nine countries treated with SOF/VEL for 12 weeks without ribavirin were included. Those with a history of decompensation or prior NS5A-inhibitor exposure were excluded. This descriptive analysis evaluated pt characteristics, time to treatment (TT [time from HCV RNA diagnosis to DAA initiation]), and sustained virological response ≥12 weeks after end of treatment (SVR), stratified by age and sex.

**Results:** Among 6356 pts, 2274 were aged <50 y, 2568 ≥65 y, and 1514 >65 y. Within these age strata, 73%, 65%, and 45%, respectively, were male. Vulnerable populations were well represented, and ~20% of all pts had a history of IV drug use. Irrespective of age, male pts were more likely to have compensated cirrhosis and to be infected with HCV genotype (GT) 3 (Table). Within vulnerable populations, higher likelihood of incarceration among male pts was restricted to those aged ≤65 y. Significantly fewer mental health disorders were seen in male pts. However, use of antipsychotics appeared similar, irrespective of sex. Median TT was shorter in male pts across the age spectrum.

In 5845 pts with a valid result, SVR was high across age ranges, with no significant differences observed between male and female pts (<50 y: female 98.7%, male 99.2%; ≥65 y: female 98.7%, male 98.1%; >65 y: female 99.3%, male 98.3%). 475 pts did not achieve SVR for a non-virological reason; mostly loss to follow-up, with no differences between males and females across age strata.

**Conclusion:** SOF/VEL shows high cure rates across different age and sex groups. Antipsychotic drug use appeared similar in males and females, despite significantly fewer mental health disorders in male pts. TT varied from 1 day to >6 months and was shorter in males.
Table: (abstract: FRI384): Characteristics of HCV pts in the overall population, stratified by age and sex

<table>
<thead>
<tr>
<th>Age Group</th>
<th>F (n = 608)</th>
<th>M (n = 1666)</th>
<th>p-value</th>
<th>F (n = 905)</th>
<th>M (n = 1663)</th>
<th>p-value</th>
<th>F (n = 833)</th>
<th>M (n = 681)</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>&lt;50 y</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>F</td>
<td>7.2</td>
<td>13.4</td>
<td>&lt;0.001</td>
<td>18.7</td>
<td>&lt;0.001</td>
<td>24.2</td>
<td>29.5</td>
<td>&lt;0.001</td>
<td></td>
</tr>
<tr>
<td>M</td>
<td>46.7</td>
<td>48.3</td>
<td>NS</td>
<td>32.5</td>
<td>&lt;0.01</td>
<td>5.3</td>
<td>10.9</td>
<td>&lt;0.001</td>
<td></td>
</tr>
<tr>
<td>≥65 y</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>F</td>
<td>30.4</td>
<td>47.6</td>
<td>&lt;0.001</td>
<td>20.0</td>
<td>&lt;0.01</td>
<td>17.3</td>
<td>13.1</td>
<td>&lt;0.05</td>
<td></td>
</tr>
<tr>
<td>M</td>
<td>6.5</td>
<td>12.0</td>
<td>&lt;0.05</td>
<td>2.2</td>
<td>&lt;0.05</td>
<td>0.0</td>
<td>4.5</td>
<td>&lt;0.05</td>
<td></td>
</tr>
</tbody>
</table>

F, females; M, males; NS, not significant; IQR, interquartile range.
*Proportions of patients belonging to vulnerable subpopulations are expressed as % of the total vulnerable population.

**FRI385**

Sofosbuvir plus velpatasvir for 8 weeks in patients with acute hepatitis C: multicenter, single arm, phase 2 study (The HepNet acute HCV-V study)

Benjamin Maasoumy1,2,3, Patrick Ingliz4, Christoph Spinner5, Christiane Cordes6, Hans-Jürgen Stellbrink7, Julian Schulze zur Wiesch6,8, Stephan M Schneeweiss10, Katja Deterding11, Tobias Müller12, Julia Kahlhöfer1, Petra Dörge3, Maria von Karpowitz13, Michael P. Manns1, Heiner Wedemeyer1, Markus Cornberg3,14,15,16, Hannover Medical School, Department of Gastroenterology, Hepatology and Endocrinology, Hannover, Germany; 12Charité Campus Virchow-Klinikum (CVK), Department of Gastroenterology and Hepatology, Berlin, Germany; 13Hannover Medical School, Department of Gastroenterology, Hepatology and Endocrinology, Hannover, Germany; 2German Center for Infection Research (DZIF), Partner Site Hannover-Braunschweig, Hannover, Germany; 3German Center for Infection Research (DZIF), HepNet Study-House, German Liver Foundation, Hannover, Germany; 4Praxis Dr. Cordes, Berlin, Germany; 5Infectiology Center Hamburg (ICH), Hamburg, Germany; 6Praxis Hohenstaufenring, Cologne, Germany; 7Infectiology Center Hamburg (ICH), Hamburg, Germany; 8University Medical Center Hamburg-Eppendorf, Medical Department, Hamburg, Germany; 9University Medical Center Hamburg-Eppendorf, Medical Department, Hamburg, Germany; 10Technical University of Munich-School of Medicine, Germany; 11Hannover Medical School, Department of Gastroenterology, Hepatology and Endocrinology, Hannover, Germany; 12Charité Campus Virchow-Klinikum (CVK), Department of Gastroenterology and Hepatology, Berlin, Germany; 13Hannover Medical School, Institute for Biometry, Hannover, Germany; 14Hannover Medical School, Department of Gastroenterology, Hepatology and Endocrinology, Hannover, Germany; 15German Center for Infection Research (DZIF), Partner Site Hannover-Braunschweig, Hannover, Germany; 16Center for Individualized Infection Medicine (CiiM), Hannover, Germany

**Background and aims:** Sofosbuvir plus velpatasvir (SOF/VEL) is highly effective for the treatment of hepatitis C virus (HCV) infection, but it is only approved in chronic hepatitis C. The EASI recommendations suggest 8-weeks of SOF/VEL for the treatment of acute or recently acquired HCV infection. However, to date there are only data published for 6 and 12 weeks for recently acquired HCV infection. The objective of this study was to evaluate the safety and efficacy of 8 weeks of SOF/VEL treatment for acute HCV monoinfection.

**Method:** In this investigator-initiated, prospective, multicentre, single-arm study, we recruited a total of 20 adults (≥18 years) with acute HCV monoinfection (proven antibody or RNA seroconversion or ALT >10 ULN with known exposure within 4 months) from nine centers in Germany between March 2019 and June 2021. Patients received SOF/VEL (400/100 mg) as a fixed-dose combination tablet once daily for 8 weeks. The primary efficacy endpoint was the proportion of patients with sustained virological response (undetectable HCV RNA 12 weeks after the end of treatment, SVR12). Other endpoints included biochemical response and safety of SOF/VEL.

**Results:** The median HCV RNA viral load at baseline was 5.0 log10 IU/ml; the distribution of HCV genotypes was as follows: GT1a/1b/2/3/4: n = 12/1/3/3/3. Thirteen (65%) of the patients were taking medication for HIV pre-exposure prophylaxis. Two patients were lost to follow-up. In the per protocol analysis, all patients achieved SVR12 (n = 18/18 [100%]). Median ALT levels were 249 U/L at baseline and 22 U/L 12 weeks after the end of treatment, with all but one patient (94%) achieving ALT normalization. Treatment was well tolerated; by 12 weeks post-treatment, there was one serious adverse event unrelated to study drug and 6 possible or probable drug-related adverse events with only mild symptoms.

**Conclusion:** The 8-week treatment with SOF/VEL was well tolerated and highly effective in patients with acute HCV monoinfection. Early treatment of hepatitis C might effectively prevent the spread of HCV in high-risk groups and should therefore be more targeted; ideally, approval for hepatitis C therapy should be pursued independently of chronic hepatitis C.

**FRI386**

Full-length genome characterization of inherently resistant African HCV genotype 1, subtype 11 in patients failing DAA-based therapy

Slim Fourati1,2,3, Erwan Vo Quang2,4, Christophe Rodriguez1,2,3, Alexandre Soulier1,2, Vanessa Demontant1,2,3, Stéphane Chevaliez1,2,3, Vincent Leroy2,3,4, Jean-Michel Pawlotsky1,2,3,4, APHP-Henri Mondor Hospital, Virology, France; 2INSERM U955, “Virus Hepatology, Cancer Team, Créteil, France; 3Paris-Est Créteil University, Créteil, France; 4APHP-Henri Mondor Hospital, Hepatology, Créteil, France

**Background and aims:** Among the so-called “unusual” HCV genotypes, genotype 1, subtype 11 (GT-11) is common in patients of African origin. GT-11 has recently been suggested to be less responsive to NSSA inhibitor-containing regimens than GT-1a or GT-1b. Here, we used shotgun metagenomics based on deep sequencing to generate full-length HCV genome sequences and characterize amino acid substitutions present at baseline and
selected by DAA therapy in regions targeted or not targeted by DAAs in GT-11 infected patients who failed to achieve SVR.

Method: Shotgun metagenomics were used to generate full-length HCV GT-11 genome sequences. Briefly, library preparation was performed using Total RNA and Nextera XT kit (Illumina). Deep sequencing was performed by means of NextSeq500 (Illumina). Full-length HCV sequences were analyzed using our original in-house MetaMIC® software (1% cutoff).

Results: Among 771 patients with HCV infection treated with DAAs who experienced a virological failure and were referred to our center between 2015 and 2019, 316 (41.0%) were infected with genotype 1, and 20 of them (6.3%) with GT-11. All GT-11-infected patients were of African origin. Deep sequencing of full-length HCV GT-11 genomes was performed in 10 patients at baseline and at time of relapse. Treatment regimens were SOF/LDV ± RBV (n = 8), SOF/VEL (n = 1) and SOF/SIM (n = 1). At baseline, all of the 10 GT-11 patients had ≥3 dominant NS5A resistance-associated substitutions (RASs), including K24G/S (>99%), L31M (>99%) and H58P (>99%). Additionally, baseline NS5A-Q30R was present in 3 patients (>99% in 2 patients; 25% in 1 patient). Sequential analysis of full-length HCV genome sequences showed enrichment of NS5A-Q30R in one patient at failure (>99%) and the selection of NS5A RASs in other patients: baseline K24S (8% and 40%, respectively) replaced by K24G (>99%) in 2 patients; selection of Y93F and Y93H RASs at failure in 2 other patients (20% and 40% respectively).

No NS5B RASs were detected. NS3 R155 K was selected in one patient failing SOF/SIM (30%). No amino acid changes of interest were observed at treatment failure in genome regions other than those targeted by the HCV DAAs administered.

Data on retreatment by triple-combination regimens are ongoing and will be presented.

Conclusion: We report the largest cohort of GT-11-infected African patients failing DAAs thus far. The large number of NS5A RASs present at baseline explains lower SVR rates with NS5A inhibitor-based therapies in these patients. Our results emphasize the need for identifying this subtype and other “unusual” subtypes (e.g. GT-4r) in Africa where they are common, and the urgent need to guarantee equal access to last-generation DAA therapies in Africa.

FR1387
Treating HCV in dual diagnosis acute psychiatric inpatients with substance use disorder
Vera Dreizin1, Yael Delayahu2, David Hovel1, Gabriela Ilionsky3, Neil Mfaria4, Eran Israeli1.
1Wolfson Medical center, Institute of Gastroenterology, Holon, Israel; 2Yehuda Abarbanel Mental Health Center, Dual Diagnosis (D) Ward, Bat Yam, Israel; 3Yehuda Abarbanel Mental Health Center, Dual Diagnosis (D) Ward, Bat Yam, Israel; 4Yehuda Abarbanel Mental Health Center, Bat Yam, Israel
Email: verpav1@yandex.ru

Background and aims: People with severe mental illness (SMI) and substance use disorder (SUD) are at increased risk for hepatitis C (HCV). However, only 4.7% receive screening for HCV. Psychiatric patients with dual diagnosis (DD) of SMI and SUD have multiple risk factors for HCV: homelessness, immigration, imprisonment, coinfections such as HIV or hepatitis B. However, few treatment approaches have been studied in this patient group.

To describe an on-going project of accessing DD patients during their stay at a psychiatric facility for diagnostic work-up, treatment and follow-up.

Method: We initiated a collaboration between Hepatology clinic of a general hospital and Dual Diagnosis acute Ward (DDW) of a psychiatric hospital for treating HCV patients. All patients admitted to the DDW are screened for HCV AB. Patients positive for HCV are examined at the facility by the project’s expert hepatologist and undergo a full diagnostic workup. Treatment is administered during hospitalization; all patients undergo monthly clinical and laboratory assessment. Patients discharged from the facility are referred for follow-up to the Hepatology Clinic. We keep close contact with family physicians, rehab centers, medical care providers and families.

Results: From January 2020 to November 2021 we allocated a cohort of 56 HCV patients at different stages of diagnosis and treatment (Table). We were able to treat 22 patients. 7 have already achieved SVR, 5 have completed treatment and are waiting for SVR, 5 are now being treated and 5 are under investigation. 13 patients had negative HCV PCR due to spontaneous recovery. Two patients died during the follow-up period not due to liver disease. 7 patients were treated for HCV before the psychiatric hospitalization, 12 were not treated. FIB 4 was measured in 30 patients; 43% (13 patients) were with FIB-4 score greater than 1.45. Fibroscan/Fibrotest examination was performed in 26 patients, with evidence of advanced fibrosis in 19% (5 patients). 19 patients were treated by Sofosbuvir/Velpatasvir for 12 weeks and 3 patients were treated with Glecaprevir/Pibrentasvir for 8 weeks. There were no severe adverse events during treatment.

<table>
<thead>
<tr>
<th>Patients M/F</th>
<th>56 (53/3)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age</td>
<td>43.6 (24-62)</td>
</tr>
<tr>
<td>Multiple psychoactive drugs</td>
<td>56</td>
</tr>
<tr>
<td>Substitute treatment</td>
<td>16 (29%)</td>
</tr>
<tr>
<td>Active drug users</td>
<td>45 (80%)</td>
</tr>
<tr>
<td>Past imprisonment</td>
<td>45 (80%)</td>
</tr>
<tr>
<td>Alcohol abuse</td>
<td>43 (77%)</td>
</tr>
<tr>
<td>Homeless</td>
<td>36 (64%)</td>
</tr>
<tr>
<td>No family</td>
<td>44 (79%)</td>
</tr>
<tr>
<td>HIV coinfection</td>
<td>1</td>
</tr>
<tr>
<td>HBV coinfection</td>
<td>3</td>
</tr>
<tr>
<td>HCV coinfection</td>
<td>1</td>
</tr>
<tr>
<td>Liver or kidney transplantation</td>
<td>1</td>
</tr>
<tr>
<td>Psychiatric comorbidity</td>
<td>56</td>
</tr>
<tr>
<td>Schizophrenia</td>
<td>28 (46%)</td>
</tr>
<tr>
<td>Dissocial personality disorder</td>
<td>9 (16%)</td>
</tr>
<tr>
<td>Other nonorganic psychosis</td>
<td>21 (38%)</td>
</tr>
<tr>
<td>Non psychiatric comorbidity</td>
<td>20 (36%)</td>
</tr>
</tbody>
</table>

Conclusion: We present our ongoing experience of treating HCV in a population of drug dependent patients with SMI during their in-hospital stay. This model has proved efficiency in facilitating their access to care and achieving SVR where no other approach proved successful.
FR1388
Eight-weeks of glecaprevir/pibrentasvir is well tolerated and yields high sustained virological response in HCV-infected treatment-naïve patients with compensated cirrhosis: the CREST study
Markus Cornberg1, Armand Aberger2, Alessio Aghemo3, Adriana Ahumada4, Massimo Andreoni5, Tarik Asselah6, Abhi Bhagat7, Isabel Butrymowicz7, Michal Carmi68, Gabriel Chodir10,11, Brian Conway12,13, Antonio Gasbarrini14, Dietrich Hüppe15, Francisco Jorquera16, Pietro Lampertico17,18, Maria Luisa Manzano Alonso19, Lindsy Myles20, Marcello Persico21, Ainoor Ramji22, Christoph Sarrazin23, Dimitri Semizarov24, Yanna Song25, Erica Villa24,25, Carla Welti15, Juan Isidro Uriz Otano26,25,26
1Hannover Medical School, Department of Gastroenterology, Hepatology and Endocrinology, Hannover, Germany; 2UMR 6602 CNRS Université d’Auvergne, CHU Estaing; 3Humanitas Research Hospital IRCCS, Department of Biomedical Sciences, Humanitas University, and Department of Gastroenterology, Rozzano, Italy; 4Hospital General Universitario Gregorio Marañón, Liver Unit; 5University of Tor Vergata, Rome; 6Hôpital Beaujon, INSERM UMR 1149, Service d’Hépatologie; 7AbbVie Inc., North Chicago, United States; 8Galilee Medical Center, Liver Unit; 9Bar-Ilan University, The Azrieli Faculty of Medicine; 10Maccabi Healthcare Services, Maccabiah; 11Tel-Aviv University, Sackler Faculty of Medicine; 12Vancouver Infectious Diseases Center; 13Simon Fraser University; 14Fondazione Policlinico Universitario A. Gemelli IRCCS, Internal Medicine and Gastroenterology; 15Gastroenterologische Gemeinschaftspraxis Herne; 16Complejo Asistencial Universitario de León, IBIOMED and CIBERehd, Digestive System Service, Spain; 17Ospedale Maggiore Policlinico, Foundation IRCCS Ca’ Granda; 18CRC ‘AM and A Migliavacca’ Centre for Liver Disease, Division of Gastroenterology and Hepatology; 19Hospital Universitario 12 De Octubre, Liver Unit, Spain; 20Barrie Ci Associates; 21AOU OO. RR. San Giovanni di Dio Ruggi e D’Aragona, Dipartimento di Medicina Clinica Medica, Epato-Pancre-Endocrinologia; 22University of British Columbia; 23Goethe-University Hospital Frankfurt, Department of Internal Medicine and Liver Center, St. Josefs-Hospital Wiesbaden and Viral Hepatitis Research Group; 24Azienda Ospedaliera Universitaria di Modena, UC Gastroenterologia, Dipartimento di SpecialitàMediche; 25Navarra Institute for Health Research (IdiSNA); 26Complejo Hospitalario de Navarra, Department of Gastroenterology, Liver Unit
Email: cornberg.markus@mh-hannover.de

Background and aims: The direct-acting antiviral glecaprevir/pibrentasvir (G/P) is approved for 8-week treatment of chronic hepatitis C genotypes (GT) 1–6 in patients with or without compensated cirrhosis (CC). To support clinical trials findings, this study assessed real-world effectiveness and safety in treatment-naïve (TN) patients with CC treated with 8-weeks G/P, with a focus on challenging-to-treat patients with advanced liver disease (platelets <150,000/μl, elasticity >20 kPa [FibroScan®, Echosens, Paris, France], or both), and special populations such as drug users, human immunodeficiency virus co-infection, and psychiatric disorders.

Method: Here we present updated interim results from the CREST study, an ongoing, noninterventional, multicenter study including data from Canada, Germany, Israel, Italy, France, and Spain. The primary endpoint was sustained virological response at posttreatment Week 12 (SVR12) based on the modified analysis set (MAS) which excluded patients who discontinued G/P for reasons other than nonvirological failure or with missing SVR12. Safety and laboratory abnormalities were assessed on the full analysis set.

Results: Of 437 patients who received ≥1 dose of G/P, 24.5% (107/437) had GT3, 46.0% (189/411) had platelets <150,000/μl, 16.4% (61/373) had elasticity >20 kPa, and 9.8% (36/376) had platelets <150,000/μl and elasticity >20 kPa. Of 375 patients in the MAS with data available, SVR12 was reached by 371 (98.9%). SVR12 was 97.7% (84/86) in patients with GT3, 99.4% (165/166) in those with platelets <150,000/μl, 98.1% (53/54) in those with elasticity >20 kPa, and 100% (32/32) in those with both elasticity >20 kPa and platelets <150,000/μl (Figure). Of 117 (26.8%) patients with an adverse event (AE), 5 (1.1%) had a serious AE (SAE), with 1 (0.2%) discontinuing the study drug due to an AE. None of the SAEs were drug related. The most common AEs (>5%) were fatigue (9.6%; 42/437) and headache (6.4%; 28/437). Of 421 patients with laboratory data available, 9 (2.1%) and 10 (2.4%) had alanine or aspartate aminotransferase, respectively, >5x upper limit of normal.

Conclusion: In this real-world cohort, 8-week G/P therapy was well-tolerated, with SVR12 rates similar to those in clinical trials. These results support the use of G/P therapy in TN patients with CC, regardless of liver disease severity or GT, including GT3. Additional efficacy data in special populations will be presented at the congress.

Acknowledgements: The authors would like to express their gratitude to the patients who participated in this study and their families, as well as the study investigators and coordinators of the study. Glecaprevir was identified by AbbVie and Enanta. Medical writing support was provided by Marta Rossi, PhD, of Fishawack Communications Ltd, and funded by AbbVie.

FR1389
HCV-RNA viral load fingerstick assay as a simplified strategy for screening and linkage to care of people who use drugs attending 3 french addiction centers
Denis Ouzañ1, Joris Herin2, Nicolas Camerlo3, Patrick Favor4, Bruno Blasi5, Maella Lebrun6, Henriette Thiercelin4, Nathalie Legros7, Teresa Namouni8, Perrine Roux9, Stéphane Chevaliez10, Arnault Institute Tzanck, Saint-Laurent-du-Var, France; 11RHECCA, NICE, France; 12Bus 31/32, Marseille, France; 13CAARUD INDU PASSAGIN, Nice, France; 14CSAPA FONDATION DE NICE, France; 15Bus 31/32, France; 16CSAPA FONDATION DE NICE, Nice, France; 17CSAPA EMERGENCE, Nice, France; 18INSERM, France; 19CNR HOPITAL MONDOR, France

Email: denis.ouzan@wanadoo.fr

Background and aims: Rational: The number of people who inject drugs (PWID) that are screened and treated for hepatitis C remains low. Many of them are lost to follow-up after serological testing. It is currently estimated that 20% of patients are treated in Harm reduction centers (CSAPAs) and in Needle exchange structures (CAARUDs). The measurement of the viral load by rapid RT-PCR from capillary blood (Xpert® HCV Viral Load Fingerstick) allows to obtain a result in <1 hour and thus to increase the percentage of HCV-seropositive patients who could benefit from treatment.

Aims: The aims of this prospective study were to evaluate the feasibility and the acceptability of HCV-RNA viral load fingerstick assay use to improve HCV screening and treatment among French PWIDs attending 3 Addiction Centers.
Method: From March 1, 2021, all HCV seropositive PWIDs (previously known positive for serology or determined using a rapid diagnostic test (RDT) simultaneous targeting HCV, HBV, and HIV) followed up in 3 Addiction Centers CAARUD/CSAPA (2 in Nice, 1 in Marseille) were offered a rapid RNA testing using a molecular point of care testing (POCT) (Xpert HCV Viral Load Fingerstick). If the RNA testing was positive, treatment was proposed.

Results: From March 1 to August 31, 2021, 119 PWID were included: 76.5% men with an average age of 45 years, 22 were without social rights, 62 with precarious housing and 22 homeless, 41 declared having injected: heroin, crack, other, 34 inhaled: cocaine, crack, other, 65 having multiple addictions of which cannabis 35 and drugs 11 and 67 excessive alcohol consumption. 46 were receiving substitution treatment. HCV serology was determined in 117 of the 119 DU and was positive in 43 (37%) of them. HBV surface antigen (HBsAg) was positive in 4 and HIV in 3 DU PWID (all previously known). Among 35/43 anti-HCV+ subjects agreed to perform a rapid RNA testing, HCV RNA was positive in 20, i.e. a prevalence of 16%. Antiviral treatment was initiated in 12. The rate of treatment success will be presented.

Conclusion: Despite the high rate of HCV infection among PWIDs, screening and linkage to care remain far from comprehensive. Our HCV-RNA screening project, highlights the feasibility and the acceptability of onsite testing performed with HCV-RNA viral load fingerstick assay in PWIDs. This easy to use approach increases the frequency of HCV RNA testing and the prescription of treatment.

FRI390
Pangenotypic and genotype-specific antivirals in the treatment of genotype 4 infected patients with HIV coinfection
Dorota Żarebka-Michałuk1, Jerzy Jaroszewicz2, Anna Wartenius-Kowalczyk3, Beata Lorenc4, Małgorzata Pawłowska5, Włodzimierz Mazu6, Marek Sikto7, Ewa Janczewska8, Hanna Berak9, Janocha-Litwin Justyna10, Jakub Klapaczynski11, Krzysztof Tomasiwicz12, Piekarska Anna13, Beata Dobrak14, Rafal Krygier15, Jolanta Cikto16, Tronina Olga17, Krystyna Dobrowolska18, Robert Flisiak1, Jan Kochanowski University, Department of Infectious Diseases, Kielce, Poland; 2Medical University of Silesia, Department of Infectious Diseases and Hepatology, Katowice, Poland; 3Medical University of Białystok, Department of Infectious Diseases and Hepatology, Białystok, Poland; 4Medical University of Gdańsk, Poland; 5Ludwik Rydygier Collegium Medicum in Bydgoszcz Faculty of Medicine Nicolaus Copernicus University in Toruń, Bydgoszcz, Poland; 6Medical University of Silesia, Katowice, Poland; 7Jagiellonian University, Kraków, Poland; 8Medical University of Silesia, Bytom, Poland; 9Hospital for Infectious Diseases, Warszawa, Poland; 10Medical University of Wrocław, Wrocław, Poland; 11Central Clinical Hospital of the Ministry of Internal Affairs and Administration, Warszawa, Poland; 12Medical University of Lublin, Lublin, Poland; 13Medical University of Łódź, Łódź, Poland; 14MED-FIX, Wrocław, Poland; 15State University of Applied Sciences, Konin, Poland; 16Regional Hospital Olsztyn, Olsztyn, Poland; 17Medical University of Warsaw, Warszawa, Poland; 18Jan Kochanowski University, Collegium Medicum, Kielce, Poland

Email: dorota1010@tlen.pl

Background and aims: The introduction of the direct-acting antivirals (DAA) has improved substantially the therapy effectiveness in patients with chronic hepatitis C and we aimed to compare the efficacy of pangenotypic and genotype-specific DAA in the cohort of genotype (GT) 4 patients with HCV mono-infection and HIV coinfection.

Method: The analysis included patients selected from the EpiTer-2 database, a large retrospective multicenter national real-world study evaluating DAA treatment in 13, 554 consecutive individuals with hepatitis C virus (HCV) infection.

Results: A total of 662 GT4-infected patients, of whom 168 (25.3%) were coinfected with HIV, treated in 2015–2020 were enrolled in the analysis. Significantly higher rate of males (67.9% vs. 57.7%), a lower proportion of liver cirrhosis (10.2% vs. 18.1%), and higher of treatment-naïve patients (87.5% vs. 76.7%) were documented in HIV coinfected individuals. The overall sustained virologic response after exclusion of non-virologic failures was achieved in 98% with no significant difference between HIV-positive and HIV-negative patients, 96.2% vs. 98.5%, respectively. While the genotype-specific regimens resulted in a similar cure rate regardless of the HIV status, the pangenotypic options were more efficacious in patients with HCV mono-infection as compared to HIV coinfected (99.3% vs. 94.4%, p = 0.05). No significant differences in demographic, clinical, and laboratory parameters were found between 13 virologic nonresponders and responders.

Conclusion: We demonstrated the high effectiveness and good safety profile of DAA regimens in GT4 infected patients with HIV coinfection. However, the current analysis demonstrated lower effectiveness of pangenotypic regimens in HIV/HCV GT4 coinfected patients compared to genotype-specific regimens.
GT1b. NS5A RASs were very common (90%–95% after EOT) in all GT and even after FU24, RASs were detectable in more than 70% of the patients. RAS patterns in GT1b were dominated by L31M and Y93H and both variants showed a stable course over time (FU24: 95% patients with RASs). Several different RASs were detected in GT1a, most common were M28 T, Q30H/R, L31M and Y93H. However, NS5A RASs slightly decreased in GT1a and GT3a which was mainly caused by the decline of high-level resistant Y93H (FU24: GT1a, 71% and GT3, 73% of patients with RASs).

**Conclusion:** After DAA failure, NS3 and NS5B RASs disappeared quickly and NS5A RASs persisted beyond two years after EOT. While NS5A RASs remained stable in HCV GT1b, patients with GT1a and GT3 showed a decrease in particular of Y93H two years after EOT.

**FRI 392**

**Real-life effectiveness and safety of sofosbuvir/velpatasvir in difficult to treat hepatitis C patients**

Hyun Young Woo1, Jeong Heo1, Young Joo Park1, 1Pusan National University Hospital, Internal Medicine, Busan, Korea, Rep. of South Email: who54@hanmail.net

**Background and aims:** In spite of recent advance in the treatment of hepatitis C virus (HCV), there are still difficult to treatment population such as prior direct antiviral agents (DAA) failure, decompensated cirrhosis or presence of hepatocellular carcinoma (HCC). Here we report our experience about these patients treated Sofosbuvir/Velpatasvir (SOF/VEL) in real world setting.

**Method:** All consecutive patients with HCV receiving SOF/VEL between August 2017–May 2021 in South Korea were enrolled. Sustained virological response (SVR) was defined as undetectable HCV-RNA 12 (SVR12) weeks after the end of treatment.

**Results:** A total of 37 patients were included: median age 65 (45–83) years, 59.5% males, median HCV-RNA 852, 500 (11, 100 000) IU/ml. HCV genotype was 1b in 67.6%, 2 in 29.7%, 1b & 2b in 2.7%. 37.8% have concomitant HCC (BCLC stage A/B/C; 4/8/2). 56.8% have underlying cirrhosis and 7.5% was decompensated cirrhosis. 70.3% have failed prior DAA treatment (Daclatasvir + asunaprevir n = 16, sofosbuvir+ribavirin n = 3, sofosbuvir + ledipasvir n = 2, glecaprevir+ pibrentasvir n = 3, boceprevir n = 1) Naive patients received SOF/VEL for 12 weeks and the patients with prior DAA failure received SOF/VEL for 24 weeks, ribavirin was added in 78.4% of treatment schedules. Undetectable HCV-RNA was achieved by 97.2% of patients at week 4 and end of treatment response was 97.2%. Overall, 36/37 (97.2%) patients by intention to treat analysis and 36/36 (100%) by per protocol analysis achieved SVR12, respectively; One patient was expired due to HCC progression during SOF/VEL treatment. Most patient well tolerated treatment without adverse events.

**Conclusion:** SOF/VEL is an effective and safe retreatment for difficult to treat HCV population in a real-life setting.

**FRI 393**

**Polypharmacy and prevalence of multi drug-drug interactions in hepatitis C patients treated with pangenotypic direct acting antivirals: an analysis from three European countries**

Frank Tacke1, Juan Turnes2, Andreas Hintz2, Stefano Fagioli2, Antoni Sícras-Mainar2, Tim Umland3, Luca Degli Esposti4, Ramón Morillo Verdugo5, Antonio García Herola6, Mehtap Guendogdu7, Maranela Mendez10, Gema Alvarez Nieto11, Kim Vanstraalen12, Candido Hernández12, Alessandra Mangia13.

1Charité-Universitätsmedizin Berlin, Berlin, Germany; 2Complejo Hospitalario Universitario de Pontevedra, Gastroenterology and Hepatology, Spain; 3Alexander Apotheke, Hamburg, Germany; 4ASST Papa Giovanni XXIII Hospital, Bergamo, Italy; 5Atrys health, HEOR, Barcelona, Spain; 6Clicon S.r.l., Health Economics and Outcomes Research, Ravenna, Italy; 7Hospital Universitario de Valme, Hospital Pharmacy, Sevilla, Spain; 8Hospital Marina Baixa, Villajoyosa, Spain; 9Gilead Sciences GmbH, Medical Affairs, München, Germany; 10Gilead Sciences S.L, Medical Affairs, Madrid, Spain; 11Gilead Sciences S.r.l, Medical Affairs, Milan, Italy; 12Gilead Sciences, Global Medical Affairs, United Kingdom; 13Fondazione “Casa Sollievo della Sofferenza” IRCCS, San Giovanni Rotondo, Italy

**Email:** a.mangia@tin.it

**Background and aims:** Current EASL, AASLD and APASL guidelines recommend a thorough drug–drug interaction (DDI) evaluation before starting pangenotypic direct-acting antiviral (pDAA) therapy. Previous studies have analyzed DDIs in HCV patients receiving pDAs and comedications only by pairwise interactions. However, this does not reflect the polypharmaceutical reality of many HCV patients. The aim of this study was to evaluate the proportion of HCV patients with multiple comedications causing potential DDIs in three European countries.

**Method:** Comedication prescription data were collected from patients treated with pDAs in Germany, Italy, and Spain. DDIs were identified using the Liverpool Hep Interaction checker. A multi-DDI profile was defined as the use of ≥2 comedications each predicted with a DDI with the administered pDAA. Potential DDI outcomes were summarized as an increase in comedication exposure (impact on safety) or a decrease in DAA exposure (impact on efficacy).

**Results:** A total of 10, 755 HCV patients (mean age: 53.6 years, 64.2% male) treated with either sofosbuvir/velpatasvir (n = 4583) or glecaprevir/pibrentasvir (n = 4583) or glecaprevir/pibrentasvir (n = 6172) were included in this multi-national analysis: 4950 from Germany, 4185 from Italy, and 1620 from Spain. Over one-half, 58.9% (6333/10, 755) received any comedication during their pDAA therapy, and 20.2% (2177/10, 755) were at risk of a DDI with their pDAA. In terms of multi-DDI risk, 566 patients were taking ≥2 comedications, each with a potential DDI with their pDAA. This represented 5.3% (566/10, 755) of the HCV patient population and 8.9% (566/6333) of patients receiving any comedication. Evaluation of predicted DDI impact revealed that approximately one-quarter (23.9%; 135/566) had a risk of increasing comedication, posing a potential safety risk. This was observed mainly in Germany and Spain. A further one-quarter of patients (26.5%; 150/566) had a risk of increasing comedication, posing a potential safety risk, mainly in cardiovascular drugs, such as statins, and nervous system drugs, such as antipsychotics.

**Conclusion:** Across Germany, Italy, and Spain, 8.9% of HCV patients taking medications concomitantly during their pDAA therapy are at risk of multiple DDIs. Accurate prediction of the impact of multiple DDIs on pDAA efficacy and safety is difficult; this should prompt a thorough pDDI assessment before HCV therapy in comorbid patients.
Use of comedication in patients with hepatitis C and addiction or drug abuse treated with direct-acting antivirals: implication in drug-drug interactions

Juan Turnes1, Antonio Garcia Herola2, Ramón Morillo Verdugo3, Marinelia Mendez Pertuz4, Cristina De Alvaro5, Candido Hernández6, Antoni Sicsas-Mainet7, 1CHU. Pontevedra, Gastroenterology and Hepatology Department, Pontevedra, Spain; 2Hospital Marina Baixa de Villajoyosa, Digestive Medicine Department, Alicant, Spain; 3Hospital de Valme, ACG Sur de Sevilla, Hospital Pharmacy, Sevilla, Spain; 4Gilead Sciences S.L., Madrid, Spain, Medical Affairs, Madrid, Spain; 5Gilead Sciences S.L., Madrid, Spain, Medical Affairs, Madrid, Spain; 6Gilead Sciences Europe Ltd, Global Medical Affairs, United Kingdom; 7Atrys Health, Health Economics and Outcomes Research, Barcelona, Spain

Email: ansicras@atryshealth.com

Background and aims: In previous studies we have analysed drug-drug interactions (DDIs) in the general population. In this sub-analysis we focus on patients with addiction to substance or drug abuse. The objective is to describe the drug use, comedication and the associated risk of drug interactions.

Method: Retrospective observational study, obtained from the BIG-PAC database (Atrys Health), on hepatitis C patients (pts) treated between 2017 and 2020. Possible DDIs with direct-acting antivirals (DAAs) (Sofosbuvir/Velpatasvir [SOF/VEL] and Gilecapersvir/Pibrentasvir [GLE/PIB]) were evaluated using the University of Liverpool Interactions for Hepatitis database. The risk of DDIs was analyzed, as well as their potential outcome: increase (↑) in comedication concentration or ↑ DAA (possible impact on safety) and decrease in DAA, ↓DAA (possible impact on efficacy).

Results: 985 pts with history or current consumption of abuse and recreational substances were included, 450 for SOF/VEL (mean age: 53 years; men 65%; F3/4 42%) and 535 with GLE/PIB (mean age: 50 years; men 65% F3/4 30%). The most consumed substances are described in the table, highlighting the higher consumption of opioids in pts treated with SOF/VEL vs GLE/PIB (13% vs 9%, p < 0.05, respectively).

The mean number of medications prescribed was 3.9 for SOF/VEL and 2.1 for GLE/PIB (p < 0.001). The most prescribed drugs belonged to the nervous system (40%); anti-infectives for systemic use (13%); cardiovascular (12%) and alimentary system (12%). GLE/PIB presented a higher percentage of potential DDIs than SOF/VEL with nervous system medication (8.5% vs 4.9%, p < 0.01) and cardiovascular (36.8% vs 13.7%, p < 0.001); and similar for alimentary system (45.4% vs 44.7%, ns) and anti-infectives (5.8% vs 6.9%, ns). The most prescribed nervous system drugs with potential DDIs were quetiapine and metamizole.

Table: Addition to substances or drug abuse for HCV patients treated with DAAs

<table>
<thead>
<tr>
<th>Study groups</th>
<th>SOF / VEL</th>
<th>GLE / PIB</th>
<th>Total</th>
<th>p</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of patients, %</td>
<td>450 (46.7%)</td>
<td>535 (54.3%)</td>
<td>985 (100%)</td>
<td></td>
</tr>
<tr>
<td>Addictions</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Chronic alcoholism</td>
<td>110 (24%)</td>
<td>105 (20%)</td>
<td>215 (22%)</td>
<td>0.068</td>
</tr>
<tr>
<td>Opioids</td>
<td>60 (13%)</td>
<td>47 (9 %)</td>
<td>107 (11%)</td>
<td>0.022</td>
</tr>
<tr>
<td>Sedative-anxiolytics</td>
<td>140 (31%)</td>
<td>136 (29%)</td>
<td>276 (28%)</td>
<td>0.048</td>
</tr>
<tr>
<td>Cannabis</td>
<td>108 (44%)</td>
<td>236 (44%)</td>
<td>345 (44%)</td>
<td>0.981</td>
</tr>
<tr>
<td>Cocaine</td>
<td>116 (26%)</td>
<td>142 (26%)</td>
<td>258 (26%)</td>
<td>0.785</td>
</tr>
<tr>
<td>Heroin</td>
<td>80 (18%)</td>
<td>77 (14%)</td>
<td>157 (16%)</td>
<td>0.148</td>
</tr>
</tbody>
</table>

Conclusion: In Spain, 9% of HCV patients with addictions to substance or drug abuse taking ≥2 comedication are at risk of multi-DDIs.

Use of comedication in patients with hepatitis C and addiction or drug abuse treated with direct-acting antivirals: implication in drug-drug interactions

Juan Turnes1, Antonio Garcia Herola2, Ramón Morillo Verdugo3, Marinelia Mendez Pertuz4, Cristina De Alvaro5, Candido Hernández6, Antoni Sicsas-Mainet7, 1CHU. Pontevedra, Gastroenterology and Hepatology Department, Pontevedra, Spain; 2Hospital Marina Baixa de Villajoyosa, Digestive Medicine Department, Alicant, Spain; 3Hospital de Valme, ACG Sur de Sevilla, Hospital Pharmacy, Sevilla, Spain; 4Gilead Sciences S.L., Madrid, Spain, Medical Affairs, Madrid, Spain; 5Gilead Sciences S.L., Madrid, Spain, Medical Affairs, Madrid, Spain; 6Gilead Sciences Europe Ltd, Global Medical Affairs, United Kingdom; 7Atrys Health, Health Economics and Outcomes Research, Barcelona, Spain

Email: ansicras@atryshealth.com

Background and aims: In previous studies we have analysed drug-drug interactions (DDIs) in the general population. In this sub-analysis we focus on patients with addiction to substance or drug abuse. The objective is to describe the drug use, comedication and the associated risk of drug interactions.

Method: Retrospective observational study, obtained from the BIG-PAC database (Atrys Health), on hepatitis C patients (pts) treated between 2017 and 2020. Possible DDIs with direct-acting antivirals (DAAs) (Sofosbuvir/Velpatasvir [SOF/VEL] and Glecaprevir/Pibrentasvir [GLE/PIB]) were evaluated using the University of Liverpool Interactions for Hepatitis database. The risk of DDIs was analyzed, as well as their potential outcome: increase (↑) in comedication concentration or ↑ DAA (possible impact on safety) and decrease in DAA, ↓DAA (possible impact on efficacy).

Results: 985 pts with history or current consumption of abuse and recreational substances were included, 450 for SOF/VEL (mean age: 53 years; men 65%; F3/4 42%) and 535 with GLE/PIB (mean age: 50 years; men 65% F3/4 30%). The most consumed substances are described in the table, highlighting the higher consumption of opioids in pts treated with SOF/VEL vs GLE/PIB (13% vs 9%, p < 0.05, respectively).

The mean number of medications prescribed was 3.9 for SOF/VEL and 2.1 for GLE/PIB (p < 0.001). The most prescribed drugs belonged to the nervous system (40%); anti-infectives for systemic use (13%); cardiovascular (12%) and alimentary system (12%). GLE/PIB presented a higher percentage of potential DDIs than SOF/VEL with nervous system medication (8.5% vs 4.9%, p < 0.01) and cardiovascular (36.8% vs 13.7%, p < 0.001); and similar for alimentary system (45.4% vs 44.7%, ns) and anti-infectives (5.8% vs 6.9%, ns). The most prescribed nervous system drugs with potential DDIs were quetiapine and metamizole.

Table: Addition to substances or drug abuse for HCV patients treated with DAAs

<table>
<thead>
<tr>
<th>Study groups</th>
<th>SOF / VEL</th>
<th>GLE / PIB</th>
<th>Total</th>
<th>p</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of patients, %</td>
<td>450 (46.7%)</td>
<td>535 (54.3%)</td>
<td>985 (100%)</td>
<td></td>
</tr>
<tr>
<td>Addictions</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Chronic alcoholism</td>
<td>110 (24%)</td>
<td>105 (20%)</td>
<td>215 (22%)</td>
<td>0.068</td>
</tr>
<tr>
<td>Opioids</td>
<td>60 (13%)</td>
<td>47 (9 %)</td>
<td>107 (11%)</td>
<td>0.022</td>
</tr>
<tr>
<td>Sedative-anxiolytics</td>
<td>140 (31%)</td>
<td>136 (29%)</td>
<td>276 (28%)</td>
<td>0.048</td>
</tr>
<tr>
<td>Cannabis</td>
<td>108 (44%)</td>
<td>236 (44%)</td>
<td>345 (44%)</td>
<td>0.981</td>
</tr>
<tr>
<td>Cocaine</td>
<td>116 (26%)</td>
<td>142 (26%)</td>
<td>258 (26%)</td>
<td>0.785</td>
</tr>
<tr>
<td>Heroin</td>
<td>80 (18%)</td>
<td>77 (14%)</td>
<td>157 (16%)</td>
<td>0.148</td>
</tr>
</tbody>
</table>

Conclusion: In Spain, 9% of HCV patients with addictions to substance or drug abuse taking ≥2 comedication are at risk of multi-DDIs.
Background and aims: We recently reported the first proof-of-concept clinical trial assessing in real-time the utility of response-guided therapy (RGT) with direct-acting antivirals (DAA) in chronic hepatitis C virus (HCV) infected patients, based on a mathematical modeling approach. The RGT modeling approach relies on measuring HCV at baseline and days 7 and 14 after initiation of DAA therapy. A simplified on-treatment viral load measurement is not necessary to predict treatment completion (TTC). Measuring HCV at baseline and days 7 and 14 after initiation of DAA therapy was sufficient to pick the optimal duration of treatment.

Method: The mathematical model used in the proof-of-concept study was re-fitted with the measured HCV kinetic data obtained from the 10 patients for whom the model was used to shorten the standard 12-week DAA therapy duration. The fitting procedure consisted of finding the best fits using corrected Akaike Information Criteria. The predicted time to cure (TTC) was defined as the time it takes during DAA therapy to reach less than 1 viral copy in the serum (i.e., $7 \times 10^{-5}$ copies/ml). The first data point below detection or lower limit of quantification (LLOQ) was assigned a value ($e_{0.2, 15}$ IU/ml) as done in the proof-of-concept study. We next removed either day 2 or day 7 from the 10 patients and repeated the same procedure projecting TTC. Modeling calibration was done using MATLAB R2021a.

Results: We first verified that fitting the model to all the measured data points measured in the proof-of-concept study were in agreement with the current modeling approach (Table 1). Excluding day 2 did not affect maximum TTC projections. TTC and TTC were significantly correlated ($r = 0.91, p = 0.0007$) with the predicted TTC based on all measured data points. Notably, while excluding day 2 caused potential non-identifiability in estimating HCV viral clearance from circulation, the estimation of TTC remained unaffected. In contrast, excluding day 7 would lead to overestimation of the maximum TTC projections ($r = 0.29, p = 0.45$) (Table 1).

Conclusion: The current analysis indicates that on-treatment day 2 viral load measurement is not necessary to predict TTC. Measuring HCV at baseline and days 7 and 14 after initiation of DAA therapy provides a simplified on-treatment monitoring procedure during modeling-based RGT. Further validation in a large-scale clinical trial, will support the routine implementation of our individualized treatment approach in patients receiving DAA for HCV.

Background and aims: Patients with hepatitis C virus (HCV) and hepatitis B virus (HBV) co-infection are at an increased risk of developing liver disease compared to mono-infected individuals. The Georgia Hepatitis C Elimination Program was established in 2015 and offers free treatment with direct-acting antivirals (DAA) to all persons with HCV infection. The program includes HBV screening for all HCV infected patients. We describe the epidemiology of HBV/HCV co-infection among patients treated within the HCV elimination program.

Method: Data for this analysis comes from the national electronic HCV elimination program treatment database. Persons aged ≥18 years with active HCV infection who initiated HCV treatment within the program during May 2015–September 2021 were included. Patients were grouped as HCV mono-infected, HCV/HBV coinfected (HBV surface antigen [HBSAg] positive), and HCV immune but not infected (HBV surface antibody or HBV core antibody positive, HBSAg negative). We present descriptive analysis and adjusted prevalence ratios (aPR) with 95% confidence intervals (CI) for HCV/HBV coinfection compared to HCV mono-infection for demographic, risk, clinical and treatment outcomes. aPRs were adjusted for age, sex, HCV genotype, and history of injection drug use in a multi-variable model.

Results: As of September 2021, 71,931 adult persons were treated for HCV and screened for HBV within the HCV elimination program in Georgia. The majority were 18–45 years old (48%; median age 46, interquartile range 39–55 years), male (78%), and did not report a history of injection drug use (57%). Overall, 70% (n = 50, 103) had HCV mono-infection, 28% (n = 2, 202) had HCV mono-infection and were immune to HBV, and 2% (n = 1, 626) had HBV/HCV co-infection. HBV/HCV co-infection was more common among persons who were 18–45 compared to 46–60 years old (aPR: 1.7, 95% CI: 1.5–2.0), male (aPR: 1.3, 95% CI: 1.1–1.6), reported a history of injection drug use (aPR: 1.3, 95% CI: 1.1–1.5), had serum end of treatment (EOT) ALT >80 U/L compared to <40 U/L (aPR: 2.3, 95% CI: 1.6–3.4), and did not achieve sustained virologic response (aPR: 1.4, 95% CI: 1.1–1.9).

Conclusion: HBV/HCV co-infection is associated with higher risk of liver disease, elevated EOTALT, and DAA treatment failure. To improve outcomes for patients with HBV/HCV co-infection, it is essential to evaluate them for HBV treatment. Promoting preventative measures, such as HBV vaccination among patients with HCV infection, is also important to reduce mortality from hepatitis.
**Background and aims:** Hepatitis B virus (HBV) reactivation may occur in chronic hepatitis C (CHC) coinfected patients using direct-acting antivirals (DAAs). However, previous studies have reported inconsistent findings on this issue. We investigated the association between DAA and HBV reactivation by conducting a meta-analysis.

**Method:** Relevant studies were identified by searching Medline, EMBASE, Cochrane Central Register of Controlled Trials, KoreaMed, KMbase, and RISS to September 4th, 2020. The primary outcome was HBV reactivation. Random effect method was used for pooling the data.

**Results:** We identified 39 articles, comprising 119,484 patients with chronic (n = 1,673) or resolved (n = 13,497) HBV infection who were treated with DAA. When all studies were pooled, the rate of HBV reactivation was 12% (95% confidence interval (CI) 0.06–0.19). When stratified by baseline HBV DNA, undetectable HBV DNA (HBV DNA <20 IU/ml) group showed significantly lower risk of reactivation compared to detectable HBV DNA group (odds ratio (OR) 0.30, 95% CI 0.11–0.86). Although patients on prophylactic anti-HBV therapy showed a lower reactivation rate, there was no significant difference (OR 0.27, 95% CI 0.07–1.01). The rate of HBV reactivation was only 0.4% in patients with resolved HBV infection.

**Conclusion:** The risk of HBV reactivation was not negligible in HCV coinfected patients using DAAs, indicating watchful attention for HBV reactivation is still needed.

**Key Words:** Direct-acting antivirals, hepatitis B virus, hepatitis C virus, reactivation

**FRI399**

**Inhibition of high fitness viruses by different antiviral strategies when the infection has started**

Carlos García-Crespo1, Lucía Vázquez-Sirvent1, Maria Eugenia Soria1, Isabel Gallego1, Ana Isabel de Ávila1, Brenda Martínez-González1,2, Esteban Domingo1,2, Celia Perales1,2,3, 1Centro de Biología Molecular Severo Ochoa, Department of Interactions with the environment, Madrid, Spain; 2Hospital Universitario Fundación Jiménez Díaz, Department of Clinical Microbiology, Madrid, Spain; 3Centro de Investigación Biomédica en Red de Enfermedades Hepáticas y Digestivas, Spain

Email: cperales@cbm.csic.es

**Background and aims:** Previous results from our laboratory have documented that high fitness hepatitis C virus (HCV) can be a determinant of multidrug resistance, including nucleotide analogues, without the acquisition of specific resistance mutations. However, we recently demonstrated using favipiravir (T-705) and ribavirin that analogue concentrations that individually did not extinguish high fitness HCV in ten serial infections, when used in combination led to extinction in a few passages. With these two nucleotide analogues, we have described for the first time a new synergy mechanism in lethal mutagenesis against HCV. Here we have investigated the effectiveness of these strategies once the infection has been initiated, as a stringent test of antiviral efficacy. Combinations of inhibitors and combinations of lethal mutagens were compared. Since new antiviral designs based on sequential inhibitor-mutagenic have proven effective for the extinction of RNA viruses, sequential versus combination therapies have been also examined for suppression of high fitness HCV infectivity once the infection was ongoing.

**Method:** Low and high fitness HCV populations were used to infect Huh-7.5 hepatoma cells in the absence and presence of mutagenic (ribavirin and favipiravir) and non-mutagenic (sofosbuvir and daclatasvir) antiviral agents. Treatment efficacy was analyzed by measuring virus progeny production when antivirals were administered at different times after infection. In addition, sequential and combination treatments were compared for the extinction these viruses.

**Results:** The results indicate that low and high fitness viruses were not extinguished by combinations of mutagenic antivirals once the infection is ongoing. Treatment efficacy was lower when time of infection increased. Sequential and combination therapies produced a similar inhibition, without achieving viral extinction.

**Conclusion:** The time at which antiviral agents were administered once the infection have been initiated influenced viral extinction independently of the mechanism of action of the antivirals (both
non-mutagenic and mutagenic agents). Also, the data reinforce that high viral fitness is a determinant of drug resistance independently of the type of therapy used (sequential and combination therapies). No significant differences were observed between both therapies for the extinction of high fitness HCV.

FRI400
Treatment of hepatitis C in primary healthcare in the country of Georgia
Tengiz Tservtadze1,2, Amiran Gamkrelidze2, Nikoloz Chkharthashvili1, Akaki Abutidze1, Lali Sharvadze2,4, Maia Butsashvili2, David Metreveli2, Lia Gvinjilja7, Tinatin Kuchuloria7, Shaun Shadaker6, Tamar Gabunia3, Ekaterine Adamia9, Stefan Ziezen10, Nezam Afshahi11, Sanjeev Arora12, Karla Thornton12, Paige A Armstrong12.

Background and aims: With technical assistance from the U.S. CDC and support from Gilead Sciences, Georgia launched the world’s first national hepatitis C elimination program in April 2015. By October 2021, more than 75 thousand persons initiated treatment, achieving >98% cure rates. Patient enrollment in hepatitis C virus (HCV) treatment sharply increased in 2016, but has since slowed due to challenges in HCV testing and linkage to care. To increase initiation of treatment, Georgia began service decentralization in 2018 by integrating HCV screening and treatment in primary healthcare centers (PHCs).

Method: By July 31 2021, a total of 10 PHCs were providing HCV care services throughout the country. The integrated model is based on “one stop shop” approach, where patients receive all HCV screening and care services in selected PHCs. Treatment naïve patients with no or mild fibrosis (FIB-4 score <1.45) receive care at PHCs and completed examinations according to a simplified diagnostic and treatment monitoring algorithm, and persons with FIB-4 score >1.45 were referred to specialized clinics. Patients received Sofosbuvir/Ledipasvir or Sofosbuvir/Velpatasvir for 12 weeks. Sustained virological response (SVR) was defined as undetectable HCV RNA 12–24 weeks after end of therapy. The Extension for Community Healthcare Outcomes (ECHO) telemedicine model was used to train and support primary healthcare providers. Regular teleECHO videoconferencing was conducted to provide primary care providers with advice and clinical mentoring.

Results: Among persons diagnosed with active HCV infection, 1, 454 were evaluated for FIB-4 score. A total of 954 patients initiated treatment, and of them 883 (92.6%) completed treatment. Of 864 patients eligible for SVR testing, 696 (80.6%) had been tested at the time of analysis, and 683 (98.1%) achieved SVR, yielding a >98% cure rate.

Conclusion: Our study reported the effectiveness of a simplified HCV treatment model in PHCs. Expanding this integrated decentralized model of HCV treatment nationwide would provide an opportunity to improve linkage to care and close gaps in the HCV cascade of care.

FRI401
Optimal screening and linkage to care model to achieve hepatitis C elimination targets in Georgia
Tengiz Tservtadze1,2, Amiran Gamkrelidze2, Nikoloz Chkharthashvili1, Akaki Abutidze1, Lali Sharvadze2,4, Vakhtang Kerashvili1, Manana Todoru2, Maia Butsashvili2, David Metreveli2, Lia Gvinjilja7, Tinatin Kuchuloria7, Shaun Shadaker6, Tamar Gabunia3, Ekaterine Adamia9, Stefan Ziezen10, Nezam Afshahi11, Sanjeev Arora12, Karla Thornton12, Paige A Armstrong12.

Background and aims: Access to care and treatment is essential to achieving hepatitis elimination, however, ensuring all patients can navigate the care pathway is challenging and involves multiple steps. Despite marked success of Georgia’s National Hepatitis C Elimination Program, with over 75, 000 persons initiating treatment April 2015–October 2021, since a peak in October 2016, patient enrollment in treatment has slowed. Developing an optimal model to ensure linkage-to-care at critical steps in the care cascade is paramount for the elimination program.

Method: We evaluated the effectiveness of various linkage-to-care modalities to assess diagnostic yield and engagement in hepatitis C virus (HCV) treatment. HCV care cascades for the period of March 2018–November 2020 were analysed and classified into 6 categories based on where the initial screening was performed: centralized and decentralized hospital sector, primary healthcare, harm reduction, specialized HCV provider sites and integrated HCV/HIV/TB screening locations. We defined linkage to care as: 1) completion of a viremia test after screening HCV antibody (anti-HCV) positive; and 2) establishment of a follow-up appointment for treatment with a hepatologist. Patients had the highest rate of viremia testing (63.6%), while the centralized hospital sector had the lowest rate of viremia testing (63.6%).

Conclusion: Our data suggest the HCV provider site screening model had been the most successful in linking persons to care, for both viremia testing and initiation of treatment. Universal inpatient screening has been effective at testing large numbers of people; among the hospital sector models, the decentralized approach to testing had higher rates of viremia testing and treatment. Decentralization of care is key to providing access to all, but the primary healthcare model showed the lowest rate of viremia testing in our study.

FRI402
Establishing a protocol for management and DAA treatment of HCV during pregnancy: adherence to a co-located care protocol
Tatyana Kushner1, Marcia Lange1, Rhoda Sperling1, Douglas T Dieterich1, 1Johns School of Medicine at Mount Sinai
Email: tatyana.kusher@mssm.edu

Background and aims: There are currently no recommendations for directly acting antiviral (DAA) therapy during pregnancy. Emerging
data suggests that DAAs are safe and effective during pregnancy. We evaluated our center experience in implementing DAA treatment during pregnancy.

**Method:** After establishment of a sub-specialty Women's Liver Clinic (WLC) co-located in the ambulatory obstetrics practice and implementation of universal antenatal HCV screening, we offered DAA treatment during pregnancy to women with active HCV. We evaluated adherence to each step in the HCV treatment cascade of care.

**Results:** Twenty-three pregnant women with active HCV infection were referred to WLC for consideration for HCV treatment; they were of median age 31 (IQR 24, 36); predominantly white (39%) non-Hispanic (52%), and medicaid-insured (78%); 30% with injection drug use as a risk factor; 9% who acquired HCV through perinatal transmission; 26% with no known risk factors. Fifteen (65%) reported that HCV was initially diagnosed during pregnancy. Adherence to cascade of care is shown in the Figure. Initial DAA ordered was ledipasvir/sofosbuvir for 7 (42%), ledipasvir/velpatasvir for 7 (42%) and glecaprevir/pibrentasvir for 2 (12%). Among those with DAA approval, nine (45%) received their DAA during pregnancy and seven (35%) initiated DAA treatment during pregnancy: eight (40%) initiated postpartum. Twelve (70%) had documented completion of DAA treatment; only 7 (35%) showed up to their SVR12 check; 6/7 who initiated treatment, 95 were available at the SVR12 time point to date. Of these, 88 achieved a cure. The main reasons an endpoint was not measured included 3 overdose-related deaths prior to SVR 12 time point and 4 disengaged from care. There were no cases of virologic failure or relapse.

**Conclusion:** Pregnancy offers an important opportunity to link women with HCV to treatment—the majority were diagnosed initially during routine screening during pregnancy. Cholestasis of pregnancy was a prevalent complication. HCV treatment during pregnancy is feasible and will likely offer benefits to maternal and child health, however significant challenges remain to ensure adherence through the vulnerable postpartum period. Similar to the management of the vulnerable postpartum period. Similar to the management of neonatal perinatal transmission, 26% with no known risk factors. Fifteen (65%) reported that HCV was initially diagnosed during pregnancy. Adherence to cascade of care is shown in the Figure. Initial DAA ordered was ledipasvir/sofosbuvir for 7 (42%), ledipasvir/velpatasvir for 7 (42%) and glecaprevir/pibrentasvir for 2 (12%). Among those with DAA approval, nine (45%) received their DAA during pregnancy and seven (35%) initiated DAA treatment during pregnancy: eight (40%) initiated postpartum. Twelve (70%) had documented completion of DAA treatment; only 7 (35%) showed up to their SVR12 check; 6/7 who initiated treatment, 95 were available at the SVR12 time point to date. Of these, 88 achieved a cure. The main reasons an endpoint was not measured included 3 overdose-related deaths prior to SVR 12 time point and 4 disengaged from care. There were no cases of virologic failure or relapse.

**FR1403**

**Sofosbuvir/Velpatasvir (S/V) for the treatment of HCV infection among vulnerable inner-city residents: the results of clinical trial**

Brian Conway1,2, David Truong1, Leo Yamamoto1, Rossitta Yung1, Shawn Sharma1, 1Vancouver Infectious Diseases Centre, Vancouver, Canada; 2Simon Fraser University, Burnaby, Canada

Email: biconway5538@gmail.com

**Background and aims:** The SIMPLIFY study demonstrated that sofosbuvir/velpatasvir (S/V) can be used to treat Hepatitis C Virus (HCV) infection among active drug users, achieving sustained virologic response (SVR) 12 rates comparable to those achieved in clinical trials enrolling other patient populations. There remains a need to replicate these results in more vulnerable populations, including those using fentanyl and not currently engaged in health care.

**Method:** Through dedicated outreach events, we identified HCV-infected patients who resided in single room occupancy dwellings who were not currently engaged in health care and who were eligible to receive government-funded antiviral treatment for HCV infection. We offered them the opportunity to enrol in a multidisciplinary program of care to address medical, psychological, social and addiction-related needs and provide S/V therapy in this context, with daily or weekly supervision of adherence, as appropriate. The endpoint of this preliminary analysis is the achievement of SVR12 in those who initiated therapy.

**Results:** We identified 172 eligible HCV-infected treatment-naïve subjects who were subsequently enrolled in the program. HCV diagnosis was documented 1–41 years before enrolment. Key demographic characteristics include: 126 (73%) male, median age 47 (23–75) years, F0/F1 (120, 70%), ≥F2 (52, 30%), opiate/cocaine/amphetamine use (126/66/112, 73%/38%/65%). Once enrolled in care, 38 (22%) initiated addiction care with opiate agonist therapy. Of 142 who initiated treatment, 95 were available at the SVR12 time point to date. Of these, 88 achieved a cure. The main reasons an endpoint was not measured included 3 overdose-related deaths prior to SVR 12 time point and 4 disengaged from care. There were no cases of virologic failure or relapse.

**Conclusion:** Through dedicated initiatives, it is possible to identify vulnerable inner-city residents who were previously diagnosed with HCV infection and had never been offered treatment for it. These initiatives, combined with dedicated programs to provide HCV treatment in an optimized manner, must be considered to achieve HCV elimination in this unique population.

**FR1404**

**High efficacy and safety of pan-genotypic direct-acting antiviral regimens in adolescents and children: a global systematic review to inform new World Health Organization recommendations**

Giuseppe Indolfi1, Sabrina Giometto2, Farah Malik3, Roger Chou4, Philippa Easterbrook5, Ersilia Lucenteforte6, 1Università di Firenze, Dipartimento Neurofarba, Firenze, Italy; 2Università di Pisa; 3UCI; 4Oregon Health & Science University; 5World Health Organization

Email: giuseppe.indolfi@meyer.it

**Background and aims:** The global hepatitis C virus (HCV) response has to date largely focused on adults who bear the greatest burden of morbidity and mortality. There had been less attention to addressing case-finding and treatment of the estimated 3.26 million HCV infected children and adolescents. The recent regulatory approval of two pan-genotypic regimens down to 3 years provides opportunity to extend treatment opportunities down to all children above 3 years. To inform new World Health Organization (WHO) guidelines, we undertook a systematic review and meta-analysis of treatment outcomes in adolescents and children down to 3 years based on the key pan-genotypic direct-acting antiviral (DAA) regimens.

**Method:** We searched two databases and key conference abstracts for studies from inception to August 2021 that evaluated three pan-genotypic DAA regimens in adolescents and children: sofosbuvir/daclatasvir, SOF/DCV, sofosbuvir/velpatasvir, SOF/VEL, glecaprevir/pibrentasvir, GLC/PIB) in HCV infected adolescents (12–18 years), older children (6–11 years) and young children (3–5 years). Randomised controlled trials (RCT), non-RCT, and prospective observational studies were eligible for inclusion. Key outcomes evaluated were attainment of sustained virological response (SVR12), any adverse events, and discontinuation. Estimates were pooled using random-effects models.

**Results:** 3 RCTS, 28 non-RCTs and 18 observational studies reported treatment experience in 167 young children (3–5 years), 472 older children (6–11 years), and 2228 adolescents (12–18 years). Across all
Effectiveness of pangenotypic retreatment of HCV infection after prior failure of pangenotypic therapies

Robert Flisiak1, Justyna Janocha-Litwin2, Anna Parfiennik-Kowerda1, Dorota Zarebska-Michaluk2, Marek Sitko2, Piekarska Anna3, Jolanta Bialkowska4, Dorota Dybowska5, Witold Dobracki3, Simon Krzysztof2, Aleksandra Murawska-Ochab6, Małgorzata Pawłowska7,8, Medical University of Białystok, Białystok, Poland; 8Medical University of Warsaw, Warszawa, Poland; 2Medical University of Białystok, Białystok, Poland; 3Medical University Wroclaw; 4Jan Kochanowski University Kielce; 5Jagiellonian University, Krakow; 6Medical University of Lodz; 7Ludwik Rydygier Collegium Medicum in Bydgoszcz Faculty of Medicine Nicolaus Copernicus University in Torun, Department of Infectious Diseases and Hepatology, Poland; 7MED-FIX Wroclaw; 8Voivodship Hospital, Kielce, Kielce
Email: robert.flisiak1@gmail.com

Background and aims: Pangenotypic therapies for HCV infections, although universal and highly effective, leave the risk of treatment failure. The aim of the analysis was to assess the effectiveness of pangenotypic re-treatment in patients with failure of previous treatment also with pangenotypic drugs; to our knowledge, the results of such real world experience studies have not been published so far.

Method: The analysis included patients selected from the EpiTer-2 database, a large retrospective, multicentre, national real-world database database, a large retrospective, multicentre, national real-world study evaluating DAA treatment during 2015–2021 in 14, 450 consecutive subjects with hepatitis C virus (HCV) infection.

Results: A total of 3, 985 patients were treated with pangenotypic regimens, of which 37 (0.9%) received them as retreatment after failure of prior pangenotypic therapy. This group was significantly dominated by males (78%), cirrhotics (49%) and genotype 3 infection (67%) compared to the general population of patients treated with pangenotypic regimens (54%, 21%, 29%, respectively). As shown in figure 1 primary glecaprevir/pibrentasvir (GP) based therapy was changed to velpatasvir/sofosbuvir (VS) based in 18, and VS to GP in 13 patients. In 6 patients, the same regimen was used, extending the duration of therapy or supplementing it with an additional drug (ribavirin (R), sofosbuvir (S), voxilaprevir (V)). The response rate at the end of treatment was 95%, while the overall SVR was 89%. There was no significant difference in SVR between patients retreated with GP (93%) and VS based regimen (87%), which included also two patients retreated with voxilaprevir (V). The response rate at the end of treatment was 95%, while the overall SVR was 89%. There was no significant difference in SVR between patients retreated with GP (93%) and VS based regimen (87%), which included also two patients retreated with voxilaprevir (V).

Conclusion: Overall, early DAA initiation (within 28 days) and late initiation (after 28 days) achieved similar SVR rates, although the early strategy reported 30% lower incidence of viremia. Early DAA initiation strategies reported a lower proportion of ACR than the delayed strategy, but this estimate was not statistically significant. On balance these results would support current guidelines recommending early treatment initiation, however randomized clinical trials may be required to more clearly define short-term responses and long-term clinical outcomes for these strategies.
Conclusion: We have demonstrated a high, almost 90% effectiveness of pangenotypic retreatment after failure of the primary pangenotypic therapy. Only men with cirrhosis, infected with genotype 3, did not eliminate HCV infection despite double pangenotypic treatment. We hope to provide data from more patients at the ILC.

FR1407
Infrequent hepatitis C genotypes/subtypes in patients treated with DAA-based regimens: successes and failures
Donald Murphy1, Isaac Ruiz2, Jean-Pierre Villeneuve2, Catherine Vincent2, Julian Hercum3, Daphna Fenyes3, Denis Marleau2, Helene Castel2, Julien Bissonnette2, Genevieve Huard2, Claire Fournier2, Jeanne-Marie Giard2, Daniel Corsilli3, Ziad Hassoun2, Philippe Willems2, Iris Soto2, Marc Bilodeau2, Bernard Willems2.

Background and aims: Patients with infrequent Hepatitis C virus (HCV) genotypes/subtypes are characterized by resistance–associated substitution (RAS) profiles that have been associated with lower sustained virological responses (SVR). Real-world data regarding efficacy of direct-acting antiviral (DAA)-based regimens are needed in order to optimize HCV therapy and to further support expert recommendations.

Method: A retrospective analysis of every patient referred to the CHUM was performed. Between 2014 and 2021, patients with an infrequent HCV genotype/subtype according to EASL guidelines definition were identified. Patients treated with at least 1 DAA-based regimen were included. Patients enrolled in clinical trials were excluded. Liver fibrosis was assessed by means of liver elastography or by histological evaluation of liver biopsy. SVR was defined as an undetectable HCV RNA 12 weeks after the end of treatment (SVR12). The choice of the DAA treatment regimen by genotype/subtype and the benefits of a rational approach based on RAS determination.

Results: Among the 801 patients of the cohort, 106 (13.2%) had an infrequent genotype/subtype. Among them, median age was 64 (17–96), 54 (50.9%) were male, 54 (50.9%) had F3-F4 fibrosis. SVR12 was 83.3% (10/12). One cirrhotic genotype 1d patient failed 2 one-DAA-based regimens (telaprevir (TPV)/pegylated interferon (pegIFN)/Ribavirin (RBV); sofosbuvir (SOF)/pegIFN/RBV) was successfully retreated with SOF/ledipasvir (LDV). One cirrhotic genotype 1k patient failed 4 DAA-based regimens (SOF/simeprevir (SIM); SOF/LDV 24/48 weeks; SOF/LDV/RBV). In a subgroup analysis of patients treated with a 2-last generation DAA (SOF/velpatasvir (VEL); SOF/VEL/RBV, glecaprevir (GLE)/pibrentasvir (PIB)), 50 patients were identified. SVR12 was 90.0% (45/50). Among the 106 treated patients, 6 were treated after liver transplantation. One patient presented with fibrosing cholestatic hepatitis. The SVR12 was 83.3% (5/6). A genotype 3b patient failed SOF/VEL for 12 weeks and was successfully retreated with SOF/VEL/voxilaprevir (VOX) for 12 weeks.

Conclusion: Our real-world data show that in patients with infrequent HCV genotypes/subtypes treated with 2 last-generation DAA the SVR rate is 90%. Although the data are limited, these results support the possibility of initially treating them with 2 last-generation DAA. More data are needed to determine optimal treatment regimen by genotype/subtype and the benefits of a rational approach based on RAS determination.

FR1408
Preemptive treatment with glecaprevir and pibrentasvir prevents HCV transmission from HCV viraemic donors to solid organ transplant recipients (single centre experience)
Sona Frankova1, Ondrej Vlklicky2, Veronika Pitova1, Janka Slatinska2, Jan Sperl1.

Background and aims: Organs from hepatitis C viraemic (HCV) donors were not used for transplantation in the past because the transmission of HCV infection to uninfected recipients used to be universal. Treatment of HCV infection in organ transplant recipients was complex and poorly effective before the introduction of direct-acting antiviral agents (DAA). More recently, the use of DAA for treatment of HCV infection has become a common practice. The aim of this study was to evaluate the efficacy of DAA-based regimens in patients infected with infrequent HCV genotypes/subtypes in a real-world cohort at the Centre hospitalier de l’Université de Montréal (CHUM), Liver Intensive Care Unit, Canada.

Method: A retrospective analysis of all patients treated at the CHUM was performed. Between 2014 and 2021, patients with an infrequent genotype/subtype according to EASL guidelines definition were identified. Patients treated with at least 1 DAA-based regimen were included. Patients enrolled in clinical trials were excluded. Liver fibrosis was assessed by means of liver elastography or by histological evaluation of liver biopsy. SVR was defined as an undetectable HCV RNA 12 weeks after the end of treatment (SVR12). The choice of the DAA treatment regimen by genotype/subtype and the benefits of a rational approach based on RAS determination.
acting antivirals (DAA) into clinical practice. Glecaprevir and pibrentasvir (GLE/PIB) represent a pan-genotypic anti-HCV DAA combination also approved for patients with severe renal impairment or on maintenance haemodialysis. The study aims to analyze the efficacy and safety of GLE/PIB combination as preemptive therapy of HCV infection when using grafts from HCV viremic donors.

**Method:** The solid organ transplant recipients, to whom an organ from HCV viremic donor was allocated, were given a single dose of GLE/PIB (300 mg/120 mg) 2–6 hours before transplant, followed by a once-daily administration for 12 weeks after transplantation, as recommended for liver and kidney transplant recipients by the manufacturer. HCV RNA levels were assessed weekly in the first four weeks post-transplant, in the treatment weeks 8 and 12, and 12 weeks after the cessation of therapy. The endpoints were negative HCV RNA levels at the end of treatment and 12 weeks post-treatment.

**Results:** Twelve organs (two liver and ten kidney grafts) from 3 HCV viremic cadaveric donors were allocated to 12 HCV uninfected recipients. All the recipients presented with an uncomplicated post-transplant course with the rapid development of graft function. None of the recipients presented with an acute rejection episode or severe graft dysfunction during the treatment and follow-up period. All the recipients completed the planned 12 weeks of preemptive antiviral treatment. None of them experienced an adverse event related to antiviral therapy or drug-drug interactions. HCV RNA was undetectable at all checked timepoints in all recipients. HCV infection was transmitted to none of the twelve recipients.

**Conclusion:** Preemptive treatment with GLE/PIB is safe and effective and allows the use of organs from HCV viremic donors, so far considered marginal, to uninfected recipients. Organ procurement from HCV viremic donors became a routine at our centre.

**FRI409**

**Hepatitis C care cascade challenges in the homeless population. A case by case model of delivering care**

Maria Guerra Veloz1, Khin Aye Wint Han1, Almuthana Mohamed1, Kathryn Oakes1, David Robertson1, Mary D. Cannon1, Ashley Barnabas1, Sital Shah1, Geoffrey Dusheiko1, Kosh Agarwala1.

1Institute of Liver Studies. King’s College Hospital, London, United Kingdom, London, United Kingdom

Email: maria.guerraveloz@nhs.net

**Background and aims:** Given the significant Hepatitis C Virus (HCV) burden, despite curative treatments, efforts focusing on the scaling up of testing and treatment in the homeless population are still needed. The aim of this project was to implement education and flexible onsite HCV incentivised testing, treatment and follow up for the homeless population and evaluate their rates of engagement, therapy initiation and cure in the South London area.

**Method:** This project was conducted by a multidisciplinary team from Jan 2018 to Sept 2021. A mobile unit “van” for onsite HCV education, flexible screening (InTec HCV Rapid Antibody Test, Cepheid GeneXpert RNA test, DBS or classic venipuncture), treatment and follow up was placed on the street in well-known homeless population areas. Homeless was defined as living in temporary- (hostel/hotel-based) or as being on the street or visiting daily soup kitchens across the area (street-based). Sociodemographic status, risk factors, comorbidities, concomitant medication, clinic data, the rates of treatment initiation and cure were recorded. Treatment adherence was defined as taking ≥75% of doses as self-reported by clients.

**Results:** 940 clients were identified as homeless and 933 (99.3%) participated. Of them 56.2% who were screened were street-based, 243 (26%) tested positive for HCV antibody and of these, 162 (67%) had detectable viremia. Clients with a positive HCV antibody had significantly higher rates of previous injection drug use (71.2 vs 8.6%), previous incarceration (12.3 vs 2.8%), previous HCV tests (28.8 vs 0.1%), as well as being active drug (36.2 vs 3.3%) and alcohol users (43.6 vs 5.2%) than those who were negative. HCV RNA positive clients had significantly more frequent psychiatric disorders, active drug use, active alcohol consumption, were on opioid substitution therapy, advanced fibrosis (23.5 vs 10%) and had lower rates of previous treatment in comparison with HCV RNA negatives (Figure 1c). The overall treatment initiation was 70.4% (114/162) and SVR 12 was 75.5% (83/110). In the multivariate analysis being screened in temporary housing (OR 2.755, 95%CI 1.356–5.600; p = 0.005) and having opioid substitution treatment (OR 2.288, 95%CI 1.041–5.026; p = 0.039) were positively associated with treatment initiation. HCV treatment adherence (OR 25.05, p < 0.001) was the only factor associated with achieving SVR.

**Conclusion:** Promoting education and having flexible onsite-testing and treatment for HCV in the homeless population improves their engagement with the healthcare system, leading to higher rates of treatment initiation and SVR. However, street based homeless people who are not linked with harm reduction services are less likely to initiate HCV treatment, highlighting that there is an urgent need for a broad health inclusion system.
Background and aims: The once-daily, oral, fixed-dose, direct-acting antiviral combination of glecaprevir/pibrentasvir (G/P) is indicated for chronic hepatitis C (CHC) infection with HCV genotypes 1–6 in patients with or without compensated cirrhosis (CC). Treatment duration of 8 weeks is recommended in most cases. Recent retrospective data from Taiwan revealed that G/P treatment resulted in high SVR12 rates according to label recommendations, comparable to those reported in the pivotal clinical trials. To further validate the data in the real-world setting, this study investigated effectiveness and safety of 8-week G/P therapy in treatment-naïve (TN), CC patients, with an emphasis on those with advanced liver disease in TAIL HCV Registry (TACR).

Method: The TACR is an ongoing nationwide registry program organized and supervised by Taiwan Association for the Study of the Liver (TASL), which aims to setup a database and biobank of patients with CHC in Taiwan. Data were analyzed as of 31 October 2021 for patients treated with G/P for TN, CC patients. In this analysis, effectiveness reported as sustained virologic response at 12 weeks post-treatment (SVR12) was assessed by modified intent-to-treat (mITT) populations that excluded patients who lost to follow-up, underwent treatment and/or traced SVR12 data. Safety profile was assessed in the ITT population.

Results: Of 806 TN, CC patients treated with G/P, 301 patients received 8-week regimen (ITT), and 275 of which had SVR12 data available (mITT). Of the 301 ITT population, mean age was 63.0 years, 53.8% were male, 27.2% were with chronic kidney disease and 2.3% were coinfection with human immunodeficiency virus. The overall SVR12 rate was 98.2% (270/275) in the mITT population. For selected special patients groups including patients with HCV genotype 3 (GT3), platelets counts  < 150,000/μl, FibroScan > 20 kPa, or both platelet counts < 150,000/μl and FibroScan > 20 kPa, the SVR12 rate was 100% (6/6), 98.0% (144/147), 100.0% (12/12) and 100.0% (7/7), respectively. Overall, 24.9% (75/301) of the patients experienced adverse events (AEs) in the ITT population. Seven patients (2.3%) experienced serious adverse events and two (0.7%) resulted in permanent drug discontinuation. None of them were considered as treatment drug related. The most frequent AEs (>5%) were fatigue (9.0%) and pruritus (7.0%). Laboratory data including international ratio of prothrombin time, total bilirubin, alanine aminotransferase, aspartate aminotransferase and albumin significantly improved after HCV eradication at SVR12.
In this real-world Taiwanese cohort, 8-week G/P therapy was well-tolerated in TN, CC patients. SVR12 rates were similarly high as in the clinical trials, including those with characteristics of advanced liver disease.

FR411
Reported safety of HCV direct-acting antivirals with opioids: 2017 to 2021
Anthony Martinez1, Tipu Khan2, Doug Dylla1, John Marcincak3, Michelle Collins3, Brad Saget3, Brian Conway4, 1State University of New York, Buffalo, New York, United States; 2Ventura County Medical Center, Ventura, United States; 3AbbVie Inc, United States; 4Vancouver Infectious Diseases Centre, Canada
Email: adm35@buffalo.edu

Background and aims: As a result of disengagement in addiction care during the COVID-19 pandemic, there has been a record increase in mortality associated with opioid overdoses (primarily fentanyl), particularly in North America. In the USA there were over 100,000 overdose deaths in 2021, while over 2000 were recorded in the province of British Columbia. As we attempt to develop novel ways to increase HCV treatment following ≥30% declines during the pandemic, we evaluated publicly available adverse events (AEs) reports for opioids and DAAs to assess whether safety concerns from potential drug interactions are warranted, particularly amongst those using fentanyl.

Method: Data were downloaded from the US Food and Drug Administration (FDA) Adverse Event Reporting System (FAERS) Public Dashboard. AEs with the DAAs glecaprevir/pibrentasvir (G/P), sofosbuvir/velpatasvir (SOF/VEL), ledipasvir/sofosbuvir (LDV/SOF), sofosbuvir/velpatasvir/voxilaprevir (SOF/VEL/VOX), and elbasvir/grazoprevir (EBR/GZR) listed as the suspect product were analyzed with an initial reporting period from July 28, 2017-December 31, 2021, as were opioid-associated AEs for all 2017–2021. Subsequently, AEs were counted based on listed concomitant use of opioids (fentanyl, oxycodone, hydrocodone), or overdose outcomes irrespective of concomitant opioid use. Data are descriptive without any statistical analyses.

Results: In the reporting period, 40 total AEs were recorded with concomitant DAA and fentanyl use, 14 resulting in death (G/p = 3, SOF/VEL = 11; Table 1); 626 total AEs were recorded with concomitant DAA and oxycodone or hydrocodone use, 28 resulting in death. Separately, overdose events were reported 186 times, 32 resulting in death. The number of overdoses declined each year from 2018 (N = 56) to 2021 (N = 29). Fentanyl AEs showed no trend year to year.

Conclusion: With the limitations of FAERS data (under or duplicate reporting, inability to establish causation or incidence), these data show that among ~58,000 fentanyl, ~189,000 oxycodone, and ~100,000 hydrocodone AEs reported to FAERS since 2017, a small proportion (<0.1%) have been reported in association with concomitant DAA therapy, with no association between recorded events and a specific DAA regimen. This should reassure HCV treaters on a lack of safety signal for concomitant opioid and DAA use.

Table 1: FAERS AEs and deaths with opioids and with concomitant HCV DAAs.

<table>
<thead>
<tr>
<th>AEs</th>
<th>Overdose AEs</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fentanyl deaths</td>
<td>Oxycodone/ Hydrocodone AEs</td>
</tr>
<tr>
<td>(N=29, 850)</td>
<td>(N=290, 224)</td>
</tr>
<tr>
<td>All DAAs</td>
<td>40</td>
</tr>
<tr>
<td>GP</td>
<td>13</td>
</tr>
<tr>
<td>SOF/VEL</td>
<td>22</td>
</tr>
<tr>
<td>LDV/SOF</td>
<td>3</td>
</tr>
<tr>
<td>SOF/VEL/VOX</td>
<td>0</td>
</tr>
<tr>
<td>EBR/GZR</td>
<td>2</td>
</tr>
</tbody>
</table>

*N represents the sum of fentanyl, oxycodone, and hydrocodone overdose AEs and deaths, whereas n’s for DAA overdose AEs and deaths are irrespective of concomitant opioids.

FR414
Impact of the presence of the infectious disease specialist in addiction services (SerD) as a point-of-care to meet WHO goal of HCV eradication
Chiara Fanelli1, Elijia Princic1, Andrea De Vito1, Claudia Marcia1, Giordano Madeddu1, Sergio Babudieri1, Ivana Rita Maida1, 1University of Sassari, Department of Medical, Surgical and Experimental Sciences, Sassari, Italy
Email: chiarfan@hotmail.it

Background and aims: The World Health Organization (WHO) aim for Hepatitis C virus (HCV) elimination by 2030 appears to be threatened by most patients remaining undiagnosed, despite the availability of effective and safe antivirals. The main reservoir of HCV is represented by people who inject drugs (PWIDs). This study aimed to assess the crucial role of the infectologist at the Addiction Services (SerDs) and its potential as a linkage to care of PWID HCV carriers.

Method: This retrospective study compares the number of new diagnoses and treatments among PWIDs before and after the introduction of an infectologist at SerDs Point of Care of Sassari, Italy. Data were collected from February 2015 to August 2020. The watershed day was the 1st of May 2019, when the infectologist was integrated in the personnel of SerD. Logistic regression analysis was performed to assess the relationship between variables before and after the introduction of the infectologist.

Results: From February 2015 to August 2020, 901 users took advantage of at least one dose of under opiate substitution treatment (OST) at the SerDs of Sassari, Italy. In total, 419 users (46.5%) underwent HCV-screening test, of which 333 (79.47%) tested positive and 191 taken in charge by the infectologist. Of 157 patients with detectable HCV-RNA, 138 (87.89%) started HCV treatment. Comparing the group treated with Direct-acting Antiviral Agents (DAA) before and after May 2019, a statistical significance was found in age (p = 0.0018) and diagnose-to-treatment prescription time (p < 0.001). When comparing PWIDs taken in charge by the infectologist of Sassari, Department of Medical, Surgical and Experimental Sciences, Sassari, Italy, and those before introduction of a SerD, Logistic regression analysis was performed to assess the relationship between variables before and after the introduction of the infectologist.
Ankita Kaushik 2, Nate Smith 3, Fadoua El-Moustaid, and more recently, Grazoprevir/Elbasvir. All were considered cured by achieving virological response 12 weeks post-treatment.

Conclusion: Our encouraging data is a result from an optimized partnership between the healthcare team in prisons and our hospital, allowing a fast diagnosis, an agile disease staging and adequate treatment, minimizing future risk of transmission and taking us closer to eliminating the infection by 2030.

FRI416

Real-world value and innovation of direct-acting antivirals for the treatment of chronic hepatitis C at Kaiser Permanente Southern California

Lisa Nyberg 1, Ankita Kaushik 2, Nate Smith 3, Fadoua El-Moustaid 3, Anders Nyberg 3, Su-Jau Yang 4, Kevin Chiang 5, Alon Yehoshua 2, Kaiser Permanente Hepatology Research, San Diego, United States; 2Gilead Sciences, Inc., Foster City, United States; 3Maple Health Group, New York, United States; 4Kaiser Permanente Research and Evaluation, Pasadena, United States; 5Kaiser Permanente Pharmacy Analytical Services, Downey, United States

Email: alon.yehoshua@gilead.com

Background and aims: Direct-acting antivirals (DAAs) have been a breakthrough therapeutic innovation in the treatment of chronic hepatitis C virus (HCV) with high efficacy rates and excellent safety and tolerability profiles. The objective of this study was to assess the long-term health and economic benefits associated with direct-acting antivirals (DAAs) vs. no treatment in the Kaiser Permanente Southern California (KPSC) healthcare delivery system.

Method: A hybrid decision-tree and Markov model was used to evaluate the long-term health and cost outcomes associated with treating HCV patients with DAAs (either sofosbuvir/velpatasvir [SOF/VEL] or ledipasvir/sofosbuvir [LDV/SOF]) vs. no treatment in the KPSC setting. A cohort of 7, 255 HCV patients, based on the total number of DAA-treated patients from 2014 to 2019, with an average age of 59 years was simulated over a lifetime (50 year) horizon. Demographic data included baseline distributions of genotype, cirrhosis, prior treatment/naive, and mix of DAAs. Treatment efficacy by subpopulation was determined from a secondary, real-world, database analysis of HCV patients in the KPSC setting. Utility values, transition probabilities, and health state costs were sourced from published literature, prioritizing data from the KPSC setting where possible. Treatment costs based on wholesale acquisition costs were sourced from publicly available databases. The model considered only direct medical costs, presented in 2021 USD.

Results: Approximately 78% of patients were treated with LDV/SOF and 22% with SOF/VEL in the DAA scenario. DAAs use led to a reduction of 3, 179 cases of compensated cirrhosis (−98%), 3, 318 cases of decompensated cirrhosis (−96%), 646 cases of hepatocellular carcinoma (−80%), 447 cases of liver transplants (−86%), and 2, 738 events of liver-related mortality (−86%) as compared to no treatment. In the DAAs scenario, life-years, and quality-adjusted life-years (QALYs) improved by +25% (+3.21 LYs) and +36% (+3.53 QALYs) vs. the no-treatment scenario. DAAs use led to a considerable change in public health.

Conclusion: Eliminating hepatitis C virus infection in prisons: 7 years of experience

Frederico Duarte 1, Luís Manuel Moura 1, Clara Batista 1, Ricardo Correia de Abreu 1, Isabel Neves 1, 1Unidade Local de Saúde de Matosinhos, Infectious Diseases, Matosinhos, Portugal

Email: frederico.duarte@gmail.com

Background and aims: Hepatitis C virus (HCV) infection is a major global health problem. The micro-elimination approach implies reaching specific populations, like people living in prisons. The introduction of direct-acting antiviral agents (DAAs) allowed a considerable change in public health.

Between 2015 and 2022 we identified 118 inmates with positive HCV infection undergoing treatment with DAAs since their availability in our healthcare unit.

Method: The authors describe the epidemiological, clinical, analytical and imaging data of inmates with confirmed HCV infection undergoing treatment with DAAs since their availability in our healthcare unit.

Results: The 79 inmates with confirmed HCV infection (51 men, 28 women) showed an average of 42 years [24–72 years], 11 years of known infection [1–30 years] and 85% had intravenous drug use in the past. HCV genotypes distribution: 1–48%; 3–30%; 4–22%. Liver fibrosis stages ranged from 4 to 6 kPa (F0–F2 85%, F3–F4 15%). All the 79 patients were initially treated with Sofosbuvir/Ledipasvir and Ombitasvir with or without ribavirin (according to criteria defined in initial protocols) and more recently, Grazoprevir/Elbasvir and pangenotypic drugs, namely Sofosbuvir/Velpatasvir, and Glecaprevir/Pibrentasvir. The 79 inmates with confirmed HCV infection (51 men, 28 women) showed an average of 42 years [24–72 years], 11 years of known infection [1–30 years] and 85% had intravenous drug use in the past. HCV genotypes distribution: 1–48%; 3–30%; 4–22%. Liver fibrosis stages ranged from 4 to 6 kPa (F0–F2 85%, F3–F4 15%). All the 79 patients were initially treated with Sofosbuvir/Ledipasvir and Ombitasvir with or without ribavirin (according to criteria defined in initial protocols) and more recently, Grazoprevir/Elbasvir and pangenotypic drugs, namely Sofosbuvir/Velpatasvir, and Glecaprevir/Pibrentasvir. All were considered cured by achieving virological response 12 weeks post-treatment.

Conclusion: Treating patients with DAAs resulted in a reduction in HCV-related morbidity and mortality and significant improvement in QALYs. Furthermore, use of DAAs was dominant (less costly and more effective) as compared to no treatment offering cost-savings within 3 years post-treatment. These findings highlight the substantial value of DAA treatment offered to HCV patients.
Abstract withdrawn

FR418
Treatment options for hepatitis C in pregnancy: a systematic review of the evidence and future research needs
Neil Gupta1, Lindsey Hiebert1, Carolyn Wester2, Paige A Armstrong1,2.
1 Task Force for Global Health, Coalition for Global Hepatitis Elimination, United States; 2 US Centers for Disease Control and Prevention, Division of Viral Hepatitis, United States
Email: ngupta-consultant@taskforce.org

Background and aims: Treatment for hepatitis C virus (HCV) infection during pregnancy has the potential to substantially increase HCV treatment coverage and prevent mother-to-child transmission. Although direct-acting antiviral (DAA) medications for the treatment of HCV infection have demonstrated excellent safety and efficacy in non-pregnant persons, HCV treatment is not recommended in pregnancy due to a lack of safety data. We assessed the published literature for information on treatment options for HCV infection in pregnancy, including linkage to care and treatment during pregnancy.

Method: We conducted a systematic literature review in PubMed for articles published in English from January 1, 2013–July 1, 2021. We searched using MESH and non-MESH equivalent search terms for “Hepatitis C virus” AND “pregnancy” AND “treatment” OR “direct-acting antivirals.” All articles were reviewed and thematically coded by dual reviewers.

Results: Overall, 486 articles were identified, of which 219 were included as relevant with full-text available. Of these, 118 contained results of primary research and 101 were secondary research. Of the 118 primary research articles, most focused on outcomes of HCV vertical transmission in infants (n = 28, 23.7%), HCV screening results (n = 25, 21.2%), epidemiology of HCV (n = 19, 16.1%), and cost-effectiveness or policies for HCV testing (n = 19, 16.1%). Fourteen (11.9%) assessed linkage to care or follow-up for persons who tested HCV positive. Five (4.2%) studies described results of DAA exposure in pregnancy. This included one prospective trial that reported minor (grade I/II) adverse events in 4 out of 9 participants, one retrospective study that reported no adverse events among 100 participants, one case study with no reported adverse events, and 2 clinical trials that reported DAA discontinuation due to pregnancy in 6 enrolled participants (no clinical outcomes reported). Of the 101 studies without primary research, 13 explicitly included the possibility of HCV treatment during pregnancy.

Conclusion: Despite a substantial body of literature on HCV infection in pregnancy, there are very few reports on maternal linkage to HCV treatment and extremely limited data regarding the safety or effectiveness of DAA treatment in pregnancy. To improve the evidence base on HCV treatment in pregnancy, additional approaches are needed to collect and report relevant data. In response, the Coalition for Global Hepatitis Elimination, with support from the US Centers for Disease Control and Prevention, developed the first clinical case registry to record maternal and infant outcomes for persons exposed to DAAs during pregnancy (“TiP-HepC” Registry). The TiP-HepC registry, in complement to clinical studies and other real-world experiences, will provide urgently needed data to inform optimal treatment options for HCV in pregnancy.
Background and aims: Primary sclerosing cholangitis (PSC) is a chronic inflammatory disorder of the biliary ducts, which leads to fibrosis and predisposes to cholangiocellular carcinoma. Although the exact pathogenesis of PSC remains unclear, proinflammatory CD4+ immune cells seem to play a pivotal role. Current treatment options are limited but over-activation of STATs (Signal Transducers and Activators of Transcription protein) was observed in CD4+ patients with PSC than in healthy controls (66.1 ± 4.6% in IFN-gamma + options are limited but over-activation of STATs (Signal Transducers and Activators of Transcription protein) was observed in CD4+ immune cells and linked to disease activity in various autoimmune diseases. Thus far, activation of STATs has been poorly studied in PSC.

Method: Using multicolor flow cytometry we analyzed activation of STAT1 and STAT3 at baseline and after in vitro stimulation with recombinant IL-6 and IFN-gamma in immune cells from peripheral blood (PBMC) and from biliary tissue specimens collected by endoscopic retrograde cholangiopancreatography (ERCP) from patients with PSC. In addition, we measured soluble factors in serum and bile via bead-based immunoassay and compared results to healthy controls.

Results: Serum levels of IL-6 (mean ± SEM; 62.1 ± 28.1 pg/ml, p = 0.0279), IFN-gamma (26.7 ± 11.7 pg/ml, p = 0.0082) and IL-17A (9.1 ± 3.0 pg/ml, p = 0.0356), were higher in PSC patients than in healthy controls (IL-6; 10.5 ± 3.6 pg/ml; IFN-gamma: 6.1 ± 2.9 pg/ml; IL-17A: 2.7 ± 1.1 pg/ml). Of note, in PSC patients, inflammatory cytokines were conspicuously higher in bile than in serum. Unlike phospho-STAT1, which was refractory to IFN-gamma and IL-6 stimulation, activation with recombinant IL-6 lead to higher frequencies of phospho-STAT3-positive cells in the IFN-gamma+ (80.2 ± 2.3%, p = 0.0055) and IL-17A+ CD4+ T cell subsets (79.0 ± 2.4%, p = 0.0197) in patients with PSC than in healthy controls (66.1 ± 4.6% in IFN-gamma+ and 68.4 ± 4.1% in IL-17A+ CD4+ T cells). Frequencies of phospho-STAT3-positive cells in the IFN-gamma+ and IL-17A+ CD4+ T-cell subsets were higher in bile duct tissue (from ERCP) when compared to peripheral blood (Fig. 1). Finally, the pan-Jak inhibitor baricitinib dose-dependently reduced IFN-gamma- and IL-17A-secretion of mitogen-stimulated PBMCs from PSC patients in vitro.

Conclusion: Patients with PSC exhibit increased phospho-STAT3 induction in pro-inflammatory CD4+ T cells from blood and bile duct tissue, suggesting enhanced responsiveness of the STAT3 pathway in PSC. Although the cause of STAT3 over-responsiveness in PSC remains to be elucidated, targeted STAT3 inhibition may offer a novel approach to modify the course of PSC.
**FR453**

Magnesium accumulation by CNNM4 GalNAc-siRNA mediated silencing reduces cholestasis-associated liver fibrosis

Marina Serrano-Macia1, Naroa Goikoetxea2, Rubén Rodríguez Agudo2, Miren Bravo4, Sofía Lachiondo-Ortega2, Marcos Fernandez Fondevila1, Petar Petrov1,2,4, Irene González-Recio2, Maria Mercado-Gómez2, Claudia Gil-Pitarqu2, Marta Romero6, Teresa Cardoso Delgado2, Luis Alfonso Martinez-Cruz2, Ruben Nogueiras3, Cesar Martin6, Piotr Milkiewicz7, Malgorzata Milkiewicz8, Ute Schaeper1,10, Daniela Bucella11, Jose Juan G. Marín1,3, Jorge Simón Espinosa1,4, María Luz Martínez-Chantar1,4, 1CIC bioGUNE-Centro de Investigación Cooperativa en Biociencias, Liver Disease Lab, Derio, Spain; 2CIC bioGUNE-Centro de Investigación Cooperativa en Biociencias, Liver Disease Lab, Derio, Spain; 3CIMUS-Centro Singular de Investigación en Medicina Molecular y Enfermedades Crónicas, Molecular Metabolism Lab, Santiago de Compostela, Spain; 4Carlos III National Health Institute, Centro de Investigación Biomédica en Red de Enfermedades Hepáticas y Digestivas (CIBERehd), Madrid, Spain; 5Instituto de Investigación Biomédica de Salamanca, Experimental Hepatology and Drug Targeting (HEVEFARM), Salamanca, Spain; 6Campus De Bizkaia-Campus of Biscay, Instituto Biofisika, Lejona, Spain; 7Medical University of Warsaw, Liver and Internal Medicine Unit, Warszawa, Poland; 8Pomeranian Medical University, Department of Medical Biology, Szczecin, Poland; 9Silence Therapeutics GmbH, Berlin, Germany; 10Silence Therapeutics GmbH, Berlin, Germany; 11New York University, Department of Chemistry, New York, United States

**Background and aims:** Primary biliary cholangitis (PBC) and primary sclerosing cholangitis (PSC) are progressive diseases that eventually culminate in cirrhosis and related complications, as liver failure or portal hypertension among others. However, cholestasis is commonly present in these patients. Hepatocytes are adversely affected by the accumulation of bile acids and trigger inflammatory and cell death responses leading to development of fibrosis. Magnesium is known to play an important role in inflammatory and immune responses. Since magnesium distribution can be modulated by silencing Cnnm4 in disease progression was characterized in an in vitro cholestasis model was set up by incubating primary hepatocytes with supraphysiological concentrations of glycodeoxycholic acid (GCDCA). Animal models of cholestasis were generated by bile-duct ligation (BDL) for 14 days and by the use of mice lacking Mdr2 (Mdr2-/-) at 3, 5 and 8 months of age. The functional role of CNNM4 in disease progression was characterized in an in vitro and in vivo models of cholestasis via GalNAc-siRNA mediated silencing approach.

**Results:** CNNM4 upregulation was detected in liver samples of patients with PBC and PSC. Furthermore, we found that CNNM4 expression was enhanced in mice that underwent BDL and in mice lacking Mdr2. GalNAc-siRNA mediated silencing of CNNM4 protected primary mouse hepatocytes from GCDCA-induced cell death, mitochondrial dysfunction, oxidative stress and endoplasmic reticulum stress. In rodent models for cholestasis, GalNAc CNNM4 siRNA treatment protected the liver from fibrotic development and inflammation. Silencing Cnnm4 in hepatocytes induced intracellular magnesium accumulation, which may protect these cells by affecting the bile acid homeostasis.

**Conclusion:** CNNM4 has been identified as a potential novel therapeutic target for bile acid-induced liver damage. Herein, we show evidence that silencing CNNM4 by a GalNAc siRNA-approach could also be a novel effective approach for treatment of cholestasis-associated liver fibrosis.

---

**FR454**

Association of bile acids composition and synthetic pathway with therapeutic effect of bezafibrate in chronic cholestatic liver disease

Manami Iida1, Atsuko Higashide2, Shuichi Ohtomo1, Naoshi Horibua1, Atsushi Tanaka3, 1Chugai Pharmaceutical Co., Ltd., Japan; 2Chugai Research Institute for Medical Science, Inc., Japan; 3Teikyo University School of Medicine, Medicine, Japan

**Background and aims:** While ursodeoxycholic acid (UDCA) and bezafibrate (BZF) are therapeutic options in primary biliary cholangitis (PBC) and primary sclerosing cholangitis (PSC), there are treatment resistance cases that do not respond to the combination. Here, we investigated the mechanism of UDCA + BZF treatment resistance in terms of the bile acid composition and synthesis pathway in patients with PBC and PSC.

**Method:** The subjects were PBC and PSC patients as well as control patients whose liver function test values were all within the normal limits. Fasting plasma was collected and the plasma levels of various bile acids, 7a-hydroxy cholesterol (7a-HC), 27-hydroxy cholesterol (27-HC), and C4 were measured by liquid chromatography-tandem mass spectrometry. In addition, various clinical test values tested on the same day and therapeutic agents were collected. The relationship between bile acid composition and synthetic pathway, UDCA and BZF treatment, and liver function tests was examined.

**Results:** Patients with PBC (n = 30, all females, mean age 67 yrs, UDCA/BZF administration: 26/8, PSC (n = 10, male/female = 7/3, mean age 44 yrs, UDCA/BZF administration: 10/5), and control patients (6 chronic hepatitis B, 23 chronic hepatitis C, 1 dyslipidemia, M/F = 16/14, 70% age 66 yrs, UDCA/BZF administration: 3/0) were enrolled in the study. The plasma level of UDCA-related bile acids were high in PBC/PSC, reflecting UDCA administration. Furthermore, GCA, TCA, and TCDCA were higher in PBC/PSC than those in the controls, and the concentrations of these three types of bile acids were significantly correlated with the liver enzymes and bilirubin levels. In terms of the bile acid synthetic pathway, 27-HC was positively correlated with liver enzyme levels, and 27-HC was high in cases with elevated liver enzymes. In relation to BZF administration, BZF-administered PBC/PSC cases (PBC 8, PSC 5) had significantly lower values of 7a-HC and C4 and higher 27-HC than non-administered cases (PBC 22, PSC 5) (Figure).

**Conclusion:** GCA, TCA, and TCDCA were higher in treatment-resistant PBC/PSC cases with elevated liver enzymes. In addition, 27-HC was elevated, suggesting that the alternative pathway was activated in these treatment resistant cases. In the BZF-administered cases, 7a-HC and C4 levels were low (Figure), indicating that Cyp7a1 was suppressed and the classical pathway was suppressed as previously reported. On the other hand, 27-HC was not decreased and the alternative pathway was not suppressed, irrespective of liver enzyme levels (Figure). Taken together, BZF treatment failed to inhibit the alternative pathway of bile acids which were activated in cases with elevated liver enzymes, possibly, in part, explaining the mechanism of treatment resistance.
Reduced hepatic expression of PPAR alpha in primary biliary cirrhosis is modulated by miR-155
Monika Adamowicz1, Agnieszka Kempińska-Podhorodecka1, Joanna Abramczyk1, Jesus María Banales2, Piotr Milkiewicz3, Małgorzata Milkiewicz1,1Pomeranian Medical University, Department of Medical Biology, Szczecin, Poland; 2Biodonostia Health Research Institute, Department of Liver and Gastrointestinal Diseases, Donostia University Hospital, Ikerbasque, CIBERehd, San Sebastian, Spain; 3Medical University of Warsaw, Liver and Internal Medicine Unit, Warsaw, Poland
Email: monika.adamowicz@pum.edu.pl

Background and aims: Peroxisome proliferator-activated receptor alpha (PPARα) regulates expression of multiple genes involving lipid metabolism, bile acids (BA) homeostasis, and shows protective effects against inflammation and apoptosis. Progressive diseases such as primary biliary cirrhosis (PBC) and primary sclerosing cholangitis (PSC) result in intrahepatic retention of toxic BA that may lead to liver dysfunction and failure. Small non-coding RNA molecules (miRNAs) regulate gene expression, and miR-155 was associated with silencing of PPARα. Since PPARα activation decreases inflammation and fibrosis we evaluated PPARα and miR-155 expressions in cholestatic livers. We have also analyzed the regulatory effect of miR-155 on PPARα expression in vitro.

Method: Liver samples were taken from biopsies at early stages (F1-F2) of PBC (n = 12) or from explanted livers in patients with cirrhotic PBC (n = 11) and PSC (n = 17). The functional role of miR-155 was characterized in vitro in hepatocytes (HepG2) and primary cholangiocytes (NHC) where overexpression of miR-155 was induced by mirVana miRNA Mimic. miR-155 expression levels were evaluated after treatment with lipopolysaccharide (LPS), glycodeloxycholic acid (GCDCA), lithocholic acid (LCA) or ursodeoxycholic acid (UDCA).

Results: When compared to controls hepatic PPARα mRNA and protein levels were reduced in cirrhotic PBC (both 50% reduction, P = 0.01), but not in PSC livers. In PBC livers this phenomenon was accompanied with induction of miR-155 (3.7-fold increase, P = 0.004 vs. control). Experimental overexpression of miR-155 in HepG2 led to the inhibition of PPARα (50% reduction, P = 0.02). LPS stimulated miR-155 expression in HepG2 (over 40-fold increase, P = 0.009), whereas the treatment with GCDCA or LCA enhanced the expression of miR-155 in NHC (2-fold p < 0.05, or 2.4 fold p < 0.05, respectively). UDCA suppressed the basal expression of miR-155 in NHC (20% reduction, p = 0.02 vs. control) as well as the LPS-induced miR-155 in HepG2 (p = 0.009 vs LPS).

Conclusion: We showed that PPARα is substantially reduced in PBC livers, and the observed concomitant overexpression of miR-155 induced either by inflammation or bile acids may be accountable for this suppression. Inhibition of miR-155 may be a potential novel therapeutic target in PBC.

Cholangiocytes-specific deletion of sphingosine-1-phospholipid receptor 1 attenuate cholestasis induced liver injury and fibrosis
Yuan Zhang1, Jie Wang1, Yingying Miao1, Haoran Zhang1, Xinliang Huang1, Luoyong Zhang1,2, QW Yu1, Zhenzhou Jiang1,3,4
1China Pharmaceutical University, New drug screening center, Jiangsu; 2China Pharmaceutical University, Key laboratory of drug quality control and pharmacovigilance, Nanjing, China; 3China Pharmaceutical University, State key laboratory of natural medicines, Nanjing, China
Email: jiangcgu@163.com

Background and aims: Cholestasis is a pathophysiological process caused by disorders involving bile secretion and excretion. Chronic cholestasis can cause bile acids (BAs) to accumulate in the liver, induce liver injury, inflammation, and liver fibrosis. Sphingosine-1-phospholipid receptor 1 (S1PR1) is distributed in various organs, it is the receptor of endogenous substance sphingosine-1-phospholipid (S1P) and participates in a variety of physiological and pathological process. But its role in cholestatic liver disease has not yet been elucidated clearly.

Method: To study the cholangiocyte-specific role of S1PR1, we generated a novel knock-out mouse strains by breeding Krt19Cre mice with S1pr1 floxed mice. S1PR1 cell specific deletion was confirmed in primary isolated intrahepatic cholangiocytes by PCR, WB, and IF, and in liver frozen section by IF. Fibrosis was established by common bile duct ligand (BDL) (14 days) and CA (0.5%) chow diet (4 months). Liver damage was determined by serum ALT, AST, ALP, TBA, and H&E staining. Fibrosis was determined by hepatic hydroxyproline, Masson trichrome staining, Sirius staining, and IHC. Comprehensive serum and liver bile acids profiling were performed using HPLC-MS/MS. RNA-seq was performed in whole liver and primary cholangiocytes after BDL.

Results: First we observed that S1PR1 was more expressed on cholangiocytes after 14 days BDL and 4 months CA chow diet. Interestingly, S1PR1(Krt19CreERT+/−) mice displayed a trend towards attenuated liver injury and liver fibrosis compared to WT mice after BDL and CA chow diet, demonstrated by significantly decrease in serum ALT, AST, ALP, TBA, hepatic hydroxyproline, Masson Trichrome, H&E, and Sirius red staining as well as immunohistochemistry staining of α-SMA. BA profiling and PCA analysis indicated that S1PR1(Krt19CreERT+/−) mice alleviates the destruction of bile acid homeostasis induced by BDL and CA chow diet. RNA-seq analysis in BDL liver showed downregulation of ROS, ER stress, and CCR1 chemokine receptor binding signalling in S1PR1(Krt19CreERT+/−) mice compared to WT mice. WB analysis showed that cholangiocytes-specific deletion of S1PR1 attenuates CHOP induction, phosphorylation of JNK, eIF2α, and PERK induced by BDL. Q-PCR analysis showed that cholangiocytes-specific deletion of S1PR1 attenuates the upregulation of Cd44, Col6, and Cdc7 induced by BDL.

Conclusion: Our results illustrate that the cholangiocytes-specific deletion of S1PR1 can alleviate liver fibrosis and injury caused by biliary obstruction or chronic cholestasis, which helps to develop S1PR1 as a target for the treatment of liver fibrosis and cholestasis.
Pruritogenic activity of these compounds was assessed by intradermal injection in wild type and TRPA1-deficient mice.

**Results:** Several fractions from bile activated the TRPA1 receptor (and several other receptors) in vitro. One of these fractions contained a compound with m/z 311.22 which could be identified as a hydrophilic isomer of hydroperoxylinoleic acid (HpODE). We could also show that in bile HpODE is rapidly converted into a hydrophilic isomer. Upon biliary diversion of a BRIC type 1 patient we could show that the initial excretion of HpODE and its metabolites is very high with gradual decrease concomitant with the disappearance of itch. In plasma of pruritic cholestatic patients HpODE concentrations were significantly increased compared to cholestatic patients without itch and healthy controls. Wild type mice exhibited scratching behavior upon intradermal injection of HpODE, whereas TRPA1 deficient mice did not.

**Conclusion:** HpODE, a pruritogen in vitro and in vivo is present in elevated levels in cholestatic patients who experience itch. This compound, and its metabolites is highly secreted into bile upon biliary diversion. Pruritceptor antagonists may be useful in the treatment of cholestatic pruritus.

**FRI458**

**Characterising the early inflammatory landscape of primary sclerosing cholangitis**

Calì Dendrou, Katie Lynch, Fabiola Curioni, Charlotte Rich-Griffin, Ling-Yueng, Nicholas Provine, Nicholas Iott, Helen Ferry, Eve Fryer, Holm Uhlig, Roger W.G. Chapman, Satish Keshav, Paul Klenerman, Roger Chapman, Satish Keshav, Paul Klenerman, Wellcome Centre for Human Genetics, University of Oxford, Oxford, United Kingdom; "Translational Gastroenterology Unit, University of Oxford, Oxford, United Kingdom; "Royal Adelaide Hospital, University of Adelaide, Australia; "Institute of Computational Biology, Helmholtz Munich, Neuherberg, Germany; "John Radcliffe Hospital, Nuffield Division of Clinical and Laboratory Sciences, Oxford, United Kingdom.

**Background and aims:** Primary sclerosing cholangitis (PSC) is a chronic inflammatory biliary disease characterised by progressive fibrosis that can lead to cirrhosis and liver failure. Over 70% of PSC patients also have gut co-morbidities, typically ulcerative colitis (UC), suggesting a link between liver pathobiology and gut microbial dysbiosis. Therapeutic options for PSC are limited, with liver transplantation being most effective, although disease may recur. Thus, there is a dire need to better understand and target the pathological mechanisms of PSC, particularly those acting early on.

A key challenge to characterising early pathology in PSC has been related to acquiring liver biopsies. However, fine needle aspiration (FNA) has emerged as a safe technique for obtaining liver infiltrating immune cells. We sought to assess the experimental efficacy of FNA to adequately sample liver immune cells, and to map the early inflammatory landscape in the liver relative to matched peripheral blood using single-cell profiling technologies. We also sought to assess how inflammation in the liver compares to pathology in the gut of PSC patients presenting with UC.

**Method:** We obtained liver-infiltrating mononuclear immune cells via FNA and peripheral blood mononuclear cells (PBMCs) from patients with PSC and with non-alcoholic fatty liver disease/steatohepatitis. Cells were analysed by polychromatic flow cytometry and by 10x Genomics single-cell RNA sequencing (scRNAseq). In addition, gut biopsies from PSC-UC patients were obtained and also analysed by scRNAseq.

**Results:** We obtained liver FNA from 38 patients (21 PSC, 17 control patients). The median pain score was 0 and no serious adverse effects were reported. Flow cytometry analysis demonstrated a significant enrichment of natural killer (NK) cells, CD8+ T cells, and CD69+ T cells in the liver (all p < 0.05). High-resolution profiling of 38,012 liver immune cells and 78,751 PBMCs by scRNAseq in a patient subset specifically showed an enrichment of CXCR6+ NK cells, CD8+ central memory T cells, and mucosal-associated invariant T cells in the liver, and a relatively lower abundance of CD4+ regulatory T cells (all p < 0.05). Among other immune cell types captured, dendritic cells were enriched in the liver whilst FOShi classical monocytes were reduced (p < 0.05). Gene expression analyses also revealed PSC-specific inflammatory pathways, such as an increase in cytokine responsiveness, and analogous analyses were applied to the PSC gut samples.

**Conclusion:** FNA sampling is a safe approach for obtaining insights into the early inflammatory landscape of the liver in PSC and other diseases, with the application of single-cell methods across tissues revealing tissue-specific and shared inflammatory pathways that may provide a basis for further experimental medicine analyses.

**FRI460**

**Copper accumulation in chronic cholestatic disease augments liver damage by impairment of mitochondrial function**

Dennis Koob, Judith Nagel, Sebastian Zimny, Jingguo Li, René Artmann, Ralph Willmer, Gerald Denk, Martin Roderfeld, Elke Roeb, Hans Zischka, Simon Hohenester, University Hospital LMU, Department of Medicine II, Munich, Germany; "Technical University of Munich, Department of Toxicology and Environmental Hygiene, Munich, Germany; "Helmholtz Center Munich, Institute of Molecular Toxicology and Pharmacology, Munich, Germany; "Affiliated University Hospital Munich, Department of Dermatology.
Hospital of Zunyi Medical University, Department of Gastroenterology, Zunyi, China; ²Justus Liebig University, Gastroenterology, Center for Internal Medicine, Giessen, Germany

Email: dennis.koob@med.uni-muenchen.de

Background and aims: Derangement of copper homeostasis, as seen in Wilson’s disease, causes liver damage. Copper accumulation also occurs in chronic cholestatic liver disease. In primary sclerosing cholangitis, copper accumulation, i.e. Orcein staining as a component of the Nakanuma score, even predicts reduced transplant-free survival. We hypothesize that copper accumulation might not only be a consequence of cholestasis, but modulate the course of disease. We aimed to investigate the role of copper accumulation in animal models of cholestasis and identify potential molecular targets of copper and bile salt co-toxicity.

Method: Hepatic copper content was determined in wild type and Mdr2<sup>−/−</sup> animals on both FVB and BALBc backgrounds. Liver damage and liver fibrosis were quantified. Mdr2/FVB animals were fed a copper-enriched diet (2 g/kg). The hepatocyte cell line HepG2 was stably transfected with Ntcp to allow for bile salt uptake and was stimulated with glycochenodeoxycholate (GCDC) and copper (5–10 μM, each). Cell survival, apoptosis, proliferation, and metabolic activity were assessed. In mitochondria from stimulated cells, oxygen consumption and ATP production were quantified.

Results: While hepatic copper content was not different from wildtype in Mdr2/FVB animals, it was increased 1.5 ± 0.2-fold in Mdr2/BALBc (wt/BALBc vs. Mdr2/BALBc, n = 5, p < 0.05). Overall, hepatic copper content correlated with liver fibrosis as determined by liver hydroxyproline (r² = 0.8, p < 0.05, n = 9). Copper feeding was well tolerated in wt animals and was associated with a slight but insignificant increase in serum ALT only in Mdr2/FVB animals. However, it led to an increase in hepatic copper content (13.5 ± 1.2 vs. 1898.3 ± 445.7 mg/kg, n = 6, p < 0.01) and liver fibrosis (Desmet score, 0.4 ± 0.5 vs. 1.3 ± 0.5, p < 0.05) in Mdr2/FVB. In HepG2, doses applied of both GCDC and copper were non-toxic in WST assays. Combination of both stimuli, however, led to a marked impairment of metabolic activity to 65.9 ± 4.3% (n = 6, p < 0.05). While caspase-3/7 assays excluded apoptosis, reduced proliferative activity was found upon dual treatment. In isolated mitochondria from stimulated HepG2 cells, ATP production was unaffected by each stimulus alone. Combined treatment, however, led to a drop in ATP production from 100 ± 4.1% to 46.1 ± 9.7% (n = 3, p < 0.05) (Figure 1), accompanied by an increase in mitochondrial oxygen consumption.

Conclusion: Hepatic copper deposition in experimental cholestasis is associated with progression of liver fibrosis, mimicking the human phenotype. On a cellular level, bile salt and copper synergistically impair ATP production. Since the respiratory chain was unaffected (increase rather than drop in oxygen consumption), the adenine nucleotide translocator (ANT) is a likely molecular target. These results encourage testing of copper chelating strategies in cholestatic liver disease.

FRJ461
The IgG4-related cholangitis autoantigen laminin 511-E8 stabilizes the biliary bicarbonate umbrella in human cholangiocytes

David Trampert¹, Renco Kersten², Dagmar Tolenaars³, Ronald Oude-Elferink¹, Stan van de Graaf¹, Ulrich Beuers¹. ¹Tytgat Institute for Liver and Intestinal Research, Amsterdam Gastroenterology Endocrinology Metabolism (AGEM), Amsterdam University Medical Centers, Department of Gastroenterology and Hepatology, Amsterdam, Netherlands

Email: u.h.beuers@amsterdamumc.nl

Background and aims: IgG4-related cholangitis (IRC) is the hepatobiliary manifestation of IgG4-related disease (IgG4-RD), a systemic, B-cell driven, fibroinflammatory disorder. To date four autoantigens with pathogenetic relevance have been described by our group and others in IgG4-RD, namely annexin A11, laminin 511-E8, galectin 3 and prohibitin 1 (PMID 28765476, 30089633). We recently demonstrated that patient anti-annexin A11 autoantibodies destabilize the ‘biliary bicarbonate umbrella’ (PMID 34718050), a protective mechanism against toxic hydrophilic bile acids (PMID 20721884). Another autoantigen, laminin 511-E8, is an extracellular matrix protein that functions as a ligand of the integrin α6β1 (ITGα6β1) receptor (PMID 28879238). Laminin 511-E8 has been shown to upregulate critical components of the ‘biliary bicarbonate umbrella’ (PMID 27103433) and ITGα6β1 signaling is important for bile duct development (PMID 22761447). Therefore, we aimed to investigate the role of laminin 511-E8 in human cholangiocytes.

Method: Laminin 511-E8 expression was confirmed in RNA sequencing datasets of human cholangiocyte organoids. Human H69 cells were subjected to shRNA knockdown using lentiviral transduction. Individual knockdown cell lines were generated targeting the mRNA transcripts encoding laminin 511-E8 (LAMAX, LAMAX, LAMC1). Knockdown of LAMAX and LAMC1 was verified on mRNA and protein level using qPCR and western blot. A parallel approach was taken selecting H69 cells to recombinant laminin 511-E8 (0.25 μg/cm²). The function of laminin 511-E8 in human cholangiocytes was assessed by three approaches: (i) intracellular pH (pHi) measurements microspectrofluorimetrically using BCECF-AM; (ii) rate of bile acid influx radiochemically by measuring 22, 23-³H-glycochenodeoxycholic acid (³H-GCDC) permeation over time; (iii) GCDC-induced apoptosis determined dynamically by real-time imaging of Caspase-3/7 Green signal and statically by conventional bulk Caspase-3/7 assays.

Results: Screening of the laminin 511-E8 constituent knockdown cell lines revealed that at least LAMAX and LAMC1 could be of functional importance in cholangiocytes. ³H-GCDC permeation was larger in LAMAX and LAMC1 knockdown H69 cells compared to Sham controls. Treatment of human cholangiocytes with the recombinant 511-E8 fragment resulted in a decreased pHi and significantly reduced the rate of ³H-GCDC permeation (Figure).

Conclusion: Collectively, our study indicates that the IgG4-RD autoantigen laminin 511-E8 has a protective role in human
cholangiocytes against toxic bile acids, similar as recently described for annexin A11. We speculate that autoantibodies against lamin 511-E8 may destabilize the biliary bicarbonate umbrella, thereby contributing to the pathogenesis of IRC.

**FR1462**
The risk-variant rs56258221 at the BACH2-locus associates with skewed polarization of naïve CD4+ T cells towards pro-inflammatory phenotypes in primary sclerosing cholangitis
Jonas Bahn1, Lilly K. Kunzmann1, Jenny Krause1, Christian Casar1,2, Silja Steinmann1, Marcell Sebode1, Samuel Huber1,3, Ansgar W. Lobse1,3, Andre Franke4, Nicola Gagliani1,3,5,6, Dorothee Schwinge1, Christoph Schramm1,6,7, Tobias Poch1.
1University Medical Center Hamburg-Eppendorf, I. Department of Medicine, Hamburg, Germany; 2University Medical Center Hamburg-Eppendorf, Bioinformatics Core, Hamburg, Germany; 3University Medical Center Hamburg-Eppendorf, Hamburg Center for Translational Immunology, Hamburg, Germany; 4Christian-Albrechts-University of Kiel, Institute of Clinical Molecular Biology, Kiel, Germany; 5Universität Medical Center Hamburg-Eppendorf, Department for General, Visceral and Thoracic Surgery, Hamburg, Germany; 6Karolinska Institute, Immunology and Allergy Unit, Department of Medicine Solna, Stockholm, Sweden; 7University Medical Center Hamburg-Eppendorf, Martin Zeitz Center for Rare Diseases, Hamburg, Germany

**Background and aims:** Primary sclerosing cholangitis (PSC) is an enigmatic disease of presumably multifactorial pathogenesis, including genetic predisposition and dysregulated immune responses as likely key contributors to the disease development. We have previously described an intrahepatic naïve-like population of CD4+ T cells in patients with PSC, prone to polarize towards a pro-inflammatory Tp17 phenotype. Genome-wide association studies (GWAS) have linked PSC to several polymorphisms in immune-related genes. We here hypothesized that genetic predisposition contributes to the observed T cell phenotype in patients with PSC.

**Method:** Patients with PSC (n = 270) were genotyped for the disease-associated risk variants rs56258221 (BACH2), rs80060485 (FOXP1), rs4147359 (IL2RA) and rs7420656 (CD28). To determine T cell function and phenotype, comprehensive immunophenotyping, in vitro experiments on polarization and proliferation, microRNA-arrays, western blots and single-cell RNA sequencing from peripheral blood naïve CD4+ T cells was performed. The data generated was correlated to the underlying genotype of the patients.

**Results:** Functional in vitro experiments with naïve CD4+ T cells from patients with PSC and healthy donors (HD) showed an increased capacity of PSC-derived cells to convert into pro-inflammatory T Helper 1 (Tbf1, 50.7% vs. 42.9%, p = 0.027) and T Helper 17 (Tb17, 5.5% vs. 2.2%, p = 0.042) subsets, which was accompanied by a lower conversion rate into induced regulatory T cells (iTREG, 9.6% vs. 17.3%, p = 0.022). The observed effects were significantly increased in carriers of the PSC-associated risk variant rs56258221 (BACH2), which was not seen for the other variants in immune-related genes assessed. Interestingly, single-cell RNA sequencing of the T cell compartment in homozygous SNP carriers vs. non-carriers identified a composition skewed towards activated phenotypes in rs56258221 carriers. Reduced expression of BACH2 itself was detected on protein but not mRNA level in naïve CD4+ T cells, which could be linked to a strongly increased expression of a microRNA located in close genomic proximity to the SNP and imputed to inhibit translation of BACH2.

**Conclusion:** We here present comprehensive data linking the risk variant rs56258221 at the BACH2-locus to the recently described dysregulated T cell phenotype in patients with PSC. Decoding how genetic risk contributes to disease pathogenesis is the first step in understanding how the environment interacts with the immune system to fuel disease pathogenesis.

**FR1463**
Single-cell profiling of liver B cells identifies distinct gene expression and reactivities of expanded B cell clonotypes in primary sclerosing cholangitis
Markus Jørdens1,2,3, Tom Hemming Karlsen1,2,4,5, Espen Melum1,2,4,5,6, Johannes R. Hou1,2,4,5, Brian K. Chung1,2.
1University of Oslo, Norwegian PSC Research Center, Oslo University Hospital and Institute of Clinical Medicine, Oslo, Norway; 2Oslo University Hospital, Research Institute of Internal Medicine, Oslo, Norway; 3University Hospital Düsseldorf, Clinic for Gastroenterology, Hepatology and Infectious Diseases, Medical Faculty, Heinrich Heine University Düsseldorf, Düsseldorf, Germany; 4University of Oslo, Institute of Clinical Medicine, Oslo, Norway; 5Oslo University Hospital, Section for Gastroenterology, Department of Transplantation Medicine, Division of Surgery, Inflammatory Diseases and Transplantation, Oslo, Norway; 6University of Oslo, Hybrid Technology Hub-Centre of Excellence, Institute of Basic Medical Sciences, Faculty of Medicine, Oslo, Norway

**Background and aims:** Primary biliary cholangitis (PBC) and primary sclerosing cholangitis (PSC) are autoimmune hepatobiliary diseases with a high prevalence of autoantibodies. In PBC, anti-mitochondrial antibodies (AMA) serve as robust biomarkers whereas autoantibodies against relevant antigens in PSC remain undefined. Using anti-mitochondrial reactivity as a proxy of disease-relevance, we assessed if expanded B cell clonotypes in PBC livers recognize AMA targets and whether analogous B cells in PSC harbour unique gene expression and antigen specificities.

**Method:** Liver B cells from PBC (n = 3) and PSC explants (n = 3) were enriched by negative bead selection (Stemcell Technologies, Canada) and assessed for B cell receptor (BCR) and total gene expression by single-cell RNA sequencing (scRNaseq). B cell clonality and differential gene expression (DEG) was analyzed by Cell Ranger and Loupe Browser (10X Genomics, USA). Monoclonal antibodies (mAb) generated from BCR sequences of expanded B clonotypes (GenScript, USA) were pooled and screened against >20,000 human proteins using HuProt v4 microarrays (Cambridge Protein Arrays, UK). A subselection of mAb microarray targets were verified by immunoblotting or enzyme-linked immunosorbent assays (ELISA).

**Results:** Cumulative frequencies of the five most-expanded B clonotypes as a percentage of total liver clonotypes were similar amongst PBC and PSC explants (mean: 16.8% vs 15.4%, range: 9.1–30.42% to 0.68–41.17%). In contrast, transcriptomes of expanded PBC clonotypes significantly differed from PSC clonotypes; plasma cell markers such as CD38, BXP1 and MZB1 were significantly higher in PBC clonotypes while the naïve and memory B cell markers MS4A1, CD79A, CD79B and HLA-DR, -DQ, -DR were significantly enriched in PSC clonotypes (log2 fold-change >2.5, p < 0.05, Benjamin-Hochberg corrected). mAbs generated from the BCR sequences of expanded B clonotypes strongly recognized the AMA targets PDC-E2, PDHA1, MS4A1, CD79A, CD79B and HLA-DR, -DQ, -DR while not recognizing mAbs of expanded PSC clonotypes.

**Conclusion:** We here present comprehensive data linking the risk variant rs56258221 at the BACH2-locus to the recently described dysregulated T cell phenotype in patients with PSC. Decoding how genetic risk contributes to disease pathogenesis is the first step in understanding how the environment interacts with the immune system to fuel disease pathogenesis.
The rs429358 apolipoprotein E (APOE) polymorphism is associated with increased liver injury in patients with autoimmune hepatitis

Maciej K. Janik1, Wiktor Smyk2, Beata Kruk3, Benedykt Szczepankiewicz4, Barbara Górnicka5, Susanne N Weber5, Piotr Milkiewicz1,2, Marcin Krawczyk1,2,5. Medical University of Warsaw, Liver and Internal Medicine Unit, Warsaw, Poland; 2Medical University of Gdańsk, Department of Gastroenterology and Hepatology, Gdańsk, Poland; 3Medical University of Warsaw, Laboratory of Metabolic Liver Diseases, Department of General, Transplant and Liver Surgery, Laboratory of Metabolic Liver Diseases, Centre for Preclinical Research, Warsaw, Poland; 4Medical University of Warsaw, Department of Pathology, Warsaw, Poland; 5Saarland University Medical Center, Saarland University, Department of Medicine II, Homburg, Germany; 6Pomeranian Medical University, Translational Medicine Group

Background and aims: The natural course of autoimmune hepatitis (AIH) varies between patients; therefore, the potential role of genetic modifiers might be suspected. Recent analyses linked the variant rs429358 in apolipoprotein E (APOE) with steatosis and liver injury in fatty liver disease (Jamialahmadi et al., Gastroenterology 2021). Here, we analyse this APOE variant in patients with AIH.

Method: The study cohort consisted of 312 non-transplanted (70% women, age 18–83 years) adults with AIH. Pure AIH and its cholestatic variants, namely AIH-primary sclerosing cholangitis (PSC) and AIH-primary biliary cholangitis (PBC), were diagnosed according to the EASL 2015 guidelines. The APOE rs429358 polymorphisms were genotyped using TaqMan assays. The liver fibrosis was assessed by liver biopsy, liver stiffness and serum indices (APRI, FIB-4), whereas liver steatosis was evaluated by controlled attenuation parameter (CAP). The effects of the APOE polymorphism were analysed in combination with the mitochondrial amidoxime-reducing component 1 (MAR1) p.A165T and adiponutrin (PNPLA3) p.I148M variants, which were previously shown to modulate liver injury in AIH.

Results: Among recruited patients, the median duration of the disease was 4 (range 0–33) years. Liver cirrhosis was present in 130 (42%) patients, and 70% of the entire cohort received steroid-based therapy. Sixty (19%) patients were therapy naïve at inclusion. In total, 26% of patients with AIH carry at least one copy of the APOE rs429358 minor allele. The APOE polymorphism was associated with more pronounced liver fibrosis according to APRI score (p = 0.035) and liver injury as reflected by increased AST (p = 0.045) and a trend for higher ALT (p = 0.055) activities in therapy-naïve patients with AIH. A trend between the genetic variant in APOE and higher ALT was also noticed in the entire cohort (p = 0.054). No link was found between the studied variant and results of liver biopsies, transient elastography or CAP (all P > 0.05). The protective effect of the MAR1 polymorphism on serum ALT (p = 0.045) and AST (p = 0.024) activities were more pronounced in patients with APOE wild-type variant. The effect of the PNPLA3 p.1148M polymorphism on liver phenotypes was not modulated by the APOE genotype.

Conclusions: Patients with AIH who carry the APOE polymorphism might manifest a more pronounced liver injury. Variant APOE (rs429358) together with previously detected MAR1 p.A165T polymorphism might help to stratify patients with AIH concerning their risk of progressive liver injury.

FRI465
Intrabiliary injection of MAIT antigens induces cholangitis in mice

Kathrine Siivertsen Nordhus1,2,3, Freeman Zheng1,2,3, Natalie Lie Berntsen1,2,4, Laura Valestrand1,2,3, Jonas Øgaard1,2,3, Tom Hemming Karlsen1,2,3,4, Xiaojuan Jiang1,2,3, Espen Melum1,2,3,4,5. 1Norwegian PSC Research Center, Division of Surgery, Inflammatory Diseases and Transplantation, Oslo University Hospital, Oslo, Norway; 2Research Institute of Internal Medicine, Division of Surgery, Inflammatory Diseases and Transplantation, Oslo University Hospital, Oslo, Norway; 3Institute of Clinical Medicine, University of Oslo, Oslo, Norway; 4Section of Gastroenterology, Division of Surgery, Inflammatory Diseases and Transplantation, Oslo University Hospital, Oslo, Norway; 5Hybrid Technology Hub-Centre of Excellence, Institute of Basic Medical Sciences, Faculty of Medicine, University of Oslo, Oslo, Norway

Background and aims: Mucosal-associated invariant T (MAIT) cells are a subset of unconventional T-cells that recognize microbial-derived vitamin B metabolites presented by MR1. Previously we have demonstrated that bile from patients with chronic biliary inflammation contains MAIT antigens. Therefore we now aimed to determine if MAIT cells could drive inflammation in the bile ducts by challenging mice with an increased frequency of MAIT cells (Mr1+ B6-MAITCAST and iV alpha beta Tg C alpha -/-/ alpha beta Tg C alpha -/-) with intrabiliary injection of MAIT cell activating antigens in terms of fixed E.coli and 5-OP-RU.

Method: E.coli, 5-OP-RU and PBS were injected into bile ducts of Mr1+ B6-MAITCAST and iValpha beta Tg C alpha -/- mice. Weight and general well-being were monitored daily. The mice were sacrificed after 2, 7 or 14 days. Isolated lymphocytes from liver and spleen were stained with monoclonal antibodies and an MR1 tetramer, then analyzed by flow cytometry. Serum was analyzed for alanine transaminase (ALT).

Results: Intrabiliary fixed E.coli injection in iValpha beta Tg C alpha -/- mice caused a biliary immune response with increased histological cholangitis score (E:colif: 1.29 vs. PBS: 0.24, p = 0.013) after 2 days, but with similar weight loss and ALT levels compared to vehicle control. Importantly, a clear activation of hepatic MAIT cells were seen after injection of fixed E.coli (MFI CD69 E:colif vs. PBS: p = 0.0015) in contrast to a minor increase in CD69 MFI for non-MAIT T-cells. In Mr1+ B6-MAITCAST mice, which has an increased frequency of MAIT cells independent of genetic manipulation, an increased cholangitis score (p = 0.0485) was also observed after injection of fixed E.coli. In experiments with intrabiliary 5-OP-RU injection in iValpha beta Tg C alpha -/- mice a clear increase in proportion of CD69+CD25+ MAIT cells was observed in the liver (5-OP-RU: 18% vs. PBS: 7%, p < 0.0001) that translated into an increased histological cholangitis score (5-OP-RU: 1.78 vs. PBS: 0.47, p = 0.021). This suggests that direct activation of MAIT cells leads to cholangitis. A systemic effect, most likely mediated by the portal circulation, was also observed as the proportion of CD69+CD25+ MAIT cells in the spleen was also increased (5-OP-RU: 6% vs. PBS: 3%, p = 0.0386).

Poster Presentations
Conclusion: We observed a clear activation of hepatic MAIT cells in a mouse model of bile duct inflammation that led to cholangitis. Biliary antigens potentially derived from gut microbiota present in the bile ducts could therefore be speculated to induce an immune response where MAIT cells play a role.

FRI466
TGF beta 2 fuels inflammation and fibrosis in cholestatic liver disease through macrophage and myofibroblast recruitment and activation

Jan Albin1, Nadja Meindl-Beinker2, Matthias Ebert1, Andreas Teufel3, Steven Dooley1, Anne Dropmann1,3, 1Medical Faculty Mannheim, Heidelberg University, Department of Medicine II, Molecular Hepatology, Mannheim, Germany; 2Medical Faculty Mannheim, Heidelberg University, Department of Medicine II, Mannheim, Germany; 3Medical Faculty Mannheim, Heidelberg University, Department of Medicine II, Clinical Bioinformatics, Mannheim, Germany

Background and aims: We have identified TGF-β2 as an important mediator and potential therapeutic target in cholestatic liver disease, in mouse and human. The aim of this study was (1) to correlate TGF-β2 expression with disease activity, fibrotic stage and degree of ductular reaction (DR), and (2) to identify the cell populations in the diseased liver that are source for and target of TGF-β2 and delineate their role in the disease course.

Method: Liver tissues from Abcb4−/− KO, CDE & DDC diet, bile duct ligated and CCl4 treated mice, as well as patient samples were stained for H&E and Sirius Red. Histologic evaluation of disease activity and fraction in the periportal area correlated with disease progression. Inhibiting TGF-β2 expression with antisense oligonucleotides leads to reduced pSmad3 positive cell numbers, suggesting that TGF-β2 is triggering Smad3 signaling.

Conclusion: TGF-β2 expression is upregulated in cholangiocytes in patients and mouse models with cholestatic liver disease. Neighboring inflammatory and fibrogenic cells display pSmad3 staining and increase in numbers. Next, we search for stress factors and upstream signals that induce TGF-β2 expression during cholestatic liver damage.

FRI467
Liver-specific Tsg101 depletion causes apoptosis, cell death and liver failure

Surui Wang1,2, Revathi Sekar1,2, Jaroslaw Cendrowski3, Ahmed Ghallab4, Karsten Motzler1,2, Yun Kwon1,2, Susanne Seitz1,2, Michael Roden2,5,6, Adriano Maida1,2, Jan G. Hengstler1,2, Jaroslaw Cendrowski3, 1Institute for Diabetes and Cancer, Helmholtz Center Munich, Joint Heidelberg-IDC Translational Diabetes Program, Inner Medicine I, Heidelberg University Hospital, Neuerberg, Germany; 2German Center for Diabetes Research (DZD), Neuerberg, Germany; 3International Institute of Molecular and Cell Biology, Warszawa, Poland; 4Leibniz Research Centre for Working Environment and Human Factors, Dortmund, Germany; 5Heinrich Heine University Düsseldorf, Division of Endocrinology and Diabetology, Medical Faculty, Düsseldorf, Germany; 6Leibniz Center for Diabetes Research at Heinrich Heine University, Institute for Clinical Diabetology, German Diabetes Center, Dusseldorf, Germany

Background and aims: The endosomal sorting complexes required for transport (ESCRT) play a key role in lysosomal degradation of membrane signaling receptors. The machinery consists four protein complexes (ESCRT –0 to –III), that are successively recruited to maturing endosomes, sorting ubiquitinated cargos into intraluminal vesicles destined for degradation. Recently, the ESCRT-I has been reported to protect mice against non-alcoholic steatohepatitis (NASH) by targeting TLR4 for degradation, suggesting its potential role for treating non-alcoholic fatty liver disease (NAFLD) and NASH. Thus, the aim of this project is to identify the function of ESCRT-I in liver physiology by interfering with the major regulator of ESCRT-I stability and function, the tumor susceptibility gene 101 (Tsg101).

Method: Tsg101 was downregulated using lipid nanoparticle induced hepatocyte-specific in vivo and adenovirus based primary hepatocytes in vitro knockdown. The in vivo experiments were conducted in time course while serum and livers are collected for functional analysis.

Results: Consistent with previous data, we found Tsg101KD leads to ESCRT-I instability, supporting an essential role of Tsg101 on ESCRT-I function. Remarkably, loss of Tsg101 induces severe liver...
inflammation and organ damage leading to animal lethality 8 days after injection. This is associated with a vast elevation of aspartate aminotransferase (AST), alanine aminotransferase (ALT) and bile acid levels in the serum accompanied by a decrease in blood glucose concentrations, indicating severe liver pathologies. Also, the size of the gallbladder is increased in Tsg101KD mice with disrupted bile canaliculi structure, pointing towards impairment of bile acid homeostasis. Initiation of the inflammatory response is dependent on the endosomal accumulation of tumor necrosis factor receptor (TNFR), which leads to the activation of canonical and non-canonical transcription factor nuclear factor kB (NF-kB) signaling and the upregulation of downstream cytokines. Moreover, we observe a time-dependent decrease in mitochondrial function, characterized by mitochondrial uncoupling and enhanced proton leak, which manifests into activation of caspase-3 cleavage and induction of apoptosis. The activation of inflammation upon Tsg101 KD is in line with data from NASH patients, where TSG101 expression is decreased and negatively correlated with interleukin 6 (IL6) and 1 beta (IL1b) levels, highlighting a potential regulatory function of Tsg101 in liver inflammation. 

Conclusion: Altogether, liver-specific Tsg101 KD causes a time-dependent activation of inflammation and apoptosis, accumulating into hepatocyte death, organ failure and ultimately a lethal phenotype. Our finding suggests a regulatory role of Tsg101 in TNFR signaling and degradation, where Tsg101 protects against liver inflammation.

FR468 Cell reactivation in autoimmune hepatitis after immunosuppression withdrawal

Elena Perpinyà1, George Koutsoudakis2, Laura Patricia Llovet3, Thais Leonel4, Mar Rivero Barciela5,Montserrat García-Retortillo6, Mercé Roget7, Alberto Sanchez-Fueyo5, Maria Carlota Londoño7,1 King's College Hospital, London, United Kingdom; 2 Hospital Clinic Barcelona; 3 Hospital Clinic Barcelona, Liver Unit, Barcelona, Spain; 4 Hospital Vall d’Hebron, Liver Unit, Barcelona, Spain; 5 Hospital del Mar, Barcelona, Spain; 6 Consorcio Sanitari de Terrassa, Terrassa, Spain; 7 King’s College Hospital, London, United Kingdom

Email: mlondono@clinical.cat

Background and aims: Long-term immunosuppression therapies increase the risk of treatment-related side effects and subsequent reduce quality of life in autoimmune hepatitis (AIH) patients. The optimal strategy for immunosuppression withdrawal (ISW) is still controversial as relapse rates vary between 25 and 100% despite previous sustained complete biochemical response. Moreover, the pathogenesis of AIH is uncertain and no studies have explored the effect of ISW on the immune response. Therefore, we aim to understand the B and T cell repertoire in AIH patients undergoing ISW.

Method: Thirty-seven patients with type 1 AIH, complete biochemical response on first-line treatment for at least 3 years and histological activity index <3 were prospectively included. Detailed characterization of peripheral B and T cell responses was performed through high-dimensional spectral flow cytometry and unsupervised clustering before and after ISW (median time of 9 months). 

Results: Fifty-one percent of patients were female (n = 19) with a median age of 60 years (22–80), and a median time on remission of 4 years (3–11). Most of the patients were on monotherapy with azathioprine at the time of ISW (n = 27, 74%). After a median follow-up of 31 months (12–34), 21 (57%) patients remained in remission and 16 (43%) patients required reinstitution of therapy (6 of them were still on low-dose immunosuppression when presented the flare). Before ISW, patients who reached remission displayed elevated frequencies of immature transitional 2 marginal zone precursor cells and early plasmablasts relative to patients who presented a flare (p = 0.02 and p = 0.03, respectively). However, both B cell populations together with the transitional T1, T2 and T3 subsets increased in all patients regardless of the outcome of ISW, and positively correlated with serum transaminases and IgG levels after discontinuation of treatment (p < 0.01). Of note, the expansion of B cell precursors was accompanied by a decrease in the frequency of switched resting memory cells (p < 0.01). In contrast, no differences were observed in the T cell compartment before or after ISW. 

Conclusion: In AIH patients, ISW results in a state of immune activation orchestrated by B cells with no detectable changes in the T cell compartment, regardless of the clinical outcome. This suggests that clinical remission does not entail the restoration of immune tolerance to liver antigens and provides an explanation for late relapses observed after ISW.

FR469 Serum steroids indicate modified cholesterol homeostasis in cirrhotic patients with PBC and correlate with response to treatment with ursodeoxycholic acid

Wiktór Smyk1, Beata Kruś2, Tadeja Rezen3, Miha Moskon4, Ewa Wunsch5, Dieter Lütjohann6, Frank Lammert7, Piotr Milkiewicz8,9, Marcin Krawczyk2,9,1 Medical University of Gdańsk, Department of Gastroenterology and Hepatology, Gdansk, Poland; 2 Medical University of Warsaw, Laboratory of Metabolic Liver Diseases, Department of General, Transplant and Liver Surgery, Centre for Preclinical Research, Warsaw, Poland; 3 University of Ljubljana, Centre for Functional Genomics and Bio-Chips, Institute for Biochemistry and Molecular Genetics, Faculty of Medicine, Ljubljana, Slovenia; 4 University of Ljubljana, Faculty of Computer and Information Science, Ljubljana, Slovenia; 5 Pomorski Medical University in Szczecin, Translational Medicine Group, Szczecin, Poland; 6 University Hospital Bonn, Institute of Clinical Chemistry and Clinical Pharmacology, Bonn, Germany; 7 Hannover Medical School (MMH), Health Sciences, Hannover, Germany; 8 Medical University of Warsaw, Liver and Internal Medicine Unit, Department of General, Transplant and Liver Surgery, Warsaw, Poland; 9 Saarland University, Department of Medicine II, Saarland University Medical Center, Homburg, Germany

Email: marcin.krawczyk@ukw.eu

Background and aims: Primary biliary cholangitis (PBC) is a chronic autoimmune cholestatic liver disease of unknown aetiology. Ursodeoxycholic acid (UDCA) is the first-line therapy in PBC however, some patients present insufficient biochemical response to UDCA, indicating worse disease course and survival. Cholesterol is involved in diverse biological activities and derives from de novo synthesis or intestinal absorption. Here, we aim to investigate and correlate serum sterol profiles and PBC phenotypes.

Method: Overall, we included 129 patients with PBC (age 32–93 years, 119 women). A total of 44 individuals presented with cirrhosis at diagnosis, and 13 were transplanted due to PBC before inclusion. Biochemical response to UDCA was assessed according to Barcelona criteria. Follow-up data (range: 1–13 years) were available in 62 (48%) patients. Serum sterol levels were measured by gas chromatography/mass spectrometry (GC/MS) at inclusion, Machine learning (ML) algorithms were used to determine a model that can predict UDCA response.

Results: Cirrhotic patients with PBC demonstrated significantly higher sitosterol (p = 0.0001), campesterol (p = 0.0042) and cholestanol (p < 0.0001) serum concentrations as compared to non-cirrhotic individuals. Patients with cirrhosis showed increased phytosterols:cholesterol but decreased lathosterol:cholesterol ratios (all p < 0.0001). Desmosterol:cholesterol ratio did not differ between patients with or without cirrhosis. Individuals after transplantation displayed increased serum concentrations of 7α-hydroxycholesterol.
Background and aims: Mucosal-associated invariant T (MAIT) cells are significant players in autoimmune liver disease (AILD), a spectrum of conditions which often starts in childhood. Biological characterisation of MAIT cells and their functional activity in children with AILD has seldom been investigated. We aim to 1) characterise the deep immunophenotype of paediatric MAIT cells in AILD compared to healthy controls and 2) assess their cytokine capabilities.

Method: We performed mass cytometry (CyTOF; Cytometry by time of flight) analysis of peripheral blood mononuclear cells (PBMC) from paediatric patients with AILD (AIH Type 1, N = 4, median age 14 yrs (range 9–14), and PSC, N = 4, median age 14 yrs (range 12–14)) and from healthy children (HC) (N = 4, median age 8.5yars (range 5–14)). These PBMC samples were treated with a cell stimulation cocktail containing phorbol 12-myristate 13-acetate (PMA) and ionomycin and incubated for 4hours prior to downstream investigation by mass cytometry with a custom MAIT cell CyTOF panel designed by the investigators. Results were compared to controls (unstimulated matched PBMCs from the same patients). Cytobank and GraphPad Prism 9 were used for data analysis.

Results: Compared to the cohort of healthy children, peripheral blood MAIT cell from children with AILD had increased expression of retinoic acid related orphan receptor gamma t (RORγt), a transcription factor of T helper 17 (Th17) cells, and the proinflammatory cytokine interleukin 17A (IL-17A). This was observed at baseline (p = 0.002) and post stimulation (p = 0.001). Higher expression of RORγt was observed in AIH Type 1 patients compared to healthy children (p = 0.005) Figure 1. There was also a significant difference between AIH Type 1 and PSC IL-17A activity post stimulation (p = 0.034). Post-stimulation IL-17A expression was highest in the PSC cohort compared to their unstimulated counterparts (p = 0.003). In addition, TNFα, IFNγ and GMCSF cytokine production were preserved in the children with AILD (AIH Type 1 and PSC), with levels comparable to those in the healthy cohort. This finding was most pronounced in TNFα production (p = 0.0042) which differs from peripheral blood MAIT cells in adults with AILD where there is decreased cytokine production.

Conclusion: Peripheral blood MAIT cell cytokine profile in children with AIH Type 1 and PSC are similar to MAIT cells from healthy children. Furthermore, MAIT cells from children with AIH Type 1 and PSC have greater RORγt expression and IL-17A activity at rest and post stimulation, suggesting that MAIT cells with a Th17-like phenotype may play a role in disease pathogenesis.
Conclusion: Decreasing portal hypertension via TIPS insertion leads to a significant improvement of SI over time, which is associated with a favorable clinical outcome.

Background and aims: Development of portal hypertension is associated with high risk of variceal haemorrhage, ascites, encephalopathy and death. In over 100,000 individuals identified with portal hypertension we identify significant comorbidities that should be addressed to improve outcomes in this vulnerable population.

Method: Individuals with features of portal hypertension were identified using the TriNetX federated health records. Three groups of patients were identified, Group 1 with confirmed variceal haemorrhage (19,454 in total, of which 12,968 were incident), Group 2 with varices but no haemorrhage (43, 583 in total, of which 30,083 were incident) and Group 3 with portal hypertension but no diagnosed varices (48,496 in total, of which 31,611 were incident). Significant comorbidities were identified across all 3 groups.

Results: Higher rates of ischaemic heart disease (IHD), heart failure and chronic kidney disease (CKD) were found in Group 3 versus the other two groups:

<table>
<thead>
<tr>
<th>CKD (%)</th>
<th>Heart failure (%)</th>
<th>Ischaemic heart disease (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Incident group 1</td>
<td>9.0</td>
<td>8.5</td>
</tr>
<tr>
<td>Incident group 2</td>
<td>11.3</td>
<td>10.2</td>
</tr>
<tr>
<td>Incident group 3</td>
<td>16.3</td>
<td>16.1</td>
</tr>
</tbody>
</table>

(76%). Median CRP and WBC were 9.2 mg/L and 5 × 103/μL, respectively. CRP levels but not WBC significantly decreased after TIPS (p < 0.001). Of note, decrease in CRP levels was significantly associated with a better survival (p = 0.012). As expected, cytokine levels were significantly higher in the cirrhotic patients as compared to healthy controls affecting 30 of 48 measured cytokines (FDR < 0.05). Pattern of SI did not differ between patients with RA and variceal bleeding except from IL-6, which was significantly higher in patients with RA (p < 0.001). One month after TIPS most cytokines were still measured at levels comparable to baseline and some, e.g. IL-2, were even increased. However, during further follow-up we documented a continuous decrease in the majority of cytokines. For 25 cytokines, including IL-6 and IL–2, levels were significantly lower at month 6 compared to the time of TIPS insertion (FDR < 0.05; figure). Moreover, 7 of the 30 cytokines (including IL-2), which were elevated prior to TIPS, did not show any statistical difference anymore compared to healthy controls. When correlating cytokine changes with the clinical status, IL-6 appeared to be of particular interest: Decrease in IL-6 was associated with a significant improvement in MAMC and numerical increase in HGS and BMI.

Conclusion: In the absence of variceal haemorrhage portal hypertension is under recognised. Comorbidities affecting patients in group 3 reported at higher levels than in groups 1 and 2 include CKD, IHD and heart failure. In patients with portal hypertension it’s important to address comorbidities in addition to the underlying liver disease.

FRI487

Durability of immune response to SARS-CoV-2 vaccination in patients with liver cirrhosis (LC) as compared to healthcare workers (HW)

Alessandra Mangia1, Valeria Piazzolla1, Maria Squillante1, Giovanna Cocomazzi1, Vito Ciciriello2, Vincenzo Giambra2, Nicola Serra3, 1Liver Unit, IRCCS “Casa Sollievo della Sofferenza”, San Giovanni Rotondo, Italy; 2ISBREMIT, IRCCS “Casa Sollievo della Sofferenza”, San Giovanni Rotondo, Italy; 3University “Federico II”, Public Health, Napoli

Email: a.mangia@tin.it

Background and aims: Patients with advanced liver disease have well recognized deficiencies in innate and humoral immunity. Phase 3 trials on both BNT162b2 and mRNA-1273 included an extremely limited number of pts with liver diseases. Real life data on vaccine response in cirrhotics is lacking. To characterize the longitudinal anti-SARS-CoV-2 response in LC as compared to an age and gender matched HW population.

Method: In pts with established diagnosis of LC ± portal hypertension, levels of binding antibodies at baseline before the first BNT162b2 dose, 7 and 31 days after the first dose and 90 and 180 days after the second dose were evaluated and compared to HW levels at similar time-points. Semiquantitative serological testing for IgG antibodies anti S1 domain was performed by anti-SARS-CoV-2 QuantiVac ELISA (EUROIMMUN); cut-off for positivity = 32.5 BAU/ml. Swab test was performed in suspected cases by RT-PCR kit (ROCHE Diagnostics). Micro neutralization test using wild type virus is ongoing. LC pts were matched 3:1 with HW. Both pts and HW had received BNT162b2 vaccine.

Results: Among 207 LC pts identified so far, 178 have results currently available at the different time-points. After a careful analysis of the swab tests results, 28 pts COVID experienced were identified. Of 150 SARS-CoV-2 naive, 86 (58%) were male, mean age 65.4 ± 4. Pts with HCV etiology were 67%, pts with portal hypertension 29%. Geometric Mean of anti-SARS-CoV-2 antibody levels overall and by gender among LC pts and HW in the Table. Higher levels of anti-SARS-CoV-2 were observed in HW as compared LC at d7 (p = 0.007) and d31 (p = 0.063), as well as at d90 (p = 0.0049) and d180 (p = 0.039). At d180, the number of pts with results lower than the assay’s threshold was higher among LC than in HW (5 vs 0, P = 0.0028). Irrespective of age, female pts were more likely to have higher anti-SARS-CoV-2 levels as compared to male at late time points.

<table>
<thead>
<tr>
<th>HW (n = 50)</th>
<th>LC (n = 150)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>d7</td>
</tr>
<tr>
<td>Timepoints</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>9.78</td>
</tr>
<tr>
<td>Male (54%)</td>
<td>1.192</td>
</tr>
<tr>
<td>Females (46%)</td>
<td>7.89</td>
</tr>
</tbody>
</table>

*after the second dose; “P = 0.028; “P = 0.024
Conclusion: Pts with LC showed an initial response to SARS-CoV-2 vaccination weaker than that of HW. An earlier antibody decline was also observed. The number of pts with absent anti-SARS-CoV-2 after 180 days was higher than in HW. This ongoing study highlights the need of a possibly more intensive vaccination schedule in LC as compared to HW.

FR1488
A simple model for predicting survival in cirrhotic patients undergoing portosystemic shunt embolization
Won-Mook Choi1, Seungbong Han2, Young Seok Kim3, Dong Hyun Sinn4, Dong Il Kwon5, Young-Suk Lim6, 1Asan Medical Center, University of Ulsan College of Medicine, Department of Gastroenterology, Seoul, Korea, Rep. of South; 2Korea University College of Medicine, Department of Biostatistics, Seoul, Korea, Rep. of South; 3Soomunghyang University Bucheon Hospital, Division of Gastroenterology and Hepatology, Bucheon, Korea, Rep. of South; 4Samsung Medical Center, Department of Medicine, Seoul, Korea, Rep. of South; 5Asan Medical Center, University of Ulsan College of Medicine, Department of Radiology, Seoul, Korea, Rep. of South; Email: limys@amc.seoul.kr

Background and aims: Portosystemic shunt embolization (PSSE) is an effective treatment for hepatic encephalopathy and gastric varix in patients with portosystemic shunt. However, some of the patients rapidly progress to hepatorenal syndrome and hepatic failure after PSSE. The aim of this study was to develop a prognostic model for predicting survival in patients treated with PSSE.

Method: We included 188 patients with portosystemic shunt who received PSSE for gastric varix or recurrent hepatic encephalopathy to develop a prediction model for 1-year mortality using a Cox proportional-hazard model incorporating significant prognostic factors, which was validated in a separate cohort of 184 patients.

Results: Using multivariable analysis, baseline serum levels of total bilirubin, albumin, and international normalized ratio (INR) were the independent prognostic factors that were significantly associated with the 1-year survival of the patients. An Albumin-Bilirubin-INR (ABI) score was developed assigning 1 point for ≥1.5 mg/dL of total bilirubin, <3.0 g/dL of albumin, and ≥1.5 for INR, respectively. Time-dependent area under the curve of the ABI score for predicting 6-month and 1-year survival were 0.851 (95% confidence interval [CI], 0.778–0.923) and 0.857 (95% CI, 0.793–0.921) in the development cohort and 0.777 (95% CI, 0.664–0.829) and 0.727 (95% CI, 0.624–0.829) in the validation cohort, which was comparable to the MELD score and the Child-Pugh score, indicating excellent discrimination performance. The ABI score showed a better calibration performance than other scores, especially in patients at high-risk.

Conclusion: The novel ABI score, which is easier to calculate than MELD or Child-Pugh scores, may help identify a proper indication for PSSE in cirrhotic patients with portosystemic shunt.

FR1489
Blunted cardiovascular effects of beta-blockers in patients with cirrhosis: relation to severity?
Puria Nabilou1, Karen Danielsen1, Nina Kimer2, Jens Hove3,4, Flemming Bendtsen1,4, Søren Møller3,5, 1Hvidovre Hospital, Gastro Unit, Medical Division, Hvidovre, Denmark; 2University of Copenhagen, Bridge Translational Excellence Program, Novo Nordisk Center for Basic Metabolic Research; 3Hvidovre Hospital, Department of Cardiology, Hvidovre, Denmark; 4Hvidovre Hospital, Department of Clinical Medicine, Hvidovre, Denmark; 5Hvidovre Hospital, Department of Clinical Physiology and Nuclear Medicine, Center for Functional and Diagnostic Imaging and Research, Hvidovre, Denmark Email: purianabilou@hotmail.com

Background and aims: Patients with cirrhosis and portal hypertension are at high risk of developing complications such as variceal hemorrhage, ascites, and cardiac dysfunction known as cirrhotic cardiomyopathy. Since non-selective betablockers may aggravate hemodynamic complications we investigated the effect of real-time propranolol infusion on cardiac function in patients with varying degrees of cirrhosis.

Method: Thirty-eight patients with Child-Pugh A (n = 17), B (n = 17) and C (n = 4) had liver vein catheterization and cardiac magnetic resonance imaging performed. We assessed the effect of real-time propranolol infusion on the hepatic venous pressure gradient, cardiac index, stroke volume, ejection fraction, heart rate, and contractility. 19 patients were classified responders to beta-blocker therapy.

Results: When pooling Child-Pugh B & C patients, the decrease in cardiac index by beta-blockade was blunted, compared to Child-Pugh A patients (−8.5% vs. −20.5%, p = 0.043). The effect of NSBB on portal pressure was inversely correlated to the changes on left atrium since the left atrial volume changed by 4 ml ± 18 in the responders compared to 15 ml ± 11 in the non-responders (p = 0.03). Finally, baseline ejection fraction correlated inversely with the decrease in portal pressure r = −0.39, p = 0.02.

Conclusion: We found a blunted effect of beta-blockade on cardiac index in patients with advanced cirrhosis compared to patients with early cirrhosis indicating impaired compensatory cardiac reserve and underlying cirrhotic cardiomyopathy with disease progression. The differential effects of beta-blockade on the left atrium may predict the beta-blocker response on portal pressure but further studies are warranted on this matter.
Background and aims: Hepatorenal syndrome (HRS)-acute kidney injury (AKI) is a rare and serious complication of cirrhosis, with serum creatinine (SCr) used diagnostically. Women generally have less muscle mass and consequently lower SCr levels than men with similar renal function. Terlipressin more effectively reverses HRS when started at lower SCr levels. The largest randomized, prospective database of placebo-controlled studies in patients (pts) with HRS-AKI was examined to assess a gender-based impact on treatment response.

Method: Pooled data from 3 phase III US studies (OT-0401, REVERSE, CONFIRM) were used; pts with HRS-AKI were treated with terlipressin plus albumin (terli) or placebo plus albumin (pbo). Associations between baseline (BL) SCr (SCr upon treatment initiation) and clinical response (complete response [CR]; HRS reversal, SCr ≥0.5 or less) or partial response [PR]; at least 30% improvement in SCr) stratified by treatment and gender were assessed. Overall response rate (ORR) comprised pts with a CR or PR; p values were calculated using a Fisher’s exact test.

Results: Males in the terli group with BL SCr ≥3 had significant improvements in CR and ORR, relative to pbo, while females did not (Figure). Among pts with a BL SCr of 3–5, both males and females had a significant improvement in ORR (terli vs pbo); however, only males had significant improvements in CR. Across genders, pts with a BL SCr >5 demonstrated limited response to treatment.

<table>
<thead>
<tr>
<th>Parameter, n (%)</th>
<th>BL SCr &lt;3</th>
<th>BL SCr 3–5</th>
<th>BL SCr &gt;5</th>
</tr>
</thead>
<tbody>
<tr>
<td>Male HRS</td>
<td>74 (46.6)</td>
<td>36 (27.7)</td>
<td>38 (10.0)</td>
</tr>
<tr>
<td>Female HRS</td>
<td>42 (56.8)</td>
<td>15 (31.9)</td>
<td>11 (11.5)</td>
</tr>
<tr>
<td>Male ORR</td>
<td>27 (51.9)</td>
<td>11 (22.7)</td>
<td>11 (22.7)</td>
</tr>
<tr>
<td>Female ORR</td>
<td>52 (52.0)</td>
<td>37 (37.0)</td>
<td>37 (37.0)</td>
</tr>
</tbody>
</table>

Conclusion: Pts in the terli group had a greater clinical response vs pbo for BL SCr of <3. Males were more likely to have a CR and ORR than females, especially those with BL SCr ≥3–5. Despite matched SCr, females had a lower response than males, likely reflecting more advanced renal dysfunction upon treatment initiation. New guidance recommending initiation of vasoconstrictor treatment based on SCr change from BL rather than absolute cut-offs may improve outcomes for female pts. Additional biomarkers to evaluate renal dysfunction should also be evaluated.

Background and aims: Ascites formation is a common manifestation of cirrhosis decompensation and heralds a poor prognosis. Refractory ascites (RA) denotes a worsened state of this condition, where pharmacotherapies are ineffective or induce significant side-effects. The current definition of RA remains largely unaltered through the past 25 years, and rests on a panel of diagnostic criteria including the introduction of intensive diuretic therapy and a modest salt-restrictive diet, and evaluations of renal sodium excretion, weight loss, ascites recurrence rate, and diuretic-induced complications. Further, the traditional binary RA classification may be too simplistic as a predictive measure. We aim to develop a prediction model that relies on easily obtainable ascites-related variables and predicts one-year mortality more accurately than the traditional RA classification.

Method: We included 478 patients from the placebo-groups of trials for the treatment of cirrhotic ascites. The outcome was mortality hazard during one year of follow-up. Fractional polynomials were included to investigate the functional form of continuous variables. We used Cox regression with stepwise backward variable selection of ascites-related predictors of mortality. Candidate variables were: age, sex, serum sodium, ascites discomfort score, and a categorical variable based on ascites accumulation and diuretic treatment (ascites accumulation with no, moderate, and intensive diuretic treatment, and no ascites accumulation with any diuretic treatment). We compared the final model’s discriminative ability (Harrell’s C index) with that of the traditional RA classification.

Results: The final prediction model included age, serum sodium, and the categorical accumulation/diuretics variable. The Cirrhotic Ascites Severity (CIRAS) score was computed as 0.041* (age-56)-0.078* (serum sodium-137) and then add 0.718 if ascites accumulation and no diuretics, or add 0.407 if ascites accumulation and intensive diuretic treatment, or subtract 0.270 if no ascites accumulation and any diuretic treatment. The CIRAS score had a C index for one-year mortality of 0.70 (95% CI: 0.64–0.75) which was statistically significantly better than the traditional RA classification with a C index of 0.60 (95% CI: 0.55–0.65) (p < 0.001, Figure).

Conclusion: The novel CIRAS score combining age, serum sodium, diuretic treatment, and ascites accumulation has better discriminative ability than the traditional RA classification during a one-year follow-up. These findings warrant validation in external cohorts.
POSTER PRESENTATIONS

Frequent hospitalisations and high mortality make prevention of OHE essential. Current treatment options for OHE include nonabsorbable disaccharides (e.g. lactulose) and antibiotics (e.g. rifaximin–alpha 550 mg). We conducted a network meta-analysis (NMA) of data from a previously published literature review (Hudson M, Schuchmann M. Eur J Gastroenterol Hepatol 2019:31:434–50) to determine the comparative long-term efficacy, in terms of number needed to treat (NNT) to prevent an additional OHE episode, of lactulose versus placebo and lactulose + rifaximin–alpha versus placebo.

Method: Literature searches were previously conducted in PubMed of titles and abstracts only, with language restricted to English and the data range unrestricted up to the cut-off date (05 March 2018), using the following search terms: ‘hepatic encephalopathy + rifaximin’ and ‘hepatic encephalopathy + lactulose’. Randomized controlled trials (RCTs) with long-term (> = 6 months) effectiveness endpoints for lactulose and/or rifaximin–alpha were selected for NNT analysis if statistically significant between-group differences were reported in the rate of OHE recurrence. In this analysis, we conducted an indirect treatment comparison analysis using the odds ratio (OR) for OHE recurrence for NNT mapping. The NMA was conducted using the Mantel–Haenszel approach, with placebo used as the reference treatment and only the fixed effect analysis considered.

Results: A total of 570 articles, including 201 with primary clinical data, were identified. Long-term treatment was reported in 8 articles for lactulose alone and in 19 articles for rifaximin–alpha, alone or in combination with lactulose. NNTs were calculated from 4 studies. When the ORs for the relative efficacy of each treatment versus each of the remaining treatments were calculated, the ORs (95% confidence intervals) for lactulose versus placebo and lactulose + rifaximin–alpha versus placebo were 0.276 (0.164–0.466) and 0.081 (0.042–0.158), respectively. The resulting NNTs were lower for lactulose + rifaximin–alpha versus placebo (2.28) than for lactulose versus placebo (3.46; Figure).

Conclusion: This NMA based on NNTs demonstrated that, in comparison with placebo, lactulose + rifaximin–alpha may be more effective than lactulose alone in preventing OHE recurrence.

FR1493
Transjugular intrahepatic portosystemic shunt versus balloon-occluded transvenous obliteration for the management of ectopic varices
Ranya Selim1, Jenna Yousif2, Daniel Hillman2, Scott Schwartz3, Kylie Springer4, Dilip Moonka1. 1. Henry Ford Hospital, Gastroenterology and Hepatology, United States; 2. Wayne State University School of Medicine, United States; 3. Henry Ford Hospital, Radiology, United States; 4. Henry Ford Hospital, Biostatistics, United States
Email: ranyaselim@gmail.com

Background and aims: Bleeding ectopic or non-gastroesophageal varices occur uncommonly in the setting of portal hypertension. Both transjugular intrahepatic portosystemic shunt (TIPS) and balloon-occluded antegrade or retrograde transvenous obliteration (BA-RTO) are potential treatment options. Our study is the first to assess and compare TIPS vs. BA-RTO for the management of ectopic varices.

Method: This is a retrospective cohort study at a tertiary liver center. All interventional radiology procedures performed for bleeding varices between 2006 and 2020 were identified. Only patients undergoing TIPS and BA-RTO for bleeding ectopic varices were included. Demographics, pre-procedural data and outcome data was collected and compared between BA-RTO and TIPS groups.

Results: Eleven patients undergoing BA-RTO were compared to seven patients undergoing TIPS. In 6 of the BA-RTO patients, TIPS was deemed unfeasible. Mean age at procedure was 55.6 ± 10.0. 55.6% were men and 83.3% were white. There were 8 rectal varices, 7 peristomal, one duodenal, one cecal and one superior mesenteric. The mean MELD-Na prior to procedures was 19.0 ± 6.4 in the BA-RTO group vs. 19.0 ± 6.4 in the TIPS groups (p = 0.69). In the BA-RTO vs. TIPS groups, respectively, the mean MELD-Na at 30 days after procedure was 18.0 ± 4.2 vs. 24.0 ± 7.5 (p = 0.39). Rebleeding rates during admission were 9.1% for BA-RTO vs. 14.3% for TIPS (p = 1.00). The mean length of stay for BA-RTO vs. TIPS was 10.6 ± 8.9 vs. 7.9 ± 8.1 days (p = 0.41), mean paracenteses 90 days prior and after procedure were 1.9 ± 3.6 vs. 0.0 ± 0.0 (p = 0.12) and 2.0 ± 3.9 vs. 0.0 ± 0.0 (p = 0.082), in the BA-RTO vs TIPS groups, respectively. The rates of hepatic encephalopathy in the BA-RTO vs TIPS groups at 90 days before and after the procedure were 45.4% vs. 57.1% (p = 1.00) and 28.6% vs 33.3% (p = 1.00), respectively. The mortality rates were 27.3% vs 28.6% (p = 1.00) in the BA-RTO vs TIPS groups.

Conclusion: Our results demonstrate that both TIPS and BA-RTO are effective treatment modalities for bleeding ectopic varices, with comparable post-procedure outcomes. Patients undergoing BA-RTO had a higher MELD at procedure but lower MELD at 30 and 90 day post-procedure and less HE though no differences were significant.

BA-RTO is an excellent option for bleeding ectopic varices, primarily rectal and peristomal, and especially in patients not candidates for TIPS.
Method: Severity of PH was assessed by HVPG measurement that served as the reference standard. Serum samples were pooled based on HVPG measurement in two groups: with and without CSPH. ECV were isolated from the serum pools using ultracentrifugation and vesicle membranes were lysed by sonication. ECV protein cargo was analyzed by Liquid Chromatography-Mass spectrometry (LC-MS). Samples were analyzed in triplicates and proteins identified with at least one peptide were considered relevant for analysis. Functional enrichment analysis of the isolated proteins was conducted using FunRich 3.1.3 analysis tool.

Results: A total of 48 patients were included (30 in the CSPH group and 18 in the non-CSPH group, 75% males; median age: 59, 9 ± 9, 8 years; majority with alcoholic (48%) and non-alcoholic fatty liver disease (23%). LC-MS analysis of ECV content resulted in identification of 733 proteins (38 distinctive for CSPH, and 75 for non-CSPH group), that were further classified based on their cellular origin and function. Proteins involved in platelet degranulation, integrin-mediated signaling pathway, receptor mediated endocytosis and regulation of cholesterol efflux were more represented, whereas those involved in opsonization, phagocytosis, complement activation, immune and inflammatory response were less represented in the CSPH group. Among the individual proteins that showed the most significant difference between the studied groups phospholipid transfer protein and beta-2-glycoprotein 1 were more represented, whereas complement C1q, C1r and C1s subcomponents and annexin A2 were less represented in the CSPH group.

Conclusion: Results of this study provide additional insights into pathophysiological processes taking place along the development of PH in patients with cALD. Distinctive protein profiles are identified between the patients with respect to the presence of CSPH. Several individual proteins are identified that should be furtherly studied as the potential non-invasive biomarkers of CSPH.

**FR495**

Factors influencing survival in cirrhotic patients with hepatic hydrothorax

Sarah Romero1, Andy Lim2, Gurpeet Singh3, Chamani Kodikara1, Rachel Shingaki-Wells1, Lynna Chen3, Samuel Hui1, Marcus Robertson1,4

1Monash Health-Clayton Hospital Main Entrance, Gastroenterology, Clayton, Australia; 2Monash University Clayton Campus; 3Department of Medicine, School of Clinical Sciences, Clayton, Australia; 4Austin Hospital, Gastroenterology & Liver Transplantation, Heidelberg, Australia

Email: s.romero.md@gmail.com

Background and aims: Hepatic hydrothorax (HH) remains a challenging complication of cirrhosis with limited treatment options. We sought to identify factors associated with mortality in hospitalised patients with confirmed HH treated with current standards-of-care.

Method: We performed a retrospective multi-center cohort study of cirrhotic patients with HH admitted to 3 tertiary hospitals (2010–2018). HH was defined as pleural effusion in the absence of cardiopulmonary disease. The primary outcomes were overall and transplant-free survival at 12-months after the index admission. Cox proportional hazards analysis was used to determine factors associated with the primary outcomes.

Results: 84 patients were included. Mean age 58.3 ± 11.5 years and 54.8% were male. The median Model for End-stage Liver Disease (MELD) score was 29 (IQR 25–33). Management of patients aligned with AASLD guidelines. Diuretics alone achieved resolution of HH in only 12% patients. At least 1 thoracocentesis was performed in 73.8% patients, of which 15% were complicated by pneumothorax. Within 12-months of the index admission, 33% patients received liver transplantation (LT) and 11.5% had transjugular intrahepatic porto-systemic shunt (TIPS) insertion, none of whom subsequently required LT. At least 1 hospital readmission was required in 63 (75%) patients, most commonly due to recurrent hydrothorax (38%) and decompensated cirrhosis (41%). Overall and transplant-free survival at 12-months were 68% and 41% respectively. The majority of deaths occurred early after the index admission, with a 45-day overall survival of 80%. The most common cause of deaths was complications of end-stage liver disease and multiorgan failure (75%). No deaths were recorded in patients receiving LT. In the multivariable analysis, increasing age (per 5-year increase, HR 1.3 (CI 1.1–1.7), p = 0.04), increasing MELD score (per 5 points, HR 1.5 (CI 1.1–1.7), p = 0.02), current smoking (HR 8.7 (CI 3.4–21.9), p = 0.01) and acute kidney injury (AKI) (HR 2.9 (CI 1.2–7.0), p = 0.01) were associated with a significantly increased risk of death. After bootstrapping and correcting for MELD score and age, a current smoker had 8.7 times the hazard of death of a non- or ex-smoker and AKI was associated with a 2.9-fold increase in the hazard of death (Figure).

Conclusion: Cirrhotic patients with HH continue to have a poor 12-month survival despite current treatments and a high-risk of treatment-related complications. LT assessment should be considered in all cases. Current smoking and episodes of AKI are potential modifiable factors affecting survival.

**FR496**

Hepatic venous pressure gradient (HVPG) measured at events is lower in non-alcoholic fatty liver disease (NAFLD) associated cirrhosis as compared to alcoholic cirrhosis

Lubomir Skladany1, Daniela Jancekova1, Michal Žilínčan2, Stanislav Okápec2, Janka Vnencakova1, Svetlana Adamcova Selcanova1, Michal Kukla3, Tomáš Koller4, 1ED.Roosevelt Teaching Hospital, HEGITO (Div Hepatology, Gastroenterology and Liver Transplant) of the Dept Internal Medicine 2, Banská Bystrica, Slovakia; 2F .D.Roosevelt Teaching Hospital, HEGITO (Div Hepatology, Gastroenterology and Liver Transplant) of the Dept Internal Medicine 2, Banská Bystrica, Slovakia; 3Faculty of Medicine, Jagiellonian University Medical College, Gastroenterology, Krakow, Poland; 4University Hospital of Bratislava, Faculty of Medicine Comenius University, Div Gastroenterology Hepatology of Dept Internal Medicine 5, Bratislava, Slovakia

Email: lubomir.skladany@gmail.com

Background and aims: In our region, alcohol-associated liver disease (ALD) and NAFLD are the most prevalent and the fastest-growing cirrhosis etiologies, respectively. We have recently demonstrated, that a natural history of cirrhosis differs in NAFLD as compared to ALD. HVPG is a strong surrogate of cirrhosis severity but its value in NAFLD is yet to be clarified. We aimed to compare HVPG in NAFLD with ALD according to the indication (compensated and decompensated disease) with a particular focus on variceal bleeding (VB) and refractory ascites (RA).

Method: In our hospital system, we have retrospectively identified patients who underwent HVPG measurement and scrutinized them
against our RH7 cirrhosis registry (NCT04767945). Then we retrieved patients’ etiologies-ALD, NAFLD and other (viral [VIR], autoimmune [AI])—as well as indications for HVPG measurement—RA (or hydrothorax), liver resection, differential diagnosis with transjugular liver biopsy, or implantation of TIPSS. We excluded patients with other etiologies, malignancies, and those with less than 6 months of follow-up.

**Results:** We enrolled 220 patients. Cirrhosis was due to NAFLD and ALD in 52 and 128 pts (VIR and AI in 26 and 14), respectively. Patients with NAFLD vs. ALD had similar age (60.4 vs. 56.9), a higher proportion of females 67.3 vs. 31.2, lower MELD scores (13.0 vs. 16.0), and a lower white blood cell count (4.9 vs. 6.15). Overall, the median HVPG in NAFLD and ALD (VIR and AI) was 14.0 and 18.0 (12.5 and 10.0) mmHg (P-value for trend <0.001), respectively. In 30 and 19 (17 and 8) compensated pts, HVPG was 11.5 and 10.0 (12.0 and 6.5) mmHg (P = 0.4). Among decompensated pts with VB, in 16 and 51 (7 and 5) the HVPG was 15.5 and 19.0 (13.0 and 18.0) mmHg, respectively. Independently of portal hypertension, the median HVPG was 16.5 and 19.0 (16.0 and 16.0) (P = 0.75). Transplant-free survival at 3 and 6 months did not differ between NAFLD and ALD (84.6 vs. 85.2, and 82.7 vs. 75.8%).

**Conclusion:** Overall, and in decompensated cirrhosis, the NAFLD etiology was associated with lower values of HVPG compared with ALD, likely reflecting a lower HVPG threshold for VB in NAFLD.

**FRI497**

**Low subcutaneous adipose tissue is associated with mortality independently from portal hypertension in patients with cirrhosis**

Xun Zhao1, Balqis Alabdulkarim1, Dana Kablawi1, Marc Deschenes1, Philip Wong1, Tianyan Chen1, Benjamin Rehany1, Mohamed Abu-Nada1, David Valenti1, Ali Bessissow1, Giada Sebastiani1, Amine Benmassaoud1, *McGill University Health Centre Glen Site (MUHC), Montréal, Canada*

Email: amine.benmassaoud@mcgill.ca

**Background and aims:** Sarcopenia and adipopenia are associated with worse outcomes in patients with cirrhosis. To this date, it is unclear if muscle and adipose tissue mass predict mortality independently from portal hypertension. The aim of our study was to investigate whether body composition could predict mortality while adjusting for the severity of portal hypertension by using the gold standard, the Hepatic Venous Pressure Gradient (HVPG).

**Method:** This was a single center retrospective cohort study of adult patients with cirrhosis who underwent HVPG measurement between November 2012 and June 2020 and had available cross-sectional imaging at the 3rd lumbar vertebrae (L3). Participants were excluded if HVPG was not reliable or if imaging was performed more than 12 months prior to HVPG measurement. HVPG was determined using CoreSlicer, a dedicated radiology software. Total psoas muscle index (PMI), total skeletal muscle index (SMI), subcutaneous and visceral adipose tissue indexes (SATI, VATI) were calculated at L3 by measuring their respective areas and dividing by the height squared (in cm²/m²). Factors associated with death were assessed using univariate and multivariate logistic regression.

**Results:** We included a total of 81 patients (mean age 60.2 years, 62% males, 31% with non-alcoholic fatty liver disease, 20% with alcohol-related liver disease and 17.3% with viral hepatitis, 52% with HVPG above 10 mmHg, 54% with decompensated cirrhosis at baseline, and median MELD 13). During follow-up, 27 (33.3%) patients died. Patients who died were older (64.6 yrs vs 58 yrs, P = 0.018), had higher HVPG (13.7 mmHg vs 9.2 mmHg, P = 0.004), lower muscle mass (PMI: 4.5 vs 5.6, P = 0.002; SMI: 41.3 vs 48.5, P = 0.002), lower SATI (45.6 vs 74.2, P = 0.002), and tended to have a higher MELD (15.3 vs 12.9, P = 0.067). Sex, BMI and VATI were not associated with mortality. In separate models for each compartment, after adjusting for age and HVPG, SATI (aOR = 0.98, 95%CI 0.97–0.99) and SMI (aOR = 0.94, 95%CI 0.88–0.99) were associated with mortality, but not PMI or VATI.

**Conclusion:** We have shown that SATI is associated with mortality independently of HVPG. Future larger studies should review the strength of this association separately for males and females and propose cut-offs.

**FRI498**

**Association of low mechano-energetic efficiency and prognosis in liver cirrhosis**

Sanna Sjøstedt1, Signe Wiese2, Flemming Bendtsen3,4, Sören Müller1,2,3, *Hvidovre Hospital, Department of Clinical Physiology and Nuclear Medicine, Hvidovre, Denmark; 4Gastro Unit, Medical Division, Hvidovre; 2Hvidovre Hospital, Gastro Unit, Medical Division, Hvidovre; 3Copenhagen University, Department of Clinical Medicine, Faculty of Health Sciences, Copenhagen, Denmark*

Email: sannia@dgdlnet.dk

**Background and aims:** In cirrhosis, cardiac systolic dysfunction as part of cirrhotic cardiomyopathy (CCM) affects development of complications and course of the disease and prognosis. Myocardial mechano-energetic efficiency (MEE) is an estimate of left ventricular performance and reduced MEE is associated with poor prognosis in heart failure patients. In this study we aimed to investigate the relation of MEE to patient characteristics and its impact on survival in patients with cirrhosis.

**Method:** We included 283 patients with cirrhosis of different severity according to the Child-Pugh classifications (A/B/C: 106/87/90). All patients had a liver vein catheterization and a hemodynamic investigation performed including determination of cardiac output (CO), stroke volume, and heart rate (HR). These data were used to assess MEE, which was defined as (stroke volume/HR)×1.666.

**Results:** Eighty-nine percent of the patients had portal hypertension (Hepatic venous pressure gradient >5 mmHg) and 80% indications of a hyperdynamic cirulatory state with increased CO and HR. There was no difference in MEE in Child-Pugh class C patients (2.03) vs Child-Pugh class A (1.98) and B (2.05) patients. In Child-Pugh class C patients, low MEE was associated with a poorer prognosis (median survival 866 days vs 2893 days).

Figure: Kaplan-Meier plot showing differences in survival in liver cirrhosis patients classified as Child C stratified by MEE (low MEE below the median value and high MEE above the median value). A significantly poorer survival is seen in patients with low MEE.

**Conclusion:** In our study, MEE does not seem to be associated with severity of the liver disease, but in patients with advanced disease low MEE is associated with a poorer prognosis. The prognostic impact of MEE should be further investigated in future prospective studies.
FR499
Long term albumin administration is associated with reduced healthcare resource use in patients with uncomplicated cirrhotic ascites: results from a simulation model
Kris Bennett1,2, Elisabet Viana3, Murat Guna4, Duncan Stacey5, Anne Davis6, David Southern7, Matthew Cramp1, 1University Hospitals Plymouth NHS Trust, South West Liver Unit, Plymouth, United Kingdom; 2University Hospitals Plymouth NHS Trust, South West Liver Unit, Plymouth, United Kingdom; 3Grifols S.A., Sant Cugat del Valles, Spain; 4Simartem, Istanbul, Turkey; 5Grifols UK, Cambridge, United Kingdom; 6Employed by Grifols SSNA, NC, United States; 7SSB Research Ltd., United Kingdom

Background and aims: Decompensated cirrhosis is associated with high rates of complications and costs. The ANSWER trial showed that long-term local albumin infusions (LTA; 40 g twice/week for 2 weeks, 40 g/week thereafter) added to standard medical treatment (SMT) led to significant reduction of complications and mortality in patients with uncomplicated ascites. We developed a discrete event simulation (DES) model to estimate economic and clinical impacts of LTA in patients with cirrhosis and uncomplicated ascites in the UK. Real-world rates of hospital visits, treatments, and complications in the UK are used as model inputs. The potential benefit of LTA is modelled on data from the ANSWER trial.

Method: We developed a DES model using Simul8 Professional 2021 software to simulate individual patients’ disease course by tracking health events (treatments, complications, hospitalizations, death) over time. We compared outputs for 2 patient cohorts: 1) SMT only, 2) SMT + LTA per ANSWER protocol. Model inputs for the SMT cohort were health event probabilities retrieved from Hospital Episode Statistics for 10 UK hospitals between April-2016 and Mar-2020. This real-world data gathered from 873 cirrhotic patients with uncomplicated ascites comprised 12-month rates for hospital visits, cirrhosis complications, treatments, and death. These were transformed into costs using NHS tariffs. Reduction in health event probabilities for the SMT + LTA cohort was based on ANSWER trial data.

Results: A hypothetical cohort of 100 patients with cirrhosis and uncomplicated ascites was simulated over 12 months, first with all patients treated with SMT, and then with 30% of patients treated with SMT + LTA; 30% was felt to represent an achievable patient volume for administering LTA in cirrhotic cohorts. In our model, the use of LTA decreased hospital admissions by 12.6% and reduced incidence of cirrhosis-related complications. The development of refractory ascites decreased from 37% to 30% in the LTA group. In the model, SMT + LTA in 30 out of 100 patients with uncomplicated cirrhotic ascites may save up to £264,589/year in total healthcare costs.

Conclusion: Our DES model suggests that, if outcomes reported in the ANSWER trial translate to similar real-world benefits in UK patients, the use of LTA in cirrhotic uncomplicated ascites could lead to cost-savings, even when administered to a proportion of those eligible.

FR500
Improved survival rates in hepatic encephalopathy after a decade of clinical practice with the addition of rifaximin-alpha to lactulose: a real-world data meta-analysis
Juha Halonen1, Roland Henrari1, 1Norgine Ltd, Harefield, United Kingdom

Background and aims: Hepatic encephalopathy (HE) is a frequent complication of liver cirrhosis with a high risk of both short-term and long-term mortality [1]. Real-world longitudinal data on mortality rates in HE are scarce. This meta-analysis of two available studies compared the survival rates attained over approximately one decade.

Method: In HE, real-world mortality rates over 5 years were initially reported in patients with alcohol-related liver cirrhosis [1] and more recently in patients with HE who received combination treatment with rifaximin-alpha plus lactulose [2, 3]. Our meta-analysis calculated survival rates at 1, 12 and 60 months in the first study, and at 12, 36 and 60 months in the more recent study. Survival rates at 12 and 60 months were compared between studies using two-sided t-tests, assuming equal variance.

Results: The first study (conducted in 1993–2006) included 169 patients with HE and survival rates at 1, 12 and 60 months were 55%, 36% and 15%, respectively. The more recent study (conducted in 2014–2019) included 136 patients with HE and survival rates after 12, 36 and 60 months were 72%, 49% and 35%, respectively. Survival rates were significantly higher in the more recent study in comparison with the previous study at both 12 months (72% vs 36%; p = 0.029) and 60 months (35% vs 15%; p < 0.001). In the more recent study, all patients received lactulose plus rifaximin-alpha 550 mg; in the previous study, treatments were not reported but were likely to consist of lactulose alone. Notably, the number needed to treat to prevent an HE death, when comparing the more recent study versus the previous study, was 2.8 at 12 months and 4.9 at 60 months.

Conclusion: Direct comparison of the two studies is limited by different countries and by expected clinical improvements over a decade. Nevertheless, these real-world results suggest that treating patients with a combination of rifaximin-alpha 550 mg twice daily plus lactulose, rather than lactulose alone, may improve both 1-year and 5-year survival rates in HE in current clinical practice.

References

FR501
Risk prediction of hepatic encephalopathy after molecular targeted therapy for hepatocellular carcinoma in patients with cirrhosis
Kisako Fujiwara1, Takayuki Kondo1, Saé Yumita1, Takamasu Ishino1, Keita Ogawa1, Mijuhyi Nakagawa1, Hidemi Unoza1, Terunaor Iwana1, Takaufumi Sakuma1, Naoto Fujita1, Hiroaki Kanzaki1, Keisuke Koroki1, Kazufumi Kobayashi1, Soichiro Kiyono1, Masato Nakamura1, Naoya Kanogawa1, Tomoko Saito1, Sadahisa Ogasawara1, Shingo Nakamoto1, Tetsuhiro Chiba1, Jun Kato1, Naoya Kato1, 1Graduate School of Medicine, Chiba University, Department of Gastroenterology, Chiba, Japan

Background and aims: The management of hepatic encephalopathy (HE) during treatment for advanced hepatocellular carcinoma is crucial because it may cause interruption of molecular targeted therapy. However, the incidence of HE and the risk of its development has not been sufficiently clarified. In this study, we investigated the incidence and risk factors of HE in cirrhotic patients with advanced hepatocellular carcinoma after the first-line chemotherapy.

Method: This retrospective study enrolled 316 cirrhotic patients with advanced hepatocellular carcinoma diagnosed by contrast-enhanced
POSTER PRESENTATIONS

computed tomography (Child-Pugh A 242 cases/B 74 cases) who received molecular targeted agents as first-line chemotherapy between July 2009 and February 2019 and measured ammonia levels before (pre-treatment) and 1 week after treatment (post-treatment). We examined the incidence and predictors of HE within 2 weeks after treatment.

Results: Incidence of HE: Pre-treatment serum ammonia levels elevated significantly compared to post-treatment (56.9 ± 30.6 vs. 79.9 ± 48.3 μmol/L, P < 0.001), and hepatic encephalopathy was observed in 14 patients (4.4%) within 2 weeks after chemotherapy. Risk factors for the development of HE: Multivariate analysis showed that higher pre-treatment ammonia levels (Odds ratio 1.022 [1.008–1.036], P = 0.002) and the greater maximum diameter of portosystemic shunts (Odds ratio 1.094 [1.014–1.179], P = 0.020) were significant predictive factors for the development of HE.

Predictive model for the development of HE using a decision-tree-based approach: The final selected tree-discriminated cases were classified according to the following 3 subpopulations; low-risk group (ammonia levels <73 μmol/L; development of HE, 0.9%), intermediate-risk group (ammonia levels ≥73 μmol/L, and portosystemic shunt diameter >6.2 mm; development of HE, 4.2%), and high-risk group (ammonia levels ≥73 μmol/L, and portosystemic shunt diameter ≥6.2 mm; development of HE, 20%).

Conclusion: The development of HE after molecular targeted therapy could be clearly risk-segmented according to the ammonia level and the diameter of portosystemic shunts. Therefore, treatment for HE should be considered in cases with higher ammonia levels and large portosystemic shunt before molecular targeted therapy.

FRI502
ABC: a novel algorithm to stratify decompensation risk in patients with cACLD (CHESS2102): an international, multicenter cohort study
Chuan Liu1, Jia Li2, Yu Jun Wang3, Qing Xie4, Masashi Hirooka5, Hirayuki Enomoto6, Tae Hyung Kim7, Amr Hanafy8, Zhujun Cao9, Lili Zhao10, Yanna Liu1, Yifei Huang11, Xiaoguo Li12, Ning Kang13, Yohei Koizumi14, Yoichi Hiasa15, Takashi Nishimura16, Hiroko Iijima17, Young Kul Jung18, Hyung Joon Yin19, Xin Li20, Qing-Lei Zeng21.

Xiaolong Qi1. 1The First Hospital of Lanzhou University, CHESs CENTER, Institute of Portal Hypertension, China; 2Department of Gastroenterology and Hepatology, Tianjin Second People’s Hospital, Tianjin, China; 3Department of Gastroenterology & Hepatology, Changi General Hospital, Singapore; 4Department of Infectious disease, Ruijin hospital, Shanghai Jiao Tong university school of medicine, Shanghai, China; 5Department of Gastroenterology and Metabolism, Ehime University Graduate School of Medicine; 6Department of Internal Medicine, Division of Gastroenterology and Hepatology, Hyogo College of Medicine, Nishinomiya, Japan; 7Division of Gastroenterology and Hepatology, Korea University-Ansan Hospital, Ansan-si, Gyeonggi-do, Republic of Korea; 8Division of Gastroenterology, Hepatology and Endoscopy, Internal Medicine, Zagazig University Faculty of Medicine, Egypt; 9Department of radiology, Tianjin second people’s hospital, Tianjin, China; 10Department of Infectious Diseases and Hepatology, The First Affiliated Hospital of Zhengzhou University, Zhengzhou, 450052, China

Background and aims: Liver-related death is preceded by clinical decompensation; therefore, the risk stratification of decompensation in compensated advanced chronic liver disease (cACLD) is extraordinary significant. This study intended to investigate a novel algorithm to stratify the decompensation risk in patients with cACLD.

Method: The international, multicenter study included two cohorts from January 2009 to August 2020. In training cohort, the unfavorable Baveno VI criteria patients were used to develop the novel CHESS criteria to stratify decompensation risk. The Algorithm based on Baveno VI criteria plus CHESS criteria (ABC model) was validated in validation cohort.

Results: A total of 1188 cACLD patients were enrolled in training cohort and validation cohort. In training cohort, multivariate analysis revealed that liver stiffness measurement (LSM), platelet count (PLT), albumin, alanine aminotransferase (ALT) and varices were the independent risk factors for hepatic decompensation. The novel CHESS criteria was produced, and <−4.4, −4.4 to −3.1 and >−3.1 indicated the low risk, medium risk, and high risk of decompensation, with a 3 year-time-dependent area under the curve (tAUC) of 0.851 (0.800–0.901) (Figure 1 A). In validation cohort, the 3 year-tAUC of ABC model was 0.843 (0.742–0.943) (Figure 1 B).

Conclusion: The ABC model can stratify the risk of decompensation in cACLD. HVPG evaluation can be waived in both low risk and high risk cACLD patients as they can be managed by Baveno VI criteria and non-selective β-blockers intervention, respectively, and the remaining medium risk patients need further HVPG evaluation.

FRI503
Quantitative parameters of esophageal varices based on computed tomography may be used for predicting severe varices in patients with liver cirrhosis
Shang Wan1, Bin Song1. 1West China Hospital, West China School of Medicine, Sichuan University, Radiology, Cheng Du, China
Email: songlab_radiology@163.com

Background and aims: Esophageal varices (EV) are the most common complication in patients with portal hypertension resulted from liver cirrhosis, and the subsequent variceal bleeding is the leading cause of death in those patients. The invasive procedure of endoscopy is now regarded as the reference standard for evaluation of EV, however, the utility of it is limited due to the invasive nature and the high-cost effectiveness. Thus, in this study, we aimed to assess whether the quantitative computed tomography (CT)-derived parameters can noninvasively predict the severity of EV and the risk of esophageal variceal bleeding (EVB).

Method: In this retrospective study, a total of 145 endoscopically confirmed EV patients were included and were divided into a conspicuous (mild-to-moderate EV, n = 39) and a non-conspicuous EV group (severe EV, n = 106), a bleeding (n = 89) and a non-bleeding group (n = 56). EV grade (EVE), EV diameter (EVD), cross-sectional surface area (CSA), EV volume (EVV), spleen volume (SV), splenic vein (SNV), portal vein (PV), diameter of left gastric vein (DLGV), and the opening type of LGV were measured independently using 3D-slicer. Univariate and multivariate logistic analysis were used to determine the independent factors and the receiver operating characteristic (ROC) curves were performed to evaluate the diagnostic performance.

Results: The difference of EVE, EVD, CSA, EVV, DLGV, SNV between the conspicuous and non-conspicuous EV group were statistically significant (p < 0.05), area under the curves (AUCs) of them for predicting severe EV were 0.72, 0.772, 0.704, 0.768, 0.707, 0.65, with correspondingly sensitivities of 70.3%, 63.5%, 50%, 74.3%, 52.7%, 48.6%, specificities
The GORE® VIATORR® Device also resulted in +0.60 QALYs versus LVP saving by 21,493 Euros versus LVP over the time frame of the analysis.

Conclusion: From the Spanish healthcare perspective, this economic analysis suggests that the GORE® VIATORR® Device was cost saving and cost-effective at two years compared to LVP. Cost-savings were primarily driven by reduced LVP sessions and decreased inpatient hospital stay. Based on this economic evaluation the consideration of the GORE® VIATORR® Device in refractory ascites is cost-saving to the hospital provider and may improve patient health-related quality of life. Further long term studies are required in providing health economic evidence in this space.

**FR1505**

**A cost-effectiveness evaluation of the GORE® VIATORR® TIPS Endoprosthesis versus large volume paracentesis in the management of portal hypertension complications in the Spanish healthcare system**

Mitesh Nakum¹, Thomas Wiersma², Francesca Di Stasi³.¹W. L. Gore & Associates (UK) Ltd., Health Economics, United Kingdom; ²W. L. Gore & Associates B.V., Tilburg, Netherlands; ³W.L. Gore & Associati Srl, Verona, Italy

Email: mnakum@wlgore.com

**Background and aims:** The GORE® VIATORR® TIPS Endoprosthesis is widely used in patients for the treatment of portal hypertension and its complications such as refractory ascites in Spain, however little is known about the cost-effectiveness of the GORE® VIATORR® Device in the Spanish healthcare system. The aim of this analysis was to establish the cost-effectiveness of the GORE® VIATORR® Device versus large volume paracentesis (LVP) in refractory ascites with the Spanish healthcare system.

**Method:** A published markov model¹ was updated to simulate economic outcomes at two years from the Spanish healthcare perspective. Clinical parameters were derived from an updated published literature review². Costing information was gathered from national tariffs, existing literature and expert opinion. Uncertainty was tested using deterministic and probabilistic sensitivity analyses.

**Results:** The GORE® VIATORR® Device was estimated to be cost-saving by 21,493 Euros versus LVP over the time frame of the analysis. The GORE® VIATORR® Device also resulted in +0.60 QALYs versus LVP and so was cost-effective. Savings with the GORE® VIATORR® Device was from reduced LVP resource utilisation costs and reduced inpatient stay. The GORE® VIATORR® Device also remained over 98% cost-effective in a probabilistic sensitivity analysis versus LVP (see figure below).

**Conclusion:** CT can be used as a noninvasive method to effectively predict the severity of esophageal varices, which may reduce the invasive screening of endoscopy and be used as a supplementary procedure in patients with portal hypertension.

**FR1504**

**A published markov model to simulate economic outcomes at two years from the Spanish healthcare perspective. Clinical parameters were derived from an updated published literature review. Costing information was gathered from national tariffs, existing literature and expert opinion. Uncertainty was tested using deterministic and probabilistic sensitivity analyses.**

**Results:** The GORE® VIATORR® Device was estimated to be cost-saving by 21,493 Euros versus LVP over the time frame of the analysis. The GORE® VIATORR® Device also resulted in +0.60 QALYs versus LVP and so was cost-effective. Savings with the GORE® VIATORR® Device was from reduced LVP resource utilisation costs and reduced inpatient stay. The GORE® VIATORR® Device also remained over 98% cost-effective in a probabilistic sensitivity analysis versus LVP (see figure below).

**Conclusion:** CT can be used as a noninvasive method to effectively predict the severity of esophageal varices, which may reduce the invasive screening of endoscopy and be used as a supplementary procedure in patients with portal hypertension.

**Postscript:**

The ratio of procoagulant factor VIII to anticoagulant protein C (FVIII/PC) is a versatile predictor of hepatic decompensation/liver-related death in patients with advanced chronic liver disease (ACLD). Of note, the association between FVIII/PC and thrombomodulin-modified thrombin generation assay (TM-TGA) results is confounded by liver disease severity.

To substantiate the notion that FVIII/PC is unrelated to coagulation potential and provide an alternative explanation for its prognostic value, we investigated its association with (i) bleeding and thrombotic events, and (ii) key pathophysiological mechanisms promoting liver disease progression.

**Method:** In cohort (i) including ACLD patients undergoing HVPG measurement at the Vienna Hepatic Hemodynamic Lab with information on FVIII/PC (n = 576), we evaluated the development of major bleeding as well as arterial/venous thrombotic events (Schulman S, et al, J Thromb Haemost 2010) during follow-up. Moreover, incidence of ACLF was assessed. In cohort (ii), associations between FVIII/PC and pathophysiology-oriented biomarkers were assessed in 142 patients from the prospective Vienna Cirrhosis Study (VICIS).

**Background and aims:** We and others have demonstrated that the ratio of procoagulant factor VIII to anticoagulant protein C (FVIII/PC) is a versatile predictor of hepatic decompensation/liver-related death in patients with advanced chronic liver disease (ACLD). Of note, the association between FVIII/PC and thrombomodulin-modified thrombin generation assay (TM-TGA) results is confounded by liver disease severity.

To substantiate the notion that FVIII/PC is unrelated to coagulation potential and provide an alternative explanation for its prognostic value, we investigated its association with (i) bleeding and thrombotic events, and (ii) key pathophysiological mechanisms promoting liver disease progression.

**Method:** In cohort (i) including ACLD patients undergoing HVPG measurement at the Vienna Hepatic Hemodynamic Lab with information on FVIII/PC (n = 576), we evaluated the development of major bleeding as well as arterial/venous thrombotic events (Schulman S, et al, J Thromb Haemost 2010) during follow-up. Moreover, incidence of ACLF was assessed. In cohort (ii), associations between FVIII/PC and pathophysiology-oriented biomarkers were assessed in 142 patients from the prospective Vienna Cirrhosis Study (VICIS).
Results: (i) During a follow-up of 31.8 (IQR: 12.0–60.3) months, major bleedings were observed in 44 (7.6%) patients and bleedings were attributed to portal hypertension in 35 (6.3%) of the first bleeding events. Non-malignant thrombotic events were diagnosed in 50 (8.7%) patients. FVIII/PC was associated with neither the incidence of major bleedings (hazard ratio [HR]: 1.03 [95% CI: 0.98–1.09]; p = 0.272), nor the occurrence of thrombotic events (HR: 1.03 [95% CI: 0.98–1.09]; p = 0.269). However, it predicted ACLF (adjusted HR: 1.10 [95% CI: 1.02–1.19]; p = 0.015) in decompensated patients, independently of CLIP-C ACLF-D.

(ii) As demonstrated in the attached Figure, FVIII/PC showed moderate to strong correlations with HVPG (Spearman’s $\rho = 0.442; p < 0.001$), von Willebrand factor ($\rho = 0.628; p < 0.001$), serum sodium ($\rho = -0.487; p < 0.001$), and renin ($\rho = 0.450; p < 0.001$), as well as associations with systemic inflammation: C-reactive protein ($\rho = 0.540; p < 0.001$), interleukin-6 ($\rho = 0.381; p < 0.001$), and procalcitonin ($\rho = 0.257; p = 0.002$). Finally, it also strongly correlated with the enhanced liver fibrosis (ELF) test, as an indicator of fibrogenesis/matrix remodelling ($\rho = 0.613; p < 0.001$).

Conclusion: Baseline FVIII/PC was associated with neither thrombotic events nor major bleedings during follow-up, i.e., the clinical correlates of coagulation. Hence, results from previous studies on FVIII/PC require reinterpretation. However, FVIII/PC was associated with key pathophysiological mechanisms involved in disease progression, including those promoting further decompensation and ACLF, which may explain its prognostic utility.

FRI506
Prognostic impact of variants in TM6SF2 and MBOAT7 in patients who have progressed to advanced chronic liver disease
Lorenz Balcar1,2, Bernhard Scheiner1,2, Markus Urhe1, Patrick Weinberger1, Rafael Paternostro1,2, Benedikt Simbrunner1,2, Georg Semmler1,2, Nicole Auer1, Claudia Willheim1, Matthias Pinter1, Michael Trauner1, Thomas Reiberger1,2, Mattias Mandorfer1,2, Albert Stättermayer1,2, 1Medical University of Vienna, Division of Gastroenterology and Hepatology, Department of Internal Medicine III, Vienna, Austria; 2Medical University of Vienna, Vienna Hepatic Hemodynamic Lab, Division of Gastroenterology and Hepatology, Department of Internal Medicine III, Vienna, Austria
Email: mattias.mandorfer@meduniwien.ac.at

Background and aims: Genome-wide association studies revealed genetic variants that modulate the susceptibility for (advanced) chronic liver disease (A)CLD. We have previously shown that a PNPLA3 variant promotes hepatic decompensation/death in ACLD, while HSD17B13 did not impact prognosis at this stage. Importantly, the impact of the transmembrane 6 superfamily 2 (TM6SF2) rs58342926 and membrane-bound O-acetyltransferase domain-containing 7 (MBOAT7) rs641738 single nucleotide variants (SNV) in patients who have already progressed to ACLD are unknown.

Method: The impact of TM6SF2/MBOAT7 variants on liver-related events was evaluated in 938 ACLD (as defined by HVPG ≥6mmHg; viral hepatitis and alcohol-related or non-alcoholic fatty liver disease) patients undergoing HVPG-measurement at the Vienna Hepatic Hemodynamic Lab.

Results: Mean age was 55 ± 11 years, mean HVPG was 15 ± 7 mmHg and mean MELD was 11 ± 5 points. The main etiologies were viral hepatitis (n = 495, 53%) alcohol-related liver disease (n = 342, 37%) and non-alcoholic fatty liver disease (n = 101, 11%). While 754 (80%) patients harboured the TM6SF2 wild-type (C/C), 174 (19%) and 10 (1%) patients had one or two T-alleles, respectively. Patients with at least one TM6SF2 T-allele had more pronounced portal hypertension (HVPG: 16 ± 7 vs. 15 ± 7 mmHg; p = 0.031), higher gamma-glutamyl transferase levels (123 vs. 97 U L$^{-1}$; p = 0.002), and more commonly hepatocellular carcinoma (HCC, 17% vs. 12%; p = 0.049). Patients with at least one MBOAT7 T-allele also tended to have a higher HCC prevalence at baseline (14% vs. 10%; p = 0.051), while other baseline characteristics were comparable. In univariable Cox regression analyses, carriers of the TM6SF2 T-allele showed a trend towards an increased risk for compensation/liver-related death during follow-up (hazard ratio [HR]: 1.26 [95% confidence interval (95%CI): 0.98–1.62]; p = 0.072); in the viral hepatitis subgroup, the association attained statistical significance (HR: 1.53 [95%CI: 1.03–2.29]; p = 0.036). After adjusting for age, HVPG, MELD, and albumin levels, neither the TM6SF2 nor the MBOAT7 genotype had an effect on decompensation/liver-related death during follow-up.

These results were unaffected by restricting our analysis to patients at increased risk of hepatic decompensation/liver-related death, i.e., those with clinically significant portal hypertension.

Conclusion: While SNVs in TM6SF2 and MBOAT7 modulate the risk of progression to ACLD, both genotypes had no independent impact on liver-related outcomes in ACLD patients but were potential risk factors for HCC development. Thus, these variants have limited value for risk stratification in patients with ACLD as HCC screening is warranted anyway.

FRI507
Hepatocellular carcinoma and number of elastic bands per session are strong predictors of bleeding after prophylactic endoscopic variceal ligation
Renato Medas1, Rodrigo Liberal1, Tiago Ribeiro1, João Afonso1, Rosa Coelho1, Hélder Cardoso1, Guilherme Macedo1, 1Centro Hospitalar Universitário São João, Gastroenterology and Hepatology, Porto, Portugal
Email: renatogmedas@gmail.com

Background and aims: Endoscopic variceal band ligation (EVL) is considered a standard care for high-risk varices treatment in cirrhosis. Despite being globally safe, procedure-related bleeding is a potential complication, with an estimated incidence up to 15% in some series, requiring hospitalization and blood transfusion. However, risk factors associated with this serious complication are not well established. The aim of our study was to evaluate factors associated with increased risk for upper gastrointestinal bleeding (UGIB) within 30 days after prophylactic EVL.

Method: We performed a single center retrospective study in a tertiary hospital during a 6-year period (between 09/2015 and 09/2021). All patients with clinically significant portal hypertension due to liver cirrhosis, submitted to prophylactic EVL, were considered eligible for the study. After EVL, all patients received oral proton pump inhibitor and sucralfate, according to an internal protocol. Statistical analysis was performed with SPSS® v.25.0.
Results: A total of 871 prophylactic EVL procedures, performed in 281 patients were analysed. Most procedures were primary prophylaxis (70.3%), 79.9% of patients were male (79.9%) and median age was 60 years (IQR 54–68). Alcohol was the main etiology for cirrhosis (57.9%), followed by hepatitis C virus (14.9%). UGIB 30–days after EVL occurred in 21 cases (2.4% of all EVLs) within a median time of 9 days (IQR 8–17) after index procedure. In 15 patients (68.2%) ligation ulcers were identified as the potential source of bleeding. On univariate analysis the number of elastic bands per session, platelets, albumin, total bilirubin, sodium, hepatocellular carcinoma (HCC) and portal venous thrombosis were associated with increased risk of UGIB 30–days after EVL. After multivariate logistic regression, only the number of elastic bands applied per session [above 7] (odds ratio [OR] 4.76, 95% confidence interval [CI] 1.97–13.02, p = 0.001), presence of HCC (OR 3.79, 95% CI 1.16–9.02, p = 0.006) and sodium (OR 0.86, 95% CI 0.78–0.95, p = 0.002) reached statistical significance. Age, sex, cirrhosis etiology, high-risk varices, concomitant gastric varices, ligation system, creatinine, international normalized ratio, antiplatelet and anticoagulant therapy were not associated with increased risk of bleeding after EVL.

Conclusion: Our study describes a relative low incidence of post-EVL UGIB in accordance with previous reports, reinforcing EVL as a safe procedure for prophylaxis of variceal bleeding. The number of elastic bands applied per session, serum sodium and presence of HCC, rather than platelets or coagulopathy, are predictors of bleeding after prophylactic EVL in patients with liver cirrhosis. These data suggest that prophylactic administration of blood or coagulation products are not necessary. In addition, a minimal EVL strategy should be considered in selected patients.

FR1509
Use of second-harmonic generation microscopy for automated detection of septa and nodules in needle liver biopsies of NASH cirrhosis
Mazen Noureddin1, Dean Tai2, Elaine Chng2, Yayan Ren2, Pol Boudes3, Harold Shlevin4, Stephen Harrison5, Guadalupe Garcia-Tsao6, Naga Chalasani1, Zachary Goodman1. 1Division of Digestive and Liver Diseases, Comprehensive Transplant Center, Cedars-Sinai Medical Center, United States; 2HistIndex Pte. Ltd., Singapore; 3Galecet Therapeutics, United States; 4Pinnacle Clinical Research, San Antonio, TX, USA; 5Section of Digestive Diseases, Yale University and CT-VA Healthcare System, Connecticut, USA; 6Division of Gastroenterology and Hepatology, Department of Medicine, Indiana University School of Medicine, USA; 7Inova Fairfax Hospital, Falls Church, Virginia, USA
Email: mazen.noureddin@cshs.org

Background and aims: Cirrhosis, previously considered irreversible, is now recognized as capable of regression or progression. Most staging systems oversimplify all degrees of cirrhosis into one category. Portal hypertension, defined by hepatic venous pressure gradient (HVPG), correlates with key histological features of cirrhotic liver tissues, including septa and nodules, which might make a biopsy an acceptable surrogate for clinical outcome. Using second harmonic generation/two-photon excitation fluorescence (SHG/TPEF), this exploratory analysis aims to develop an artificial intelligence (AI) tool based on septa and nodule microscopy for use in natural history monitoring and evaluate treatment response in cirrhotic NASH trials.

Method: 25 liver biopsies from 15 NASH patients with compensated cirrhosis were included from a phase 2a trial. Digitized images stained with Sirius red and immunostain for smooth muscle actin were used by an expert pathologist to identify all septa and cirrhotic nodules. 2 image algorithms were developed to automatically detect septa and nodules based on pathologist’s annotations, named qSepta and qNodes, respectively. Agreement between the algorithm detection results and annotations were determined, and the images were rotated to establish repeatability.

Results: Concordance between the pathologist annotations and algorithm identification was determined after excluding technical artifacts. 284 septa were annotated by the pathologist (“true septa”) and 294 septa were detected from the SHG/TPEF images using qSepta algorithm. Comparing the qSepta results versus true septa, 91% of the true septa were detected by the algorithm and 85% of the algorithm
Hepcidin is higher in patients with more severe liver disease independent of portal hypertension

Robin Greinert1, Alexander Zippriech2, Laura Popp3, Cristina Ripoll2.
1Martin-Luther-University Halle-Wittenberg, Department for Internal Medicine I, Halle (Saale), Germany; 2University of Jena, Department for Internal Medicine IV, Jena, Germany; 3Kreiskrankenhaus Delitzsch GmbH, Innere Medizin, Delitzsch, Germany

Email: cristina.ripoll@med.uni-jena.de

Background and aims: Hepatocytes are the main source of hepcidin. Hepcidin expression is driven by iron load, although also inflammation, hypoxia and erythropoietic drive. The aim of this study is to evaluate hepcidin in cirrhosis and its association to the main pathophysiological drivers of cirrhosis: portal hypertension, liver insufficiency and systemic inflammation.

Method: Prospective study including consecutive patients between 2014 and 2016 who underwent a hepatic hemodynamic study. Measurement of ferritin, transferrin saturation and hepcidin (in hepatic vein and in peripheral blood) were performed besides standard measurements of liver function. Portal hypertension was estimated by means of HVPG, liver insufficiency was quantified by means of MELD score. SPSS v21 was used. Results are presented as proportions or median with IQR. Categorical variables were evaluated by means of the Chi-square test. Continuous variables were evaluated by the U-Mann Whitney or Spearman correlation as appropriate.

Results: Fifty-one patients (31 male, median age 62 [56–67] years, Child Pugh A 12 (23%), B 28 (55%) C 11 (22%) were included. Median hepcidin (nmol/L) in the peripheral vein was 2.2 (0.5–7.6) and in the hepatic vein 2.1 (0.5–9.2) with a positive correlation between both (rho Spearman 0.85, p < 0.001). 31 and 36% of the patients had levels of hepcidin ≤0.5 nmol/l (lower limit of detection) in peripheral and hepatic vein respectively. Those with hepcidin >0.5 nmol/l had vs those below: greater MELD [16 [11–19] vs 10 [19–12] and Ferritin (229 [154–473] vs 37 [26–80]). No differences were observed according to CRP & leukocytes. Hepcidin was higher in patients with more severe liver disease [MELD: r = 0.436, p = 0.003; Child B&C vs A: 2.7 (0.5–11.8) nmol/l vs 0.5 (0.5–3.3) nmol/l p = 0.05]. No relevant association to HVPG.

Conclusion: No significant differences in peripheral and hepatic vein can be observed, suggesting that the liver remains a main source of hepcidin production even in end-stage liver disease. Increased levels of hepcidin are associated to more severe liver disease and ferritin and have no relevant association to portal hypertension.

FRI511

Effect of thrombocytopenia and platelet transfusion on outcomes of acute variceal bleeding: a real world experience

Sagnik Biswas1, Manas Vaishnav2, Piyush Pathak1, Aditya Vikram Pachisia3, Rithvik Golla4, Amit Goel2, Dr. Shalimar1.
1All India Institute of Medical Sciences, New Delhi, Gastroenterology and Human Nutrition, New Delhi, India; 2Sanjay Gandhi Post Graduate Institute of Medical Sciences, Gastroenterology, Lucknow, India

Email: drshalimar@yahoo.com

Background and aims: Thrombocytopenia is a feature of portal hypertension. In patients with thrombocytopenia and acute variceal bleeding (AVB), platelet transfusion is recommended by few guidelines and is common in routine clinical practice. However, the effect of thrombocytopenia and platelet transfusion on acute variceal bleeding (AVB) outcomes is unclear. We aimed to assess the outcomes in AVB patients with thrombocytopenia and the effect of platelet transfusion on rebleeding and mortality.

Method: Prospectively maintained database of the patients who presented with AVB were reviewed to study their outcome. Patients were grouped as platelet count <20,000/mm³, 20,000–50,000/mm³ and >50,000/mm³. The outcomes were assessed as the risk of rebleeding at days 5 and 42, and risk of death at day 42 from the onset of AVB. Outcomes were compared among patients with and without platelet transfusion during AVB management. Statistical comparisons were done using Kaplan-Meier curves with log-rank tests for rebleeding and logistic regression for 42-day mortality.

Results: A total of 913 patients- males 762 (83.5%); mean age 44.4 ± 12.8 years, MELD 16.6 ± 7.9; Child Class A 374 (41%), B 361 (39.5%) and C 178 (19.5%); platelet count <20,000/mm³, 20,000–50,000/mm³ and >50,000/mm³. The outcomes were assessed as the risk of rebleeding at days 5 and 42, and risk of death at day 42 from the onset of AVB. Outcomes were compared among patients with and without platelet transfusion during AVB management. Statistical comparisons were done using Kaplan-Meier curves with log-rank tests for rebleeding and logistic regression for 42-day mortality.

Results: A total of 913 patients- males 762 (83.5%); mean age 44.4 ± 12.8 years, MELD 16.6 ± 7.9; Child Class A 374 (41%), B 361 (39.5%) and C 178 (19.5%); platelet count <20,000/mm³, 20,000–50,000/mm³ and >50,000/mm³. The outcomes were assessed as the risk of rebleeding at days 5 and 42, and risk of death at day 42 from the onset of AVB. Outcomes were compared among patients with and without platelet transfusion during AVB management. Statistical comparisons were done using Kaplan-Meier curves with log-rank tests for rebleeding and logistic regression for 42-day mortality.

Conclusions: Median platelet count was 50,000/mm³. Five patients had two rebleeds at 5 days with 3 (13%), 7 (5.1%) and 38 (21.3%) patients in each group respectively. Among patients with platelet count <20,000/mm³, 20,000–50,000/mm³ and >50,000/mm³, 5 (21.7%), 25 (18.2%) and 108 (14.3%) patients respectively had 42-days rebleeding (p = 0.296, log-rank test; figure 1a); similarly, 42-day mortality was 3 (13.0%), 33 (24.1%) and 130 (17.3%), respectively (p = 0.137, log-rank test; figure 1b). Ninety-one patients received platelet transfusions-Child A/B/C 8.8%/9.4%/13.5%, respectively; MELD score 16.6 ± 8.0 vs 16.4 ± 7.6, p = 0.252). Among three platelet groups, 10/23 (43.5%), 51/167 (30.6%) and 130/253 (51.3%) patients, respectively. Forty-eight (5.2%) patients experienced a rebleed at 5 days with 3 (13%), 7 (5.1%) and 38 (21.3%) patients in each group respectively. Among patients with platelet count <20,000/mm³, 20,000–50,000/mm³ and >50,000/mm³, 5 (21.7%), 25 (18.2%) and 108 (14.3%) patients respectively had 42-days rebleeding (p = 0.296, log-rank test; figure 1a); similarly, 42-day mortality was 3 (13.0%), 33 (24.1%) and 130 (17.3%), respectively (p = 0.137, log-rank test; figure 1b).

Discussion: No differences were observed according to CRP & leukocytes. Hepcidin was higher in patients with more severe liver disease and ferritin and have no relevant association to portal hypertension.

Conclusion: No significant differences in peripheral and hepatic vein can be observed, suggesting that the liver remains a main source of hepcidin production even in end-stage liver disease. Increased levels of hepcidin are associated to more severe liver disease and ferritin and have no relevant association to portal hypertension.

FRI510

Hepcidin expression is driven by iron load, although also inflammation, hypoxia and erythropoietic drive. The aim of this study is to evaluate hepcidin in cirrhosis and its association to the main pathophysiological drivers of cirrhosis: portal hypertension, liver insufficiency and systemic inflammation.

Method: Prospective study including consecutive patients between 2014 and 2016 who underwent a hepatic hemodynamic study. Measurement of ferritin, transferrin saturation and hepcidin (in hepatic vein and in peripheral blood) were performed besides standard measurements of liver function. Portal hypertension was estimated by means of HVPG, liver insufficiency was quantified by means of MELD score. SPSS v21 was used. Results are presented as proportions or median with IQR. Categorical variables were evaluated by means of the Chi-square test. Continuous variables were evaluated by the U-Mann Whitney or Spearman correlation as appropriate.

Results: Fifty-one patients (31 male, median age 62 [56–67] years, Child Pugh A 12 (23%), B 28 (55%) C 11 (22%) were included. Median hepcidin (nmol/L) in the peripheral vein was 2.2 (0.5–7.6) and in the hepatic vein 2.1 (0.5–9.2) with a positive correlation between both (rho Spearman 0.85, p < 0.001). 31 and 36% of the patients had levels of hepcidin ≤0.5 nmol/l (lower limit of detection) in peripheral and hepatic vein respectively. Those with hepcidin >0.5 nmol/l had vs those below: greater MELD [16 [11–19] vs 10 [19–12] and Ferritin (229 [154–473] vs 37 [26–80]). No differences were observed according to CRP & leukocytes. Hepcidin was higher in patients with more severe liver disease [MELD: r = 0.436, p = 0.003; Child B&C vs A: 2.7 (0.5–11.8) nmol/l vs 0.5 (0.5–3.3) nmol/l p = 0.05]. No relevant association to HVPG.

Conclusion: No significant differences in peripheral and hepatic vein can be observed, suggesting that the liver remains a main source of hepcidin production even in end-stage liver disease. Increased levels of hepcidin are associated to more severe liver disease and ferritin and have no relevant association to portal hypertension.
**Conclusion:** Platelet counts and platelet transfusion is not associated with the risk of rebleeding and mortality during follow-up in patients with A/V.B. Endotherapy is safe in patients with severe thrombocytopenia and not associated with higher rebleed rates.

**Background and aims:** To evaluate whether individualized treatment effect prediction approach can assist in personalized treatment of acute variceal bleeding (A/VB) with pre-emptive transjugular intrahepatic portosystemic shunt (p-TIPS) among patients with Child-Pugh B cirrhosis.

**Method:** Data of 1021 consecutive patients with Child-Pugh B cirrhosis and A/VB from 13 university hospitals in China who were treated with p-TIPS (p-TIPS group, n = 297) or standard of care (medical group, n = 724) were used to predict treatment effects for individual patients in terms of absolute risk reduction (ARR) of death. Predictions were based on a refitted Chronic Liver Failure Consortium Acute Decompensation score (CLIF-C ADs) and on a newly developed prediction model. The net benefit of different p-TIPS treatment-strategies was compared: (i) treat none, (ii) treat all, (iii) risk-stratification strategy (i.e. selective treatment of patients at high-risk of death), and (iv) prediction-based treatment strategy (i.e. selective treatment of patients whose predicted treatment effect exceeds a decision threshold).

**Figure: (abstract FRI511)**

**Figure: (abstract FRI512)**

---

**Table:**

<table>
<thead>
<tr>
<th>Total Points</th>
<th>6−Week Mortality</th>
<th>1−Year Mortality</th>
</tr>
</thead>
<tbody>
<tr>
<td>Points</td>
<td>Age (years)</td>
<td>Active bleeding</td>
</tr>
<tr>
<td></td>
<td>INR</td>
<td>Bilirubin (mg/dL)</td>
</tr>
<tr>
<td></td>
<td>Platelet (×109)</td>
<td>Albumin (g/L)</td>
</tr>
<tr>
<td></td>
<td>Creatinine (mg/dL)</td>
<td>Sodium (mmol/L)</td>
</tr>
</tbody>
</table>

---

**Nomogram of optimal fit model for predicting mortality on medical treatment and treatment effect from pre-emptive TIPS**

**6-week risk-benefit plot**

**1-year risk-benefit plot**

**Calibration plot for 1-year mortality risk**

**Calibration plot for 1-year treatment effect**

---

---
Results: After propensity score matching, the probability of death was significantly lower in p-TIPS group (15.5% vs 25.6% at 1 year, HR 0.52, 95%CI: 0.35–0.78; p = 0.002) compared with medical group. A Cox proportional hazards model comprising 9 easy-to-measure clinical predictors (age, active bleeding, albumin, bilirubin, creatinine, INR, sodium, platelet, and treatment status) was built for predicting treatment effects of p-TIPS, which had higher values of concordance-statistic-for-benefit and better calibration compared with the refitted CLIF-CADs model. Net benefit analyses showed that prediction based treatment strategy were associated with more net benefit than other treatment strategies.

Conclusion: The treatment effects of p-TIPS can be predicted for individual patients based on routinely available patient characteristics. Individualized prediction treatment strategy is associated with optimal net benefit.

FRI513
Real-world survival outcomes in patients with decompensated cirrhosis receiving long term human albumin infusions
Nicholas Hannah1,2, Douglas Tjandra1, Ashwin Patwardhan3, Kelsey Rutland1, Siddharth Sood1,2. 1The Royal Melbourne Hospital, Department of Gastroenterology, Parkville, Victoria; 2University of Melbourne, Medicine, Dentistry and Health Sciences, Parkville, Australia
Email: nick.m.hannah@gmail.com

Background and aims: The ANSWER study demonstrated the benefit of long term outpatient human albumin (HA) infusions in patients on diuretics for cirrhosis related ascites. HA is commonly used at our institution for cirrhotic patients with refractory ascites requiring repeated paracentesis, including those with ongoing alcohol consumption and renal impairment. We evaluated patient survival outcomes on HA infusions in an unwell but real-world cirrhotic cohort.

Method: We present a single-centre cohort study of patients receiving outpatient HA infusions at The Royal Melbourne Hospital between April 2017–June 2021. Inclusion: age >18 years and cirrhosis with ascites requiring paracentesis. Demographics, clinical data, including outcomes such as time on HA, trans-jugular portosystemic shunt (TIPS), liver transplant and death were recorded. Child-Pugh and Model for End-Stage Liver Disease-Sodium (MELD-Na) score were calculated. Patients received regular outpatient HA infusions up to 40 g/week. Primary outcomes were assessed 12 months after first HA infusion.

Results: 24 patients received at least 1 month of HA infusions (range 1.2–28.2, median 9.3 months). Median age 59.5 years, and 7 were female (29.2%). Aetiology included alcohol (50%), non-alcoholic steatohepatitis (NASH) (16.7%) and viral/algohol (12.5%). Median MELD-Na 18.5, with Child-Pugh Scores A (4.2%), B (50%) and C (45.8%). Comorbidities included chronic kidney disease 37.5% and Type 2 diabetes mellitus (T2DM) 41.7%. Median follow-up was 16 months and median TIPS/transplant-free survival (TTFS) 10.5 months. Median serum sodium (134 mmol/L to 136.5 mmol/L, p = 0.014) and albumin (28.5 g/L to 39 g/L, p = 0.003) increased significantly over 12 months, whilst Child-Pugh score improved from 9 to 7.5 (p = 0.0172). On multivariate analysis, T2DM (not NASH) had a significant TTFS disadvantage (HR 6.16; 95% CI 1.23–30.84, p = 0.027), while time on HA infusions showed a TTFS advantage (HR 0.84, 95% CI 0.72–0.99, p = 0.031). Median TTFS improved in patients with a change in MELD-Na <1 at 1 month; 29.4 months versus 7.7 months (p = 0.011).

Conclusion: Outpatient HA infusions are associated with increased sodium and albumin levels and improvement in Child-Pugh score in a real-world cohort representing a more unwell population than the original ANSWER trial. T2DM was significantly associated with poorer outcomes, whilst an improvement in MELD-Na score at 1 month may predict those likely to benefit from HA. These results may help targeting of regular HA in decompensated cirrhotic patients.

FRI514
Impact of non-selective beta-blockers on survival and liver-related complications after TIPS-Insertion
Anja Tiede1, Lena Stockhoff1, Hannah Schneider1, Bernhard Meyer2, Heiner Wedemeyer1, Jan Hinrichs2, Markus Cornberg1,1,1, Benjamin Maasoumy1,3,1, Hannover Medical School, Gastroenterology, Hepatology and Endocrinology, Hannover, Germany; 2Hannover Medical School, Diagnostic and Interventional Radiology, Hannover, Germany; 3Centre for Individualised Infection Medicine (CIIM), Hannover, Germany
Email: maasoumy.benjamin@mh-hannover.de

Background and aims: Non-selective beta-blockers (NSBB) are commonly used to treat portal hypertension in patients with liver cirrhosis. An even more effective reduction and often normalization of portal pressure can be achieved by insertion of a transjugular intrahepatic portosystemic shunt (TIPS). So far, it remains unclear whether NSBB should be stopped immediately after TIPS. Recent data suggest that NSBB exert some additional e.g. anti-inflammatory effects that are independent from pressure reduction and may contribute to a favourable clinical outcome. The aim of this study was to evaluate if NSBB treatment is linked to survival and/or liver-related events after TIPS-insertion.

Method: A number of 235 consecutive cirrhotic patients receiving a TIPS between 2009 and 2019 were included. Patients were followed up for acute kidney injury (AKI), acute-on-chronic liver failure (ACLF), hepatic encephalopathy (HE), infections and mortality for one year after TIPS insertion. Intake of NSBB was assessed prior to TIPS insertion and at the time of hospital discharge. Incidence of perinterventional complications until hospital discharge was analyzed with binary logistic regression adjusting for the recently introduced FIPS-Score. Link between NSBB intake at hospital discharge and further survival and the development of liver-related complications was tested using a multivariable Cox Regression adjusting for TIPS indication (refractory ascites) and FIPS-Score.

Results: Median age of the patients was 59 years, median FIPS −0.15 and median MELD 12.0. TIPS insertion effectively treated portal hypertension in 234 patients (99.6%) as indicated by pressure reduction of >50% or a PSV value <12 mmHg after TIPS. At baseline 136 patients received NSBB therapy (57.9%). Patients in the NSBB group were younger (57 vs 61 years, p = 0.030) and had lower FIPS (−0.34 vs −0.02, p = 0.002) and MELD (11.5 vs 12.6, p = 0.014). Varicose bleeding as TIPS indication was more common in the NSBB group (38.2% vs 8.1%, p < 0.001). Perinterventional development of AKI, infections and HE as well as in-hospital mortality did not differ between the two groups. In contrast, NSBB therapy prior to TIPS-insertion was associated with a significantly lower incidence of ACLF.
Real world validation of B/BENO-7 non-invasive diagnosis for clinically significant portal hypertension in compensated advanced chronic liver disease: international cohort study

Yu Jun Wong1,2, Junhui Garrett Kang3, Elisabeta Degasperi4, Giulia Tosetti4, Massimo Primignani4, Anoop Saraya3, Sanchit Sharma5, Chuan Liu6, Jia Li7,8, Xiaolong Qi6, Yu Jun Wong1,2, Junhui Garrett Kang3, Elisabeta Degasperi4, Giulia Tosetti4, Massimo Primignani4, Anoop Saraya3, Sanchit Sharma5, Chuan Liu6, Jia Li7,8, Xiaolong Qi6, Yu Jun Wong1,2, Junhui Garrett Kang3, Elisabeta Degasperi4, Giulia Tosetti4, Massimo Primignani4, Anoop Saraya3, Sanchit Sharma5, Chuan Liu6, Jia Li7,8, Xiaolong Qi6, Yu Jun Wong1,2, Junhui Garrett Kang3, Elisabeta Degasperi4, Giulia Tosetti4, Massimo Primignani4, Anoop Saraya3, Sanchit Sharma5, Chuan Liu6, Jia Li7,8, Xiaolong Qi6, Yu Jun Wong1,2, Junhui Garrett Kang3, Elisabeta Degasperi4, Giulia Tosetti4, Massimo Primignani4, Anoop Saraya3, Sanchit Sharma5, Chuan Liu6, Jia Li7,8, Xiaolong Qi6.

Background and aims: The presence of clinically significant portal hypertension (CSPH) confers a 10-fold higher risk of decomposition in compensated advanced chronic liver disease (cACLD) patients. Recent B/BENO-7 consensus proposed that non-invasive criteria may be used to identify cACLD patients with CSPH using liver stiffness measurement (LSM) and platelet count. Whether non-invasive diagnosis of CSPH could predict clinically meaningful outcomes such as decomposition, hepatocellular carcinoma (HCC) and death remained unclear. We aim to validate the real-world performance of Baveno-7 CSPH criteria to predict liver decomposition in cACLD patients.

Method: We analysed cACLD patients from 4 countries (Singapore, China, India and Italy). cACLD was diagnosed based on LSM > 10 kPa, and platelet < 110 (China, India and Italy). CSPH was diagnosed based on LSM > 10 kPa, with or without histological, radiological or clinical features of liver cirrhosis. CSPH was defined as either LSM between 15 and 20 kPa and platelet count < 110 (CSPH-1), LSM 20–25 kPa and platelet count < 150 (CSPH-2), or LSM > 25 kPa (CSPH-3). Absence of CSPH was defined as LSM < 15 kPa and platelet count > 150. Patients who did not fulfill either of the above criteria were categorized as borderline CSPH. Exclusion criteria were: prior or current liver decomposition, use of non-selective beta-blocker, untreated viral hepatitis and active alcohol drinking. Primary outcome was liver decomposition; secondary outcome were HCC and death. Overall, 91 patients (40.3%) were still on NSBB treatment at the time of discharge. NSBB therapy at discharge was neither linked to survival nor to development of AKI, ACLF or incidence of infections during further follow-up in the univariable and multivariable analysis.

Conclusion: Intake of NSBB prior to TIPS is not linked to the risk of perinterventional complications. Use of NSBB after TIPS has no impact on the risk for AKI, ACLF, infections and mortality. Thus, NSBB may be stopped in patients achieving sufficient pressure reduction after TIPS.

FRIS15

Real world validation of B/BENO-7 non-invasive diagnosis for clinically significant portal hypertension in compensated advanced chronic liver disease: international cohort study

Conclusion: Decompensation risk in cACLD patients varied across different non-invasive definitions of CSPH. LSM > 25 kPa is a reliable, non-invasive diagnosis for CSPH, which correlates with significantly higher risk of decomposition in cACLD patients.

FRIS156

Derivation of machine learning histologic scores correlating with portal pressures and the development of varices in NASH patients with cirrhosis

Mazen Noureddin1, Dean Tai2, Elaine Chng2, Yayan Ren3, Pol Boudes4, Harold Shlevin5, Stephen Harrison6, Guadalupe Garcia-Tsao, Zachary Goodman4, Naga Chalasani2.

Background and aims: In clinical trials of non-alcoholic steatohepatitis (NASH) cirrhosis, primary efficacy endpoints have been hepatic venous pressure gradient (HVPG), liver histology and clinical outcomes. Conventional histological assessment of cirrhosis do not include important features such as septa thickness, nodules features, and fibrosis area. We have assessed these with a machine learning (ML) model.

Method: NASH patients with compensated cirrhosis and HVPG ≥ 6 mm Hg (n = 143) were included from the Belapectin phase 2b trial (NCT02462967). Liver biopsies, HVPG measurements, and upper endoscopy were performed at baseline (BL) and at end of treatment (EOT). A second harmonic generation/two-photon excitation fluorescence (SHG/TPEF) imaging-based tool provided an automated quantitative assessment of histologic features: 252 related to septa, 21 related to nodules, and 184 related to fibrosis (SNOF). We also created ML scores and tested their association with HVPG and clinically significant portal hypertension (CSPH: HVPG ≥ 10 mm Hg) and its changes as well as with the presence of varices (SNOF-V).

Results: Samples were divided into training (BL) and validation (EOT). We found that septa [r = 0.55 (training) and 0.56 (validation)], nodule [r = 0.52 (training), and 0.53 (validation)], and fibrosis [r = 0.57 (training) and 0.62 (validation)] parameters correlated individually with HVPG (Ps < 0.05). Combining these parameters in the SNOF score showed better correlations of r of 0.57 (training) and 0.70 (validation) with HVPG (Ps < 0.05). The SNOF score (≥ 11.78) distinguished CSPH at BL and in the validation cohort (BL + EOT) [AUC = 0.85 and 0.74, respectively]. The SNOF-V score (≥ 0.57) distinguished the presence of varices at BL and in the same validation cohort [AUC =
0.86 and 0.73, respectively]. The SNOF-C score differentiated those who had >20% change in HVPG against those who did not, with an AUROC of 0.89.

Table: Metrics of SNOF and SNOF-V scores at predicting HVPG and presence of varices

<table>
<thead>
<tr>
<th></th>
<th>BL</th>
<th>BL + IOT</th>
</tr>
</thead>
<tbody>
<tr>
<td>AUC</td>
<td>Sensitivity</td>
<td>Specificity</td>
</tr>
<tr>
<td>SNOF score ≥ 11.78</td>
<td>0.85 73%</td>
<td>86%</td>
</tr>
<tr>
<td>10 (CSPH)</td>
<td>0.86 77%</td>
<td>86%</td>
</tr>
<tr>
<td>SNOF score ≥ 0.57 to predict varices</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**Conclusion:** The ML algorithm accurately predicted HVPG, CSPH and its changes, development of varices in patients with NASH cirrhosis. Use of ML histology model in NASH cirrhosis trials may improve the assessment of key outcome changes.

**FRI517**

Ruling out varices needing treatment with a non-invasive score in patients with compensated HBV cirrhosis

Giulio Emanuele Maria Rizzo¹, Pietro Gracella², Fabrizio Bronte¹, Giuseppe Falco¹, Gabriele Rancatore¹, Ciro Celsa¹, Giada Reina¹, Fabio Simone¹, Sergio Peralta¹, Antonio Craxi¹, Vito Di Marco¹, Vincenza Calvaruso¹, 1University of Palermo, Gastroenterology and Hepatology Unit, PROMISE, Palermo, Italy

Email: vincenza.calvaruso@unipa.it

**Background and aims:** Non-invasive criteria to rule-out oesophageal varices needing treatment (VNT) in patients with compensated HBV cirrhosis on long-term treatment with nucleoside analogs (NUCs) are lacking. We have assessed the performance of an algorithm combining platelets and albumin (PLT-ALB) in a cohort of such patients under endoscopic (EGD) surveillance.

**Method:** All consecutive patients with compensated HBV cirrhosis who achieved HBV DNA suppression on NUCs since at least 1 year were classified at the moment of EGD as:-PLT-ALB IN (low risk for VNT) if platelets were >120 × 10^9/L plus serum albumin >3.6 g/dL.-PLT-ALB OUT (high risk for VNT) if platelets were <120 × 10^9/L and/or serum albumin <3.6 g/dL. Primary outcome was the finding of VNT at EGD. Performance of PLT-ALB scoring to predict the outcome was assessed measuring the area under the receiver operating characteristic (AUROC) curve.

**Results:** Among the 41 PLT-ALB IN patients (47.1%) no VNT were found (NPV 100%). The PLT-ALB algorithm showed an AUROC of 0.76, potentially saving 47% of EGDs, with a false negative rate (FNR) of 0% and a false positive rate (FPR) of 48.1%.

**Conclusion:** PLT-ALB algorithmic approach based on widely available noninvasive parameters can avoid up to 50% EGDs aimed to screen for high-risk varices patients with compensated HBV cirrhosis under NUC suppression. Further validation in larger cohorts are needed before translating this approach into practice.

**FRI518**

Evaluation of clinically significant portal hypertension with a novel spleen-dedicated probe using transient elastography

Aitor Odriozola Herrán¹, Jose Ignacio Fortea², Anaña Angela Penut³, Antonio Cuadrado⁴, Emilio Fabrega⁴, Maria Teresa Arias Loste⁴, Paula Izurzubieta⁴, Coral Rivas⁴, Juan Carlos Rodriguez Duque⁴, Ines García⁴, Marina Cobreros⁴, María Del Barrio⁴, Álex García Tellado⁴, Javier Crespo⁴, 1University Hospital Marqués de Valdecilla, Gastroenterology and Hepatology Service, Santander, Spain; 2University Hospital Marqués de Valdecilla, Internal Medicine, Santander, Spain

Email: aodrihe94@gmail.com

**Background and aims:** Most studies evaluating the association between spleen stiffness (SS) by transient elastography and the presence of portal hypertension (PH) have used the 50 Hz probe (range: 15–75 kPa). Whether the previously reported cut-off values can be extrapolated to those obtained by the spleen-dedicated 100 Hz probe (SSM@100 Hz, range: 6–100 kPa; FibroScan® Expert 630) is uncertain since there is only one study that has assessed its correlation with the hepatic venous pressure gradient (HVPG). In the current study, we aimed to examine its diagnostic accuracy for PH in comparison to other non-invasive tests.

**Method:** Retrospective single-center study. Patients with available liver stiffness (LSM)-SSM and HVPG within 12 months were included. Patients with unstable liver disease (i.e., new decompensated events or any intervention that may impact PH between SSM and HVPG), non-cirrhotic PH, hepatocellular carcinoma (CHC) outside Milan criteria, liver transplants and transjugular intrahepatic portosystemic shunts were excluded. AUROC analysis was conducted to identify dual cut-offs (rule in and out) associated with the presence/absence of clinically significant PH (CSPH).

**Results:** A total of 56 patients were included with a median interval between HVPG and LSSM of 3.3 months (interquartile range (IQR) 0.4–72). LSM and SSM were not feasible in 1 (2%) and 4 (7%) patients. Median age was 60 years (54–70), 71% were males and non-alcoholic fatty liver disease was the most prevalent underlying etiology (50%). Most patients were Child–Pugh A (82%, none C) with a median MELD score of 8 (8–10). A history of decompensation and CHC had occurred in 14 (25%) and 2 (4%) patients. CSPH was present in 29 patients (51.8%), 69% of whom had HVPG ≥12 mmHg. Median (IQR) LSM and SSM were 19.2 (10.5–30.8) and 46, 5 (31, 0–62, 5) kPa, and both showed positive correlation with HVPG (Figure 1A/1B). For CSPH, the AUROC of SSM was 0.81 (95% CI 0.68–0.93) and was lower than LSM (0.89 [0.79–0.98], APRI [0.84 [0.74–0.95]], and FIB-4 [0.87 [0.77–0.98]]) (Figure 1C). The SSM cutoffs to rule in and out CSPH were 55, 8 (positive predictive value 83, 8%) and 31, 3 kPa (negative predictive value 93.8%) (Figure 1D).

**Conclusion:** SSM@100 Hz constitutes a good non-invasive test for portal hypertension and can be used to rule in and out clinically significant portal hypertension. However, in our cohort its diagnostic performance was lower than other non-invasive tests, showing LSM the highest accuracy.

**FRI519**

Are psychometric tests helpful for the prediction of hepatic encephalopathy after TIPS insertion?

Alena Friederike Ehrenbauer¹, Hannah Schneider², Lena Stockhoff², Anja Tiede², Meike Dirks³, Jennifer Witt³, Katja Deterding³, Henning Pflugrad³, Maria Magdalena Gabriel³, Denise Menti³, Bernhard Meyer³, Heiner Wedemeyer³, Jan Hinrichs³, Karin Weissenborn³, Benjamin Maasoumy⁴,³, A Hannover Medical School, Hannover, Germany

Email: aodrihe94@gmail.com

**Background and aims:** Most studies evaluating the association between spleen stiffness (SS) by transient elastography and the presence of portal hypertension (PH) have used the 50 Hz probe (range: 15–75 kPa). Whether the previously reported cut-off values can be extrapolated to those obtained by the spleen-dedicated 100 Hz probe (SSM@100 Hz, range: 6–100 kPa; FibroScan® Expert 630) is uncertain since there is only one study that has assessed its correlation with the hepatic venous pressure gradient (HVPG). In the current study, we aimed to examine its diagnostic accuracy for PH in comparison to other non-invasive tests.

**Method:** Retrospective single-center study. Patients with available liver stiffness (LSM)-SSM and HVPG within 12 months were included. Patients with unstable liver disease (i.e., new decompensated events or any intervention that may impact PH between SSM and HVPG), non-cirrhotic PH, hepatocellular carcinoma (CHC) outside Milan criteria, liver transplants and transjugular intrahepatic portosystemic shunts were excluded. AUROC analysis was conducted to identify dual cut-offs (rule in and out) associated with the presence/absence of clinically significant PH (CSPH).

**Results:** A total of 56 patients were included with a median interval between HVPG and LSSM of 3.3 months (interquartile range (IQR) 0.4–72). LSM and SSM were not feasible in 1 (2%) and 4 (7%) patients. Median age was 60 years (54–70), 71% were males and non-alcoholic fatty liver disease was the most prevalent underlying etiology (50%). Most patients were Child–Pugh A (82%, none C) with a median MELD score of 8 (8–10). A history of decompensation and CHC had occurred in 14 (25%) and 2 (4%) patients. CSPH was present in 29 patients (51.8%), 69% of whom had HVPG ≥12 mmHg. Median (IQR) LSM and SSM were 19.2 (10.5–30.8) and 46, 5 (31, 0–62, 5) kPa, and both showed positive correlation with HVPG (Figure 1A/1B). For CSPH, the AUROC of SSM was 0.81 (95% CI 0.68–0.93) and was lower than LSM (0.89 [0.79–0.98], APRI [0.84 [0.74–0.95]], and FIB-4 [0.87 [0.77–0.98]]) (Figure 1C). The SSM cutoffs to rule in and out CSPH were 55, 8 (positive predictive value 83, 8%) and 31, 3 kPa (negative predictive value 93.8%) (Figure 1D).

**Conclusion:** SSM@100 Hz constitutes a good non-invasive test for portal hypertension and can be used to rule in and out clinically significant portal hypertension. However, in our cohort its diagnostic performance was lower than other non-invasive tests, showing LSM the highest accuracy.
Background and aims: Hepatic encephalopathy (HE) is a frequent and severe complication in patients after transjugular intrahepatic portosystemic shunt (TIPS) insertion. Of note, risk factors for post-TIPS HE remain poorly defined. Presence of minimal HE (mHE) is a well-known risk factor for development of overt HE in cirrhotic patients without TIPS. Different psychometric tests, which differ in their diagnostic performance, have been suggested to diagnose mHE. However, their role for the prediction of post-TIPS HE still needs to be determined. We aimed to evaluate the value of three different psychometric tests for the prediction of HE after TIPS.

Method: We prospectively recruited 85 consecutive cirrhotic patients before TIPS insertion and monitored them for 180 days after TIPS insertion for development of HE. 65 patients underwent all psychometric tests: the Portosystemic Encephalopathy Syndrome Test (PSE, Version 2.0; 2020) (cut off <4), the Animal Naming Test (ANT) (cut-off of <23 animals/minute) and the Critical Flicker Frequency (CFF) (cut-off <39 Hz). Association to HE development was tested using multivariable cox-regression analysis adjusting for all additional parameters with p-value<0.05 in univariable analysis.

Results: Median age was 59 and MELD 12. Indication for TIPS was refractory ascites in 75% of patients. Evaluation for mHE at baseline yielded pathological results in 67%, 24% and 66% of patients according to PSE (gold standard), CFF and ANT, respectively. The highest concordance was observed between PSE and ANT and lowest between PSE and CFF. After TIPS insertion, 24 patients (28%) developed at least one HE episode in the first 180 days. Among all parameters, a larger stent diameter (p = 0.049), higher serum-creatinine (p = 0.022) and pathological CFF (p = 0.001) were significantly associated with HE development in univariable analysis. Of note, pathological CFF values at baseline remained significant in the multivariable model (p = 0.001). In contrast, pathological PSE and pathological ANT values were not significantly associated with HE after TIPS neither in univariable (PSE p = 0.357 and ANT p = 0.098) nor in multivariable analysis (PSE p = 0.495 and ANT p = 0.050). However, also CFF had a limited value in predicting HE: sensitivity was 61%, specificity 80%, positive predictive value 45% and negative predictive value 85%. Predictive value slightly improved by combining all psychometric tests (figure). Among the 12 patients with normal results in all tests HE incidence was 8% (n = 1) compared to 44% (n = 7) among those 16 patients with concordant pathological values.

Conclusion: Development of HE after TIPS is a multifactorially influenced event. Psychometric tests, which were designed for diagnosis of mHE, have limited value for predicting HE after TIPS insertion. The relatively good predictive value of CFF could implicate altered pathomechanism of HE after TIPS.
EVL in patients with high-risk varices treated to prevent first bleeding, stratifying risk according compensation/decompensation of cirrhosis.

Method: A systematic review was performed to identify RCTs comparing NSBBs vs EVL, either in monotherapy or combined, for 1yr prevention of bleeding in cirrhosis. We performed a competing-risk time-to-event meta-analysis using individual patient data (IPD) obtained from principal investigators of RCTs, using an Inverse Probability of the Treatment Weights (IPTW) approach. Analyses were stratified according to present or previous decompensation (bleeding, ascites or encephalopathy). Outcomes included death, prevention of bleeding and prevention of ascites. OLT and death were competing-events.

Results: Among 25 RCTs eligible, 11 providing IPD were included. Overall, 1400 patients were included (656 compensated), 625 treated with NSBB, 546 with EVL and 229 with NSBB+EVL. There were no differences in baseline characteristics between groups. Over 19 months of follow-up, bleeding occurred in 16% compensated vs 16% decompensated (SHR = 1.09, 95% CI = 0.83–1.44, P = 0.537), and death in 15% vs 28% respectively (SHR = 2.58, 95% CI = 1.02–3.28, P < 0.0001). Overall, risk of death was similar with EVL vs NSBB (SHR = 1.04, 95% CI = 0.71–1.52, P = 0.848) and with EVL+NSBB vs either alone, with heterogeneity (P² = 77%). In compensated patients, mortality risk was lower with NSBB vs EVL (SHR = 0.57, 95% CI = 0.36–0.90; P = 0.016) and with EVL+NSBB vs EVL (p = 0.104), without heterogeneity (P² = 0.0%). In decompensated patients, mortality risk was similar with EVL vs NSBB (SHR = 0.81, 95% CI = 0.52–1.26, P = 0.350) and with NSBB+EV vs NSBB (p = 0.469) and vs EVL (p = 0.357), without heterogeneity (P² = 34%). The risk of first bleeding was similar with EVL vs NSBB in compensated (p = 0.85) and decompensated patients (p = 0.64). The risk of ascites was higher with EVL vs NSBB (SHR = 2.68, 95% CI = 1.36–5.19, P = 0.004) in compensated patients and was similar in decompensated (p = 0.316).

Conclusion: In patients with compensated cirrhosis and high-risk varices treated to prevent bleeding, NSBB achieved better survival than EVL, without additional benefit by adding EVL to NSBB. The risk of bleeding was similar with both therapies but risk of developing ascites was lower with NSBB. In decompensated patients, survival was similar using NSBB or EVL or combining both. The NSBB may be preferable in compensated patients for prevention of bleeding, while either NSBB or EVL can be used in decompensated.

FRIS21
Baseline plasma renin activity (PRA) predicts risk of AKI in patients with cirrhosis: a prospective observational study
Srinivasa Reddy Golamari1, ILBS/Vasant Kunj Sector A, Hepatology, New Delhi, India
Email: srinivasaredgyolamari@gmail.com

Background and aims: Plasma renin activity (PRA), is a measure of the activity of the plasma enzyme renin; which plays a major role in the body’s regulation of blood pressure, thirst, and urine output. The degree of impairment in renal function, mainly decrease in renal perfusion and glomerular filtration rate (GFR) correlates with the activity of the endogenous vasoconstrictor system and both correlate with the severity of portal hypertension. Overactive RAAS system leads to renal vasoconstriction, renal injury and failure. We aimed to study the effect of PRA on organ injury/failure in cirrhosis.

Method: A total of 63 patients with cirrhosis, presenting for the first time with grade II/III ascites and no prior ascitic tap, were enrolled in a cross sectional study. At admission and during the hospital stay, presence and development of acute kidney injury (AKI) was studied and correlation with baseline serum PRA was determined.

Results: Altogether, 63 patients with ascites [62% males, with mean age 46.56 ± 12.59 years, CTP, 8.4 ± 1.1, MELD 18.4 ± 4.1, and MAP 74 ± 8.2 mmHg] were included. Forty two percent of patients had AKI at baseline. Ninety percent of the patients were on diuretics with a median dose of furosemide 15 mg (10–20) and spironolactone of 37.5 mg (25–50) per day. Mean PRA levels at presentation were 16.07 ± 1.4 (Normal-0.6–4.3 ng/ml/hr.). Baseline serum PRA levels were significantly associated with the presence or development of AKI during the hospital stay (p = 0.001, OR=1.22 95% CI: 1.096–1.36). A PRA value of 16.7 ng/ml/hr increased the risk of AKI with AUC = 0.95, with a sensitivity of 0.83, and specificity of 0.87. Every 1 ng/ml/hr increase in the PRA level was associated with 0.03 mg/dl increase in serum creatinine from baseline.

Figure 1: Correlation of serum PRA with AKI-A Kaplan-Meier analysis. [AUC = 0.95, Sensitivity = 0.83, Specificity = 0.87, 95% CI:79.8–97.5].

Conclusion: The serum PRA levels closely correlate with the acute kidney injury. Patients with high serum PRAs have a much higher risk of developingAKI. Therefore, baseline serum PRA can serve as a simple and reliable laboratory marker to assist in the prognosis of renal injury in decompensated cirrhosis patients.

FRIS22
Performance of spleen stiffness measured by point-shear wave elastography in esophageal varices screening
Mauro Giuffre1,2,3, Alessia Visentin1,2,3, Cristina Abazia1,2,3, Flora Masutti2,3, Saveria Lory Croce1,2,4, Università Degli Studi Di Trieste, Dipartimento Universitario Clinico Di Scienze Mediche Chirurgiche e Della Salute;2 Fondazione Italiana Fegato Onlus, Basovizza, Italy; 3 ASUGI Clinica Patologie del Fegato, Trieste, Italy; 4 ASUGI Clinica Patologie del Fegato, ospedale cattinara, Trieste, Italy
Email: gff.mauro@gmail.com

Background and aims: According to Baveno VI guidelines, esophageal-gastro-duodenoscopy (EGD) to stage esophageal varices (EVs) can be avoided in patients with chronic advanced liver disease who have a liver stiffness (LS) <20 kPa and a platelet count >150 × 10³/μL. Current evidence suggests that spleen stiffness (SS) <46 kPa, measured by transient elastography, can safely predict absence of high-risk varices (HRV). Our aim is to externally validate those data by performing SS measurement with point-shear wave elastography.

Method: We enrolled 500 consecutive patients with compensated liver cirrhosis, of which n = 208 (40.4%) had esophageal varices (150 EVs, 58 HRV).

Results: Median SS values were 36 (28.5;45.3) kPa. Patients with EVs had higher median SS values if compared to patients without EVs (45.5 vs. 30 kPa, p < 0.001). A similar trend was detected in LS values (23 vs. 15 kPa, p <0.001).

SS showed an AUROC of 0.88 (95% CI. 0.85–0.9, p < 0.001) to discriminate between patients with and without EVs of any kind. Also, SS <30 kPa showed the highest sensitivity to rule-out EVs of any kind (sensitivity 100%, specificity 64%, accuracy 77%); SS >38.5 can rule-in the presence of EVs of any kind with a sensitivity of 87%,
Portal pressure decreasing effect of beta blockers in cirrhosis with clinically significant portal hypertension, according to the components of metabolic syndrome

Anna Brujats,1 Berta Cuyas,1 Edilmar Alvarado-Tapias,1,2 Claudia Pujol,1 Antoni Mombiela,1 Cristina Roig,1 Maria Poca,1,2 Xavier Torras,1 Àngels Escorsell,1,2 Candíd Villanueva,1,2 1Hospital de la Santa Creu i Sant Pau, Gastroenterology and Hepatology Department, Biomedical Research Institute Sant Pau (IIB Sant Pau), Universitat Autònoma de Barcelona; 2Centro de Investigación Biomédica en Red de Enfermedades Hepáticas y Digestivas (CIBERehd), Instituto de Salud Carlos III

Background and aims: Patients with cirrhosis due to metabolic associated fatty liver disease (MAFLD) have higher risk of complications related to portal hypertension at any HVPG threshold than patients with HCV cirrhosis. MAFLD is associated with metabolic comorbidities such as obesity, diabetes mellitus (DM), arterial hypertension (AHT) and dyslipidemia (DLP), which may affect vascular response to beta blockers (NSBB). However, whether the unfavorable outcomes in patients with MAFLD can be related to an impact of metabolic comorbidities on the hemodynamic response to NSBB has not been clarified. We aimed to investigate whether the effect of NSBBs on portal pressure may be worse with metabolic comorbidities.

Method: Patients with cirrhosis and high-risk varices, were consecutively included. Hemodynamic measurements were performed at baseline and were repeated 15 to 20 minutes after intravenous administration of propranolol (0.15 mg/Kg). The HVPG response was investigated by grouping patients according to obesity, DM, AHT and DLP. The effect of propranolol was adjusted for baseline differences between groups using propensity score (PS).

Results: 585 patients were included (71% male, mean age 62 ± 11 years), 41% were Child Pugh class A and 59% class B/C, with MELD score of 12 ± 4. The etiology of cirrhosis was alcohol in 48%, HCV in 36% and MAFLD in 19%. 178 (30%) patients had DM, 116 (20%) obesity, 220 (38%) AHT and 100 (17%) DLP. 191 (33%) had ≥1 metabolic comorbidity. After propranolol, mean decrease in HVPG was lower in patients with DM than in those without DM (9 ± 10% vs 13.4 ± 10%, p < 0.01). Lower in obesity vs normo-weight (10.7 ± 5% vs 13.5 ± 10%, p = 0.04) and in AHT vs without (10.7 ± 10% vs 13.1 ± 10%, p = 0.02) and lower in DLP vs without (9.7 ± 8% vs 12.7 ± 10%, p = 0.03). Adjusting by PS only HVPG changes in DM were significant (p = 0.03). Among metabolic comorbidities, only DM was independently associated with HVPG decrease by multivariable logistic regression (OR = 0.64, 95% CI = 0.41–0.99; p = 0.049). Patients with DM had lower rates of HVPG decrease ≥10% from baseline (46% vs 59%, p = 0.01) and of HVPG decrease ≥20% (8% vs 25%, p < 0.01). Patients with MAFLD also had lower decrease in HVPG after propranolol than those with cirrhosis not MAFLD related (9 ± 6% vs 14 ± 10%, p < 0.01). By multivariable logistic regression, only MAFLD and not metabolic comorbidities, was independently associated with HVPG decrease (p < 0.01). Among patients with MAFLD, HVPG decrease was <10% in all cases, either with or without each metabolic comorbidity.

Conclusion: Patients with MAFLD cirrhosis had worse hemodynamic response to NSBB than those with cirrhosis not MAFLD related. Among metabolic comorbidities, only the presence of DM has an independent negative influence on acute hemodynamic response to NSBB. However, the influence of MAFLD on hemodynamic response to NSBB was independent of DM or other metabolic comorbidities.
Conclusion: In elderly patients, TIPS implantation is an effective option for the treatment of complications of PH. In this population, the incidence of post-derivative encephalopathy and deterioration of liver function is similar to the one observed in younger patients.

FRI525
Endoscopic glue injection v/s endoscopic human thrombin injection for bleeding gastric varices - a randomized controlled trial
Ashok Jhajharia1, 1SMS Medical College, Gastroenterology, Jaipur, India Email: drashokjhajharia@gmail.com

Background and aims: Acute gastric variceal bleeding (AGVB) is a potentially fatal consequence of portal hypertension, accounting for 10–30% of all variceal bleeding. Although endoscopic cyanoacrylate glue injection is a common treatment for acute hemorrhage, it has been linked to significant side effects. In the treatment of AGVB, there is limited evidence of the efficacy and relative safety of endoscopic human thrombin injection over glue injection.

Method: A total of 52 AGVB patients were randomized to receive either thrombin injection (25 patients) or glue injection (27 patients). The primary outcome was the incidence of any glue or thrombin injection-related post-therapy complications. Initial hemostasis, rebleeding, and mortality were all secondary end goals.

Results: Both groups had comparable baseline data. Hemostasis of active bleeding at endoscopy was 100.0% (10/10) in the thrombin group and 87.5% (7/8) in the glue group (p = 0.44). Treatment failure after 5 days occurred in two patients (6.1%) in the glue group compared to none in the thrombin group (p = 0.165). Between 6 and 42 days after index bleeding, rebleeding occurred in 4 patients in the thrombin group compared to 12 patients in the glue group (p < 0.03). In the thrombin group, none of the patients had post treatment ulcers on gastric varices compared to 14.81% (4/27) that occurred in the glue group (p = 0.045). Overall, complications occurred in 4 (20%) and 11 (40.7%) patients in the thrombin and glue groups, respectively (p = 0.105). Two patients in glue group died.

Conclusion: In order to achieve successful AGVB hemostasis, endoscopic thrombin injection was identical to glue injection. However, glue injection may be linked to a higher rate of rebleeding and post-therapy gastric varices ulcerations.

FRI526
Updating target PPG value to reduce clinical events in patients receiving covered-TIPS for the prevention of variceal rebleeding
Qiuheng Wang1, Bohan Luo1, Wei Bai1, Kai Li1, Wengang Guo1, Zhengyu Wang1, Jie Yuan1, Xiaomei Li1, Yong Lv1, Dongdong Xia1, Zhanxin Yin1, Jielai Xia2, Guohong Han1, 1Department of Liver Diseases and Interventional Radiology, Digestive Diseases Hospital, Xi’an International Medical Center Hospital, Northwestern University, Xi’an, China; 2Department of Medical Statistics, Fourth Military Medical University Email: 13991969930@126.com

Background and aims: A portosystemic pressure gradient (PPG) value of ≤12 mm Hg or ≥20% decrease has long been established as the target for TIPS in preventing variceal rebleeding. However, this value was defined in the era of bare stents, when dysfunction rate was high with constantly increased PPG. Moreover, not reaching this target does not necessarily indicate rebleeding. We aimed to confirm the optimal time point to measure PPG as an outcome predictor and update its target value in the scenario of covered TIPS for the prevention of variceal rebleeding.

Method: Consecutive patients receiving TIPS for acute variceal bleeding or secondary prophylaxis of rebleeding during January 1st, 2017 to October 31st, 2019 were included. TIPS procedures with local anesthesia and 8 mm covered stents were performed. PPG was measured preoperatively, immediately after stenting (immediate PPG), within 24–72 h post-operatively (early PPG), and at 1 month (late PPG).

Results: TIPS indications were secondary prophylaxis of rebleeding in 463 (93.7%) patients and pre-emptive TIPS in 31 (6.3%) patients. Median follow-up was 24.4 (17.2–36.7) months. Baseline, immediate, early, and late PPG values were 24.4 ± 5.8, 8.2 ± 3.0 mm Hg, 8.9 ± 3.1 mm Hg, and 8.7 ± 3.2 mmHg, respectively (Fig. 1A). Absolute early and late PPG were independent predictors of rebleeding in multivariate analyses, with similar HRs (1.11 [1.10–1.12], p = 0.015, vs. 1.09 [1.01–1.10], p = 0.029) and restrictive cubic spline curves (Fig. 1B). Given the easy access of early PPG before discharge, it was designated as the preferred timepoint. The cut-off value with the best discrimination for early PPG in predicting rebleeding was 14 mm Hg (Fig. 1C). Patients were then stratified into three subgroups: early PPG ≤12 mmHg, >12 mm Hg but ≤14 mmHg, and >14 mmHg. Patients with early PPG ≤14 mm Hg, whether lower than 12 mm Hg or not, had similar rates of variceal rebleeding, yet both strata exhibited lower rebleeding rates compared to that with early PPG >14 mm Hg (log-rank p = 0.011, Fig. 1D). As for HE, multivariate analyses indicated that early PPG reduction ([baseline PPG-early PPG]/baseline PPG) was an independent predictor (HR 1.05 [1.03–1.07], p < 0.001, Fig. 1E), with optimal cut-off being 55% (Fig. 1F). Given these results, the optimal window of PPG should be an absolute early PPG value ≤14 mm Hg (to control rebleeding), with early PPG reduction ≤55% (to avoid excessive HE). Indeed, this subgroup of patients present the most satisfying results regarding both rebleeding and HE, as compared with other subgroups (Fig 1G, and 1H).

Conclusion: The optimal timepoint to measure PPG as an outcome predictor should be early after the procedure (within 24–72 h). Raising the bar of absolute early PPG value from ≤12 mm Hg to
Background and aims: Alcohol-related liver disease (ALD) is a leading cause of liver-related mortality worldwide. Alcohol abstinence is a major determinant of its natural history. However, the impact of abstinence on the disease course in patients who have already progressed to cirrhosis and clinically significant portal hypertension (CSPH) is less well-established. The aim of this study was to examine the impact of alcohol abstinence on decomposition and mortality in ALD patients with CSPH.

Method: Alcohol abstinence, CSPH-related decomposition and mortality were assessed in a cohort comprised of retrospectively and prospectively (Vienna Cirrhosis Study, NCT03267615) recruited ALD patients diagnosed with CSPH (hepatic venous pressure gradient (HVPG) ≥10 mmHg). Patients were classified into four groups according to alcohol abstinence during follow-up and the presence of low (HVPG 10–19 mmHg) or high (HVPG ≥20 mmHg) risk portal hypertension at baseline: abstinent-low (n = 97), abstinent-high (n = 120), active-low (n = 35) and active-high (n = 36).

Results: We included 288 ALD patients (mean age: 56.7 ± 9.9 years; 74.7% male; 88.2% decompensated), who were followed for a median of 21.8 (IQR: 9.1–41.8) months. During the study period, 217 patients (75.3%) remained abstinent, while 71 patients (24.7%) showed continuous alcohol consumption. The mean baseline HVPG of the overall cohort was 20.2 ± 5.0 mmHg (abstinent: 20.2 ± 5.1 vs. active: 20.1 ± 4.8 mmHg; p = 0.858).

First/further hepatic decomposition was less frequent in abstinent patients compared to patients with continued alcohol consumption (26.5% vs. 42.4% at one year; 32.8% vs. 53.0% at two years; log-rank p < 0.001). Importantly, abstinent patients survived significantly longer, with a median transplant-free survival time of 68.2 (95%CI: 37.3–99.1) vs. 41.9 (95%CI: 27.7–56.0) months in patients with ongoing alcohol intake (log-rank p = 0.006).

Following the sub-stratification according to HVPG, the cumulative incidence of hepatic decomposition varied significantly between the subgroups, with 19.0%/23.5% in abstinent-low, 32.8%/40.2% in abstinent-high, 35.7%/48.6% in active-low and 48.9%/57.4% in active-high at one and two years respectively (log-rank p < 0.001). HVPG ≥20 mmHg and continued alcohol intake negatively impacted survival, as demonstrated by a median transplant-free survival time of 94.7 (95%CI: 40.1–149.3) months in abstinent-low, 63.3 (95%CI: 34.1–92.4) months in abstinent-high, 61.3 (95%CI: 32.8–88.9) months in active-low and 36.5 (95%CI: 27.5–45.4) months in active-high (log-rank p = 0.034) ALD patients.

Conclusion: Alcohol abstinence and severity of CSPH are key determinants in the clinical course of ALD patients with cirrhosis and CSPH. ALD patients with low-risk CSPH but a continued alcohol consumption still have a poor prognosis that is similar to abstinent patients with high-risk CSPH.

Background and aims: Abstinence from alcohol constitutes the removal of the primary aetiologic factor in alcohol-related cirrhosis and has been linked to an improved outcome. However, the extent and prognostic value of clinical improvements after achieving alcohol abstinence in decompensated alcohol-related cirrhosis have not been sufficiently characterised. Thus, the aim of this study was to examine the impact of hepatic recompensation according to the novel Baveno VII criteria on liver-related mortality and the development of hepatocellular carcinoma (HCC) in patients with decompensated alcohol-related cirrhosis.

Method: Recompensation during follow-up was assessed in patients with decompensated alcohol-related cirrhosis and persistent alcohol abstinence who underwent a baseline hepatic venous pressure gradient (HVPG) assessment. Recompensation was defined according to Baveno VII criteria as resolution of ascites and hepatic encephalopathy (absence of clinical signs and cessation of medical therapy), absence of variceal bleeding and improvement in liver function. Achieving recompensation was regarded as a time-dependent covariate and analysed using Cox proportional-hazards models.

Results: 204 patients with alcohol-related cirrhosis (age: 56.9 ± 9.8 years, 75.0% male) and a median HVPG of 20 (18–24) mmHg were followed-up over a median of 24.4 months. Overall, 37 patients (18.1%) achieved hepatic recompensation. Baseline parameters linked to a higher probability of recompensation in a competing risk analysis included a lower HVPG, a lower Child-Pugh score, higher albumin, higher mean arterial pressure and a lower BMI. Achieving hepatic recompensation nearly abolished the risk of liver-related mortality (HR: 0.071 [95% CI: 0.010–0.527]; p = 0.010), even after adjusting for baseline HVPG, MELD, albumin, C-reactive protein and age (adjusted HR: 0.091 [95% CI: 0.012–0.677]; p = 0.019; Table 1). With regard to
HCC development, we observed a trend towards a reduced risk in recompensated patients, yet this finding did not reach statistical significance (HR: 0.398 [95% CI: 0.884–1.878], p = 0.245).

<table>
<thead>
<tr>
<th></th>
<th>Univariate analysis</th>
<th>Multivariate analysis</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>HR</td>
<td>95% CI</td>
</tr>
<tr>
<td>Recompensation</td>
<td>0.071</td>
<td>(0.010–0.527)</td>
</tr>
<tr>
<td>MELD (per point)</td>
<td>1.072</td>
<td>(1.018–1.129)</td>
</tr>
<tr>
<td>Albumin (per g/L)</td>
<td>0.957</td>
<td>(0.917–0.999)</td>
</tr>
<tr>
<td>HVPC (per mmHg)</td>
<td>1.301</td>
<td>(1.040–1.616)</td>
</tr>
<tr>
<td>CRP (per mg/dL)</td>
<td>1.257</td>
<td>(1.079–1.464)</td>
</tr>
<tr>
<td>Age (per year)</td>
<td>1.042</td>
<td>(1.012–1.074)</td>
</tr>
</tbody>
</table>

Conclusion: Hepatic recompensation according to Baveno VII criteria occurred in a considerable proportion of patients with decompensated alcohol-related cirrhosis and was associated with a significantly reduced risk of liver-related mortality. Of note, recompensated patients remain at risk of HCC.

**FRI529**

Covered TIPS reduces the risk of further decomposition: results from an individual patient data meta-analysis of 3924 patients with cirrhosis

Hélène Larrue1,2, Pol Olivas3,4, Yong Ly5, Guohong Han6, Theresa Bucsics7,8, Thomas Reiberger7,8, Tilman Sauerbruch9, Virginia Hernandez-Gea3,4,10,11,12, Dominique Thabut13,14, Marika Rudler13,15, Jean Marie Peron1,2, Gennaro D’Amico16,17, Juan Carlos Garcia Pagan3,4,11,12, Christophe Bureau1,2.

Background and aims: Baveno VII conference introduced the concept of further decomposition as a prognostic stage of cirrhosis that is associated with an even higher mortality than first decomposition. The effectiveness of transjugular intrahepatic portosystemic shunt (TIPS) has already been demonstrated for the prevention of rebleeding and recurrent ascites. Nevertheless, the effect of TIPS to decrease the overall incidence of further decomposition events remains unclear—mainly because of the risk of encephalopathy and liver failure. The aim of this study was to assess the incidence of further decomposition after TIPS, defined as new or worsening ascites, new or worsening encephalopathy or new portal hypertension (PH)-related bleeding or rebleeding, in comparison to standard of care (SOC).

Method: We conducted a review of the medline literature searching for controlled studies (randomized control trials (RCT) and cohorts) assessing TIPS in comparison to SOC in the indication of recurrent ascites, refractory bleeding, and secondary prevention of bleeding since the use of polytetrafluoroethylene-covered stents and until 2020. We collected individual patient data (IPD) to perform an IPD meta-analysis also using a propensity score (PS) matching by multivariate logistic regression. The comparisons were performed by stratified log-rank test by PS quintiles. The primary outcome was the incidence of further decomposition. The secondary outcome was overall survival.

Results: 12 databases among the 14 selected studies (5 RCT, 9 cohorts) were available. The whole population included 3924 patients (SOC: n = 3077; TIPS: n = 847). After PS matching, 2415 patients (SOC: n = 1802; TIPS: n = 613) were analyzed: 70% men, mean age 54 ± 12, alcohol-related cirrhosis 42%, mean Child-Pugh 9 ± 2, mean MELD score 14 ± 6 without significant differences between groups. The cumulative incidence function of further decomposition at 2 years in the PS-matched population was 0.45 (0.41–0.50) in the TIPS group vs. 0.62 (0.59–0.65) in the SOC group (stratified log-rank p = 0.00001), with mortality and liver transplantation as competing risk (figure). The benefit of TIPS was confirmed by IPD meta-analysis adjusted for age, treatment, history of ascites, of encephalopathy, of hepatocellular carcinoma, serum albumin and MELD (hazard ratio 0.47 (0.39–0.57)) without significant heterogeneity (I² = 8.4%; p = 0.365) and was consistent across study subgroups according to TIPS indication. The overall survival was significantly better in TIPS group: 74% (69–78%) vs 63% (59–66%) in SOC group (stratified log rank p < 0.0001).

Conclusion: This IPD meta-analysis demonstrates that TIPS decreases the risk of further decomposition in comparison to SOC, in patients with cirrhosis treated for recurrent ascites or in secondary prevention of PH-related bleeding and importantly, also improves survival.
Sarcopenia increases the risk of cirrhosis disease progression and death in patients with cirrhosis

Puneeta Tandon1, Sarah Wang1, Moon Young Kim2, Bart Van Hoek3, Daphne Bot4, Jeroen van Vugt5, Berend Beumer5, Jan Ijzermans5, Sunil Taneja6, Surender Singh6, Maryam Ebadi6, Aldo J Montano-Loza1, 1Division of Gastroenterology (Liver Unit), University of Alberta, Edmonton, Canada; 2Department of Internal Medicine, Yonsei University Wonju College of Medicine, Wonju, Korea, Rep. of South; 3Department of Gastroenterology and Hepatology, Leiden University Medical Center, Leiden, Netherlands; 4Department of Dietetics, Leiden University Medical Center, Leiden, Netherlands; 5Department of Surgery, Division of HPB & Transplant Surgery, Erasmus MC Transplant Institute, Erasmus MC, University Medical Centre Rotterdam, Rotterdam, Netherlands; 6Department of Hepatology, Postgraduate Institute of Medical Education and Research, Chandigarh, India

Email: ptandon@ualberta.ca

Background and aims: Sarcopenia in cirrhosis has been operationalized as low muscle mass. The skeletal muscle index (SMI) is a well-validated tool to identify sarcopenia in cirrhosis and has been associated with increased mortality in patients awaiting liver transplant (LT). To date, the impact of sarcopenia on cirrhosis progression is unknown. In this study, we aimed to explore the relationship between sarcopenia and the risk of: (i) a combined outcome of cirrhosis progression or mortality or (ii) mortality alone.

Method: The SMI was measured at baseline using abdominal CT imaging at the 3rd lumbar vertebra (L3). Sarcopenia was defined using established cut-offs in patients with cirrhosis awaiting LT as SMI <39 cm²/m² in females and <50 cm²/m² in males. Progression of cirrhosis was defined by an increase in clinical stage from baseline using the D'Amico classification. Factors associated with progression or death or death alone were evaluated using univariate and multivariate Cox regression models.

Results: 1624 adult patients with cirrhosis from five centers across Europe, North America and Asia were included. Mean age was 54 ± 9 years, 26% of patients were female, 31% had compensated disease at baseline, and the mean MELD-Na was 15 ± 7 years. Data on ethnicity was available in 1354 patients (48% Caucasian/European, 46% Asian, and the remainder other ethnicities). The top three etiologies of liver disease were alcohol (40%), hepatitis C (19%) and hepatitis B (13%). Both the SMI as a continuous variable and presence of sarcopenia were associated with the combined outcome of cirrhosis progression or mortality (HR 0.98, 95% CI 0.97–0.99, p < 0.001; and HR 1.37, 95% CI 1.17–1.61, p < 0.001; respectively) and mortality alone (HR 0.98, 95% CI 0.97–0.99, p < 0.001; and HR 1.39, 95% CI 1.16–1.67, p < 0.001; respectively). In multivariate analysis, sarcopenia was associated with increased risk of progression to the next cirrhosis stage or death (HR 1.25, 95% CI 1.06–1.47, p = 0.007) and increased risk of death alone (HR 1.25, 95% CI 1.04–1.50, p = 0.02), after adjusting for age, sex, and MELD score. The 1-year, 5-year and 10-year probabilities of death or mortality (HR 0.98, 95% CI 0.97–0.99, p < 0.001; and HR 1.37, 95% CI 1.17–1.61, p < 0.001; respectively); and mortality alone (HR 0.98, 95% CI 0.97–0.99, p < 0.001; HR 1.39, 95% CI 1.16–1.67, p < 0.001; respectively). Substantial reduction of the diagnostic grey zone of the Baveno-VII CSPH criteria by sequential consideration of VITRO score.

Conclusion: Sarcopenia was an independent predictor of cirrhosis progression or death or death alone. Future studies are needed to evaluate the possibility of slowing cirrhosis disease progression by reversing or preventing sarcopenia.

SUBSTANTIAL REDUCTION OF THE DIAGNOSTIC GREY ZONE OF THE BAVENO-VII CSPH CRITERIA BY SEQUENTIAL CONSIDERATION OF VITRO

Lukas Hartl1,2, Mathias Jachs1,2, Benedikt Simbrunner1,2,3, David JM Bauer1, Rafael Paternostro1,2, Bernhard Scheiner1,2, Lorenz Balcar1,2, Georg Semmler1,2, Albert Stättermayer1,2, Matthias Pinter1,2, Peter Quehenberger4, Michael Trauner1, Thomas Reiberger1,2,3, Mattias Mandorfer1,2,1Medical University of Vienna, Division of Gastroenterology and Hepatology, Department of Medicine III, Vienna, Austria; 2Medical University of Vienna, Vienna Hepatic Hemodynamic Lab, Division of Gastroenterology and Hepatology, Department of Medicine III, Vienna, Austria; 3Medical University of Vienna, Christian Doppler Lab for Portal Hypertension and Liver Fibrosis, Vienna, Austria; 4Medical University of Vienna, Department of Laboratory Medicine, Vienna, Austria

Email: mattias.mandorfer@meduniwien.ac.at

Background and aims: Baveno-VII proposed liver stiffness measurement (LSM) and platelet count (PLT) criteria for non-invasive clinically significant portal hypertension (CSPH) diagnosis in compensated advanced chronic liver disease (cACLD); CSPH ‘ruled-out’: LSM ≤15 kPa plus PLT ≥150 G/L; CSPH ‘ruled-in’: LSM ≥25 kPa. However, a substantial share of patients remains in the diagnostic ‘grey-zone’. We aimed to refine these criteria by sequential application of von Willebrand factor antigen (VWF)/thrombocytes (VITRO) score.

Journal of Hepatology 2022 vol. 77(S1) | S389–S664 S631
POSTER PRESENTATIONS

Method: Patients with evidence of cACLD (LSM ≥10 kPa) undergoing hepatic venous pressure gradient (HVPG) measurement at the Vienna General hospital between 2004 and 2021 were included. The performance of non-invasive tests (NIT) including VITRO, i.e., the ratio between VWF (%) and PLT (G/L), for the diagnosis of CSPH (HVPG ≥10 mmHg) were evaluated in a derivation (2004–2016; n = 221) and a validation (2017–2021; n = 81) cohort. A particular focus was put on patients who were unclassifiable by Baveno-VII criteria.

Results: Overall, viral hepatitis was the predominant etiology (50.7%), followed by alcoholic liver disease (15.2%) and non-alcoholic steatohepatitis (13.2%). CSPH prevalence was 62.3%.

According to Baveno-VII criteria, 45.7% of patients in the diagnostic cohort remained in the diagnostic ‘grey-zone’ for CSPH, in which VITRO showed an excellent performance for the detection of CSPH with an area under the receiver operator characteristic curve (AUROC) of 0.909 (95% confidence interval [95%CI]: 0.823–0.965). VITRO ≤1.5/≥2.5 ‘ruled-out’ (negative predictive value [NPV]: 97.5%; specificity: 97.7%) and ‘ruled-in’ (positive predictive value [PPV]: 91.2%; sensitivity: 94.7%) CSPH in patients who were unclassifiable by Baveno-VII criteria.

The application of a sequential Baveno VII-VITRO algorithm re-allocated 73% of initial ‘grey-zone’ patients to the ‘ruled-in’/‘ruled-out’ group, whilst maintaining a PPV/NPV >90%. Finally, 87.8% of patients were classifiable in regard to CSPH by the Baveno-VII-VITRO sequence. Importantly, all findings were confirmed in a temporal validation cohort.

Of note, not a single patient (0.0%) allocated to the ‘CSPH ruled-out’ group by the Baveno-VII-VITRO sequence developed decomposition within five years, while 5-year decomposition rates were substantial (23.9%) among ‘CSPH ruled-in’ patients and negligible (4%) in remaining ‘grey-zone’ patients.

Conclusion: The sequential application of VITRO ≥2.5 to patients who are unclassifiable by Baveno-VII-criteria improves the identification of cACLD patients with a high risk of CSPH and subsequent decomposition. In turn, VITRO ≤1.5 ‘ruled-out’ CSPH in Baveno-VII ‘grey zone’ patients and indicated a favorable prognosis. Less than 15% of cACLD patients remained in the final ‘grey zone’ when applying the sequential Baveno VII-VITRO algorithm.

FR1532

Causes and predictors of 30-day readmission in patients with gastric varices requiring Balloon-occluded retrograde transvenous obliteration (BRTO)

Mohamed Ahmed1, Vinay Jahagirdar1, Wael Mohamed1, Ifrah Fatima1, Kevin Kennedy2, Alisa Likhitups1, 1University of Missouri-Kansas City Volker Campus, Internal medicine, Kansas City, United States; 2Saint Luke’s Hospital of Kansas City, Kansas City, United States; 3University of Missouri-Kansas City

Email: mohamedfayez1991@gmail.com

Background and aims: Variceal bleeding is one of the major complications of portal hypertension. Though gastric variceal bleeding is less common, it has a higher mortality than esophageal variceal bleeds. Endoscopic management of gastric varices (GV) is less effective, and Transjugular Intrahepatic Portosystemic Shunts (TIPS) and balloon-occluded retrograde transvenous obliteration (BRTO) are used. In BRTO, the portosystemic gastrorenal shunt is accessed via the left renal vein, from a trans-jugular or transfemoral approach. The shunt is occluded by a balloon and a sclerosing agent is injected into the variceal system. Studies have shown that BRTO can effectively control active gastric variceal bleeding and is a good alternative to TIPS. Diverting the blood towards the liver improves hepatic function and patient survival, but increased portal pressures may also worsen esophageal varices and ascites.

Method: Patients with GV who underwent BRTO were identified from the 2016–2018 Healthcare Cost and Utilization Project databases (HCUP) using the National readmission database (NRE) by using the International Classification of Diseases Code, 10th Revision Clinical Modification (ICD-10), 30-day readmission rate and diagnosis were identified. Multiple logistic regression model was used to identify the factors associated with readmission. SAS 9.4 was used for data analysis.

Results: Total of 608 patients who underwent BRTO were identified between 2016 and 2018. Mean age was 58.2 ± 12.6. 39.8% of patients were females. The 30- and 90-days readmission rate was 20.4% and 28.2% respectively. Significant increase length of stay (10.5 ± 10.1 vs 8.4 ± 6.5; p < 0.004) and total charges (238765 vs 185972; p = 0.001) was associated with the 30-day readmission patients. Most common diagnosis for 30-day readmissions were hepatic encephalopathy (13%), acute liver failure (8%), gastric varices (6%), Ascites (5%), systemic infection (4%), and acute blood loss anemia (4%). Multiple logistic regression analysis showed that 30-day readmission was associated with renal failure (OR 3.25, 95% CI 1.72–6.16, P = 0.003) but not associated with presence of bleeding esophageal varices (OR 1.27, 95%CI 0.81–1.98), hepatic encephalopathy (OR 1.2, 95% CI 0.75–2.17), liver failure (OR 2.16, 95% CI 0.93–4.99) and DM with chronic complications (OR 1.39, 95% CI 0.91–2.14) at the index admission.

Conclusion: BRTO procedures are associated with high 30-day readmission rate. Patients with renal failure undergoing BRTO are at significantly higher risk of 30-day readmissions with OR of 3.25. Hepatic decomposition, Acute liver failure and systemic infections appears to be the most common causes of 30-days readmission in patient having BRTO.

FR1533

Carvedilol is associated with superior hemodynamic response and rebleeding rates in comparison to propranolol in secondary prophylaxis of variceal bleeding

Mathias Jachs1, Lukas Hartl1, Benedikt Simbrunner1, David JM Bauer1, Rafael Paternösto1, Lorenz Balcar1, Benedikt Hofer1, Nikolaus Pfisterer1, Michael Schwarz1, Bernhard Scheiner1, Albert Stättermayer1, Matthias Pinter1, Michael Trauner1, Mathias Mandorfer1, Thomas Reiberger1, 1Medical University of Vienna, Division of Gastroenterology and Hepatology, Department of Internal Medicine III, Vienna, Austria

Email: thomas.reiberger@meduniwien.ac.at

Background and aims: In primary prophylaxis of variceal bleeding, carvedilol offers more profound decreases in hepatic venous pressure gradient (HVPG) as compared to propranolol. However, limited data exists on its efficacy and safety after the first variceal bleed, i.e., in secondary prophylaxis.

Method: For this retrospective evaluation, patients who had previously bled and underwent paired HVPG measurements at our centre between 2004 and 2021 to guide non-selective betablocker (NSBB) therapy were included. All patients underwent band ligation in addition to NSBB therapy. The effects of NSBB treatment on HVPG and mean arterial pressure (MAP) was compared between...
propranolol and carvedilol users. Long-term follow-up data on rebleeding, acute kidney injury (AKI) and ascites development/progression was recorded and analysed comparing competing risk regression.

**Results:** Eighty-seven (carvedilol) patients: n = 45 (n = 42) patients were included. Patients underwent their baseline HVPG measurement after a median of 2.2 months following their initial bleed and had a median (NSBB-naive) baseline HVPG of 21 (IQR: 18; 24) mmHg. Ascites was present in 62% of patients, and 39%, 48% and 13% had Child-Turcotte-Pugh stage A, B and C cirrhosis, respectively. Carvedilol induced more marked reductions in HVPG as compared to propranolol (relative change: −20 [−29; −10] % vs. −11 [−22; −5] %, p = 0.027), resulting in a higher proportion of patients achieving chronic HVPG response, i.e., a reduction by ≥20% or an absolute value ≤12 mmHg (53.3% vs. 28.6%, p = 0.034). Carvedilol was thus, associated with a lower cumulative incidence of rebleeding (2.4%/9.5%/10.4% vs. 9.5%/21.6%/34.9% at 1/3/5 years, Gray’s test: p = 0.015) and liver-related death (5.0%/10.7%/10.7% vs. 7.4%/23.8%/33.9% at 1/3/5 years, p = 0.032) during long-term follow-up, as compared to propranolol. Notably, the incidence of AKI did not differ between the two groups (p = 0.139) despite more pronounced decreases in MAP induced by carvedilol (relative change: −12 [−17; −6] % vs. −6 [−17; 2]% , p = 0.044), and ascites development or worsening was less commonly observed in patients on carvedilol therapy (p = 0.034). Stratifying patients by HVPG response status yielded similar results.

Conclusion: Carvedilol was associated with higher rates of HVPG response and lower rebleeding rates in our retrospective study. Of note, the use of carvedilol was also linked to lower rates of non-bleeding further decompensation, i.e., ascites development/progression, whilst having similar impact on the incidence of AKI in our cohort, despite more marked reductions in MAP.

**FRIS34**

**Impact of early nasogastric tube feeding after endotherapy for acute variceal bleeding in patients with cirrhosis: a randomized controlled trial**

Jatin Yegurla¹, Sanchit Sharma 1,2, Namrata Singh¹, Samagra Agarwal¹, Sumaira Qamar¹, Deepak Gunjan¹, Anoop Saraya¹, 1, All India Institute of Medical Sciences, Department of Gastroenterology and Human Nutrition Unit, New-Delhi, India; ²John Radcliffe hospital, Translational Gastroenterology Unit, Oxford, United Kingdom

Email: ansaraya@yahoo.com

**Background and aims:** Limited data exist on safety of early feeding in patients with cirrhosis after endotherapy for acute variceal bleeding (AVB). We studied the impact of early nasogastric (NG) tube feeding on relevant outcomes in these patients in a randomised controlled trial.

**Method:** Consecutive patients with cirrhosis undergoing endotherapy for AVB were randomized to receive either liquid diet through an NG tube (n = 40) [early-feeding (EF) group] or sips of water and lemon water orally (n = 40) [standard-of-care (SOC) group] for 48 hours after endotherapy. In early feeding group, 14 Fr NG tube (Ryle’s tube) was placed immediately after endotherapy under endoscopic guidance and liquid diet was started one hour later which consisted of commercial polymeric formula feed for first 6 hours followed by home-made milk-based formula feed. Solid diet was resumed 48 hours later in both the groups. Primary end-point was 5-day rebleeding and secondary end-points included incidence of infections, hepatic encephalopathy during hospitalization and 6-week mortality.

**Results:** Eighty patients [Mean age: 41 ± 11.5 years; males (82.5%); Alcohol etiology (55%)] were included. Baseline characteristics were comparable in both the groups. The 5-day rebleeding rates in EF and SOC groups were 2.5% and 5%, respectively (p = 0.55). The incidence of infection [2.5% (EF) vs 2.5% (SOC), p = 1.00] and development of HE [5% (EF) vs 2.5% (SOC), p = 0.36] during hospitalisation were comparable. One patient in EF group developed mild epistaxis following NG tube insertion. Average calorie and protein intake by patients in EF group during the 48 hours was 1318 ± 240 Kcals and 43.4 ± 9.2 g of proteins per day. No patient in EF group developed feed intolerance. No significant difference was observed in mortality, rebleeding, infections or decompensations during the 6-week follow-up.

**Table:** Comparison of baseline characteristics and outcomes between early-feeding (EF) and standard-of-care (SOC) groups. All values are expressed as mean ± SD or frequency (percentage).

<table>
<thead>
<tr>
<th>Age (years)</th>
<th>EF group (N = 40)</th>
<th>SOC group (N = 40)</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>39.4 ± 12.3</td>
<td>42.6 ± 10.5</td>
<td>0.23</td>
<td></td>
</tr>
</tbody>
</table>

- **Etiology**
  - 8 (20%)
  - 5 (16.25%)

- **Others**

**Conclusion:** Early NG tube feeding in patients with cirrhosis after AVB is safe and does not lead to increased risk of rebleeding or encephalopathy. (CTRI/2021/05/043590).

**FRIS35**

**A multi-compartmental model of the HepQuant SHUNT test can quantify anatomic shunting and stratify risk for varices: combined results from the HALT-C and SHUNT-V studies**

Michael McRae¹, Steve Helmeke², Greg Everson¹. ¹Custom Diagnostic Solutions LLC; ²HepQuant, Denver, United States

Email: michaelpmcrae@gmail.com

**Background and aims:** In chronic liver disease (CLD), persistent inflammation and fibrosis impair hepatocyte function and increase portal pressure, resulting in portal venous collaterals and portal-systemic shunting. The HepQuant SHUNT test uses stable nonradioactive isotopes of carbon-13 cholate (13C-CA) intravenously and deuterium cholate (D4-CA) orally to simultaneously measure clearance from both portal and systemic circulations. The aim of this study was to determine whether compartmental analysis of the HepQuant SHUNT test could quantify anatomic shunting in patients with CLD and esophageal varices.

**Method:** A compartmental model was developed from the HepQuant SHUNT test results from 26 lean controls and 492 CLD patients with esophage-gastro-duodenoscopy findings (291 no varices, 143 small varices, and 58 large varices). Transfer between systemic, portal, and
liver compartments was modeled by a system of 18 first-order ordinary differential equations along with assumptions from measured or literature-derived values. The compartmental model and PK parameters were solved for each subject with three parameters estimated by nonlinear least-squares regression including the anatomic shunt flow (kPS). Compartamental analysis was completed using MATLAB Simbiology.

**Results:** The compartmental model (Fig 1A) fit the data with median adjusted R-squared across all patients of 0.99 for 13C-CA IV curves and 0.95 for d4-CA oral curves. Population-averaged oral curve simulations (Fig 1B) (mean and 95% confidence) from the compartment model show significant differences between controls, no varices, small varices, and large varices. The estimated median anatomic shunt flow, kPS, was 0, 0, 411, and 566 ml/min for controls, none, small, and large varices, respectively with significant difference between all groups (Wilcoxon rank-sum p < 0.05) (Fig 1C). In parallel, the model demonstrated reduced portal inflow to the liver (kPT) among varices groups, with median kPT values of 784, 676, 380, and 156 ml/min for controls, none, small, and large varices, respectively with significant difference between all groups (p < 0.001) (Fig 1D).

**Conclusion:** The compartmental model discriminated patients with small and large varices. The model also distinguished the individual contributions of hepatocyte function and anatomic shunting to the hepatic clearance of cholate. The individualized PK parameters estimated from this compartmental model, when combined with artificial intelligence or machine learning algorithms, have significant potential to enhance the diagnostic performance and clinical utility of the HepQuant test of global liver function.

**FRIS36**

**Expandable constrained 6 mm transjugular intrahepatic portosystemic shunt: an alternative approach for high-risk patients?**

Hannah Schneider1, Anja Tiede1, Alena Friederike Ehrenbauer1, Lena Stockhoff1, Johanna Luise Charlotte Lorenz1, Heiner Wedemeyer1, Richard Taubert1, Jan Hinrichs2, Benjamin Maasoumy1,1 Hannover Medical School, Dept. of Gastroenterology, Hepatology and Endocrinology; 2 Hannover Medical School, Dept. of Interventional Radiology

**Background and aims:** A transjugular intrahepatic portosystemic shunt (TIPS) can effectively overcome portal hypertension in patients with liver cirrhosis. However, in a considerable proportion of the respective patients relative or absolute contraindications such as cardiac impairment, recurrent hepatic encephalopathy (HE) or advanced hepatic impairment prevent TIPS insertion. In this study, we investigated whether a response-guided step-up approach using a constrained TIPS with a diameter of 6 mm may pose as an option for otherwise ineligible or high-risk patients.

**Method:** A number of 38 patients, considered to have a high risk for TIPS related complications due to the presence of relative contraindications, received a constrained 6 mm TIPS at Hannover Medical School between 10/2020 and 03/2022. During the TIPS procedure, a 6 mm stent graft was placed into the parenchymal tract to constrain expansion of the later inserted TIPS endoprosthesis. The 6 mm stent graft can be revised to >8 mm via balloon expansion in case of an insufficient clinical response, increasing shunt volume gradually. A control cohort of patients with conventional (8 mm) TIPS was generated using propensity score matching considering the FIPS (Freiburg index of post TIPS survival), history of HE and diastolic dysfunction. A caliper of 0.25 resulted in 28 patients per group. Patients were followed up for 6 months. Competing risk analysis was performed to evaluate clinical complications.

**Results:** Median age of patients with constrained TIPS was 61, the majority was male (60.7%), median FIPS was 0.12. Within the high-risk group indication for the constrained TIPS was cardiac impairment, poor liver function or history of HE in 15, 9, and 4 patients, respectively. The constrained TIPS procedure was successful in all patients without any major complication. However, TIPS dysfunction was significantly more frequent in the constrained TIPS cohort (n = 1 vs. 6; p = 0.03). In 2 patients constrained TIPS did not achieve adequate symptom control. Importantly, in all cases the constrained TIPS was successfully revised and/or dilated to 7/8 mm. While no constrained TIPS had to be reduced or occluded due to clinical complications, TIPS diameter had to be decreased in 2 of the control patients due to recurring HE and cardiac decompensation. Patients treated with the response-guided step-up approach less frequently developed overt HE during follow up (n = 15 vs. 5; p = 0.02). There was no significant difference concerning the development of cardiac decompensation (n = 6 vs. 9; p = 0.25) and survival (n = 4 vs. 6; p = 0.38) between the two groups.

**Conclusion:** The constrained 6 mm TIPS may offer a more careful step-up approach for selected high-risk TIPS patients. The technical procedure appeared to be safe and well feasible. Larger studies are needed to further explore promising results on TIPS related complications i.e. with regard to HE development.

**FRIS537**

**Early treatment with terlipressin in patients with hepatorenal syndrome yields improved clinical outcomes in 3 phase III North American studies**

Michael Curry1, Hugo E. Vargas2, Alex Refetoff3, Nikolaos T. Pyrsopoulos4, Vilas Patwardhan1, Khurram Jamil3,1 Beth Israel Deaconess Medical Center; 2Mayo Clinic; 3Saint Louis University; 4Rutgers-New Jersey Medical School University Hospital; 5Mallinckrodt Pharmaceuticals

**Email:** mcurry@bidmc.harvard.edu

**Background and aims:** Hepatorenal syndrome (HRS), a serious complication of advanced cirrhosis and a potentially reversible form of acute kidney injury, is associated with a rapid deterioration in kidney function. The vasopressin analogue, terlipressin, successfully reverses HRS. Patients (pts) with higher baseline serum creatinine (Scr) levels have a reduced response to terlipressin. The largest randomized, prospective database of placebo-controlled studies in pts with HRS was examined to assess terlipressin treatment response in pts with varying baseline Scr levels.

**Method:** Pooled data from 3 Phase III North American-centric, placebo-controlled clinical studies (OT-0401, REVERSE, and CONFIRM) were used. Post hoc analyses examined pooled data from terlipressin-treated pts with HRS (type 1; n = 352)—across 3 Scr subgroups (<3, ≥3 to <5, and ≥5 mg/dL)—to
delineate their correlation with HRS reversal (defined as at least 1 SCr level of ≤1.5 mg/dL on treatment), renal replacement therapy (RRT)-free survival, transplant-free survival (TPS), and overall survival (OS). Statistical analyses included the Wald test (logistic regression analysis), Chi-square/Fisher’s exact test (HRS reversal), and the log rank test (survival estimates).

**Results:** SCr levels were significantly associated with HRS reversal in univariate and multivariate logistic regression analyses (p < 0.001) (Figure). Among pts with HRS, the incidence of HRS reversal inversely correlated with SCr subgroup: <3 mg/dL, 49.2%; ≥3 to <5 mg/dL, 28.0%; ≥5 mg/dL, 9.1% (p < 0.001). At Day 30 follow-up, RRT-free survival was significantly higher for pts with HRS in the lower SCr subgroups versus the highest subgroup (<5 mg/dL vs ≥5 mg/dL; p = 0.01). Terlipressin-treated pts with HRS who had a lower baseline SCr level had higher OS (p < 0.001) and TPS at Day 90 (p = 0.04).

**Results:**

<table>
<thead>
<tr>
<th>Baseline parameters</th>
<th>Terlipressin n</th>
<th>Odd ratio</th>
<th>95% CI</th>
<th>p value</th>
</tr>
</thead>
<tbody>
<tr>
<td>SCr</td>
<td>312</td>
<td>0.516</td>
<td>0.35&lt;1.794</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>&lt;3 mg/dL</td>
<td>312</td>
<td>0.939</td>
<td>0.902&lt;0.977</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>≥3 mg/dL</td>
<td>1,949</td>
<td>1.106&lt;1.091</td>
<td>0.19</td>
<td></td>
</tr>
</tbody>
</table>

**Conclusion:** Terlipressin-treated pts with HRS and a lower baseline SCr level experienced higher HRS reversal and survival outcomes. It is important to identify and treat pts with HRS early when they have lower SCr levels and a greater probability of clinical response to terlipressin.

**Non-invasive tools are suboptimal to predict the presence of varices needing treatment and risk of clinical decompensation in patients with autoimmune hepatitis related cirrhosis**

Randeep Rana, Samagra Agarwali, Sanchit Sharma, Ujjwal Sonika, Syed Ahmed, Srikanth Gopi, Deepak Gunjan, Anoop Saraya, All India Institute Of Medical Sciences New Delhi, Gastroenterology and Human Nutrition Unit, New Delhi, India; 2Translational Gastroenterology Unit, John Radcliffe Hospital, Oxford, United Kingdom; 3Govind Ballabh Pant Hospital, Gastroenterology, New Delhi, India

Email: ansaraya@yahoo.com

**Background and aims:** Baveno VII consensus recommend the use of non-invasive tools (NITs) to predict the risk of clinical decompensation (CD) and detecting varices needing treatment (VNTs) in patients with compensated cirrhosis. The present study aimed to validate these recommendations in patients with autoimmune hepatitis (AIH) related cirrhosis.

**Method:** Diagnostic performance of Baveno-VI (LSM >20 kPa or platelet <1 50 000/mm³), expanded Baveno-VI (LSM >25 kPa or platelet <1 10 000/mm³) and platelet-albumin (albumin <3.6 g/dl <1 20 000/mm³) criteria for detecting VNTs was assessed. Standard supportive treatment included non-selective beta-blockers (40–60 mg daily) and UDCA (500–1000 mg daily) with dose adjustment according to BMI.

**Results:** One hundred ten (110) patients with AIH-related cirrhosis were included, with 37 patients having VNTs. At a threshold probability of 10% missed VNTs, platelet-albumin criteria was the most beneficial among NITs to detect VNTs with a potential to avoid 44 additional endoscopies before 1 additional VNT is missed. Rest of the NITs had similar benefit to performing endoscopy in all patients. At lower thresholds (<10% missed VNTs), performing endoscopy in all patients was the most beneficial strategy. Over a median follow-up of 30 months (IQR913–39 months), 30 of 96 patients with available follow-up developed clinical decompensation. The 1-year and 3-year rate of clinical decompensation in patients with definite CSPH, possible CSPH and no CSPH was (29.2%, 29.0%, 19.8%) and (35.6%, 39.5%, 29.0%), respectively (log rank test, p = 0.75).

**Conclusion:** The strategy of endoscopy for all to screen large varices using the Baveno VII criteria for predicting clinical decompensation is suboptimal to stratify patients of AIH.
functions (protein synthesis and ammonia purification) demonstrated considerable improvement in the long-term observation period due to combined treatment. 65 (54.2%) of 120 patients had no bleeding episodes at the endpoint of 12 months. 39 (32.5%) were hospitalized with 1 (28) or more (11) minor bleedings. Fatal bleedings took place in 11 (9.2%) patients and not related to bleeding deaths in 4 cases.

**Conclusion:** From our point of view, the improving of HE manifestations after SAE procedure could be explained by synergistic effects of reduction of the excessive splenic flow, restoring of liver synthetic function due to ameliorating splenic artery steal syndrome, and, as a result, liver tissue rearterialization. SAE showed a long-term reliable prophylactic effect in high-risk patients with CSPH and HE.

**FRIS40**

Sequential algorithm of spleen stiffness measured by a dedicated 100 Hz examination and Baveno VII criteria for clinically significant portal hypertension in compensated cirrhosis

Ruiling He1,2, Chuan Liu1, Li jie5, Jianzhong Ma5, Ying Guo5, Xiaoqing Guo5, Shiqing Liu2, Bo Gao6, Ning Liu6, Mingkai Chen7, Hongwei Zhou8, Tianyu Tang9, Yu Shi10, Shenghong Ju9, Yan Huadong11, Xiaolong Qi1. 1The First Hospital of Lanzhou University, CHESS Center, Institute of Portal Hypertension, China; 2The First Clinical Medical College of Lanzhou University, China; 3Nanjing Drum Tower Hospital, The Affiliated Hospital of Nanjing University Medical School, Department of Infectious Diseases, China; 4The third people’s Hospital of Taiyuan, Department of Hepatology, China; 5Qufu People’s Hospital, Department of Infectious Diseases, China; 6Qufu People’s Hospital, Medical Laboratory, China; 7Renmin Hospital of Wuhan University, Department of Gastroenterology, China; 8Zhujiang Hospital, Southern Medical University, Department of Laboratory Medicine, China; 9Zhongda Hospital Affiliated to Southeast University, Department of Radiology, China; 10Shengjing Hospital, China Medical University, Department of Radiology, China; 11Shulan (Hanzhou) Hospital Affiliated to Zhejiang Shuren University Shulan International Medical College, Department of Infectious Diseases, China

**Background and aims:** The renewing Baveno VII consensus proposed that liver stiffness measurement (LSM) and spleen stiffness measurement (SSM) can be used to rule in and rule out clinically significant portal hypertension (CSPH) in patients with compensated cirrhosis; however, the thresholds of SSM should be further validated with spleen-dedicated 100 Hz examination. This study aims to assess the performance of sequential algorithm of SSM measured by a dedicated 100 Hz FibroScan® and Baveno VII criteria for CSPH in patients with well-characterized compensated cirrhosis.

**Method:** This is a prospective multi-center study (NCT05251272). Patients with well-characterized compensated cirrhosis undergoing a 100 Hz specific FibroScan® to evaluate SSM and LSM were consecutively enrolled between August 2021 and March 2022. CSPH was defined as the threshold of hepatic venous pressure gradient measurement above 15 mmHg.

**Results:** A total of 101 patients (71 male) with a mean age of 52 ± 9 years were recruited from 5 university centers, and 50 (49.5%) patients had CSPH. Applying the Baveno VII criteria for exclusion of CSPH (LSM ≤15 kPa and platelet count ≥150 × 10^9/L), 24/101 (23.8%) patients could rule out CSPH with 8.3% of patients being missed, and the negative predictive value (NPV) and sensitivity were 91.7% and 96.0%. The sequential algorithm for SSM and Baveno VII criteria [SSM <21 kPa OR (LSM ≤15 kPa and platelet count ≥150 × 10^9/L)] showed that 28/101 (27.7%) patients could rule out CSPH with 7.1% of patients being missed, and the NPV and sensitivity were 92.9% and 96.0%, respectively. Furthermore, the Baveno VII criteria for identification of CSPH (LSM ≥25 kPa) had 100% positive predictive value (PPV) and specificity, yet merely 5/101 (5.0%) patients would enable to identify correctly. Comparing with the former, the sequential algorithm of SSM >50 kPa OR LSM ≥25 kPa improved the proportion of ruling in CSPH (22.8% vs 5.0%, p < 0.001) with only 4.3% of patients misclassified, and the PPV and specificity were 95.7% and 98.0%, respectively.

<table>
<thead>
<tr>
<th>Rule out</th>
<th>Rule in</th>
</tr>
</thead>
<tbody>
<tr>
<td>CSPH</td>
<td>Non-CSPH</td>
</tr>
<tr>
<td>SSM ≤15 kPa and PLT ≥150 × 10^9/L</td>
<td>2/23 (8.3%)</td>
</tr>
<tr>
<td>LSM &lt;21 kPa OR (LSM ≤15 kPa and PLT ≥150 × 10^9/L)</td>
<td>2/28 (7.1%)</td>
</tr>
<tr>
<td>LSM ≥25 kPa</td>
<td>-</td>
</tr>
<tr>
<td>SSM &gt;50 kPa OR LSM &gt;25 kPa</td>
<td>-</td>
</tr>
</tbody>
</table>

**Conclusion:** The sequential algorithm of SSM measured by a dedicated 100 Hz examination and Baveno VII criteria is useful to assess CSPH accurately, especially in ruling in CSPH compared to Baveno VII criteria only.

**Liver tumors: Experimental and pathophysiology**

**FRIS42**

NGK2A hampers tumor surveillance of liver-infiltrating natural killer (NK) cells via TLR4 signaling pathway after liver transplantation

Xinxiang Yang1,2, Kwan Man1,3. 1The University of Hong Kong, Surgery, Hong Kong

**Background and aims:** Liver transplantation (LT) provides the best option for selected hepatocellular carcinoma (HCC) patients. However, tumor recurrence occurs at a rate of 10–20% within 5 years. Graft injury during LT significantly affects the outcome of tumor recurrence by changing the regional immune microenvironment. However, the immunological mechanism of hepatic natural killer (NK) cells in graft injury was not completely understood.

**Method:** 349 HCC patients who underwent LT in Queen Mary Hospital, Hong Kong were recruited in this study. The correlation among the number of intra-graft NK cells, liver function, recurrence free survival (RFS) rate was analyzed. The cytotoxic function of NK cells was evaluated by co-culture with primary HCC cells. Hepatic ischemia–reperfusion injury plus major hepatectomy (IRI + Hx) was performed in C57bl/6 mice to mimic the pathological changes during human LT. Tumor cells (Hepa 1–6) were injected into the liver via portal vein after IRI + Hx in TLR4 knockout and wild-type mice.

**Results:** The frequency of intra-graft NGK2A+NK cells was significantly increased in patients with tumor recurrence after LT, along with increased expressions of its ligand HLA-E and inflammation signatures (IL-1β, IL-6, NLRP3, HMGB1, and TLR4). GWR (the ratio of graft volume to estimated standard liver volume) <60% was an independent risk factor for tumor recurrence after LT. The frequency of circulating NGK2A + NK cells was significantly increased in the patients with GWR <60% compared with GWR ≥60% at 3, 6, 9, and 12 months post-LT. The cytotoxic function of NGK2A + NK cells was significantly decreased compared to NGK2A-NK cells when co-cultured with primary HCC cells, characterized by decreased expressions of Granzyme B and CD107a. In IRI+Hx mouse model,
NKG2A+ hepatic (NK1.1+) NK cells were increased at 6, 24, and 48 hours. Interestingly, the expression of NKG2A was increased in liver-infiltrated (CD45a-CD45b+) NK cells but not liver-resident (CD45a-CD45b-) NK cells. In TLR4 knockout mice subjected to IRI+Hx and tumor cell injection, the tumor growth was significantly hindered and the expression of NKG2A on liver-infiltrated NK cells was significantly decreased compared to wild-type mice at week 4.

Conclusion: Hepatic IRI increased expression of NKG2A on liver-infiltrated NK cells via TLR4 signaling pathway, which provided a favorable immune microenvironment for late-phase tumor recurrence. Understanding the broad spectrum of NK cell functional diversity would help to explore NK cell-based immunotherapy against tumor recurrence.

FR543
Cancer-associated fibroblasts nurture LGR5 marked liver tumour-initiating cells and promote their metastasis
Jiajie Liu1, Qiuwei Pan1, Erasmus University Medical Center Rotterdam, Department of Gastroenterology and Hepatology, Rotterdam, Netherlands
Email: q.pan@erasmusmc.nl

Background and aims: Tumor-initiating cells (TICs) are thought to be the main drivers of cancer development, progression and treatment resistance. We have recently identified the LGR5+ compartment as an important TIC population in liver cancer, representing a viable therapeutic target. Given that cancer-associated fibroblasts (CAFs) constitute a key component of the tumor microenvironment, this study aims to investigate the impact of CAFs on LGR5 marked TICs in liver cancer.

Method: Liver tumor organoids and CAFs were cultured from Diethylnitrosamine-induced liver tumors of LGR5-diphtheria toxin receptor (DTR)-GFP knock-in mice and Rosa 26-mT mice, respectively. 3D co-culture models of LGR5+ TICs with CAFs, based on cell-receptor (DTR)-GFP knock-in mice and Rosa 26-mT mice, respectively. Diphtheria toxin treatment for specific depletion of LGR5+ cells. Consistently, subcutaneous co-engraftment of liver tumor organoids with CAFs resulted in significantly high number of LGR5+ cells in formed tumors when compared with engrafting LGR5+ tumor cells alone (0.6 ± 0.2 VS. 0.3 ± 0.2 g, n = 40, p < 0.001). Although there is no statistical significance in the number of formed organoids. In vitro, co-culture of LGR5 tumor cells with CAFs, in both cell-cell contact or trans-well system, were established in vitro. Immunodeficient mouse-based xenograft model was used to investigate the role of CAFs on tumor formation and metastasis, as well as diphtheria toxin treatment for specific depletion of LGR5+ cells.

Results: In primary tumors formed in the liver of LGR5-GFP reporter mice, we found high frequency of CAFs marked by alpha-smooth muscle actin surrounding LGR5 expressing cancer cells. In xenograft model, co-engraftment of liver tumor organoids with CAFs resulted in substantially higher number of LGR5+ cells in formed tumors when compared with engrafting tumor organoids alone. Furthermore, ex vivo culture of isolated LGR5+ cells from tumors of co-engrafted mice formed significantly larger size of organoids (68.1 ± 36.1 VS. 35.2 ± 18.3 um, n = 40, p < 0.001), although there is no significant statistical significance in the number of formed organoids. In vitro, co-culture of LGR5 tumor cells with CAFs, in both cell-cell contact and paracrine signaling based trans-well system, resulted in significantly larger size and number of formed organoids, when compared with culturing LGR5+ cells alone. This promoting effect was eliminated by diphtheria toxin treatment which specifically deplete LGR5 cells due to transgenic expression of DTR. Consistently, subcutaneous co-engraftment of LGR5 tumor cells with CAFs formed significantly larger tumors compared with engrafting LGR5+ cells alone (0.6 ± 0.2 VS. 0.3 ± 0.2 g, n = 8, p = 0.05). Most importantly, co-engraftment dramatically increased the probability of abdominal metastasis (7/8) compared with engraftment of LGR5+ tumor cells alone (1/8). Diphtheria toxin treatment mediated depletion of LGR5+ cells effectively inhibited tumor growth and metastasis in this xenograft model.

Conclusion: We here revealed robust nurturing effects of CAFs in promoting growth and metastasis of LGR5 marked TICs in experimental liver cancer. Understanding their intimate interactions shall help to decipher the mechanistic insight of liver cancer progression and to develop effective treatment for reducing tumor burden and preventing metastasis.
Conclusion: Our work provides insights into how PP2A-B5delta suppresses human hepatocarcinogenesis and progression, and how its tumor suppressor activity is impaired in human HCC. Specifically, we show that PP2A-B5delta prevents c-MYC protein stabilization via regulation of AKT and GSK3beta, and PP2A-B5delta inactivation is mediated by CIP2A overexpression.

FRI545
Identification of new dominant neoantigens in hepatocellular carcinoma based on a single plasmid system with co-expressing patient’s HLA and antigen
Pu Chen1, Dongbo Chen1, Shaoping She1, Yao Yang1, Liying Ren2, Bigeng Zhao3, Ruieng Yang3, WeiJia Liao3, Hongsong Chen1, 1Peking University Hepatology Institute, Beijing Key Laboratory of Hepatitis C and Immunotherapy for Liver Disease, Peking University People’s Hospital, China; 2Laboratory of Hepatobiliary and Pancreatic Surgery, Affiliated Hospital of Guilin Medical University, China
Email: chenhongsong@bjmu.edu.cn

Background and aims: Hepatocellular carcinoma (HCC) is the sixth most common malignancy worldwide. Compared with plentiful neoantigens in melanoma, the paucity and inefficient identification of effective neoantigens in HCC remain enormous challenges in effectively treating this malignancy. Therefore, we tried to identify new dominant neoantigens in HCC based on an innovative plasmid system.

Method: We established a single plasmid system with co-expressing patient’s human leukocyte antigen (HLA) and antigen. To verify whether the system works normally, we connected a reported KRAS G12D neoantigen sequence in HCC and its corresponding wild antigen sequence to the antigen linker regions of the vectors respectively, which carry the corresponding HLA sequence. Subsequently, they were inserted into viral vectors and transduced to the target cells. Moreover, T cell receptor (TCR) T cells that could recognize the neoantigen were constructed and co-cultured with the target cells. Then, the cytotoxicity was detected by enzyme-linked immunosorbent assay (ELISPOT) and enzyme-linked immunosorbent assay (ELASA). Finally, the proliferation of TCR-T cells was detected by flow cytometry assay.

Besides, next-generation sequencing (NGS) was performed for the samples such as HCC tissue, portal vein tumor thrombosis (PVTT) and tumor infiltrating lymphocyte (TIL) to analyse gene variations, candidate neoantigens and tumor immune microenvironment (TIME). Then, tetramer staining assay was used to detect the specific T cells induced by the predicted candidate neoantigens. Finally, the positive candidate neoantigens were further validated by the single plasmid system.

Results: An innovative plasmid system was established, which includes 39 high-frequency HLA vectors for Asian. Then, we successfully constructed TCR-T cells which could recognize KRAS G12D neoantigen in HCC and used the single plasmid system to verify the immunogenicity of the neoantigen. Interestingly, we found TCR-T cells co-cultured with the target cells which express KRAS G12D could be specifically activated and proliferate. Hence, the single plasmid system works normally, which provides an efficient molecular tool for immunogenicity validation of antigen.

We found some new gene variations in 14 HCC patients and predicted candidate neoantigens. Moreover, we produced some tetramers for the detection of the specific T cells and identified several positive candidate neoantigen-specific T cells. Finally, we successfully identified several new dominant neoantigens produced by ALG1 A555 mutation (ENST00000586840) and other gene variations in HCC, based on our single plasmid system.

Conclusion: Based on our single plasmid system with co-expressed patient’s HLA and antigen, we successfully identified several new dominant neoantigens in HCC. These neoantigens could be as potential immunotherapeutic targets for HCC.

FRI546
Polypeptide N-acetylgalactosaminyltransferase 14 mediated O-glycosylation on prohibitin-2 serine 161 modulates cell growth, migration and drug susceptibility in hepatocellular carcinoma
Chau-Ting Yeh1, Yu-De Chu2, 1Chang Gung Memorial Hospital, Liver Research Center, Taoyuan, Taiwan; 2Chang Gung Memorial Hospital, Liver Research Center, Taoyuan
Email: chautingy@gmail.com

Background and aims: Worldwide, hepatocellular carcinoma (HCC) remained a leading cause of cancer-related death. A single nucleotide polymorphism (SNP), rs9679162, located on Polypeptide N-Acetylgalactosaminyltransferase 14 (GALNT14) gene, differentially predicted the therapeutic outcomes for various gastrointestinal cancers including HCC, while the molecular mechanisms remained largely unknown.

Method: For clinical outcome analysis, 300 HCC patients having received surgical resection were retrospectively enrolled. Their paired liver tissue samples were subjected for SNP genotyping, RNA isolation, western blot, and immunohistochemical analysis. The key GALNT14 substrate was identified by the differential lectin capture method. Functional assessments of the candidate substrate protein were performed following site-directed mutagenesis.

Results: GALNT14 level was significantly upregulated in the cancerous parts of HCCs. Higher cancerous/noncancerous ratios of GALNT14 were associated with rs9679162-GG genotype and unfavourable postoperative prognosis. A novel exon-6-skipped GALNT14 mRNA variant was identified preferentially in the rs9679162-TT genotype, and was associated with lower GALNT14 expression and favourable clinical outcomes. Cell-based experiments showed that elevated GALNT14 levels promoted HCC growth, migration, and anticancer-drugs susceptibility. Differential lectin capture analysis identified prohibitin-2 (PHB2) as a major GALNT14-mediated O-glycosylation substrate. Site-directed mutagenesis experiments revealed serine-161 (Ser161) as the O-glycosylation site. Complementation assays demonstrated that PHB2-Ser161 O-glycosylation was required for GALNT14-mediated modulation of cell growth, migration, and anticancer drugs susceptibility. PHB2 O-glycosylation was positively correlated with GALNT14 expression in HCC. Finally, PHB2-Ser161 O-glycosylation was crucial for its interaction with Insulin-like Growth Factor-Binding Protein-6 (IGFBP6) and Insulin-like Growth Factor-1 Receptor (IGFIR) mediated signalling activation.

Conclusion: GALNT14 SNP genotypes were associated with GALNT14 levels and differential expression of a novel GALNT14 mRNA variant, linking to postoperative prognosis in HCC. The elevated GALNT14 level promoted HCC growth via O-glycosylation on PHB2-Ser161, leading to activation of the IGFIR-mediated cascade.
FRI547
Gut bacteria modulate anti-tumour immunity in patients with hepatocellular carcinoma
Dhruvi Devshi1,2, Sandra Phillips1,2, Helen Edwards1,2, Nicola Harris1,2, Melissa Preziosi3, Abid Suddle1, Antonio Riva1,2, Shilpa Chokshi1,2,3, The Roger Williams Institute of Hepatology (Foundation for Liver Research), United Kingdom; 4Faculty of Life Sciences and Medicine (King's College London), United Kingdom; 5King's College Hospital, London, United Kingdom

Email: s.chokshi@researchinliver.org.uk

Background and aims: The gut microbiota and their metabolites play a key role in the response to checkpoint receptor (CR) inhibitors. Interestingly, antibiotics can also limit cancer progression by modulating the gut microbiota and their metabolites. The role of bacteria and their metabolites in modulating anti-tumour immunity in hepatocellular carcinoma (HCC) is not understood and is the focus of this study.

Method: Peripheral blood mononuclear cells (PBMCs) from HCC patients were stimulated in vitro with a peptide pool spanning seven HCC tumour-associated antigens with/without priming with formaldehyde-fixed Escherichia coli DH5a (EC, 50 bacteria-per-cell) or EC with non-alcoholic steatohepatitis (NASH) which systematically resulted in HCC development.

Results: Induced liver damage was more severe in Trim21-KO mice after 12 weeks on HFHCD, as attested by serum transaminase levels. In addition, higher number of HCC nodules arose at 12 weeks. At an earlier stage (4 weeks of HFHCD), a more pronounced pro-inflammatory hepatic microenvironment was already detected in Trim21-KO mice. However, 8 weeks later, the number of hepatic macrophages and lymphocytes significantly decreased in Trim21-KO mice. At the same timing, the spleen of Trim21-KO mice contained more CD4+ T cells than in Trim21-WT mice. Further analysis showed a higher proportion of CD4+PD1+ and CD8+PD1+ T cells in Trim21-KO mice spleen.

Conclusion: The E3 ubiquitin ligase TRIM21 limits the emergence of HCC nodules in mouse developing NASH. The establishment of an effective anti-tumour immune response may require TRIM21, potentially by restricting the expression of PD-1 in lymphocytes and of PDL-1 in cancerous cells.

FRI549
Role of autophagy-mediated neuropilin-1 degradation on lenvatinib efficacy in human hepatocarcinoma
Paula Fernández-Palanca1,2, Tania Payo-Serafin1,2, Flavia Fondevila1,2, Carla Ménendez-Blanco1,2, Javier González-Gállego1,2, José Luis Mauriz1,2, 1Institute of Biomedicine (IBIOMED), University of León, León, Spain; 2Centre of Investigation Biomédica en red de enfermedades hepáticas y digestivas (CIBERehd), Instituto de salud Carlos III, Madrid, Spain

Email: pferp@unileon.es

Background and aims: Hepatocarcinoma (HCC) is one of the main causes of cancer-related death. Despite the effectiveness of therapeutics such as tyrosine kinase inhibitors, loss of efficacy that leads to resistance acquisition is a frequent problem that needs to be addressed. Neuropilin-1 (NRP1) is a transmembrane glycoprotein whose role in cancer has become of special interest. We aimed to identify the in vitro role of NRP1 in the underlying mechanisms of lenvatinib efficacy in human HCC.

Method: The human HCC cell lines Huh-7 and Hep3B were employed. Lenvatinib was used for treatments and 100 nM bafilomycin A1 as specific autophagy inhibitor. Protein expression was analyzed by Western blot and immunocytochemistry, cell viability by Ki67 proliferation index, showing also a decrease in NRP1 protein expression in both HCC cell lines. To identify the mechanism responsible of lenvatinib-derived NRP1 downregulation, a time-course with bafilomycin A1 alone and combined with lenvatinib was done. Autophagy inhibition prevented the reduction of NRP1 expression when combining with lenvatinib, thus blocking lenvatinib effect. Specific NRP1 gene silencing reduced cell viability.
showing even greater results when combining with lenvatinib. Interestingly, NR1 silencing also blocked the loss of lenvatinib sensitivi

Conclusion: Autophagy-dependent NR1 degradation seems to play a key role in lenvatinib efficacy in HCC, highlighting the potential interest of NR1 silencing as a novel strategy to prevent therapeutic failure in advanced HCC.

**FR550**

Different acylcarnitines tissue profiles as metabolomics signatures of human hepatocellular carcinoma in non-alcoholic fatty liver disease according to fibrosis level


*Chu Estang, Service de médecine digestive et hépatobiliaire, Clermont-Ferrand, France; 2Université Clermont-Auvergne, Unité de Nutrition Humaine, UMR 1019, Clermont-Ferrand, France; 3INRA PFEM, PFEM, Saint-Géens-Champapelle, France; 4Chu Estang, Service d'anatomopathologie, Clermont-Ferrand, France*

Email: benjamin.buchard@gmail.com

**Background and aims:** The incidence and prevalence of non-alcoholic fatty liver disease (NAFLD) are rising worldwide with the increase of obesity and diabetes. NAFLD is becoming a growing cause of hepatocellular carcinoma (HCC). NAFLD-HCC may rise in the absence of severe liver fibrosis in 20 to 50% of patients. However, current evidence does not support routine screening for HCC in this population. The aim of this study was therefore to identify metabolic pathways and putative biomarkers of NAFLD-HCC according to fibrosis level (F0F1 vs. F3F4).

**Method:** A non-targeted metabolomics strategy was applied to two groups of NAFLD-HCC according to fibrosis level. We investigated 45 pairs of human HCC and adjacent non-tumoral tissues (NTT) which included 30 HCC developed in severe fibrosis or cirrhosis (HCC-F3F4) and 25 HCC developed in no or mild fibrosis (HCC-F0F1). Most of samples were provided by the French Tumor Biobank. Aqueous tissue extracts were analyzed using liquid chromatography coupled to mass spectrometry analysis. HCC was compared to its own NTT in these two groups.

**Results:** The comparison between HCC and NTT in each group revealed acylcarnitines (AC) as the main discriminant metabolites (figure). AC are known to allow the transportation of fatty acids (FA) across the mitochondrial membrane preceding mitochondrial beta oxidation for energy production. In HCC-F3F4 we found an accumulation of both medium chain acylcarnitines (MCAC, Carbon 12) and long chain acylcarnitines (LCAC, Carbon 14 -18 - 20) while short chain acylcarnitines (SCAC-derived from Isoleucine and leucine) were decreased in comparison with NTT- F3F4. In contrast HCC-F0F1 was characterized by a significant increase of LCAC (Carbon 16 -18 - 20) in comparison with NTT-F0F1. Notably, unlike HCC-F3F4, MCAC and SCAC were not detected in HCC-F0F1 group when compared to its own NTT.

**Conclusion:** Our results are the first one to highlight differences in AC metabolism in NAFLD-HCC and confirm the existence of two distinct metabolomics phenotypes according to underlying non tumoral fibrosis (Buchard et al, Metabolites 2021).

**FR551**

Hepatocellular carcinoma alters granulopoiesis to produce neutrophils with an immature phenotype

Daniel Geh1, Erik Ramon-Gil1, Maja Laszczyńska Saimir Luli1, Amy Collins1, Fiona Oakley1, Jack Leslie1, Helen L. Reeves2,3, Derek A Mann1.

1Newcastle Fibrosis Research Group, Biosciences Institute, Faculty of Medical Sciences, Newcastle University, Newcastle upon Tyne, United Kingdom; 2Translational and Clinical Research Institute, Faculty of Medical Sciences, Newcastle University, Newcastle upon Tyne, United Kingdom; 3Hepatopancreatobiliary Multidisciplinary Team, Newcastle upon Tyne Hospitals NHS Foundation Trust, Freeman Hospital, Newcastle upon Tyne, United Kingdom

Email: daniel.geh@newcastle.ac.uk

**Background and aims:** Despite immunotherapy being the first line treatment for advanced hepatocellular carcinoma (HCC), the majority of HCCs are resistant, especially in the context of non-alcoholic fatty liver disease (NAFLD). Neutrophils have emerged as important drivers of HCC, exerting pro-tumour functions such as creating an immunosuppressive tumour microenvironment. Despite this little is known about how HCC influences neutrophils. Here we aim to characterize the effect HCC has on neutrophil phenotype.

**Method:** In vivo model. High fat diet induced steatohepatitis plus orthotopic tumour implantations were conducted in C57BL/6J mice. Sham surgeries were conducted for controls. Neutrophils were isolated from the bone marrow, blood, spleen, liver and tumours. Patient study. HCC, chronic liver disease and healthy control patient blood samples were collected and neutrophils isolated by density gradient centrifugation. Neutrophils were analyzed by flow cytometry.

**Results:** In the murine HCC model neutrophil frequency increased across all compartments with disease progression (A). HCC induced altered granulopoiesis with a preferential increase in early neutrophil progenitor populations such as granulocyte-monocyte progenitor cells (GMPS) and pre-neuts (B). Overall neutrophil phenotype mainly corresponded to the tissue of residence and maturation (C), however...
POSTER PRESENTATIONS

A. Neutrophil frequency
B. Bone marrow neutrophil progenitor frequencies

C. LY6G expression

D. UMAP 1
E. UMAP 2

F. HCC n=19
Control n=8

G. Neutrophil frequency
H. CXCR2 expression

Figure: (abstract: FRI551)
across all compartments HCC gave rise to a more immature neutrophil phenotype as demonstrated by a reduction in Ly6G expression (D). There were also HCC-associated changes in neutrophil immune checkpoint and chemokine receptor expression. In patient blood samples 3 neutrophil populations were identified; low density (LD) CD16 low, LD CD16 high and high density (HD) neutrophils (E). These populations could be distinguished based on activation marker and chemokine receptor expression (F). Similar to the murine model there was an increase in neutrophil frequency in HCC patients compared to controls (G) with HCC neutrophils displaying a more immature phenotype as demonstrated by a reduction in CXCR2 expression (H).

Conclusion: HCC induces large shifts in neutrophil dynamics starting during granulopoiesis causing an increase in neutrophil frequency and giving rise to a more immature neutrophil phenotype. We hypothesize that these immature neutrophils have tumor-promoting functions, utilized by the HCCs to promote tumour progression. Manipulation of neutrophil maturation may represent an important immune-therapeutic strategy.

FR553
RNA-Seq based transcriptome analysis revealed inhibiting methionine aminopeptidase 2 prevented hepatocellular carcinoma with inhibited angiogenesis
Yongtao Wang1, Mozdeh Soojoodi2, Shijia Zhu2, Wei Tang3, Guoliang Qiao3, Shike Wang4, Stephen Barrett5, Michael兰uti2, Motaz Qadan1, Yujin Hoshida5, Kenneth K. Tanabe1.1Massachusetts General Hospital and Harvard Medical School, Division of Gastrointestinal and Oncologic Surgery, Boston, United States; 2University of Texas Southwestern Medical Center, Department of Internal Medicine, Dallas, United States; 3National Cancer Institute, Center for Cancer Research, Bethesda, United States; 4The University of Texas MD Anderson Cancer Center, Departments of Thoracic/Head and Neck Medical Oncology, Houston, United States; 5Massachusetts General Hospital and Harvard Medical School, Division of Thoracic Surgery, Boston, United States
Email: ktanabe@partners.org

Background and aims: In our previous experiments with molecular and histologic assessments, we demonstrated that in a diethylnitrosamine (DEN)-induced rat hepatocellular carcinoma (HCC) model, inhibition of methionine aminopeptidase 2 (MetAP2) decreased HCC development by inhibiting cirrhosis progression, which was involved with inhibiting angiogenesis and neo-vascularization. In this study we investigated the hypothesis with RNA-Seq analysis, MetAP2 inhibition can reverse the global transcriptomic landscape of DEN-induced HCC with inhibited angiogenesis.

Method: Male Wistar rats received weekly intraperitoneal injections of 50 mg/kg DEN for 18 weeks, and were randomly assigned to 4 groups starting from 9th week: 1) water (control); or 2) MetAP2 inhibitor ZGN-1136 (0.3 mg/kg) by daily subcutaneous injection. Global transcriptomic landscape between DEN-induced rat HCC and normal rat liver, DEN-induced rat HCC before and post-MetAP2 inhibitor treatments were investigated with RNA Sequencing and Gene Set Enrichment Analysis (GSEA) analysis.

Results: Compared with normal rat liver, regulatory signatures of protein maturation, and signatures of collagen containing extracellular matrix, DEN-induced up-regulated genes in liver cancer and cancer keratinization, angiogenesis and vascular invasion in liver cancer were positively enriched in DEN-induced rat HCC. After inhibiting MetAP2 with ZGN1345 treatment, these signatures reflecting enhanced protein maturation, HCC and angiogenesis were significantly reversed in DEN-induced rat HCC. More detailed, regulatory signatures of protein mature were negatively enriched, indicating MetAP2-catalyzed protein maturation and MetAP2 function were inhibited. Signatures of collagen containing extracellular matrix and up-regulated genes in carcinoma associated fibroblast were negatively enriched and suppressed after inhibiting MetAP2. Of notable importance, signatures of cancer keratinization were also negatively enriched and inhibited. Moreover, negative enrichment of signatures of angiogenesis were observed after inhibiting MetAP2, indicating inhibited HCC development was involved with suppressed angiogenesis. Inhibiting MetAP2 with ZGN1136 treatment closely matched and further supported these observations.
Conclusion: On the global transcriptomic level, MetAP2 inhibition effectively prevented HCC development, which was involved with inhibited angiogenesis. These data further suggest that inhibition of MetAP2 may represent a new prevention target for HCC.

FRI554
Proteomic analysis of bile in the rat thioacetamide model reveals new mechanisms in human cholangiocarcinogenesis
Leticia Colyn1, Gloria Álvarez-Sola1,2, María U Latasa1, Ilker Uriarte1,2, Jose María Herranz1,2, María Arecchederra1,2,3, Juan Falcon-Perez1,2, Antonio A Pineda4, Andrea Casadei Gardini5, Coral Barbás2, Jesús M Urman1,8, Bruno Sangro2,3,4, Jesús María Banales2,10, María Luz Martinez-Chantar11,13, Jose Marin1,2,12, Fernando Corrales1,13, María Iarribar Elizalde14, Francisco Javier Cubero15, Carmen Berasain1,2,3, Maite G Fernandez-Barrena1,2,3, Matías A Avila1,2,3,4, CIMA, Universidad de Navarra, Hepatology Program, Pamplona, Spain; 2CIBERERHD, Madrid, Spain; 3Instituto de Investigaciones Sanitarias de Navarra IdISNA, Pamplona, Spain; 4CIC-BioGune, Metabolomics Platform, Derio, Spain; 5CIMA, Universidad de Navarra, Molecular Therapies Program, Pamplona, Spain; 6San Raffaele Hospital, Oncology, Milano, Italy; 7Universidad CEU-San Pablo, Centre for Metabolomics and Bioanalysis, Madrid, Spain; 8Hospital Universitario de Navarra, Gastroenterology, Pamplona, Spain; 9Clinica Universidad de Navarra, Hepatology Unit, Pamplona, Spain; 10Bio-Donostia Research Institute, San Sebastian, Spain; 11CIC-BioGune, Liver Research Laboratory, Derio, Spain; 12Universidad de Salamanca, Physiology and Pharmacology Department, Salamanca, Spain; 13CNB-CSIC, Proteomics Unit, Madrid, Spain; 14Universidad de Navarra, Department of Biochemistry and Genetics, Pamplona, Spain; 15Universidad Complutense de Madrid, Department of Immunology, Ophthalmology and ENT, School of Medicine, Madrid, Spain
Email: icolyn@alumni.unav.es

Background and aims: Cholangiocarcinoma (CCA) is a deadly disease usually diagnosed at advanced stages. Animal models enable the understanding of pathological processes and its translation into diagnostic and therapeutic advances. Thioacetamide (TAA)-induced CCA in rats captures key features of the human carcinogenic process, including chronic liver injury, inflammation and stromal reaction. Molecular analysis of bile is an excellent liquid biopsy approach and may also help understanding CCA pathogenesis. Here we performed proteomic analyses of bile from control and TAA-CCA rats. Our findings provide further support to the clinical relevance of this model and allowed us to identify new molecular interactions in CCA.

Method: Male Sprague-Dawley rats were treated with TAA in drinking water for 30 weeks. Serum, bile and liver tissues were collected. We performed LC-MS based proteomic analysis of bile. Most relevant hits were validated by qPCR and immunohistochemistry. In vitro mechanistic studies were performed in human CCA cell lines, including Huh28 cells transduced with KRAS-G12D. Cell signaling, cell growth, gene regulation and C13-glucose-serine fluxomics analyses were performed.

Results: All TAA-treated rats developed liver fibrosis and CCA. More than 200 proteins were differentially represented in bile from TAA rats. Ingenuity Pathway Analysis highlighted pathways related to inflammation, cell signaling, oxidative stress and glucose metabolism. The most relevant hits were confirmed by qPCR in rat liver tissues and in human CCA (TCGA). Activation of interleukin-6 (IL6) and epidermal growth factor receptor (EGFR)-ERK1/2 pathways, critical in CCA biology, as well as key genes in cancer-related glucose-serine metabolic reprogramming, were confirmed in TAA-CCA tissues. TAA-CCAs also showed increased expression of G9a histone-methyltransferase and DNA methyltransferase 1 (DNMT1), epigenetic pro-CCA effectors. In CCA cell lines we showed that IL6 expression can be triggered by EGFR-pathway activation and the presence of KRAS-G12D. We also show that the serine-glycine pathway, critically involved in cancer, is enhanced in CCA cells and can be inhibited upon G9a/DNMT1 pharmacological targeting. Mechanistically, KRAS-G12D promoted G9a binding to chromatin in CCA cells, and this was prevented by the inhibition of G9a self-methylation. Finally, we demonstrated that tumorigenic properties confered by KRAS-G12D to CCA cells such as anchorage-independent growth are highly sensitive to G9a/DNMT1 inhibition.

Conclusion: Our study confirms the rat TAA-CCA model as a key resource for basic and translational CCA research. This model led us to identify the EGFR-ERK1/2 pathway as a critical driver for IL6 production, and to establish the relevance of the glucose-serine pathway in CCA. The G9a/DNMT1 epigenetic complex is further validated as a target for CCA therapy.

FRI555
Expression of hepatitis B surface antigen in vivo and in vitro induces endoplasmic reticulum stress, impairs autophagy and promotes proliferation
Yaojie Liang1, Xufeng Luo1,2, Stefan Schefczyk1, Hideo Baba3, Mengli Lu4, Ruth Broering1, 1University Duisburg-Essen, Medical Faculty, Dept. of Gastroenterology, Hepatology and Transplant Medicine, Essen, Germany; 2The Affiliated Cancer Hospital of Zhengzhou University, Henan Cancer Hospital, Institute for Lymphoma Research, China; 3University Duisburg-Essen, Medical Faculty, Institute for Pathology, Essen, Germany; 4University Duisburg-Essen, Medical Faculty, Institute for Virology, Essen, Germany
Email: ruth.broering@uni-due.de

Background and aims: Hepatitis B surface antigen (HBsAg) has been identified to increase the risk and contribute to hepatocellular carcinoma (HCC). However, factors and mechanisms that drive HBsAg-induced hepatocarcinogenesis remain poorly defined, thus hindering the development of new therapeutic strategies. Therefore, we explore how HBsAg mechanistically facilitates the transformation from normal liver cells to HCC.

Method: Data mining of the microarray set GSE84429 (from GEO datasets) indicated the potential candidate signatures of HBsAg-driven intracellular events. Hemizygous tg (Alb1HBV/J4Bri/J) mice were investigated for this HBsAg-driven carcinogenic events by western blotting, immunohistochemical (IHC) staining. Finally, the findings were verified in HBsAg-overexpressing Hepa1-6 cells, in which functional analysis was performed to study the contribution of these events in hepatocarcinogenesis.
Results: Gene set enrichment analysis identified significant signatures in HBsAg-transgenic mice correlating with ER stress, unfolded protein response (UPR), autophagy, cell cycle and proliferation. Clustered heatmap visualized distinct gene expression pattern for endoplasmic reticulum (ER) stress and autophagy in HBsAg-transgenic mice, compared to wild type. These events were further investigated in 2-, 8- and 12-month-old HBsAg-transgenic mice. Elevated BiP expression in HBsAg-transgenic mice indicated induction of UPR. Furthermore, our study indicates that HBsAg impaired the autophagic flux. In HBsAg-transgenic mice autophagy was enhanced at the early stage (increased Beclin1) and blocked at the late stage (increased p62 and LC3B-II). These ER stress and autophagy events could be verified in Hepa1-6 cells overexpressing HBsAg for up to 72 hours. In addition, HBsAg expression changed lysosomal acidification, visualized by acidine orange staining, and promoted proliferation, indicated by Ki67 staining of paraffin-embedded sections and CCK-8 staining and colony formation assay in vitro. IHC staining of cleaved caspase3, an apoptosis marker, revealed a slight increase in HBsAg-transgenic mice, indirectly indicating hepatocyte proliferation due to HBsAg accumulation.

Conclusion: Our findings revealed that HBsAg directly induces ER stress, impairs autophagy and promotes proliferation thereby driving hepatocarcinogenesis. Moreover, this study expanded the understanding of HBsAg-mediated intracellular events in carcinogenesis.

FR1556
Cross-talk between cholangiocarcinoma cells and extracellular microenvironment drives desmoplastic matrix deposition
Gilles van Tienderen1, Oskar Rosmark2, Ruby Lieshout1, Jørke Willensem2, Tfhör de Weijer1, Linda Elowsson Rendin2, Gunilla Westergren-Thorsson2, Michael Doukas2, Bas Groot Koerkamp3, Martin van Royen1, Luc J.W. van der Laan1, Monique M.A. Verstegen1, ErasmusMC Transplant Institute, Department of Surgery, Rotterdam, Netherlands; Lund University, Department of Experimental Medical Science, Lund, Sweden; Erasmus MC, Department of Pathology, Rotterdam, Netherlands
Email: g.vantienderen@erasmusmc.nl

Background and aims: Cholangiocarcinoma (CCA) is a highly aggressive tumor which arises from the biliary duct epithelium. Currently available models fail to recapitulate the full complexity of CCA, particularly the desmoplastic environment and the interplay between cancer cells and the extracellular matrix (ECM). We aimed to study the role of tumor cells in ECM deposition and desmoplasia by combining patient-derived CCA organoids (CCAOs) and native liver and tumor scaffolds, obtained by decellularization.

Method: Native human CCA matrix (CCA-M) and tumor-free liver matrix (TFL-M) were decellularized and subsequently recellularized with CCAOs. The decellularized scaffolds were biochemically and mechanically assessed. Tumor cell behavior of CCAOs in CCA-M, TFL-M and basement membrane extract (BME), was assessed by bulk mechanically assessed. Tumor cell behavior of CCAOs in CCA-M, TFL-M with CCAOs. The decellularized scaffolds were biochemically and matrix (TFL-M) were decellularized and subsequently recellularized Native human CCA matrix (CCA-M) and tumor-free liver and tumor scaffolds, obtained by decellularization. Combining patient-derived CCA organoids (CCAOs) and native liver study the role of tumor cells in ECM deposition and desmoplasia by between cancer cells and the extracellular matrix (ECM). We aimed to explore the migration of CCAOs in CCA-M, the expression profile of differentially expressed genes much compared to TFL-M (correlation coefficient (CC) CCA-M 0.83 ± 0.03 vs CC TFL-M 0.70 ± 0.03, p = 0.004) and BME (CC CCA-M 0.88 ± 0.04 vs CC BME 0.63 ± 0.06, p < 0.0001). Furthermore, CCA-M induced specific extracellular matrix protein production in CCAOs, such as fibronectin 1 (FN1), which is related to desmoplasia and patient survival. In TFL-M, lacking desmoplasia, CCAOs were able to initiate a desmoplastic reaction directly through increased production of multiple collagen types (e.g. COL1A1, COL1A2, COL6A1, COL6A3). Conclusion: This improved model of cholangiocarcinoma recapitulates key aspects of CCA tumor biology, including transcription profiles and ECM protein production. The increased production of extracellular matrix proteins suggests that tumor cells can contribute to their own desmoplastic environment.
data showed that their loss of expression was significantly associated with worse survival and poor tumor differentiation, supported by the lower expression of hepatic specific genes such as Albumin, CYP3A4, MAT1A or HNF4alpha. Accordingly, in vitro downregulation of a set of these IncRNAs in well-differentiated HepaRG cells resulted in the loss of hepatic specific markers.

Conclusion: All together, our results demonstrate that hepatocarcinogenesis is associated to the downregulation through DNA methylation of a set of IncRNAs essentials to ensure hepatic differentiation.

FR1558  
Inhibiting IRE1a-endonuclease activity potentiates the effect of doxorubicin in hepatocellular carcinoma

Maria Kopsida1, Femke Heindryckx1, Natasa Pavlovic1, Hans Lennernäs2, Jaafar Khaled1. 1Uppsala Universitet, Medical Cell Biology, Uppsala, Sweden; 2Uppsala Universitet, Pharmaceutical Biosciences, Uppsala, Sweden

Email: maria.kopsida@mcb.uu.se

Background and aims: Hepatocellular carcinoma (HCC) is the most common form of liver cancer, characterized by a high resistance to chemotherapeutic agents, such as doxorubicin (DOX). One potential contributing factor to this drug resistance, is the activation of the endoplasmic reticulum (ER) stress pathways. This is a cellular stress mechanism that becomes activated when the cell’s need for protein synthesis exceeds the ER’s capacity to ensure accurate protein folding, and has been implicated in creating drug-resistance in several solid tumors. However, its role in HCC remains unclear and requires further investigation.

Method: Publicly available data from the Human Protein Atlas (HPA) was used to find correlated expression of drug resistance/ER-stress markers in HCC-patients. A chemically induced mouse model for HCC was used and mice were treated twice per week with the ER-stress inhibitor 4u8C and/or DOX for 3 weeks, after the occurrence of tumors. Liver samples were taken for histological and molecular biology analyses.

Results: Data-mining of the HPA revealed that ER-stress markers are highly intertwined with different drug-resistance mechanisms in HCC-patients. Mice with HCC experienced a statistically significant weight loss compared to healthy mice. This was further exacerbated after DOX-treatment, while co-treatment with 4u8C restored weight levels to nearly those of healthy mice. All treatments significantly decreased the number of tumors, with the strongest reduction in the 4u8C + DOX combination treatment. Staining for Ki-67 showed a significant increase in the number of Ki-67 positive cells in mice with HCC, which was significantly reduced in all treatment groups, with the strongest reduction in the 4u8C+DOX combination treatment. In mice with HCC, 4u8C and the combination of 4u8C and DOX significantly increased apoptosis compared to untreated mice. Interestingly, no increase of apoptosis was seen in the DOX-treated group, which could suggest an alternative form of cell death. As DOX is known to induce ferroptosis, Transferrin Receptor-staining in liver tissue was quantified. This showed that DOX increased the area of Transferrin Receptor positive staining, suggesting a possible increase in ferroptosis. Interestingly, treatment with 4u8C reduced this effect, which is in line with previous findings that ferroptosis is-at least in part-dependent on ER-stress pathways.

Conclusion: By using an in vivo model known for its similarity to human HCC, we show that using an ER-stress inhibitor can potentiate the cytotoxic effect of DOX. The long-term impact of our study could open the possibility of ER-stress inhibitors as adjuvant treatments for HCC-patients.

FR1559  
Genetic ablation of miR-22 fosters hepatic carcinogenesis in mice

Monika Gjorgjieva1, Cyril Sobolewski1, Anne-Sophie Ay1, Daniel Abegg2, Marta Sousa1, Flavien Berthou1, Margot Fournier1, Christine Maeder1, Xavier Montet2, Alexander Adibekian2, Michelangelo Foti1. 1University of Geneva, PHYME, Geneva, Switzerland; 2The Scripps Research Institute, Chemistry, Jupiter, United States

Email: monika.gjorgjieva@unige.ch

Background and aims: We previously reported that microRNA-22 (miR-22) deficiency exacerbated diet-induced obesity, hepatomegaly, and liver steatosis in mice by promoting hepatic glycolysis and lipid uptake. In HCC, miR-22 expression/activity is strongly downregulated in both mouse models of HCC and human HCC, suggesting an important role for this microRNA also in pre-cancerous stages and tumourigenesis. Herein, we investigated the role of miR-22 deficiency in HCC development associated or not with diet-induced obesity.

Method: Mir22-knockout (miR22KO) mice were used to investigated hepatic carcinogenesis induced either by DEN, or PTEN-deficiency, in mice fed a normal or obesogenic diet. Proteomic analyses of liver tissues from miR22KO mice were performed and metabolic alterations and cancer processes under the influence of miR-22 were investigated in transformed hepatic cancer cells.

Results: In vivo, the genetic deletion of miR-22 triggers a significant increase in the onset of hepatic tumour nodules and multiplicity induced by DEN. This miR-22-associated phenotype was further exacerbated in diet-induced obese mice. A similar tumour promoting effect of miR-22 deficiency was observed in a genetic model of HCC spontaneous development induced by the liver specific deletion of the tumour suppressor PTEN (liver-specific miR-22/PTEN double KO mice). Consistent with these phenotypes, proteomic analyses of hepatic tissues from miR-22 KO mice indicate that miR-22 exerts tumour suppressive function in vivo by restraining the expression/activity of several oncogenic factors. Surprisingly, overexpression of miR-22 in Huh7 hepatic cancer cells triggers, in contrast to our in vivo observations, a clear induction of a Warburg effect with an increased glycolysis and an inhibited mitochondrial respiration consistent with an oncogenic role for miR-22 in these cells.

Conclusion: Our study indicates that in vivo miR-22 behaves as a strong tumour suppressive miRNA restraining tumour initiation. Our data further indicate that miR-22 may have a dual role in hepatic carcinogenesis by promoting tumour initiation but inhibiting then tumour progression when cells are already transformed.

FR1560  
Focal nodular hyperplasia: a response to portal vein thrombosis followed by a sequence of arterio-portal shunting, hyperperfusion, focal retrograde sinusoidal blood and Wnt flow, and Wnt-induced activation of the bud maturation sequence

IanR Wanless1, Ashley Stueck1. 1Anatomic Pathology, Halifax, Canada

Email: ian2460@gmail.com

Background and aims: Focal nodular hyperplasia (FNH) is a hyperplastic lesion with abnormally high arterial blood flow. Subsequent events in the pathogenesis have not been elucidated. In studies of cirrhosis, we showed that regeneration occurs in the sequence: 1) activation of hepatocyte progenitor cells (HPCs) identified by glutamine synthetase activation (GSA), 2) Hepatocyte (HC) buds with tubular plates, and 3) HC remodeling into single-cell plates. This budding sequence may be initiated by local Wnt secretion. Wnt activates the Wnt/beta-catenin pathway causing regeneration and GSA. GSA in a “map-like pattern” is a defining feature of FNH.

We hypothesize that increased delivery of secreted Wnt to HPCs initiates focal HC hyperplasia. We studied morphology of FNH for an explanation of how Wnt, produced in hepatic veins, could be distributed to the HPC niche in portal tracts.
Method: A consecutive series of 50 resected FNH lesions were serially sectioned and stained with GS, CD34, CK19, reticulin.

Results: Most lesions had a large arterio-portal shunt (APS). Proximal sinusoids were mostly lined by CD34-positive sinusoidal endothelial cells (SEC), indicating a high-flow/high-pressure state. HPC activation and tubular HC plate structure confirmed that hyperplasia resulted from budding. Within FNH, GSA was markedly increased near small hepatic veins and absent in high flow areas revealed by CD34-positive SEC. This map-like distribution of GSA suggests that an APS focally pressurizes hepatic veins resulting in focal retrograde sinusoidal flow, delivering increased Wnt concentration to local parenchyma and small bile ducts, inducing HC hyperplasia by activation of budding sequence.

Conclusion: In FNH, hyperperfusion and focal retrograde sinusoidal flow, can explain the map-like distribution of Wnt effects, such as GSA and bud-derived hyperplasia. Most lesions likely begin with a local portal vein thrombosis, with shunt forming during recanalization. Downstream arterialization and A-HV shunting provide the focal and variable HV-to-sinusoidal pressure gradients that determine direction of blood flow. Budd-Chiari lesions likely begin with HV thrombosis giving a distinct lesion (FNH-type 2).

FNH serves as a model for Wnt causing hyperplasia and GSA. Similar blood flow abnormalities occur in chronic liver disease, although in a less predictable and focused pattern. Thus, local Wnt concentration may be an important driver for regeneration in many liver diseases.

Method: 275 subjects (72 healthy; 42 chronic liver disease controls; 161 with HCC-all with Childs Pugh ‘A’ liver function-of whom 84 had tumor biopsy tissue available). Neutrophil immunohistochemistry (IHC), digital image analysis, serum cyto/chemokine 65-Plex panel (Eve Technologies), FACS, cytospin nuclear maturity, reactive oxygen species (ROS) generation, proteome (Orbitrap Fusion Lumos Tribrid mass spectrometer; MaxQuant and Perseus software) and patient data were analysed.

Results: The IHC density of intra-tumor (IT) CD66B+ neutrophils was higher in earlier TNM stage cancers (p = 0.007), associated with significantly better responses to therapies and independently with better survival (Figure 1). In contrast, peri-tumor (PT) neutrophils rose as cancers progressed, significantly associated with circulating neutrophil number (0.436; p = 0.002), size and vascular invasion. Four serum cytokines (IL-8, CXCL10, CXCL13, CCL21) were significantly elevated with HCC, regardless of cirrhotic state. Elevations in IL-8 were early and striking (up to 5X, p < 0.001), correlating with tumor number (0.531; p = 0.001), size (0.493; p = 0.020) and vascular invasion (0.595; p = 0.004). IT neutrophils correlated with IL-18 (0.587; p = 0.035) and PT neutrophils with CXCL10 (0.645; p = 0.032) and MCP-1 (~0.645; p = 0.032).

In the presence of cirrhosis, reductions in nuclear mature (>70%>55%) and immature (25%>10%) circulating neutrophils, with increases in hypersegmented (5%<35%) were evident, with a proteome revealing reduced degranulation (MPO, AZU1, CTSG, GM2A, RNASE3). In cancers there was a sharp recovery in immature neutrophils, with a proteome supporting haem metabolism and oxidative phosphorylation (highly significant changes in multiple cytochrome oxidase and haemoglobin subunits and carbonic anhydrase). Functionally, ROS...
production was elevated by the NADPH oxidase activator PMA, but less responsiveness to IML/Receptor signaling.

**Conclusion:** The development and progression of cancer is associated with changes in chemokines, restoration/elevation in circulating immature neutrophils, metabolic reprogramming and elevated ROS capacity. Elevations in IT neutrophils associated with better responses and outcomes, while accumulation of PT neutrophils associated with circulating neutrophils, and tumor progression.

**FRIS562**

Dynamic organotypic culture of primary liver cancer as a personalised immunocompetent drug screening platform for immuno-oncology

Ravi Jagatia,1,2,3 Ewald Doornebal1,2,3 Lorenzo Caciolli1,2,4 Nicola Harris1,2, Una Rastovic1,2, Sara Campioni1,2, Melissa Preziosi5, Marjorie Yumol6, Rosa Miquel7, Yoh Zen8, Andreas Prachalias9, Krishna Menon9, Sara Mantero9, Sandra Phillips1,2, Nigel Heaton9, Luca Urban1,2, Elena Palma1,2, Shilpa Chokshi1,2,6. Kings College London, Faculty of Life Sciences and Medicine, London, United Kingdom; 2The Roger Williams Institute of Hepatology, London, United Kingdom; 3Contributed Equally; 4Politecnico di Milano, Department of Chemistry, Materials and Chemical Engineering “Giulio Natta,” Milano, Italy; 5Institute of Liver Studies, Kings College London, London, United Kingdom; 6Corresponding Author Email: s.chokshi@researchinliver.org.uk

**Background and aims:** Current primary liver cancer (PLC) models fail to truly encompass the human tumour immune microenvironment, exacerbating a recognised discord between the preclinical and clinical successes of emerging (immuno)therapeutics. The organotypic culture of 3D human Precision Cut Tumour Slice (PCTS) is a cancer explant model which retains tumour specific histoarchitecture, aetiological background, disease phenotype, resident immune landscape, and checkpoint (CP) expression for >5 days ex-vivo. Our study aims to (1) validate PCTS to assess patient-specific therapeutic responses and (2) advance culture conditions using a proprietary Multi-well Plate (MuPL) perfusion bioreactor to extend PCTS lifetime and allow perfusion of immune cells through PCTS.

**Method:** PCTS generated from PLC (HCC & CCA) were treated with approved single agent or combinatorial checkpoint inhibitor (ICI), monocolonal antibody (mAb) or kinase inhibitor (KI) therapy for up to 7 days. Therapeutic response was determined by evaluating histology (H&E and Sirius red), apoptosis/cell death (TUNEL, lactate-dehydrogenase release, cytokeratin 18), and proliferative capacity (PC, Ki67). Gene expression was assessed using QuantiGene RNA Assay. Resident immune cells were assessed by immunofluorescence and FACS. In addition, PCTS/immune cells co-cultured in the MuPL bioreactor were longitudinally assessed for viability, histology, and tissue integrity.

**Results:** Doxorubicin was used as a positive cell death control in all treated patients, decreasing PCTS viability and PC by day 5. Overall immunotherapy response was patient specific. Compared to monotherapy, nivolumab + regorafenib therapy decreased the tumour to stroma ratio and PC in all patients by day 7. Also, significantly increased apoptosis was detected in one patient, who comparatively showed higher CP expression including PD-1, PD-L1 and CTLA-4. Other combinatorial immunotherapies, including atezolizumab + bevacinumab and nivolumab + ipilimumab, reduced PC without affecting histology or viability. Additionally, PCTS and immune cells cultured in the MuPL bioreactor maintained viability, structural integrity and histoarchitecture for >7 days.

**Conclusion:** PCTS can be used as a powerful tool to study personalised responses to (immuno)therapeutics. In addition, PCTS can be successfully cultured in a perfusion system, recapitulating tumour-immune cell interactions, allowing assessment of response to cell and vaccine therapy ex-vivo.

**FRIS563**

High plasma level of osteopontin, a potential biomarker in hepatocellular carcinoma, is associated with weakened anti-tumour immunity

Tengfei Si1, Zhenlin Huang2, Shirin Elizabeth Khorsand1,3,4, Wayel Jassem1,3, Xiaohong Huang1, Abd Suddie1, Mark W McPhail1, Francesca Trovato1,5, Salma Mujib1, Salvatore Napoli1, Ellen Jerome1,2, Yun Ma1, Nigel Heaton1,3. Kings College Hospital, Institute of Liver Studies, London, United Kingdom; 3Kings’ College Hospital, Transplant Service, London, United Kingdom; 4the Roger Williams Institute of Hepatology, London, United Kingdom; 5Kings’ College Hospital, Liver Intensive Therapy Unit, London, United Kingdom

**Background and aims:** It has been shown that osteopontin (OPN) is closely associated with tumour invasion and metastasis in hepatocellular carcinoma (HCC). The mechanisms for the role of OPN in HCC has been defined in both animal models and carcinoma cell lines, but direct evidence derived from human studies are lacking. We aim to explore OPN’s association with clinical outcome and anti-tumour immunity through a comprehensive analysis in a large cohort of HCC patients.

**Method:** A total of 92 HCC patients, 81 non-HCC patients with underlying liver cirrhosis (NASH/ARLD/HBV/HCV) and 25 healthy controls (HC) were recruited from our centre. Plasma levels of OPN, Th1/Th17 cytokines, soluble PD-1, PD-L1, CTLA-4, CCL17 and CXCL-9 were measured by ELISA. mRNA expression of OPN and ligands for immune checkpoint were assessed by quantitative real-time PCR across HCC and paired adjacent liver tissue (n = 16). Immunofluorescence staining was performed to co-stain OPN with CD8 and PD-L1 in HCC, paired adjacent tumour and healthy liver tissues.

**Results:** The plasma OPN level in untreated HCC (n = 48) was significantly higher than other groups (Fig 1A). ELISA results showed good diagnostic performance when compared with both healthy controls (AUC = 0.90, p < 0.0001) and cirrhotic group (AUC = 0.90, p < 0.0001) (Fig 1B). For patients receiving ablation (radiofrequency ablation, RFA; microwave ablation, MWA) or liver resection (LR) (n = 16), the OPN levels were much lower than those treated with radiotherapy (selective internal radiation therapy, SIRT; stereotactic ablative radiotherapy, SABR) or chemotherapy (transarterial chemoembolization, TACE) (n = 22). In some patients, low OPN level represented better treatment response to TACE and longer...
progression free survival (PFS) (>1 year) after liver resection (Fig 1 C). PCR results showed high expression of OPN in HCC tumour tissue (Fig 1 D) and there was a positive correlation between OPN with the ligands of CTLA-4 (CD80/CD86) and TIM-3 (LGALS9) (Fig 1 E). Plasma PD-L1 and CCL-17 levels in untreated HCC (n = 48) were both higher when compared to other HCC treated groups (n = 25; n = 19) and positively correlated with OPN. Furthermore, immunofluorescent staining showed that the expression of both OPN and PD-L1 were upregulated in tumour, with high signal of OPN around tumour vasculature. While CD8 was downregulated in tumour and paired adjacent tumour tissue.

**Conclusion:** OPN has been shown as a potential marker for both diagnosis and prognosis in HCC. The positive correlations between OPN, PD-L1 and chemokine of T-regulatory cells CCL-17 in plasma, suggest that high OPN levels is associated with a weakened anti-tumour immunity. This indication was further confirmed by PCR results and immunofluorescent staining.

FR564

**The uptake of extracellular lipids promotes cholangiocarcinoma progression**

Mikel Ruiz de Gauna 1, Francesca Biancaniello 2,3, Francisco González-Romero 1, Pedro Miguel Rodrigues 3,4, Ainhoa Lapitz 2, Beatriz Gómez Santos 3, Paula Olaiola 2, Sabina Di Matteo 2,3, Igor Aurrekoetxea 1,5, Ibone Labiano 2, Luis Bujanda 2,4, Jesus Maria Banales 2,4,11,12, Diego Calvisi 9, Jesper Andersen 10, Domenico Alvaro 3.

**Faculty of Medicine and Nursing, Department of Phisiology, Leioa, Spain; 2Department of Liver and Gastrointestinal Diseases, Biodonostia Health Research Institute, Donostia University Hospital, University of the Basque Country UPV/EHU, San Sebastian, Spain; 3Department of Translational and Precision Medicine, “Sapienza” University of Rome, Rome, Italy; 4National Institute for the Study of Liver and Gastrointestinal Diseases (CIBERehd, Instituto de Salud Carlos III); 5Biocruces Health Research Institute, Cruces University Hospital, Barakaldo, Spain; 6Department of Molecular Biophysics, Biofisica Institute (University of Basque Country and Consejo Superior de Investigaciones Científicas (UPV/EHU, CISC)), Leioa, Spain; 7Department of Biochemistry and Molecular Biology, University of the Basque Country (UPV/EHU), Leioa, Spain; 8Proteomics Platform, Center for Cooperative Research in Bioscience (CIC Biogune), ProteoRed-ISCIII, Bizkaia Science and Technology Park, Derio, Spain; 9Institute for Pathology, Regensburg University, Regensburg, Germany; 10Department of Health and Medical Sciences, Biotech Research & Innovation Centre (BRIC), University of Copenhagen, Copenhagen, Denmark; 11IKERBASQUE, Basque Foundation for Science, Bilbao, Spain; 12Department of Biochemistry and Genetics, School of Sciences, University of Navarra.

Email: patricia.aspichueta@ehu.eus

**Background and aims:** One of the hallmarks of cancers is metabolic reprogramming, and its regulation is a possible therapeutic target. There is little information about rearrangements of lipid metabolism in cholangiocarcinoma (CCA), characterised by great heterogeneity and poor prognosis. Previous evidence suggests that de novo synthesis of fatty acids (FAs) is decreased in CCA, pointing to exogenous lipids as the main source of FAs. Here, we investigated the alterations in lipid metabolism in CCA and their role in tumour proliferation.

**Method:** In vitro proliferative and migration capacities and in vivo tumorigenic capacity of 5 human CCA cell lines were analyzed. Proteome, lipid content and metabolic fluxes were studied in CCA cells, using primary cultures of normal human cholangiocytes (NHC) as a control. Lipid content and metabolic fluxes were analyzed in liver samples of a mouse model of CCA based on the overexpression of Akt1 and NOTCH1 intracellular cytoplasmic domain (Nicd1).

**Results:** The proteome of CCA cells showed a dysregulation of pathways involved in lipid and lipoprotein metabolism. The EGI1 CCA cell line showed the highest proliferative and migration capacity. We studied metabolic fluxes with radioisotopes and measured lipid content in high (EGI1) and low (HUCCT1) proliferative cell lines, and in liver tumor tissue from the mouse model of CCA. Both EGI1 and HUCCT1 incorporated more oleic and palmitic acid than NHCs, which resulted in an increased triglyceride storage. Similarly, the CCA mouse model showed a faster clearance and increased liver uptake of intravenous [3H]-oleate. Highly proliferative EGI1 cells showed an increased uptake of very-low density lipoproteins (VLDL) and high density lipoproteins (HDL) than NHC and HUCCT1. This increased uptake of lipids was accompanied by a higher expression of CD36 and fatty acid binding protein FABP5. Unlike glucose or glutamine oxidation, fatty acid oxidation (FAO) rate was increased in EGI1 and downregulated in HUCCT1. Accordingly, FAO-related proteins showed a higher expression in the proteome of EGI1 and, therefore, pharmacological inhibition of FAO induced a more pronounced inhibition on proliferation in EGI1 than in HUCCT1. Expression of the first enzyme involved in FAO, the acyl-CoA dehydrogenase ACADM, whose protein levels are specifically increased in EGI1, was found to correlate with that of the proliferation marker PCNA in tumour tissue from CCA patients.

**Conclusion:** Highly proliferative human CCA cells are highly dependent on lipid and lipoprotein uptake to sustain an active catabolism of FAs. These results suggest that inhibition of FAO and/or lipid uptake may provide a novel therapeutic strategy for patients of this subclass of CCA.
Background and aims: Metabolic liver disease and hepatocellular carcinoma (HCC) are major global health burdens with unsatisfactory treatment options. HCC is the third most common cause of cancer-related death and the leading cause of death among cirrhotic patients. While new treatments for HCC have been recently approved, chemopreventive strategies for advanced fibrosis are lacking. By combining a cell-based system predicting liver disease progression and HCC risk and transcriptome analysis of fibrotic/cirrhotic patient liver tissues, we identified peroxiredoxin 2 (PRDX2) as a driver of disease progression and HCC risk. Here we aimed to uncover the role of PRDX2 in liver disease progression and HCC development.

Method: The role of PRDX2 in liver disease progression and HCC development was investigated by Prdx2 KO in a state-of-art CRISPR/Cas9 mouse model for NASH-induced hepatocarcinogenesis and a cell-line-derived xenograft (CDX) mouse model. The mechanism of action was explored using RNA-Seq analyses of mouse liver tissues and validated by perturbation studies in human liver cell-based models.

Results: In patient liver tissues, PRDX2 expression is increased in tumor, suggesting a role of PRDX2 in hepatocarcinogenesis. In the CRISPR/Cas9 NASH-induced HCC mouse model, KO of Prdx2 improved metabolic liver functions, robustly reduced liver steatosis through improvement of the AMPK/LXRα axis and significantly decreased HCC development. RNA-Seq analyses of mouse liver tissues confirmed that Prdx2 KO restored liver metabolic pathways (i.e. cholesterol, fatty acid and bile acid metabolism), decreased inflammation (IL6/STAT3) and suppressed proliferative and pro-inflammatory pathways (i.e. EGFR/p38/MAPK, PI3 K/AKT/mTOR). Finally, PRDX2 loss-of-function studies in hepatoma cell-based models and a Huh7-CDX mouse model unraveled that PRDX2 mediates cancer cell proliferation, migration, invasion, and survival.

Conclusion: Our findings demonstrate an important functional role of PRDX2 in metabolic liver disease and hepatocarcinogenesis. Therefore, targeting PRDX2 may be a previously undiscovered therapeutic option for the treatment of metabolic liver diseases and to prevent NASH-induced HCC.
POSTER PRESENTATIONS

Method: CCA cells (HuCCT-1 or CCLP1) were treated with monoun-
saturated FA (132mCM oleic or 100mCM palmitoleic acid). Responsiveness of CCA cells to cytotoxic drugs was tested with
crystal violet staining. Epithelial-mesenchymal transition program,
stem-like markers, ABC transporters and metabolic markers, were
tested with real-time PCR. Self-renewal ability was tested with a
colony formation assay. Cancer stem cell- (CSC)-enriched spheres were
obtained growing cells in anchorage-independent conditions and
selective medium. Five-year overall survival (OS) was analyzed in
104 patients with cholangiocarcinoma sub-grouped based on fatty
acid synthase (FASN) expression. NSG mice were injected with
spheres obtained from CCLP1 cells and treated for four weeks with
the FASN inhibitor orlistat (240 mg/kg).

Results: Exposure of CCA cell lines to FAs increased cell proliferation and
activated growth and survival pathways, including AKT and
ERK1/2. Exposure to FA before treatment with chemotherapeutic agents made CCA cells less sensitive to their toxic effects, and
modulated the expression of ABC transporters involved in drug
resistance. The colony forming ability of CCA cells was increased by
FAs, and was associated with upregulation of genes controlling
epithelial-mesenchymal transition and stemness. Expression levels of
genes involved in lipid metabolism were upregulated in CSC-
enriched spheres. In a series of CCA patients, the expression of FASN correlated with OS. FASN inhibition by orlistat decreased cell
proliferation and CSC or EMT markers. In a xenograft model of CCA,
tumor volume of mice treated with orlistat was significantly lower
than in control mice.

Conclusion: Exposure of CCA cells to FA increases growth, invasive-
ness and resistance to antineoplastic drugs, and modulates stem-like
features and self-renewal abilities. In the CCA stem-like subset, several key genes involved in FA synthesis and transport were
upregulated, and FASN inhibition decreased cell proliferation and
downregulated CSC markers. FASN expression levels correlate with survival in patients with CCA. These data indicate that lipid metabolism could be a new potential target to affect CCA progression, especially in CSC subset.

FRI568
Cyclophilin D knockout promotes cell death pathways in
preventing HCC development in a streptozotocin-induced mouse model of diabetes-linked NASH
Winston Stauffer1, Joseph Kuo2, Daren Ure2, Robert Foster3, Philippe Gallay4, Scripps Research, Immunology and Microbiology, La Jolla, CA, United States; 2Arena Pharmaceuticals, San Diego, United States; 3Hepion Pharmaceuticals, Edison, NJ, United States.

Background and aims: Cyclophilins are a diverse family of peptidyl
prolyl isomerases which promote protein folding and perform a
variety of functions in the liver and other tissues. We have previously
reported that the pan-cyclophilin inhibitor (CypI) compounds, CRV-431, NV565 and Debio-025/Alisporivir, decreased the severity of non-alcoholic steatohepatitis (NASH) and hepatocellular carcinoma (HCC) in a streptozotocin (STZ)-induced HCC murine model. However, it is not known which cyclophilin family member(s) whose inhibition is causing this effect. Here, we report the effects of this HCC model in Ppif−/− mice lacking cyclophilin D (CypD), an important component of the mitochondrial permeability transition pore.

Method: 6-week-old male Ppif−/− and wild-type (WT) mice were
injected with 200 mg/kg STZ to destroy pancreatic beta cells and
induce a diabetic phenotype. Mice were nourished with chow with
21.1% fat, 41% sucrose, and 1.25% cholesterol by weight and high sugar
solution (23.1 g/L fructose and 18.9 g/L glucose), which continued
throughout. After 30 weeks on this diet, mice (n = 10 per group) were
sacrificed. Body and liver weight were recorded. Livers were scored
for HCC tumor burden. Histological sections of livers stained with
H&E were scored for inflammation, steatosis, and ballooning. Liver
sections were also stained with Sirius Red for examination of collagen
fibrosis. RNA was extracted from frozen liver tissue for qRT-PCR
analysis. PCR apoptosis arrays were purchased from Qagen. Unpaired
Student’s t-tests were conducted with GraphPad Prism.

Results: Tumor burden scores were three times higher in WT mice compared to Ppif−/− mice, significant by Student’s t-test (p = 0.03). Average tumor number was also significantly decreased with Ppif−/− mice, of which 8 out of 10 mice had no tumors, compared to just 3 of 10 in WT mice. A trend of reduced collagen deposition was also observed in livers of Ppif−/− mice relative to WT, but this was not significant. Inflammation, steatosis, and ballooning were similar between groups. Mechanistically, qPCR arrays for apoptosis genes revealed that the tumor suppressor Fhit was significantly elevated in Ppif−/− livers, while apoptosis inhibitor and oncogene Birc5 was decreased.

Conclusion: Cyclophilin inhibition represents a promising avenue for the
treatment of HCC development in mouse models. These data show for the first time that mice without CypD are significantly protected from HCC development, suggesting CypD inhibition is at
least partly responsible for the previously established anti-tumor
effects of Cyp1 antagonist compounds. Molecular analyses suggest CypD inhibition may promote cell death pathways which act as tumor suppressors.

FRI569
Ribosomal protein encoding genes: potential drivers of primary
sclerosing cholangitis associated cholangiocarcinoma
Megan Illingworth1,2,3, Yoh Zen4, Jeremy Nayagam5, Deepak Joshi4, Luca Urbani5,6, Neil Youngson1, Nigel Heaton1, Shirin Elizabeth Khorsandi1,2,3, The roger williams institute of hepatology, foundation for liver research, London, United Kingdom; 4King’s college london, faculty of life sciences and medicine, London, United Kingdom; 5The institute of liver studies, kens college hospital, London, United Kingdom.

Email: megan.illingworth@kcl.ac.uk

Background and aims: Primary sclerosing cholangitis (PSC) patients have a 20% lifetime risk of cholangiocarcinoma (CCA), equating to a
250–1500 fold higher risk than that of the average population. Despite this, stratification of PSC patients at risk of CCA is currently
not possible, with PSC patients who progress to CCA facing insufficient and unsuccessful treatment options and thus, a poor
diagnosis. The degree of similarity between CCA in PSC patients and
non-PSC patients is unclear, and therefore the applicability of research into CCA targeted therapeutic for PSC associated CCA (PSC-
CCA) patients remains unknown. This work aims to provide novel
insight into gene expression in PSC-CCA to aid in the development of
biomarkers for risk stratification and targeted therapeutics for this
patient cohort. Additionally, this work aims to highlight novel
differences in PSC-CCA and CCA not on a PSC background.

Method: Massive analysis of cDNA end (MACE) sequencing of
formalin fixed and paraffin embedded tissue from CCA (n = 10),
PSC-CCA (n = 10), PSC-CCA surrounding liver (n = 7), PSC bile ducts
(n = 9), PSC surrounding liver (n = 9) and CCA adjacent liver (n = 6)
was undertaken. Standard bioinformatic analysis was undertaken
differential gene expression determined.

Results: A total of 2567 genes were differentially expressed between PSC-CCA and CCA tumours. Ribosomal processes were significantly
downregulated in PSC-CCA tumours when compared to both CCA
tumours and PSC bile ducts and ion transport was significantly
upregulated. Additionally, 849 of the 2567 genes were long non-
coding RNAs, all of which were downregulated in CCA. Analysis of
differential expression in the background liver identified 357 genes
differentially expressed in PSC-CCA when compared to non-malignant
PSC background livers. Apoptotic pathways were upregulated, and
ribosomal processes downregulated in PSC-CCA background
livers. Comparison of PSC-CCA tumours to PSC bile ducts identified
1717 differentially expressed genes. Ribosomal processes, the
complement cascade and extracellular matrix organisation were all
downregulated in PSC-CCA tumours, while mitotic nuclear division and migration were upregulated in PSC-CCA tumours.

**Conclusion:** This transcriptomic dataset provides novel mechanistic insight into PSC-CCA and highlights a unique role for ribosomal proteins in PSC progression to CCA. The precise mechanism of this is currently unclear, warranting further investigation.

**FR1570**

**Stemness features during cholangiocarcinoma progression in vivo: characterization of primary and metastatic stem-like cells**

Margherita Correnti1,2,3, Marco Erreni4, Roberta Avigni4, Marina Sironi2, Matteo Ramazzotti1, Caterina Peraldo Neia1, Giuliana Cavalloni1, Stefania Recalcati1, Fabio Marra1, Chiara Raggi1, 1Humanitas clinical and research center, Center for autoimmune liver diseases, Rozzano, Italy; 2University of Milan, Dept. of biomedical sciences for health, Milan, Italy; 3University of Milan, Department of Biomedical Sciences for Health, Milan, Italy; 4Humanitas clinical and research center, Dept. of immunopharmacology, Rozzano, Italy; 5Humanitas clinical and research center, Dept. of immunopharmacology, Rozzano, Italy; 6University of Florence, Dept. of Experimental and Clinical Biomedical Sciences, Florence, Italy; 7Department of Molecular Biophysics, Biofisika Institute (University of Basque Country and Consejo Superior de Investigaciones Científicas (UPV/EHU, CSIC)), Leioa, Spain; 8Department of Biochemistry and Molecular Biology, University of the Basque Country (UPV/EHU), Leioa, Spain; 9Email: margherita.correnti@gmail.com

**Background and aims:** Cholangiocarcinoma (CCA) is an extremely heterogeneous adenocarcinoma arising from malignant transformation of biliary tree. Spread of tumor cells in blood or lymphatic circulation as circulating tumor cells (CTCs) plays a major role in recurrence, metastasis and drug unresponsiveness. Assuming that CTCs are heterogeneous, we hypothesized the existence of CCA stem-like relapse-initiating cells. Consistent with cancer stem cells (CSC) hypothesis, stem-like CTCs might represent the potential source for cancer relapse and distant metastasis. The present study aimed to explore the evolution of stemness features during CCA progression.

**Method:** Enrichment of CCA stem-like subset by sphere culture (SPH) in established CCA cell line (HUCCT1) and primary CCA cell culture (MTCHC-01). Adherent monolayer (MON) cells as control. Set up of CCA orthotopic mouse model by intrahepatic injection of Luciferase-GFP transfected SPH and MON cells. Analysis of GFP+ disseminating tumor cells in target organs and bloodstream by FACS. Isolation of GFP+ tumor cells from primary and metastatic tumors by FACS sorting. Molecular characterization by qRT-PCR arrays focus on CSC, epithelial-to-mesenchymal transition (EMT), angiogenesis and drug resistance. Expression of CSC-like surface markers evaluated by FACS. Molecular data validation in human CCA samples.

**Results:** CCA SPH-primary tumor derived GFP+ cells showed CSC and EMT-related gene enrichment compared to MON-primary tumors. In accordance, SPH cells were responsible for enhanced tumor spread in secondary organs (lungs, spleen, peritoneum, mesenteric lymph nodes). CD45−/GFP+ tumor cells were detected in bloodstream of very few samples, suggesting that lymphatic circle is the preferential via to CCA dissemination. Notably, lung SPH-disseminated cells showed up-regulation of most of tested CSC, EMT, angiogenesis and drug resistance related genes compared to SPH-primary tumor cells. Despite some differences between cell lines and different mice, a panel of 35 genes commonly up-regulated was found in SPH-disseminated cells. Some of these genes were significantly up-regulated in 13 recurrent CCA tumor specimens compared to paired primary tumors.

**Conclusion:** These findings suggest that CCA SPH cells are enriched in stem-like disseminating tumor cells responsible for recurrence and metastasis formation. Moreover, our data indicate that a stemness core is stably maintained during CCA-evolution starting from primary tumor initiation through disseminating process.

**FR1571**

miR34a-5p is a target of E2F2 transcription factor in MAFLD-related HCC

Maider Apodaka-Biguri1, Francisco Gonzalez-Romero1, Daniela Mestre Congrádo1, Igor Aurrekoetxea1, Beatriz Gómez Santos1, Igotz Delgado1, Xabier Buque1,2,2, Ana Nieva-Zuluaga1, Mikel Ruiz de Gauna1, Idioia Fernández-Puertas1, Ainhoa Iglesias3, Ana María Aransay4,5, Juanjo Lozano4,5, Cesar Augusto Martin5,8, Imanzu Bernales6, Ana Zubia1, Patricia Aspichueta1,2,5, 1Department of Physiology University of the Basque Country UPV/EHU, Faculty of Medicine and Nursing, Leioa, Spain; 2Biocruces Bizkaia Health Research Institute, Cruces University Hospital, Barakaldo, Spain; 3Department of Genetic, Physical Anthropology and Animal Physiology, Faculty of Science and Technology, University of Basque Country UPV/EHU, Leioa, Spain; 4Genome analysis platform, Center for Cooperative Research in Biosciences (CIC bioGUNE), Dero, Spain; 5National Institute for the Study of Liver and Gastrointestinal Diseases (CIBERehd, Carlos III Health Institute), Madrid, Spain; 6Bioinformatic Platform, Clinic Hospital, Barcelona, Spain; 7Department of Molecular Biophysics, Biofisika Institute (University of Basque Country and Consejo Superior de Investigaciones Científicas (UPV/EHU, CSIC)), Leioa, Spain; 8Department of Biochemistry and Molecular Biology, University of the Basque Country (UPV/EHU), Leioa, Spain; 9SICKER, University of Basque Country UPV/EHU, Leioa, Spain

**Background and aims:** Metabolic associated fatty liver disease (MAFLD) is the most common cause of chronic liver disease in Western countries and a risk factor for hepatocellular carcinoma (HCC). E2F2 is a metabolic driver in MAFLD development and progression to HCC. A relationship between E2F2 and microRNAs (miRNAs) expression has been described in different pathologies, but not in liver disease. The aims here were: 1) to identify if liver E2F2 regulates miRNAs involved in MAFLD development and progression to HCC; 2) to investigate the metabolic relationship between E2F2 and the identified miRNAs in liver pathology.

**Method:** To induce MAFLD-related HCC, diethylnitosamine (DEN) (25 mg/kg) was administrated to 14 day-old E2F2−/− and wild-type mice (WT), which were fed a high-fat diet (HFD) until sacrificed at 9 months. Chow diet-fed (CD) 3 month-old E2F2−/− and WT mice were also used. E2F2 was specifically upregulated in liver with adeno-associated viruses-serotype 8. miRNA sequencing and transcriptome analysis was performed in 9-month-old DEN-HFD WT and E2F2−/− mice. Selected differentially expressed liver miRNA candidates and genes were further validated by RT-qPCR analysis. Metabolic fluxes and lipid content were analyzed.

**Results:** The results obtained from miRNA sequencing and later validation by qPCR showed that in 9 month-old DEN-HFD E2F2−/− mice, resistant to MAFLD-related HCC, expression of miR-122-5p was upregulated while that of miR34a-5p, miR155-5p and miR146a-5p were downregulated. Among all, miR34a-5p was the only one decreased in CD-fed E2F2−/− while increased when E2F2 was specifically overexpressed in liver, as compared to the corresponding controls. The crosstretched analysis between the upregulated transcriptome genes underlying the resistance to develop MAFLD-related HCC in E2F2−/− mice and the miR34a-5p predicted interacting genes showed, among others, the enrichment in “Bile acid transport” and “lipid metabolism” pathways. Given the relevance of
cholestasis in liver disease, the expression and protein levels of HNF4, a critical regulator of bile metabolism, and of Etnk2 and Chtp1, modulators of the synthesis of phosphatidylethanolamine (PE) and phosphatidylcholine (PC), required for bile secretion, were analyzed. The results showed higher levels of the regulators of bile metabolism in revertant mice than in DEN-HFD WT mice together with increased PE and PC synthesis which led to higher PE, but not PC liver content, suggesting increased elimination into bile. 

**Conclusion:** miR34a-5p is a target of E2F2 in MAFLD-related HCC. The results suggest that the E2F2-miR34a-5p axis induce inefficient bile secretion during MAFLD development and progression to HCC promoting development of the disease.

**FRI572**

TIA1 in fatty liver disease and hepatocellular carcinoma

Dobrochina Dolicka1, Szabolcs Zahoran2, Marta Sousa1, Monika Gjorgjieva1, Christine Sempoux 3, Margot Fournier 1, Christine Maeder1, Martine Collart3, Michelangelo Foti1, Cyril Sobolewski1,4, 1University of Geneva, Faculty of Medicine, Department of Cell Physiology and Metabolism, Switzerland; 2University of Geneva, Faculty of Medicine, Department of Microbiology and Molecular Medicine, Switzerland; 3Lausanne University Hospital, University Institute of Pathology, Switzerland; 4Institute for Translational Research in Inflammation, Inserm, U1286, Faculty of Medicine, Pole Recherche, France

**Email:** cyril.sobolewski@univ-lille.fr

**Background and aims:** Adenylate-Uridylate-rich elements binding proteins (AUBPs) contribute to the development of non-alcoholic fatty liver disease (NAFLD) and hepatocellular carcinoma (HCC) by regulating the expression of genes important for metabolic, inflammatory, and cancerous processes. This effect is mediated by their binding to target mRNAs, which elicits their recruitment into processing bodies (P-bodies) or stress granules (SGs), where mRNAs are degraded or kept translationally silent, respectively. Herein, we aimed at characterizing the role of TIA1, an AUBP with a poorly known function in the liver, in NAFLD and HCC.

**Method:** TIA1 expression was analyzed in datasets of mouse and human samples of NAFLD and HCC. The role of TIA1 in vivo was investigated in mice fed a methionine-choline-deficient (MCD) diet and in a liver-specific PTENKO mouse model of hepatic carcinogenesis, where TIA1 was silenced using AAV8 viruses. Finally, TIA1 functions were characterized in vitro in human hepatic cancer cells and a translational-based approach was used to identify the network of potential TIA1 targets.

**Results:** In vitro analyses indicate that TIA1 promotes cell proliferation and migration. In vivo, its silencing worsens NASH induced by the MCD diet and increases tumor number in LPTENKO mice. In agreement, the analysis of polysomal RNAs indicates that TIA1 regulates a whole network of tumor suppressors and oncogenes as well as genes related to lipid metabolism. Finally, TIA1 protein level is strongly downregulated in human HCC and represents an important marker of stress granules upon sorafenib treatment.

**Conclusion:** Our data emphasize TIA1’s dual role in liver carcinogenesis and indicate that its downregulation and association with stress granules may represent potential diagnostic tools and/or therapeutic targets.

**FRI573**

Mitochondrial damage, revealed as key factor in cabozantinib efficacy against hepatocellular carcinoma, is potentiated by the BH3-mimetic navitoclax

Anna Tutusaus1, Blanca Cucarull1, Patricia Rider1, Carlos Cuño1, Pablo García de Frutos1, Loreto Boix2,3,Montserrat Mari1, Albert Morales1,1 1IBB-CSIC/IDIBAPS, Barcelona; 2Unidad de Hepatología, Hospital Clinic, IDIBAPS, CIBERHID, Barcelona, Barcelona, Spain; 3Barcelona Clinic Liver Cancer (BCLC), Barcelona, Spain  

**Email:** amorales@clinic.cat

**Background and aims:** The mitochondrial damage induced by sorafenib and regorafenib plays an important antitumor role in hepatocellular carcinoma (HCC). Both Tyrosine Kinase Inhibitors (TKIs) induce mitochondrial dependent cell death that may be potentiated by specific BH3-mimetics, selective inhibitors of BCL-2 proteins. ABT-263, navitoclax, is a BCL-2 and BCL-xl inhibitor studied in clinical trials, such as with sorafenib in solid tumors (NCT02143401). Mitochondrial effects of cabozantinib have not been previously reported in HCC therapy.

**Method:** Hepatoma cell lines (HepG2, Hep3B, PLC5) were treated with cabozantinib and BH3-mimetics (ABT-263, navitoclax: BCL-2 and BCL-XL, ABT-199: BCL-2, A-1331852: BCL-xl). Western blots, qPCR and microarrays were performed. Mitochondrial functionality, caspase activation and induction of apoptosis were analyzed. Tumor growth was determined in a mouse syngeneic model after subcutaneous injection of Hepa-1-6 cells treated with cabozantinib and/or ABT-263.

**Results:** Cabozantinib induced mitochondrial Reactive Oxygen Species (ROS) generation and cell death that was potentiated by BH3-mimetics in hepatoma cells. Cabozantinib induced loss of mitochondrial membrane potential, release of apoptogenic proteins and apoptotic cell death, particularly triggered after navitoclax addition. Sorafenib-resistant cells, which exhibited altered levels of BCL-2 proteins, were less sensitive to cabozantinib; effect that was suppressed by navitoclax co-administration. Moreover, the decreased tumor growth in an immunocompetent mouse model induced by cabozantinib was potentiated in combination with navitoclax, promoting mitochondrial-dependent death as observed after tumor genetic and proteomic analysis.

**Conclusion:** Cabozantinib efficacy may be reduced following other TKIs treatments with mitochondrial impact, such as with sorafenib or regorafenib. In contrast, cabozantinib-induced cell death is potentiated in experimental HCC by mitochondrial directed drugs, such as navitoclax, providing a novel strategy for therapy.
ATP assay (CellTiterGlo). BAP1 protein and markers for apoptosis (cleaved caspase 3) and necroptosis (phosphorylated MLKL) were determined by immunostaining and immunoblotting.

**Results:** The three different CCAOs each harbor distinct BAP1 phenotypes: wild type (CCAOWT), loss of heterozygosity (CCAOLOH), and missense mutation combined with LOH (CCAO Mut/LOH). Compared to PDOWT, BAP1 protein expression could not be detected in CCAOMut/LOH and was greatly declined in CCAOLOH. The cell viability analysis and immunostaining showed that the resistance to either apoptotic or necrotic induction was significantly increased in CCAOMut/LOH (p<0.001) compared to CCAOWT. In contrast, CCAOLOH were more sensitive to cell death induction (p<0.001). Similar increased sensitivity was also observed in ICO BAP1-KO compared to wild-type ICOs. Gemcitabine evoked extensive apoptosis in PDOWT (IC50 0.06 μM), but the sensitivity of both PDOLOH (IC50 0.34 μM) and PDO Mut/LOH (IC50 0.12 μM) was significantly lower. Likewise, ICO BAP1 KO displayed drastic resistance to gemcitabine compared to normal ICOs.

**Conclusion:** Mutations in the BAP1 gene causing loss of function, are associated with a lower sensitivity of CCAOs to extrinsic apoptosis, necroptosis, and gemcitabine cytotoxicity. Correction of the mutation in BAP1 using prime editing is currently effectuated to confirm the role of BAP1 in programmed cell death in CCA. Our findings reveal a promising strategy in CCA precision medicine by targeting BAP1 mutations.

**FR1575**

*Integrative clustering of multiple genomic data using organoid model with application to subtype analysis in intrahepatic cholangiocarcinoma*

Hee Seung Lee1, Dai Hoon Han2, Kyung Joo Cho3, Soo Been Park3, Chanyang Kim2, Galam Leem1, Soon Sung Kwon4, Chul Hoon Kim4, Jung Hyun Jo2, Hye Won Lee1, Si Young Song1, Jun Yong Park1. 1Yonsei University College of Medicine, Division of Gastroenterology. 2Department of Internal Medicine; 3Yonsei University College of Medicine, Division of Hepatobiliary and Pancreatic Surgery, Department of Surgery; 4Yonsei University College of Medicine, Department of Pharmacology

**Email:** drpjy@yuhs.ac

**Background and aims:** Intrahepatic cholangiocarcinoma (ICC) has increased rapidly, and the 5-year survival rate is less than 20%. As the genomic analysis technology has been advanced, subgrouping is possible at the histological or molecular level in ICC. But, there was no well-representative model for subtypes of ICC to study developmental differences, carcinogenesis, and personalized drug response. We aimed to develop ICC organoid models that reflect phenotypical, molecular and genetic properties and performed integrative clustering of multiple genomic data using organoid models with subtype analysis.

**Method:** We enrolled a total of 16 patients who were pathologically diagnosed with cholangiocarcinoma. We made ICC organoid following the previous organoid culture protocol in nature protocol. In accordance with histological characteristics, S100P, N-cadherin, and CD56 expression, the ICC patients were subclassified into small duct type and large duct type. Immunofluorescence (IF), whole exome sequencing, and transcriptomic analysis were performed to characterize and investigate all cancer tissues and matched ICC organoids.

**Results:** We successfully established ICC organoids within a month. The morphology of ICC organoid was similar to matched primary cancer. Organoid derived xenograft also showed similar phenotype in H&E stain. IF stains showed the expression of cholangiocyte marker (CK19 and Sox9) but negative expression in liver cell marker (AFP and Albumin). The cancer immunotherapy marker, Programmed death-ligand 1 expression between the organoid and tumor tissue was similar. Large and small duct type organoids showed their typical histologic phenotype and stain. ICC organoids shared somatic mutations and showed high concordance of somatic mutation between primary tumor and organoids. Through the unsupervised PCA clustering showed the separation of each type of ICC. Using the differential gene expression between types, KRAS signaling pathway, TGFβ and ERBB2 pathway were significantly enriched in large duct type compared to small duct type (p<0.05). GSEA demonstrated that cholangiocarcinoma class2 signature by Andersen et al. was significantly enriched with LD type (enrichment score = 2.19, p<0.001). Protein-protein interaction network analysis indicated that the significant hub proteins were ZNF217 (Odd’s ratio 4.96, P=0.0105).

**Conclusion:** We succeeded in prospective modeling of histological subtype specification in patient-derived ICC organoids. Identification of type specific targetable pathway was possible through gene expression profile of ICC organoids.

FR1576

*Role of soluble adenylyl cyclase in the formation and growth of liver tumours*

Jung-Chin Chang1,2, Suzanne Duijst1, Simei Go1, Dagmar Tolenaars1, Rachel Thomas1, Alain de Bruin2, Arthur Verhoeven2, Ronald Oude-Eferink1. 1Amsterdam University Medical Centers, Tytgat Institute for Liver and Intestinal Research, Amsterdam, Netherlands; 2Utrecht University, Department of Biomolecular Health Sciences, Utrecht, Netherlands

**Email:** j.chang1@uu.nl

**Background and aims:** Soluble adenylyl cyclase (ADCY10, sAC) mediates the cAMP signaling in the cytoplasm, mitochondria, and the nucleus. sAC is activated by metabolic signals (Ca2+, ATP, and bicarbonate) and was recently shown to regulate AMP-activated kinase (AMPK) and transcriptional factor TAZ (WW domain-containing transcription regulator protein 1). The YAP (Yes-associated protein 1)/TAZ signaling pathway regulates the liver size, promotes liver regeneration, and is hyper-activated in liver cancers. Using human liver hepatoma cells HepG2, we recently showed that sAC-cAMP-Epac1 (exchange proteins activated by cyclic AMP 1) signaling regulates mitochondrial Complex I activity and is a metabolic switch between glycolysis and oxidative phosphorylation (PMID: 33412125). We observed that inhibition of sAC activity promotes a Warburg-like metabolic phenotype. Therefore, we hypothesized that reduced sAC activity could promote hepatic tumorigenesis.

**Method:** Liver carcinogenesis was evaluated in hepatocyte-specific sAC knockout mice (Adcy10Δ/Δ × Alb-Cre) and littersmate controls (Adcy10+/−) following a single dose of 25 mg/kg diethylnitrosamine (DEN) injection at 3–4 weeks of age. Tumor formation was monitored by plasma α-fetoprotein (Afp). Tumor burden was evaluated by liver-to-body weight index. Histologic grading was performed on hematoxylin-eosin stained, formalin-fixed tissues. HepG2 cells were used for the in vitro mechanistic study. Cell proliferation was evaluated by dSNA quantification; pharmacological agents and intermediate metabolites of lipid and nucleotide synthesis were used to dissect the underlying mechanisms.

**Results:** Contrary to our expectation, hepatocyte-specific sAC deletion delayed the rise of plasma Afp and reduced the tumor burden in the liver. Preliminary results from histopathology analysis did not suggest a strong correlation between liver-specific sAC deletion and the histological grading of the liver tumors. The in vitro mechanistic study revealed that the suppression of sAC-cAMP-Epac1 signaling activates AMPK and inhibits proliferation of HepG2 cells, which could not be rescued by supplementing intermediates of lipid synthesis or nucleotide. Consistent with AMPK being an established regulator of YAP, we found that sAC inhibition suppressed YAP nuclear translocation.
Conclusion: Hepatocyte-specific sAC deletion delays DEN-induced liver carcinogenesis in mice and reduced the overall tumor burden. Pharmacological inhibition of the sAC-cAMP-Epac1 signaling suppresses the growth of human liver cancer cells. The anti-tumor effect of sAC inhibition is likely mediated by the AMPK-dependent suppression of YAP signaling.

FRI577
A targeted screen identifies Dmbt1 as an oncogene in cholangiocarcinoma
Pooya Shokouhi1, Saumya Manmadhan1, Christian Lechler1, Birgit Kohnke-Értel1, Carolin Mogler2, Thomas Engelbrecht3,4, Rupert Òllinger1-4, Roland Raef1-4, Roland M Schmid1, Ursula Ehmer1.
1Klinikum rechts der Isar der Technischen Universität München, Internal Medicine II, München, Germany; 2Klinikum rechts der Isar der Technischen Universität München, Institute of Pathology and Unit of Comparative Experimental Pathology, München, Germany; 3Technische Universität München, Institute of Molecular Oncology and Functional Genomics, School of Medicine, München, Germany; 4Technische Universität München, Center for Translational Cancer Research (TranslatTUM), School of Medicine, München, Germany
Email: ursula.ehmer@tum.de

Background and aims: Activation of Ras signaling is a common event in human cholangiocarcinoma (CCA). With direct targeting of Ras signaling in its infancy, identification of relevant pathways and genes in Ras-activated cholangiocarcinoma is a prerequisite to the development of novel therapies. To model Ras-activated cholangiocarcinoma, we generated the RKp mouse model that combines liver-specific expression of oncogenic Kras with genetic inactivation of the tumor suppressors Rb and p53. Upon Cre-mediated gene recombination, adult mice developed liver tumors resembling human intrahepatic CCA. To identify potential target genes in the context of activated Ras signaling we performed a targeted screening approach.

Method: Liver tumors from Rb<sup>lox/lox</sup>, p53<sup>lox/lox</sup>, Kras<sup>LSL-G12D</sup>Δ<sup>+/−</sup> (RPK) mice and liver tissue of age-matched control mice were micro-dissected and analyzed for RNA and protein expression. A curated subset of top upregulated genes in mRNA microarray analysis of RPK liver tumors were chosen for further investigation. Primary cells lines from RPK mice were transfected with lentiviral shRNA or sgRNA constructs to induce gene knock-down or CRISPR/Cas9-mediated gene mutation, respectively. Cells were analyzed for proliferation and clonogenic assay, followed by RNAseq, GSEA, and cell cycle analysis of cells mutated for the candidate gene Dmbt1.

Results: Microarray analysis showed several highly upregulated genes in RPK tumors in comparison to controls. shRNA constructs targeted against top upregulated genes showed a striking decrease in cell proliferation and clonogenic capacity with constructs targeting Dmbt1. RPK cells mutant for Dmbt1 showed an enrichment of gene sets for E2F and G2/M checkpoint activation. Further analysis revealed that reduced proliferation upon inactivation of Dmbt1 is associated with a G2/M cell cycle arrest.

Conclusion: Activation of RAS signaling is a common change in human CCA. In our screen, we identified Dmbt1 as a potent oncogene in a model of Ras-mutant cholangiocarcinoma. While DMBT1 has been described as a tumor suppressor in other cancers by interacting with the immune system, we were able to identify a novel cell-autonomous oncogenic role of DMBT1 in CCA. Our results show that DMBT1 is essential for cell cycle progression and proliferation in RPK cancer cells. DMBT1 expression is upregulated in a large subset of human CCA and its potential as a therapeutic target are currently under investigation.

FRI578
ACSL4-dependent ferroptosis promotes HCC progression
Julia Piche1, Antje Mohs1, Stephanie Erschfeld1, Christian Trautwein1, Tobias Otto1,1 Uniklinik RWTH Aachen, Aachen, Germany
Email: jppiche@ukaachen.de

Background and aims: In industrialized countries the prevalence of non-alcoholic fatty liver disease, ranging from steatosis to non-alcoholic steatohepatitis (NASH), is increasing. Mechanisms triggering disease progression towards cirrhosis and hepatocellular carcinoma (HCC) are only incompletely understood. A newly discovered mode of cell death, ferroptosis, is triggered by accumulation of lipid peroxides and is iron-dependent. According to in vitro studies, acyl-CoA synthetase long-chain family member 4 (ACSL4) is an essential enzyme for ferroptosis. Interestingly, ACSL4 expression was shown to be upregulated in HCC tissue indicating that ferroptosis might play a role in HCC pathophysiology. Here, we aimed to investigate the relevance of ferroptosis for disease progression using hepatocyte-specific ACSL4<sup>hspa</sup> knockout mice.

Method: We used a well-established fibrosis-driven HCC model. Tumor formation was induced by injecting the carcinogen diethylnitrosamine (DEN), followed by weekly injections of carbon tetrachloride (CCL<sub>4</sub>). As a second model we applied the Streptozocin/HFD model. Wild-type (WT) and hepatocyte-specific ACSL4 knockout (ACSL4<sup>hspa</sup>) mice were included to investigate the role of ferroptosis for cancer development.

Results: Our analysis in both models demonstrated that ACSL4-dependent ferroptosis is not involved in HCC initiation, but important for tumor progression. After DEN-CCL<sub>4</sub> treatment, serum transaminase levels were increased, but without significant differences upon ACSL4 deletion. Interestingly, the number of tumors, as well as overall tumor burden were significantly reduced in ACSL4<sup>hspa</sup> mice compared to WT mice. This was accompanied by significantly decreased liver-to-body-weight-ratio in ACSL4<sup>hspa</sup> mice. However, immune cell infiltration was not altered. Furthermore, ACSL4 deletion caused reduced proliferation in the liver and diminished tumor-promoting fibrosis.

Conclusion: Our results demonstrate that ACSL4-dependent ferroptosis promotes tumor progression by enhancing tumor-promoting fibrosis. Therefore, inhibition of ferroptosis or key molecules regulating cell death represents a possible therapeutic treatment for human HCC.

FRI579
Identification of risk factors for HBV-derived HCC using HLA-DPB1 genotype and HBV peptides for genome medicine
Masaya Sugiyama1, Naoko Nishida1, Katsushi To Kunaga1, Mizokami Masashi1.1 National Center for Global Health and Medicine, Japan
Email: msugiyama@hosp.ncgm.go.jp

Background and aims: Hepatocellular carcinoma (HCC), caused by hepatitis B virus (HBV) infection, is a major problem worldwide. However, no biomarkers for early diagnosis have been discovered so far. In the present study, we focused on the genetic factors associated with HBV-derived HCC. To discover the genetic factors, we analysed the combined genomes of both humans and HBV.

Method: The genome-wide SNPs array and Lumines were applied to 2,996 individuals (408 chronic hepatitis B (CHB) patients, 307 HCC patients with HBV and 2,281 healthy volunteers (HVs)) from 10 hospitals. The obtained SNPS data were filled by imputation: the HBV genome was extracted from sera of CHB or HCC patients and prepared...
for next generation sequencing (NGS). All sequence reads were converted into amino acid (AA) sequences to assess the effect of HBV mutations on replication and antigen expression in vitro.

**Results:** HLA-DPB1*02:01 allele was associated with protection against HCC development (p < 4.53 × 10^{-9}, OR = 0.53). We then analysed the whole HBV genome of patients carrying the HLA-DPB1*02:01 allele. HLA-DPB1*02:01 homoyzgous patients were divided into HCC and non-HCC groups, matched for age, sex and HBV genotype. HCC with HLA-DPB1*02:01 The proportion of S166 in CHB and HCC was 51.5% and 0%, respectively (p < 0.05). In contrast, the proportion of L166 was 34.3% in CHB and 99.4% in HCC (p < 0.05). This variation was confirmed using a validation sample set (p < 0.02, OR = 18.2). Next, we prepared HLA-DPB1*05:01 homoyzgous patients and examined the AA variations of HBV protein. We then detected that the K130M and V131I mutations were associated with the HCC group (p < 0.05, OR = 8.8); the OR value of the 05:01 population was stronger than that of all patients with HCC (OR = 4.1). Interestingly, mutations in K130M and V131I (nt A1762T and T1764A) were strongly associated with the HLA-DPB1*05:01 homoyzgous population.

**Conclusion:** We have identified genetic factors, both host and viral, that are associated with clinical outcome. As only a small proportion of CHB patients develop HCC, these risk factors may be useful in optimising clinical diagnosis and follow-up time. The finding that certain combinations of HLA-DPB1 alleles and viral mutations are associated with a higher risk of developing HCC is novel, and this study is a proof-of-concept study to use genomic data from hepatitis B patients to predict prognosis.

**FRI580**

**Early Kupffer cell depletion does not affect hepatocellular carcinoma progression in mice**

Bart Van Derborght1,2, Kevin De Muynck1,2, Charlotte Scott3,4, Alain Beschin5,6, Martin Guiliams3,7, Hans Van Vlierbergh5,8, Lindsey Devisscher6,1 Ghent University, Internal Medicine and Pediatrics (Liver Research Center Ghent; Hepatology Research Unit), Ghent, Belgium; 2Ghent University, Basic And Applied Medical Sciences (Liver Research Center Ghent; Gut-Liver Immunopharmacology Unit), Ghent, Belgium; 3Ghent University, Biomedical Molecular Biology, Ghent, Belgium; 4VIB-UGent Center for Inflammation Research, Laboratory of Myeloid Cell Biology in Tissue Damage and Inflammation, Ghent, Belgium; 5Vrije Universiteit Brussels, Laboratory of Cellular and Molecular Immunology, Brussels, Belgium; 6Vrije Universiteit Brussels, Myeloid Cell Immunology Laboratory, Brussels, Belgium; 7VIB-UGent Center for Inflammation Research, Laboratory of Myeloid Cell Biology in Tissue Homeostasis and Regeneration, Chent, Belgium; 8Ghent University Hospital, Gastroenterology and Hepatology, Ghent, Belgium.

**Email:** lindsey.devisscher@ugent.be

**Background and aims:** Hepatocellular carcinoma (HCC) represents the majority of primary liver cancer cases. Its aggressive disease behavior and poor prognosis substantiate the critical need to urgently address the lack of effective HCC treatment options. HCC usually occurs in a background of chronic liver disease (CLD), characterized by chronic hepatic inflammation and fibrosis, in which Kupffer cells (KCs), resident liver macrophages, have been proposed to play a role. However, the role of KCs in HCC initiation and progression remains unknown.

**Method:** In order to investigate the role of KCs in HCC initiation, transgenic Clec4F-diphtheria toxin receptor mice were used. Diphtheria toxin (DT)-mediated KC depletion was performed prior to the introduction of chronic liver damage in both a fibrosis-associated and a non-alcoholic steatohepatitis (NASH)-induced HCC mouse model.

**Results:** At the time of sacrifice, macroscopic hepatic tumors were present in approximately 100% of the cases in both HCC mouse models without differences between groups. Flow cytometric analysis of the liver tissue showed depletion of KCs and infiltration of monocytes and monocyte-derived macrophages (MoMFs), confirming previous literature, and the presence of monocyte-derived KCs (MoKCs) in both models. DT-mediated KC ablation at the initiation stage of HCC induction resulted in a decreased number of KCs and MoKCs at end-stage disease in fibrosis-associated HCC but not in the model of NASH-induced HCC. This altered hepatic macrophage pool composition was however not associated with significant changes in tumor burden, KC markers or inflammatory, angiogenic and fibrotic components of the tumor microenvironment (TME). In NASH-induced HCC, depletion of the KCs resulted in decreased hepatic expression of alpha-smooth muscle actin and vascular endothelial growth factor, however, no differences were detected on histology for tumor burden, steatosis, inflammation and fibrosis, substantiating the limited effect of KC depletion in the initiation phase of HCC pathogenesis.

**Conclusion:** Despite the tolerogenic function of KCs in homeostasis and the reported role as early activators during inflammation, depletion of KCs during the initiation phase of HCC pathogenesis only has minor effects on the TME and does not affect disease severity or progression in HCC mouse models with different underlying backgrounds.

**FRI581**

**RELB activation drives tumour aggressiveness and predicts prognosis in hepatocellular carcinoma**

Luisa Nader1, Federico Nichetti2,3, Anna-Lena Scherr1, Christin Eissner1, Dirk Riddel4, Sarah Fritzschke4, Sofia Weiler5, Thomas Albrecht5, Annika Kessler1, Nathalie Schmitt1, Felix Korell5, Liangtao Ye1,2, Toni Urbanik1, Christoph Heilig5, Mohammad Rahbar5, Lydia Brandl6, Christoph Springfield1, Todd Longrich5, Henning Schulze-Bergkamen12, Dirk Jäger19, Stefan Fröhling7, Peter Schirmacher3,9, Beate Straub11, Achim Weber14, Mathias Heikenwälder1, Enrico de Toni15, Benjamin Goeppe1,11, Stephanie Roesler1,11, Kai Breuhahn5,11, Bruno Köhler1,11, National Center for Tumor Diseases (NCT) Heidelberg, University Hospital Heidelberg, Department of Medical Oncology, Heidelberg, Germany; 2Fondazione IRCCS Instituto Nazionale Dei Tumori, Medical Oncology, Milan, Italy; 3National Center for Tumor Diseases (NCT) and German Cancer Research Center (DKFZ), Computational Oncology, Molecular Diagnostics Program, Heidelberg, Germany; 4University Hospital Heidelberg, Institute of Pathology; Heidelberg, Germany; 5Ludwig-Maximilians-University Munich, Department of Internal Medicine II, Munich, Germany; 6German Cancer Consortium (DKTK), Heidelberg, Germany; 7NCT Heidelberg and German Cancer Research Center Heidelberg (DKFZ), Department of Translational Medical Oncology, Heidelberg, Germany; 8German Cancer Research Center Heidelberg (DKFZ), Division of Chronic Inflammation and Cancer, Heidelberg, Germany; 9Ludwig-Maximilians-University Munich, Medical Faculty, Institute of Pathology, Munich, Germany; 10University Hospital Heidelberg, Liver Cancer Center Heidelberg, Heidelberg.
Background and aims: Hepatocellular carcinoma (HCC) is the fourth leading cause of cancer death worldwide with increasing incidence rates. Better molecular understanding to identify prognosticators and tailored therapy are urgently needed. The canonical nuclear factor kappa B (NF-kappaB) signaling branch has been shown to play a role in chronic liver disease and hepatocarcinogenesis. However, the role of the non-canonical part with its key transcription factor RELB remains unclear.

Method: Three tissue microarrays (TMA) were immunohistochemically (IHC) stained for NF-kappaB signaling components including RELB and scored for intensity. The TCGA-LIHC cohort served as a third validation set, to comparatively analyze mRNA expression and protein activity as inferred by the VIPER algorithm. Patients were grouped in RELB high and RELB low (expression) and RELB active and RELB inactive (inferred activity). Kaplan-Meier method and Cox proportional hazard models were used for overall survival (OS) analysis. Gene Set Enrichment Analysis (GSEA) was performed on differentially expressed (DE) genes between RELB active and RELB inactive cases.

Results: A total of 1462 (TMA) and 371 (TCGA-LIHC) cases were included. RELB was nuclear enriched in HCC compared to control tissue (IHC score 1.2 vs 6.3, p < 0.0001). The increase of RELB activity correlated with tumor grading (control vs. G1: p = n.s.; control vs. G2: p = 0.0193; control vs. G3/G4: p = 0.0004). Patients with a high nuclear RELB expression score had poorer overall survival (OS) compared to those with low RELB expression score (p = 0.0333; HR 2.129; 95% CI = 1.087 to 4.17). In the TCGA-LIHC cohort, RELB active cases showed worse OS compared to RELB inactive ones (46 vs 81 months; HR 1.69; 95%CI = 1.20 to 2.39; p = 0.003). Through GSEA of DE genes and clustering of functional terms, RELB active tumors showed a significant enrichment of pathways related to cell proliferation, differentiation and metabolic disregulation.

Conclusion: Non-canonical NF-kappaB signaling drives hepatocarcinogenesis by inducing proliferation and tumor aggressiveness. Activation of its key transcription factor RELB is a prognostic factor for HCC, identifying patients with poor overall survival.
FR1583
Single cell RNAsequencing derived signature of hepatocyte de-differentiation predicts development of hepatocellular carcinoma in patients with liver cirrhosis

Mikhail Gromak1, Hendrik Luxenburger1, Tobias Böttler1, Robert Thimme1, Maike Hofmann1, Natascha Röhlen1, University Medical Center Freiburg, Department of Medicine II, Freiburg, Germany

Email: natascha.roehlen@uniklinik-freiburg.de

Background and aims: Hepatocellular carcinoma (HCC) represents a major complication of liver cirrhosis, occurring at a rate of 1–5% per year. Hepatocytes are believed to represent the origin of malignant transformation in HCC. However, the molecular events determining HCC risk are poorly defined accounting for absence of chemopreventive strategies. Frequent overexpression of immature liver progenitor cell or bile duct markers in HCC suggests de-differentiation of hepatocytes to be involved in its pathogenesis.

Method: Applying single cell RNAsequencing (scRNAseq) derived marker genes of mature hepatocytes, cholangiocytes and progenitor cells we aimed to characterize hepatocyte de-differentiation in liver transcriptome data from different cohorts of patients with chronic liver disease (Geo database: GSE33814, GSE15654, GSE10140). To assess whether hepatocyte-de differentiation can be investigated non-invasively, serum levels of individual markers were determined by enzyme-linked immunosorbent assay (ELISA) in a cohort of patients with liver cirrhosis with (n = 31) or without (n = 74) HCC development.

Results: Stratification of healthy liver scRNAseq data derived cell cluster marker genes (GSE124395) was used to generate a transcriptional signature of mature hepatocytes and bile duct-like cells. Gene set enrichment analysis (GSEA) of these scRNAseq derived signatures in liver tissue microarray data of patients with non-alcoholic steatohepatitis (NASH) and Controls suggested enrichment of bile duct-like cells in chronically diseased livers (GSE33814, n = 44, FDR < 0.001). Similar upregulation of progenitor markers on the single cell level in hepatocytes from cirrhotic livers (GSE136103, n = 5 donors) further support this enrichment to occur via de-differentiation of hepatocytes during chronic liver injury. Interestingly, transcriptional signatures of hepatocyte de-differentiation strongly correlated with risk of HCC development. Indeed, cirrhotic livers of patients with no HCC development within a follow-up period of >10 years showed enrichment of mature hepatocyte marker genes (GSE15654, n = 216, FDR < 0.001), while immature bile duct marker genes were strongly enriched in cirrhotic livers of patients with HCC de novo development or recurrence (GSE10140, n = 82, FDR < 0.001). Among the top markers of hepatocyte de-differentiation, we could identify MCAM or recurrence (GSE10140, n = 82, FDR < 0.001). Similar upregulation of progenitor markers on the single cell level in hepatocytes from cirrhotic livers (GSE136103, n = 5 donors)

Conclusion: Our results indicate hepatocyte de-differentiation to occur during chronic liver disease progression and serve as a putative risk factor for HCC development. Detectable serum levels of multiple markers of our scRNAseq derived signature raise the outlook for non-invasive assessment of hepatocyte de-differentiation and its associated clinical HCC risk.

FR1584
Detection of cholangiocarcinoma in mice with protease activity probes

Jesse Kirkpatrick1,2, Pinzhu Huang3, Yury Popov3, Sangeeta Bhatia1,2,4, Massachusetts Institute of Technology, Cambridge, United States; 2Koch Institute For Integrative Cancer Research, Cambridge, United States; 3Beth Israel Deaconess Medical Center and Harvard Medical School, Division of Gastroenterology and Hepatology, Boston, United States; 4Howard Hughes Medical Institute, Cambridge, United States

Email: jessekirk11@gmail.com

Background and aims: Patients with primary sclerosing cholangitis (PSC) are at a 400-fold increased risk of cholangiocarcinoma (CCA), and are thus subjected to regular screening with magnetic resonance cholangiopancreatography (MRCP) (Lazaridis et. al. 2016). Unfortunately, MRCP findings are nonspecific for CCA in the setting of biliary fibrosis, and even invasive endoscopic retrograde cholangiopancreatography with brush cytology and fluorescence in situ hybridization often fails to yield a definitive diagnosis (Barr Fritcher et. al. 2015). We have previously developed a novel class of diagnostic agents, activatable zymography probes (AZPs), analogous to immunofluorescence probes for protease activity, that can be used to visualize tumour-associated protease dysregulation in situ and in vivo (Soleimany and Kirkpatrick et. al. 2021). Upon proteolytic cleavage, these probes electrostatically bind to positively charged tissue domains, thereby tagging and labelling proteolytically active cells (Fig. 1A). Because matrix metalloproteases (MMPs), including MMP1 (Leelawat et. al. 2010) and MMP1 (Metzger et. al. 2012) have been shown to be dysregulated in CCA, we aimed to develop MMP-sensitive AZPs to enable the differential diagnosis of CCA and benign biliary fibrosis.

Method: We induced CCA tumour formation in Mdr2/-/- mice via hydrodynamic injection of sleeping beauty transposon-transposase plasmids encoding for Akt and Yap1 (Fig. 1B), and harvested livers of tumour-bearing and untreated Mdr2/-/- mice 5 weeks later. We then synthesized a panel of nine AZPs with peptide sequences designed to be cleaved by MMPs and applied them to fresh frozen liver tissue sections from CCA and Mdr2/-/- mice.

Results: We found that four AZPs, most notably AZP6, specifically bound to CCA tumours, and that this binding was significantly abrogated by pre-treatment with broad-spectrum protease inhibitors (p = 0.00015 for AZP6) (Fig. 1C, D). Furthermore, these four AZPs bound significantly less efficiently to fibrotic portal tracts of Mdr2/-/- mice (p = 4.9 × 10^-8 for AZP6) (Fig. 1C, D). Finally, we incubated a panel of recombinant MMPs, including the CCA-associated MMP1, with a quenched fluorescent version of the AZP6 peptide substrate and found it be efficiently cleaved (Fig. 1E).

Figure 1: Activatable zymography probes specifically label CCA tumours. A) Principle of AZP mapping method. B) Hydrodynamic injection of Akt and Yap1 plasmids. Immunohistochemical staining of tumour-bearing livers for Ck18 is shown below. C) Fluorescence microscopy images of AZP1/2/3/4/5 (AZPs) or CD68 (TAMs) stained cryosections from tumour-bearing (T) and control (C) livers. Scale bar = 100 μm. D) Quantiﬁcation of AZP1 staining. Each point represents one tumour (CCA) and (CCA + bile) or one portal tract (‘Tumour’; *** p < 0.001, **** p < 0.0001; by two-tailed test). E) A quenched fluorescent version of the AZP6 peptide substrate was incubated with MMP1, 3, or 12 and fluorescence fold change was measured by ﬂuorometry.
Conclusion: MMP dysregulation in a mouse model of CCA is detected by AZPs, enabling differentiation of benign and malignant biliary disease in situ. Our next steps will be to adapt these probes for in vivo administration and assess their ability to noninvasively distinguish biliary malignancy from fibrosis in mouse models of CCA.

FRI585
Critical investigation on the usability of hepatoma cell lines HepG2 und Huh7 as models for the metabolic representation of resectable hepatocellular carcinoma
Andrea Scheffschick1,2, Gerda Schicht1,2, Lena Seidemann1,2, Sebastian Sperling3, Julia Nerusch1,2, Natalie Herzog4, Jonas Babel5, Jan Küpper3, Daniel Seehofer1,2, Georg Damm1,2,1, Saxonia Incubator of Clinical Translation (SIKT), Leipzig, Germany; 1University Hospital, Department of Hepatobiliary Surgery and Visceral Transplantation, Leipzig, Germany; 2Charité University Medicine Berlin, Department of General, Visceral and Transplantation Surgery, Berlin, Germany; 3Brandenburg University of Technology Cottbus-Senftenberg, Faculty of Science, Senftenberg, Germany
Email: georg.damm@medizin.uni-leipzig.de

Background and aims: Changes in energy metabolism are a known feature of hepatocellular carcinoma (HCC). Therefore, addressing the energy metabolism in hepatoma cells as a potential treatment is work in progress. Here, we compared the hepatoma cell lines HepG2 and Huh7 with appropriate controls based on primary cells to evaluate their usability in HCC research.

Method: We isolated control primary human hepatocytes (PHHs) from resected livers from non-HCC patients and primary human hepatoma cells (PHCs) and corresponding PHHs (HCC-PHs) from HCC patients. As a model of proliferating PHHS we used Upcyte® hepatocytes (HepaF3 clone) generated by lentiviral transduction of PHHS with proliferation-inducing genes. Cell types were characterized for specific HCC markers, enzymes and signaling proteins of the energy metabolism on RNA, protein and functional level.

Results: The characterization for established HCC markers revealed that advanced PHCs are closely related to hepatoma cell lines Huh7 and HepG2 which showed lower expression in PHCs in comparison to hepatoma cell lines and PHHs. Hepatoma cell lines did not reflect anaerobic and fasting characteristics of PHCs. In line with that, clinical data of our donors indicated that their HCC were slowly growing tumors. In contrast, hepatoma cell lines showed similar metabolic characteristics to proliferating PHHs suggesting that the Warburg effect is a general feature of energy shortage in rapidly proliferating cells.

Conclusion: We show that HepG2 and Huh7 cells do not reflect the energy metabolism of PHCs. In particular anaerobic and fasting states of HCCs were not covered by cell lines under standard cell culture conditions.

FRI586
Different immunological microenvironment in patients with different cirrhosis etiology and hepatocellular carcinoma
Andrea Dalbeni1, Leonardo Natale1, Filippo Cattazzo1, Antonio Vella2, Marta Garbin3, Michele Bivliaquà3, Anna Mantovani1, Giovanna Zanoni2, Alfredo Guglielmi3, Michele Millela4, David Sacerdoti3, 1AOUI Verona, Medicine, Verona, Italy; 2University of Verona, Immunology Department, Italy; 3University of Verona, Surgery, Verona, Italy; 4Università of verona, Oncology, Italy
Email: andrea.dalbeni@aoavr.veneto.it

Background and aims: Hepatocellular carcinoma (HCC) is the second leading cause of cancer-related death. Most cases (90%) of HCC arise in the setting of a chronic liver disease. The advanced stages of HCC are amendable only to systemic treatment. Systemic therapy has been revolutionized by immune-based therapies. However, a recent meta-analysis of three randomized phase III clinical trials that tested inhibitors of PD-L1 or PD1 in more than 1, 600 patients with advanced HCC, revealed that immune therapy did not improve survival in patients with non-viral HCC. The aim of the study was to identify differences in immune cell population of patients with HCC, according to etiopathogenesis of cirrhosis, in order to identify different patterns that may be targeted for immunotherapy.

Method: We analyzed 50 leukocyte sub-populations, using flow cytometric technique, in a cohort of 111 consecutive HCC cirrhotic patients with different etiopathogenesis. Differences between groups were analyzed with the Mann-Whitney U test.

Results: We divided HCC patients with cirrhosis into five groups according to etiology of liver disease: alcoholic, viral (HCV/HBV), metabolic (NAFLD/NASH), overlap between etiological factors and other etiology. Leukocyte sub-populations were significantly different in two groups. Specifically in the group of alcoholic etiology there were increased levels of PMN (p < 0.01), monocytes (p < 0.01) and NKT cells CD57+RA- (4-8-) (p = 0.011), while in viral etiology group there were increased levels of CD57+RA- (4-8-) (p = 0.007) and T cell CD3+ (4-8-) (p = 0.009). No specific leukocyte subpopulation was significantly increased in the other groups, in particular in the metabolic one.

Conclusion: These data suggest that in liver disease with different etiopathogenesis there are different immunological microenvironments. Innate and innate-like cells are the principal regulators of immune response in alcoholic HCC, while adaptive immune system is predominant in viral etiology. This suggests that differences in cancer-mediated immune escape could explain the different response to immunotherapy and may be helpful in identification of responder patients to new HCC therapy.

FRI587
Cytokine levels and circulating DNA in plasma could be used as serological biomarkers of response to immunotherapy in hepatocellular carcinoma
Elena Vargas Accarino1,2, Monica Higuera1, Maria Bermúdez1,2,3,4, Monica Pons1,2,3,4, María Torrens1, Gloria Torres1, Marta Viã1, Francisco Rodríguez-Frias4,5, Xavier Merino6, Beatriz Minguéz1,2,3,4
1Liver Diseases Research Group, Vall d’Hebron Research Institute, Barcelona, Spain; 2Department of Medicine, Universitat Autònoma de Barcelona, Barcelona, Spain; 3Liver Unit, Vall d’Hebron University Hospital, Barcelona, Spain; 4CIBERehd, Instituto Carlos III, Barcelona, Spain; 5Biochemistry and Microbiology Department, Clinical Laboratories Hospital Universitari Vall d’Hebron, Barcelona, Spain; 6Radiology Department, Vall d’Hebron University Hospital, Barcelona, Spain
Email: bminguez@vhebron.net

Background and aims: Immunotherapy and, in particular, immune checkpoint inhibitors (ICIs) have revolutionized the therapeutic landscape for advanced hepatocellular carcinoma (HCC). As monotherapy, they have shown antitumor activity in a subgroup of patients and the combination of anti-PDL1 antibody (atezolizumab) and VEGF-neutralizing antibody (bevacizumab) have become treatment of choice in first-line. One of the unsolved challenges is to identify and validate predictive biomarkers of response to these treatments in patients with HCC. The objective of this study was to identify potential serological markers of response to ICIs.

Method: Prospective cohort of 21 patients treated with ICIs (Nivolumab monotherapy (n = 15), Atezolizumab/Bevacizumab combination (n = 5) and Durvalumab/Tremelimunab combination (n = 1)). Plasma samples were collected at the beginning of ICI treatment and after three months of treatment. Twenty-four inflammatory cytokine levels were analyzed by ELISA as well as the levels of circulating cell free DNA (cfDNA) and its percentage of TERT mutation by ddPCR, at baseline and at 3 months of treatment.

Results: 86% of the study patients were male, with a mean age of 72 years and 76% were BCLC-C at starting ICIs treatment. 48% presented progression (PD), 9% complete response (CR), 14% partial response
(PR) and 29% stable disease (SD) as best radiological response. The underlying liver disease in most cases was hepatitis C virus (HCV) infection (62%). Lymphocyte Activation Gene type 3 (LAG-3) levels measured 3 months after starting ICIs treatment were significantly higher in PD [median (IQR)] 231.4 pg/ml (2668.3) than in CR, PR SD (median [IQR] 126.7 pg/ml (245.5) (p = 0.031). Interleukin-21 (IL-21) levels after three months of treatment were significantly different between patients who presented the best radiological response at follow-up CR/PR (195.5 (159.9) pg/ml), SD (62.7 (29)) or PD (290.6 (686.9) pg/ml) (p = 0.05). The analysis of MCP-1 (monocyte chemotactic protein 1) also showed significantly different levels depending on the response to treatment (CR/PR or SD (3 pg/ml (2.9)) (p = 0.024). Changes in TERT mutation percentage after 3 months of treatment showed a trend to significance between patients experiencing PD and CR/PR/SD patients (p = 0.083).

Conclusion: Our findings suggest that LAG-3, IL-21 and MCP-1 levels depending on the response to treatment (CR/PR or SD) can be used as biomarkers of response in patients with advanced HCC. Validation studies are currently ongoing.

**FRI588**

**RuvBL1 haploinsufficiency improves mTOR-driven NASH-HCC development in mice**

Alice Guida1,2, Irene Simeone1,2, Simone Polvani1, Elisabetta Ceni1, Lucia Picariello1, Gabriele Dragoni1,2, Andrea Galli1, Tommaso Mello1, Mario Serio1

1University of Florence, Clinical and Experimental Biomedical Sciences
2University of Florence, Clinical and Experimental Biomedical Sciences “Mario Serio”, Florence, Italy; 3University of Siena, Genetics, Oncology and Clinical Medicine “GenOmeC” PhD programme, Siena, Italy Email: tommaso.mello@unifi.it

Background and aims: The AAA+ ATPase RuvBL1 participates in several cellular processes relevant to oncogenic transformation, including DNA repair, gene expression, telomerase complex assembly and mTOR pathway activity. RuvBL1 expression correlates with a worse prognosis in HCC patients, however its role in HCC is largely unexplored. We have previously demonstrated that RuvBL1 haploinsufficiency impairs insulin signalling affecting the PI3K/Akt/mTOR pathway in vivo. Considering the relevance of mTOR pathway hyperactivation in human HCC, we aimed to reduce mTOR-driven hepatocarcinogenesis by targeting RuvBL1 in Ptenhep+/− mice, a genetic model of NASH progression to HCC.

Method: Ptenhep+/− and Ruvbl1hep+/− mice were crossed to generate Ptenhep+/− Ruvbl1hep+/− mice. The impact of RuvBL1 haploinsufficiency on NASH development was assessed by histology at 12 weeks of age. Metabolic and inflammatory markers were evaluated by qPCR and IHC. mTOR pathway cascade was analysed by western blot of liver lysates.

HCC development was assessed in mice aged to 15 months by multiplicity evaluation of macroscopic tumours and by histological classification by Edmondson-Steiner grading system.

Results: Oil red, Sirius red histological stain and F4/80 IHC revealed a significant reduction of steatosis, fibrosis, and inflammation in Ptenhep+/− Ruvbl1hep−/+ compared to Ptenhep+/− at 12 weeks of age. Quantification of triglycerides extracts confirmed the reduced lipid content in Ruvbl1 haploinsufficient mice livers. Surprisingly, similar mRNA expression of mTOR-driven lipogenic targets was found in the two mice models. However, expression of Ppara and its target CPT1 was increased in Ptenhep+/−, Ruvbl1hep+/−, indicating a lipid-lowering action mediated by PPARalpha in this mouse model. Western blot revealed an increase of p-AMPK and p-RAPTOR protein levels in Ptenhep+/−, Ruvbl1hep−/+ suggesting a role of RuvBL1 at the interplay between mTOR and AMPK in hepatic lipid metabolism. Ptenhep+/−, Ruvbl1hep−/+ mice aged to 15 months developed significantly less macroscopic tumours, which resulted better differentiated and of lower grade than Ptenhep−/− ones. qPCR analysis showed a significant upregulation of key lipolytic genes, such as Cpt1a, Acadl, Acadvl and Ppara in Ptenhep+/−, Ruvbl1hep−/+ at 15 months of age.

Conclusion: Targeting RuvBL1 mitigates the NASH metabolic and tumorigenic phenotype driven by mTOR hyperactivation in Ptenhep+/− mice, likely promoting the switch from mTOR-driven lipogenesis to AMPK-induced fatty acid catabolism.

**FRI589**

**Cold shock protein YB-1 upregulates MDR1 transcription and thus contributes to chemoresistance against cisplatin treatment in cholangiocarcinoma**

Tao Lin1, Jonathan A. Lindquist2, Peter Rene Mertens2, Matthias Ebert3, Steven Dooley1, Jun Li4, Stefan Munker4, Honglei Weng1, UMM; 2uni-magdeburg; 3University Medical Center Hamburg-Eppendorf; 4LMU Email: steven.dooley@medma.uni-heidelberg.de

Background and aims: Cholangiocarcinoma is a liver cancer with high mortality. Chemotherapy with cisplatin or gemcitabine is currently the main approach to treat cholangiocarcinoma patients with advanced stage. However, efficiency of these drugs is poor due to chemoresistance. To date, detailed mechanisms underlying chemoresistance in cholangiocarcinoma are largely unknown. In this study, we demonstrate a crucial role for the cold shock protein Y-box binding protein-1 (YB-1) in cholangiocarcinoma chemoresistance to cisplatin.

Method: Expression of YB-1 was examined by immunohistochemistry in 28 cholangiocarcinoma patients receiving surgery. Among them, 10 patients underwent chemotherapy following operation. Functional studies on the YB-1 effects were performed in cholangiocarcinoma cell lines to delineate the underlying mechanisms.

Results: YB-1 expression in cancer cells, in particular in nuclei, was closely associated with survival of patients. From 10 patients receiving chemotherapy, 2 patients without YB-1 expression, but only 3 out of 8 patients with YB-1 expression survived a 5-year follow-up. In vitro, immunofluorescence staining showed that cisplatin administration induced YB-1 nuclear translocation. ChIP assays demonstrated YB-1 binding to the multidrug resistance gene MDR1 promoter prior to induction of gene expression. Impressively, administration of cisplatin significantly increased MDR1 promoter binding activity of YB-1. Functionally, knockdown of YB-1 by RNAi inhibited cancer cell proliferation and increased cisplatin-dependent apoptosis.

Conclusion: YB-1 nuclear expression plays a crucial role in cholangiocarcinoma chemoresistance to cisplatin treatment through upregulating MDR1 expression. YB-1 expression in cancer cells might be a useful biomarker to predict chemotherapy efficacy in cholangiocarcinoma. Further, disrupting YB-1 function in cholangiocarcinoma is a promising treatment approach in clinical practice.
**FRI590**

**Synergistic anti-tumor activity with a combination of anti-PD1 antibody and the cyclophilin inhibitor, rencofilstat, in the Hep53.4 fatty liver model of hepatocellular carcinoma**

Daren Ure1, Jack Leslie2, Bhavesh Varia3, Robert Foster1, Jelena Mann1, Derek A Mann2,3. 1Hepion Pharmaceuticals, Canada; 2Newcastle University, United Kingdom; 3Fibrofarm Ltd, United Kingdom

Email: dure@hepionpharma.com

**Background and aims:** Cyclophils are a class of protein folding and regulatory enzymes that have been shown in preclinical studies to contribute to progression of several types of cancer, including hepatocellular carcinoma (HCC). Immunomodulation is one of the many therapeutic activities ascribed to cyclophilin inhibition and was the rationale for investigating the clinical phase cyclophilin inhibitor, rencofilstat (CRV431), in combination with anti-PD1 in a murine orthotopic model of HCC.

**Method:** Murine Hep53.4 HCC cells were implanted into either normal livers or fatty livers of C57BL/6 mice. Fatty livers were generated by feeding mice a western diet with sugar water for 3 months prior to surgical Hep53.4 implantation. Treatments included rencofilstat by once-daily oral gavage and anti-PD1 IgG twice weekly, alone or in combination, starting 2 weeks post-implantation. Anti-cancer effects were assessed by measuring tumor volumes at Week 4 post-implantation, immunohistochemical tumor analysis, and mouse survival in additional cohorts of mice.

**Results:** Rencofilstat and anti-PD1 IgG treatments, alone or in combination, similarly decreased tumor growth in non-fatty livers by 76–83% over 2 weeks of treatment compared to vehicle treatment. Immunohistochemical analysis showed that rencofilstat and anti-PD1 independently doubled CD4 and CD8 lymphocyte infiltration into tumors. Additionally, rencofilstat decreased the number of tumor neutrophils by 55%, whereas anti-PD1 had no effect on neutrophil infiltration. In the fatty liver model, neither rencofilstat nor anti-PD1 alone produced statistically significant reductions in tumor growth, but the combination decreased tumor growth by 84% compared to 2 weeks of vehicle treatment. Survival analyses in separate cohorts in the fatty liver-HCC model mirrored the tumor measurements in that monotherapies had no effect on survival whereas rencofilstat plus anti-PD1 extended median survival time by 26%.

**Conclusion:** The different outcomes for fatty versus fatty liver HCC models align with previous reports stating that HCC in fatty livers is more resistant to immune checkpoint inhibitor therapy. Combination treatment with rencofilstat and anti-PD1 synergistically decreased tumor growth and extended survival time, which supports clinical investigation in HCC.

**FRI591**

**Rencofilstat, a pan-cyclophilin inhibitor, exerts diverse metabolic and transcriptional anti-tumor activities in a murine NASH-HCC model**

Daren Ure1, Joseph Kuo2, Winston Stauffer2, Lacey Haddon1, Patrick Mayo3, Robert Foster1, Philippe Gallay2. 1Hepion Pharmaceuticals, Canada; 2Scirps Research Institute, United States

Email: dure@hepionpharma.com

**Background and aims:** Cyclophils are protein folding and regulatory enzymes that have been shown in preclinical studies to contribute to progression of several types of cancer, including hepatocellular carcinoma (HCC). They are elevated in most types of cancer, and overexpression is prognostic of shorter survival. Current pharmacologic cyclophilin inhibitors exert anti-cancer activities but target multiple cyclophilin isoforms. The aim of the current study was to elucidate the predominant anti-cancer mechanisms of the pan-cyclophilin inhibitor, rencofilstat (CRV431), in an experimental murine HCC model.

**Method:** Rencofilstat was studied in a murine NASH-HCC model (streptozotocin + Western diet) characterized by a high mutational burden and spontaneous liver tumor development. Rencofilstat was administered by once-daily oral gavage from Weeks 20–30 following initiation of Western diet. Liver tumor and non-tumor tissue from vehicle-treated and rencofilstat-treated mice were analyzed by genomic, transcriptomic, and metabolomic methods.

**Results:** Once-daily, oral rencofilstat treatment decreased tumor burden at Week 30 by 50%. Whole exome sequencing of tumors and non-tumor liver tissue revealed a diverse repertoire of somatic mutations that far exceeded the mutation burden of human HCC tumors. This was accompanied by extensive dysregulation of metabolic and transcriptional processes, i.e. changes in approximately 25% of all metabolites and gene expression. Rencofilstat treatment produced many alterations of the metabolic and transcriptional signatures in tumor and non-tumor, NASH tissue consistent with anti-cancer effects. At a systems level, 47% of the differential metabolites and 59% of the differential gene expression in tumors were normalized by rencofilstat treatment to levels observed in nontumor specific. Metabolism-related effects of rencofilstat in tumors included normalization of the oncometabolite, fumarate, and the principal byproduct of methylation reactions, s-adenosylhomocysteine. At the transcriptional level, rencofilstat altered the expression of genes across a spectrum of cellular processes, including oncogetic signaling, cell cycle, cell death, unfolded protein responses, ubiquitination, and several metabolic processes. Noteworthy rencofilstat effects included attenuation of Wnt-β-catenin, Myc, C/EBPβ, Nupr1, Eif2ak3 (PERK), and Rac1.

**Conclusion:** The clinical phase drug candidate, rencofilstat, decreased tumor burden in an aggressive, hypermutated model of HCC, which was associated with a wide range of metabolic and transcriptional effects. These results suggest that pan-cyclophilin inhibition may be therapeutic across multiple tumor types in HCC or other cancers.
HCC mouse model is suitable for profiling novel drug therapies for tumor burden following extended GAN dieting. The GAN DIO-NASH-transcriptome signatures demonstrated enhanced fibrogenesis (col- (number of inflammatory foci, galectin-3), fibrosis (PSR, collagen steatosis (lipids, hepatocytes with lipid droplets), inflammation further highlighted by increased quantitative histological markers of and hepatic biliary/progenitor cells (CK19). Disease progression was increased quantitative histological markers of proliferation (Ki67), lin-stained fibers. Progressive HCC development was supported by architectural and cytologic features of HCC, notably loss of reticu-

Notably, advanced fibrosis (stage F3, bridging fibrosis) was observed discovering tumour specific TME features and pave way for the discovery of novel prognostic and therapeutic targets.

FR1593 Development of hepatocellular carcinoma in the extended GAN diet-induced obese mouse model of NASH with advanced fibrosis Andreas Nygaard Madsen 1, Denise Oró 1, Martin Rønn Madsen 1, Mogens Vyberg 2, Henrik B. Hansen 1, Michael Feigh 1, Gubra, Hørsholm, Denmark; 2Aalborg University, Center for RNA Medicine, Department of Clinical Medicine, Copenhagen, Denmark

Background and aims: Non-alcoholic steatohepatitis (NASH) predispose to the development of severe fibrosis and hepatocellular carcinoma (HCC). Preclinical animal models resembling NASH-driven HCC development are important tools for exploring novel pharmacological interventions for HCC. The present longitudinal study aimed to characterize disease progression in the extended GAN (Gubra-Amylin NASH) diet-induced obese (DIO) mouse model of NASH.

Method: Male C57Bl/6J mice were fed the GAN diet (40% fat, 22% fructose, 10% sucrose, 2% cholesterol) for up to 88 weeks (n = 12–15/ group). Disease progression in DIO-NASH mice was evaluated using the clinical NAFLD Activity Score (NAS) and fibrosis staging system, quantitative histology, macroscopic tumor evaluation and liver transcriptomics. Tumor histopathological classification was performed by an expert clinical pathologist.

Results: DIO-NASH animals demonstrated progressive NASH (NAS ≥5) and fibrosis (stage ≥F1) from 28 weeks of GAN diet feeding. Notably, advanced fibrosis (stage F3, bridging fibrosis) was observed ≥80% of animals from 48 weeks of GAN diet. Development of liver tumors was progressively observed with 100% tumor burden after 58 weeks of GAN diet-induction. Tumors demonstrated consistent architectural and cytoligic features of HCC, notably loss of reticulin-stained fibers. Progressive HCC development was supported by increased quantitative histological markers of proliferation (Ki67), and hepatic biliary/progenitor cells (CK19). Disease progression was further highlighted by increased quantitative histological markers of steatosis (lipids, hepatocytes with lipid droplets), inflammation (number of inflammatory foci, galectin-3), fibrosis (PSR, collagen 1α1), activated stellate cells (alpha-SMA). Finally, liver whole-tissue transcriptome signatures demonstrated enhanced fibrogenesis (collagens, matrix metalloproteins) and tumorigenesis activity (cell cycle control, growth factors).

Conclusion: DIO-NASH mice show advanced fibrosis and high HCC tumor burden following extended GAN dieting. The GAN DIO-NASH-HCC mouse model is suitable for profiling novel drug therapies for advanced fibrosing NASH-driven HCC.

FR1504 Non-canonical TGF-β signalling contributes to pro tumorigenic Smad3 linker phosphorylation in cholangiocarcinoma

Sophie Alex 1, Jan Albin 1, Diego F. Calvisi 2, Stefan Munker 3, Honglei Weng 1, Nuh N. Rahbari 4, Matthias Ebert 5, Anne DROPMANN 1, Steven DOOLEY 1, 1Medical Faculty Mannheim, University Heidelberg, Molecular Hepatology, Department of Medicine II, Mannheim, Germany; 2University Regensburg, Department of Pathology, Regensburg, Germany; 3Hospital of the University of Munich, Department of Medicine II, Munich, Germany; 4Medical Faculty Mannheim, University Heidelberg, Department of Surgery, Mannheim, Germany; 5Medical Faculty Mannheim, University Heidelberg, Department of Medicine II, Mannheim, Germany

Email: S.Alex@stud.uni-heidelberg.de

Background and aims: TGF-β signal transduction commences with receptor-mediated C-tail phosphorylation of Smad3, complex formation with Smad4 and nuclear translocation for cytostatic target gene regulation in epithelial cells. Regulatory phosphorylation steps at serine/threonine residues in the Smad linker (L) domain generate phosphorylated forms with mitogenic functions by interfering with transcriptional activity and proteasomal degradation. TGF-β signalling is impaired in several human tumors. We now show that in intrahepatic cholangiocarcinoma (iCCA) pSmad3L levels are increased and we aimed at identifying if this may facilitate tumorigenesis.

Method: We examined 180 healthy and tumorigenic liver tissues from iCCA patients for their Smad3 phosphorylation status, discriminating C-tail (S423 and S425)- and linker residues (S204 and S213), using immunoblotting, immunofluorescence and immunohistochemistry with Smad phosphorylation site-specific antibodies and correlated these with clinical data. For functional studies, we treated cultured iCCA cells with inhibitors for Smad3 and non-Smad TGF-β signalling pathways in combination with TGF-β1 stimulation and the chemotherapeutics Cisplatin, Gemcitabine, Doxorubicin and 5-FU, and tested chemosensitivity and proliferative activity.

Results: C-tail Smad3 phosphorylation was evident similarly in healthy and tumorigenic liver tissue samples. Elevated pSmad3L levels were exclusively present in tumour tissue with 86% of CCA samples showing increased pSmad3L S213 and only 5% being positive for pSmad3L S204. CCA cell lines show decreased pSmad3C and increased pSmad3L (S213 and 204) levels as compared to non-tumorous cholangiocytes which show strong pSmad3C and weak pSmad3L staining. Treatment with inhibitors indicate a counter regulation of C-terminal versus linker phosphorylation. Intrins pSmad3L (S204 and S213) is decreased by treatment with a GSK-3β inhibitor. In this setting, TGF-β1 leads to a stronger phosphorylation of Smad3C. When instead inhibiting ALK5, TGF-β1 treatment enhances nuclear pSmad3L. High pSmad3L and low pSmad3C levels result in enhanced proliferation and robust chemoresistance. Interfering with linker phosphorylation of Smad3 by targeting GSK-3β reduces proliferative activity and sensitized the cells for chemotherapy. MMP-9, p21 and c-Myc mRNA expression levels correlate with the respective proliferative activity.

Conclusion: pSmad3L (S204 and S213) phosphorylation is predominant in CCA tissue and interferes with cytostatic pSmad3C (S423/425) signaling in cultured iCCA cells, thereby facilitating proliferative activity and chemoresistance of cancer cells. Canonical ALK5/C-terminal Smad3 phosphorylation and non-canonical Smad3 linker phosphorylation are counterregulated in vitro. A similar scenario in patient samples is currently not confirmed and requires further studies.
**Background and aims:** It was found that secretory SCUBE3 protein is highly expressed in lung cancer and osteosarcoma, is associated with proliferation, invasion and metastasis of lung cancer cells and breast cancer cells. Therefore, the aim is to explore the clinical significance of SCUBE3 in HCC and the specific molecular mechanism of SCUBE3 on the biological function.

**Method:** TCGA database and IHC were used to detect the SCUBE3 of cancer and paracancerous. CCK8, Clone formation and cell elongation experiment were used to detect the regulation of SCUBE3 on the proliferation of hepatoma cells. The apoptosis and cell cycle after knockdown of SCUBE3 were detected by flow cytometry. Cell migration and invasion were detected by cell scratch and Transwell. The invasion and EMT markers were verified by confocal species assay was used to evaluate the effect of SCUBE3 on cell movement was observed by the RTCA system. ROS reactive oxygen species assay was used to evaluate the effect of SCUBE3 on cell adhesion. The xenograft tumour and metastasis model of liver cancer was constructed. The interacting proteins were verified by confocal and IP assay. TGF-β was added on the basis of knocking down SCUBE3, SCUBE3 recombinant protein induced EMT formation. The interaction between Sox9 and SCUBE3 was verified by Chip experiment.

**Results:** SCUBE3 in hepatocellular carcinoma was different from that in adjacent tissues (p = 0.017), and SCUBE3 was related to age and stage and grade of hepatocellular carcinoma. SCUBE3 knockdown inhibit the HCC cell proliferation and colony formation, migration and invasion. The apoptosis increased and the transformation of the cell cycle from the G1 phase to S phase inhibited in KD group. The degree of ROS in different cells was different. The lung metastasis model of liver cancer evaluated the regulative ability of SCUBE3 on the invasion and metastasis of liver cancer cells. The overexpression of metastatic tumors in the upper lung group was more than that in the control group. Akt and TGFβ were the pathways related to the regulation of hepatoma cell proliferation, metastasis and EMT β/Smad2/3 pathway. SCUBE3 and TGFβ R II has interaction. Smad2/3 pathway was also inhibited in KD group. VEGF, N-cadherin also increased, E-cadherin decreased and Smad2/3 expression increased when TGFβ was given in KD group. Sox9 and Runx1 were inhibited with SCUBE3 knockdown. The function of Sox9 was related to the prognosis of liver cancer. Chip experiment showed that there was SCUBE3 binding site in chromosome 1657–1665 region of Sox9 transcription factor.

**Conclusion:** TGF-β- Sox9-SCUBE3 axis regulates the Akt pathway and EMT to promote the proliferation, invasion and metastasis of HCC cells. SCUBE3 may become a new target for clinical diagnosis and treatment of HCC.

**Keywords:** SCUBE3, Signaling pathway, animal model, hepatoma cells, proliferation and metastasis.

---

**Inhibition of Wee1 induces antitumoral effects in preclinical models of hepatocellular carcinoma independently of p53 mutational status**

Julia Sophie Schneider1, Liangtao Ye1,2, Najib Ben Khaled1, Helke Hermanns1, Claude Haan3, Andreas Geier3, Enrico de Toni1, Florian P Reiter1. 1University Hospital, LMU Munich, Department of Medicine II, Munich, Germany; 2The Seventh Affiliated Hospital, Sun Yat-sen University, Center for Digestive Diseases, Shenzhen, China; 3University Hospital Würzburg, Division of Hepatology, Department of Medicine II, Würzburg, Germany; 4Faculty of Science, Technology and Medicine (FSTM), University of Luxembourg, Department of Life Sciences and Medicine (DLSM), Belvaux, Luxembourg

**Conclusion:** Wee1 inhibition induces antitumoral effects in HCC by induction of autophagy and impairment of cell cycle control. Further research should address the hypothesis that Wee1 mutational status and/or Wee1 protein expression may serve as biomarkers of response to Wee1 inhibition in systemic HCC treatment.
Extracellular concentration of nicotinamid adenine dinucleotide modulates CD203a on TH17 cells and is associated with recurrence of hepatocellular carcinoma

Felix Krenzien1, Julia Babigan1, Alexander Arnold2, Philipp Brunnauer1, Can Kamali1, Karl Hillebrandt1, Katrin Spilth1, Moritz Schmelzel1, Johann Pratschke1, Christian Benzing1, 1Campus Charité Mitte and Campus Virchow-Klinikum, Charité-Universitätsmedizin, corporate member of Freie Universität Berlin, Humboldt-Universität zu Berlin, and Berlin Institute of Health, Department of Surgery, Berlin, Germany; 2Charité-Universitätsmedizin, Corporate Member of Freie Universität Berlin, Humboldt-Universität zu Berlin, Institute of Pathology, Berlin, Germany

Email: felix.krenzien@charite.de

Background and aims: T helper 17 cells (TH17 cells) are a subtype of T helper cells that are involved in a number of pathological processes, one of them being the carcinogenesis of malignant tumors through the secretion of cytokines. Herein, we investigated the influence of extracellular nicotinamide adenine dinucleotide (eNAD⁺) on the ecto-nucleotide pyrophosphatase/phosphodiesterase 1 (CD203a, ENPP1 or PC-1) on Th17 cells with respect to the probability of HCC recurrence following liver resection.

Method: Heparinised blood plasma samples and liver specimen of 59 patients who underwent curative liver resection were compared with 10 control patients free of liver disease. The eNAD⁺ concentration of blood plasma was determined by a heat-based dichotomous pH extraction with a combined enzymatic cycling method. While fibrosis was histologically graded (Desmet score, F0–F4). Flow cytometry was used for cell analysis. Overall, an alpha value of p < 0.05 was applied.

Results: Plasma eNAD⁺ concentrations were significantly reduced with increasing liver fibrosis grade (p < 0.05). The expression of CD203a on CD4+, CCR4+, and CCR6+ T cells was found to correlate significantly with eNAD⁺ concentrations (p < 0.05). Patients with a postoperatively high proportion of CD203a expressing Th17 cells (CD4+, CCR6+, CCR4+) showed a 6-fold increased risk of HCC recurrence and a median recurrence-free survival of 233 days (p < 0.05), when compared to low expression CD203a Th17 cells (CCR6+, CCR4+). Similarly, patients with a postoperatively high proportion of CD203a expressing Th17 cells (CD4+, CCR6+) showed a 5-fold increased risk for recurrence and a median recurrence-free survival time of 334 days (p < 0.05), when compared to low CD203a expressing Th17 cells (CCR6+).

Conclusion: Our data show that eNAD⁺ decreases in patients with liver fibrosis/cirrhosis and also correlates with the expression of the ectoenzyme CD203a on TH17 cells. Moreover, the probability of recurrence was significantly increased in patients with high expression of CD203a on TH17 cells, suggesting their potential as valuable prognostic markers and, furthermore, future therapeutic targets.
~22 nucleotides. They play an important role in gene regulation and can exert tumor suppressive or oncogenic functions. p53 is known to regulate miRs in a range of cancer entities, but little is known about p63- and p73-dependent control of miRs in HCC. Aim of this study was to evaluate regulation of tumorsuppressive miRs by TAp63 and TA/DNp73 in HCC alone or in combination with HCC-relevant therapeutics.

Method: Hep3B cells were transduced with adenoviral vectors rAd-TAp63, -TAp73, -DNp73 or -GFP to induce expression of the respective p53 family member. (Non-)transduced cells were stimulated with different HCC therapeutics (Doxorubicin, Bleomycin, Regorafenib, Sorafenib, Tivantinib) for up to 72 hours. Expression profiles of tumorsuppressive miRs miR-34a, −145, −149, −192 and −194 were analyzed by RT-qPCR.

Results: Tivantinib induced an increase of all miRs analyzed in non-transduced Hep3B cells, with most effective induction of miR-34a and miR-145 (3.6×/7.4×), while other drugs had no effect. TAp63 transduction moderately increased miR-34a, −145, −192, and −194. TAp73 time-dependently induced miR-34a, −145 and −149, but had no effect on miR-192 and −194. Noteworthy, DNp73 did not induce any of the miRs, underlining the divergent functions of TA and DN isoforms. HCC therapeutics led to a moderate increase of all analyzed miRs in TAp63-transduced cells. In contrast, Tivantinib treatment highly increased (up to 15×) miR-34a, −145 and −149 in TAp73-transduced cells, whereas all other drugs resulted in induction rates of 4–8×. Importantly, in TAp73-transduced cells this reinforcing effect of Tivantinib also displayed a dose-dependency.

Conclusion: TAp63 and TAp73 regulate expression profiles of tumorsuppressive miRs and interact with HCC-relevant therapeutics to control miR expression profiles in HCC. In concordance with our previous data, DNp73 displayed divergent effects regarding miR regulation. Thus, specific combinations of p53 family members and HCC therapeutics—especially TAp73 and Tivantinib—have the capacity to reinforce tumorsuppressive miR expression. These findings provide novel knowledge to the complex network of p53 family-mediated tumor suppression and suggest novel therapeutic scope for the clinical management of HCC.

FR600

Trust your gut—a new direction in multikinase inhibitors therapy in hepatocellular carcinoma

Iuliana Nenu1, Diana Tudor1, Horia Stefanescu1, Bogdan Procopet1, Zeno Sparchez1, Gabriela Adrian Filip1, Iuliana Nenu1, Diana Tudor1, Horia Stefanescu1, Bogdan Procopet1, Zeno Sparchez1, Gabriela Adrian Filip1.

Background and aims: Hepatocellular carcinoma (HCC) has become a worldwide burden and its incidence is rising. The intestinal microbiota is responsible for inducing resistance to antitumoral drugs. The present study investigated the effects of the combined treatment of Regorafenib (Rego) and probiotic Streptococcus rhamnosus (Pro) on HCC bearing mice.

Method: We have induced cirrhosis and hepatocellular carcinoma on two-week Swiss male mice using diethylnitrosamine (DEN- 1 mg/kg) one intraperitoneal injection following carbon tetrachloride (CCL4-0.2 ml/kg) intraperitoneal administration two times per week for six weeks (between weeks 8 and 14). Abdominal ultrasound was performed to validate the presence of cirrhosis and liver tumors. Afterward, the mice were divided into four groups: in the first group (control group), the mice were treated with vehicle, the second group received Regorafenib (Rego) (10 mg/kg one time per day for one week), in the third group probiotic (100 mg/day for one week) was administered, and the last group received the combination of Rego and Pro. After the last treatment, liver and intestine fragments were taken for biochemical and histopathological analysis. Liver tumour and intestinal inflammation quantified by ELISA and western blot, oxidative stress and apoptosis markers, histopathological necrosis rate were assessed.

Results: IL-6 and IL-1 levels from both liver and intestine fragments decreased in the groups treated with probiotic compared to control but statistically insignificant (p>0.05). Similarly, malondialdehyde levels dropped when Pro was added to Rego (p<0.05). Tumor necrosis factor-alpha (TNF-α) and TLR-4 have a decreased levels in the combined regimen (p<0.05) and in the Rego group (p<0.05) when compared to the control group and correlate with the histological findings. Likewise, nuclear factor-kB (NF-kB) and IKKα expression decreased in the combined regimen. Intestinal inflammation assessed by determination of lipopolysaccharide (LPS) is reduced in the groups where probiotic was administered compared to the control and Rego group (p<0.05). In addition, inducible nitric oxide synthase (iNOS) expression evaluated in intestine homogenate diminished in Rego and Rego associated with the probiotic groups (p<0.05).
NAFLD: Experimental and pathophysiology

SAT001
The DNA damage response is involved in the metabolic dysregulation of MAFLD patients via inefficient fatty acid oxidation
Beatriz Gómez Santos 1, Idoia Fernández-Puertas 1, Ane Nieva-Zuluaga 1, Mikel Ruiz de Gauna 1, Maider Apodaka-Biguri 1, Francisco González-Romero 1, Diego Saenz de Urturi 1, Igotz Delgado 1, Igor Aurrekoetxea 1,2, Lorena Mosteiro González 2, Gaizka Errasti Olartekoetxea 2, Sonia Gaztambide 2, Luis A Castaño González 2, Luis Bujanda 3, Jesus María Banales 3, Ana Zubiaga 1, Xabier Buque 1, Patricia Aspichueta 1,2. 1 Faculty of Medicine and Nursing. University of the Basque Country UPV/EHU, Department of Physiology, Leioa, Spain; 2 Biocruces Bizkaia Health Research Institute, Barakaldo, Spain; 3 Biodonostia Health Research Institute-Donostia University Hospital, University of the Basque Country (UPV/EHU), Department of Liver and Gastrointestinal Diseases, San Sebastián, Spain; 4 Faculty of Science and Technology, University of Basque Country UPV/EHU, Department of Genetics, Physical Anthropology and Animal Physiology, Leioa, Spain
Email: patricia.aspichueta@ehu.eus

Background and aims: A feature of the metabolic associated fatty liver disease (MAFLD) is the imbalance between processes that regulate lipid input and output. A chronic lipid–rich environment alters the oxidative capacity of the mitochondria generating species involved in the DNA damage response (DDR). The DDR is linked to MAFLD and to E2F transcription factors; however, the effect that the DDR plays in the altered lipid metabolism of MAFLD and the E2F involvement are still unknown. Aims: 1) Evaluate if DDR could be involved in the metabolic dysregulation of MAFLD identifying the involvement of E2F1 and E2F2; 2) Elucidate if the metabolic dysregulation induced by the lipid-rich environment is exacerbated by the DDR.

Method: An obese patient cohort with liver biopsies was used. The activity of mitochondrial complexes, pH2AX (marker of DNA damage) and E2f1 and E2f2 activity of mitochondrial complexes, pH2AX (marker of DNA damage) were analyzed. A cohort of C57/BL6 mice of different ages was also used. E2f1 (E2f1−/−) and E2f2 (E2f2−/−) knockout mice and their controls, injected with diethylnitrosamine (DEN), were fed a high-fat diet (HFD-DEN) for 10 weeks to induce progressive MAFLD. In vitro, mouse primary hepatocytes were used.

Results: Liver pH2AX levels, increased in obese non-alcoholic steatohepatitis patients (NASH), correlated positively with metabolic features of worse prognosis. Mitochondrial activities were higher in NASH, mainly in those with increased DDR, in which liver triglycerides and diglycerides (DG) were higher; however, serum ketone bodies, an indirect marker of fatty acid oxidation (FAO), remained unchanged when compared with no-NASH patients, suggesting that the increased mitochondrial activity was not linked to increased FAO. In the mouse cohort, pH2AX levels also correlated with insulin resistance and liver DG content. Interestingly, E2f1−/− and E2f2−/− mice, protected from steatosis due to an efficient FAO activation, showed decreased pH2AX when treated with HFD-DEN. When hepatocytes were treated with the DDR inducers UV or H2O2, they were not able to catabolize the increased intracellular lipid levels when facing a lipid-rich environment. Finally, treatment with fatty acids alone was enough to activate DDR in hepatocytes.

Conclusion: DDR activation triggers metabolic changes related with mitochondrial dysfunction and facilitates lipid accumulation, both linked to disease progression. The results suggest that E2F1 and E2F2 might be intermediates promoting the DDR induced metabolic dysregulation.

SAT002
Hepatic miR-144 drives fumarase activity preventing NRF2 activation during obesity
Valerio Azzimato 2, Ping Chen 1, Emelie Barreby 1, Cecilia Morgantini 2, Laura Levi 1, Ana Vankova 1, Jennifer Jager 3, André Sulen 1, Marina Diotallevi 4, Joanne X. Shen 1, Ewa Ellis 2, Mikael Ryden 3, Erik Naslund 3, Anders Thorell 3, Volker Lauschke 2, Keith M. Channon 4, Mark J. Crabtree 3, Arvand Haschemi 10, Siobhan M. Craige 11, Marina Diotallevi 4, Joanne X. Shen 5, Ewa Ellis 6, Mikael Ryden 7, Erik Naslund 8, Anders Thorell 8, Volker Lauschke 9, Keith M. Channon 4, Mark J. Crabtree 3, Arvand Haschemi 10, Siobhan M. Craige 11, Mattia Mori 12, Francesco Spallotta 13, Myriam Aouadi 1, Center for Infectious Medicine, Medicine, Huddinge, Sweden; Karolinska Institutet, Medicine, Huddinge, Sweden; Université Côte d’Azur, Inserm, Centre Méditerranéen de Médecine Moléculaire (C3M), Team « Cellular and Molecular Pathophysiology of Obesity and Diabetes », Nice, France; John Radcliffe Hospital, University of Oxford, Medicine, Oxford, United Kingdom; Karolinska Institutet, Department of Physiology and Pharmacology, Stockholm, Sweden; Karolinska Institutet, Department of Clinical Science, Huddinge, Sweden; Karolinska Institute, Medicine, Huddinge, Sweden; Karolinska Institutet, Department of Physiology and Pharmacology, Stockholm, Sweden; University of Wien, Department of Laboratory Medicine, Austria; Virginia Tech, Human Nutrition, Food, and Exercise Department, United States; University of Siena, Department of Biotechnology, Chemistry, and Pharmacy, Italy; National Research Council (IASI-CNR), Institute for Systems Analysis and Computer Science “A. Ruberti,” Italy
Email: myriam.aouadi@ki.se

Background and aims: Oxidative stress is central in the development of obesity-associated metabolic complications, including insulin resistance and non-alcoholic fatty liver disease. We recently discovered that microRNA miR-144 regulates the master mediator of the antioxidative response, NRF2. Upon miR-144 silencing, NRF2 target genes were significantly upregulated, suggesting that miR-144 controls NRF2 protein expression and activity. Here we explored a mechanism whereby obesity-related increased miR-144 inhibited NRF2 activity regulating a tricarboxylic acid (TCA) metabolite, fumarate.

Method: Transcriptomic analysis in liver macrophages (LMs) of obese mice identified the immuno-responsive gene 1 (Irg1) as a target of miR-144. Irg1 catalyzes the production of a TCA derivative, itaconate, which inhibits succinate dehydrogenase (SDH). TCA enzyme activities and kinetics were analyzed after miR-144 silencing in obese mice and human liver organoids using single cell assay in situ and molecular dynamic simulations.
Results: miR-144 upregulation in obesity was associated with reduced expression of Irg1, which was restored upon miR-144 silencing in vitro and in vivo. Furthermore, miR-144 overexpression reduces Irg1 expression and the production of itaconate in vivo. In alignment with the reduction in Irg1 and itaconate levels, SDH activity was upregulated during obesity. Surprisingly, also fumarate hydratase (FH) activity was upregulated in obese livers, leading to fumarate depletion. miR-144 silencing selectively reduced the activities of both SDH and FH resulting in the accumulation of their related substrates succinate and fumarate. Moreover, molecular dynamics analyses revealed the potential role of itaconate as a competitive inhibitor of not only SDH but also FH. Combined, these results demonstrate that miR-144 inhibits the activity of NRF2 through decreased fumarate production in obesity.

Conclusion: miR-144 triggers hyperactivation of FH in the TCA cycle and consumption of its substrate fumarate, eventually inhibiting NRF2 activity. Therefore, herein we unraveled miR-144 immunometabolic role in obesity in the regulation of endogenous antioxidant response.

SAT003
TNFR1 inhibition reduces lipogenesis and improves insulin resistance and fibrosis in NAFLD
Katharina John1, Stephanie Liebig2, Silke Marhenke1, Heiner Wedemeyer1, Heike Bantel1.
1Hannover Medical School, Department of Gastroenterology, Hepatology and Endocrinology, Hannover, Germany
Email: bantel.heike@mh-hannover.de

Background and aims: Non-alcoholic fatty liver disease (NAFLD) shows an increasing prevalence and can result in the development of liver fibrosis/cirrhosis with associated complications. The molecular mechanisms of NAFLD progression remain largely unknown. TNFalpha has been implicated as an important mediator of NAFLD progression. TNF-mediated liver injury mainly occurs via TNFR1. We therefore investigated the role of TNFR1 signaling for development of steatosis, insulin resistance and fibrotic liver injury in NAFLD. TNFR1 inhibition might therefore represent a promising therapy for fibrotic NASH.

Conclusion: The results implicate an important role of TNFR1 signaling for development of steatosis, insulin resistance and fibrotic liver injury in NAFLD. TNFR1 inhibition might therefore represent a promising therapy for fibrotic NASH.

SAT004
Obesity alters the partitioning of glycerol metabolism pathways in NAFLD
Jack Carruthers1, Patricia Nunes1, Paul Driscoll2, Jim Ellis2, James Macrae2, Massimo Pazzini3, Dimitrios Anastasiou1. 1Francis Crick Institute, Cancer Metabolism Laboratory, London, United Kingdom; 2Francis Crick Institute, Metabolomics Science Technology Platform, London, United Kingdom; 3University College London, Institute of Immunity and Transplantation, United Kingdom
Email: jack.carruthers@crick.ac.uk

Background and aims: Circulating glycerol can originate from the diet and adipose tissue lipolysis, amongst other sources. Glycerol is metabolised by the liver and kidney, both of which express glycerol kinase, an enzyme that phosphorylates glycerol to produce glycerol 3-phosphate. Glycerol is a substrate for gluconeogenesis (GNG) and glycolysis, and can form the backbone of lipids such as triglycerides (TAG). It has been shown that glycerol supports augmented glucose production in type 2 diabetes and provides carbons for circulating TAGs in patients with non-alcoholic fatty liver disease (NAFLD). It is still unclear how glycerol metabolism is partitioned into downstream pathways as these pathological conditions develop. In this study we investigated how risk factors for NAFLD, such as age and obesity, affect the use of glycerol in hepatic glucose and lipid synthetic pathways whilst promoting NAFLD.

Method: C57BL/6j mice were fed either normal chow (NC) or a Western diet (WD) for 12, 25 or 50 weeks. Visceral adiposity and hepatic TAG content were evaluated by magnetic resonance imaging (MRI) and magnetic resonance spectroscopy (MRS). Hepatic insulin signalling was assessed by Western blotting. To measure the capacity of these animals to convert exogenous glycerol into glucose, glycerol tolerance tests were used. To understand whole-body and hepatic glycerol metabolism, mice were infused with 13C-glycerol and 13C-glucose tracers followed by metabolic analysis using gas chromatography-mass spectrometry (GC-MS) and nuclear magnetic resonance (NMR). Mass-isotopomer distribution analysis was applied to estimate the contribution of glycerol to GNG and TAG esterification.

Results: As expected, WD-fed mice had greater visceral adiposity and higher intrahepatic TAG content at all time points, consistent with the development of NAFLD. Whole-body glycerol turnover increased with age, particularly in WD-fed mice. After 50 weeks, WD-fed mice showed augmented glycaemia in response to a glycerol bolus compared to NC-fed animals. Also at 50 weeks, stable isotope tracing revealed that glycerol to glucose flux was higher in WD- than NC-fed mice. The flux of glycerol carbons into the TAG backbone was higher in WD- than NC-fed mice peaking after 25-50 weeks of diet. The proportionate contribution of glycerol to TAG was decreased in WD-fed animals. The transition of glycerol flux from TAG esterification to glucose production coincides with the development of changes in hepatic insulin signalling as judged by decreased PI3 K signaling.

Conclusion: Chronic exposure to a WD alters the partitioning of glycerol from TAG to glucose. This transition coincides with the onset of alterations in hepatic insulin signalling. These observations present the possibility that glycerol metabolism could be targeted to alter the pathogenesis of obesity-related NAFLD and insulin resistance.
**Background and aims:** Non-alcoholic fatty liver disease (NAFLD) is one of the most common chronic liver diseases worldwide, but its pathophysiology is not fully understood due to the complexity of the mechanisms involved in the disease. Moreover, pharmacological therapy for NAFLD is not yet available. We investigated therapeutic potential of induced pluripotent stem cell-derived mesenchymal stem cells (iPS-MSCs) on hepatic steatosis and mitochondrial oxidative function.

**Method:** HepG2 cells were treated with palmitic acid (PA) and then co-cultured with iPS-MSCs. Intracellular lipid accumulation was measured by oil red O staining. The mitochondrial oxidative function was assessed by quantifying mitochondrial mass and measuring reactive oxygen species (ROS) and activity of antioxidant enzymes. C57BL/6 mice were chronically fed with choline-deficient, L-amino acid-defined, high-fat diet (CDAHFD). At week 20, mice were injected with either phosphate-buffered saline (nontransplanted) or iPS-MSCs (transplanted: 1 × 10⁶ cells). Four weeks later, liver histology and function were assessed.

**Results:** PA-induced intracellular lipid accumulation was attenuated when co-cultured with iPS-MSCs (Figure 1A). The functional mitochondrial mass was reduced by PA treatment and then was restored following co-culture with iPS-MSCs (Figure 1B). Increased cellular ROS production by PA treatment was attenuated after co-culture with iPS-MSCs. The activity of superoxide dismutases (SODs) and the ratio of reduced/oxidized glutathione were decreased by PA treatment and then were restored by co-culture with iPS-MSCs. After infusion of iPS-MSCs, a successful engraftment of transplanted stem cell was confirmed, leading to amelioration of severe hepatic steatosis in CDAHFD-fed mice (Figure 1C). Decreased mitochondrial DNA content in CDAHFD-fed mice was reinstated to near-control level after transplantation of iPS-MSCs. Augmented hepatic ROS accumulation caused by CDAHFD was attenuated after transplantation of iPS-MSCs with dynamic changes in the activity of SODs and the ratio of glutathione.

**Conclusion:** Hepatic steatosis and mitochondrial oxidative dysfunction in NAFLD can be ameliorated by transplantation of iPS-MSCs. Our study findings suggest the therapeutic potential of iPS-MSCs in NAFLD and help understanding alterations in hepatic lipid metabolism, which may be restored by iPS-MSCs transplantation.
SAT007
Patient-derived liver organoids to reveal PNPLA3 I148M role in Non-alcoholic Fatty Liver Disease
Elia Casirati1, Alessandro Cherubini2, Melissa Tomas1i, Ilaria Marin2, Daniele Prati3, Daniele Dondossola3, Luca Valentl1,2, 1Università degli Studi di Milano, Department of Pathophysiology and Transplantation, Italy; 2Fondazione IRCCS Ca’ Granda Ospedale Maggiore Policlinico, Transfusion Medicine and Hematology, Milano, Italy; 3Fondazione IRCCS Ca’ Granda Ospedale Maggiore Policlinico, General and Liver Transplant Sugery Unit, Milan, Italy
Email: e.casirati@gmail.com

Background and aims: Non-alcoholic fatty liver disease (NAFLD) heritability is estimated to be within 25–75% and PNPLA3 rs738409 C > G, encoding for the p.I148M protein variant, accounts for a large fraction of disease susceptibility. The p.I148M variant promotes intrahepatic lipid accumulation and progression to advanced fibrosis and hepatocellular carcinoma. A comprehensive human model to study the role and mechanisms of genetic variability in liver disease is still lacking. Aim of this study was therefore to generate patient-derived human liver organoids (HLOs) to clarify the impact and role of PNPLA3 variation in NAFLD onset and progression.

Method: We isolated HLOs from 14 surgical resection specimens. PNPLA3 rs738409 was genotyped by 5′ nucleic Taqman assays. Single cells were embedded in Matrigel and a complete organoid medium to instruct signaling cues crucial for the growth of liver epithelial cells. To model fatty liver, HLOs were differentiated toward a hepatocyte-like phenotype (modified from Broutier L, Nat Protoc 2016) and exposed to free fatty acids (FFAs, 300/300 uM palmitic/oleic acid) for 5 days.

Results: We successfully isolated, grew for >150 days and biobanked organoids with different PNPLA3 p.I148M genotypes (7, 1% were CG, 42, 8% were CG, 50, 1% were CC). HLOs showed a monolayer epithelial phenotype with a well-defined apical-basal polarity surrounding a central hollow lumen, and a cholangiocyte-like phenotype expressing KRT19 and SOX9. Differentiated HLOs showed high levels of hepatocyte markers mRNA (albumin, CYP2D6 and ApoA1, Fold Increase 85.8, p = 0.0307; 1.27, p = ns and 324.8, p = 0.0035 respectively; n = 5), while the epithelial staminal marker LGR5 was suppressed. The persistent expression of KRT19 suggests the presence of both hepatocellular and cholangiocyte populations, both involved in fibrogenesis. HLOs showed a high expression of PNPLA3 after isolation, which was maintained after hepatocyte differentiation (0.41±0.1 fold compared to liver tissue). When exposed to FFAs, differentiated organoids showed an accumulation of lipid droplets, as examined by Oil Red O (ORO) staining (2.3 fold increase in organoid exposed vs. non-exposed).

Conclusion: We isolated, characterized and biobanked HLOs from 14 patients with different PNPLA3 genotypes, obtaining a 3D in vitro model to investigate NAFLD within a personalized medicine framework with high translational potential.

SAT008
Transcriptomic analysis confirms that PNPLA3 I148M variant is associated with impaired mitochondrial function and antioxidant response in 3D cultured human hepatic stellate cells and liver tissue of patients with NAFLD
Elisabetta Caon1, Maria Martins1, Kessarin Thanapirom1, Ana Levi1, Walid Al-Akkad1, Jeries Abu-Hanna2, Pernille Juhi1, Ida Villesen1, Diana Leeming1, Guido Alessandro Baselli4, Jan-Willem Taanman5, Michele Vaca6, Luca Valentl2, Stefano Romeo2, Giuseppe Mazza2, Massimo Pinzani3, Krista Rombouts1, 1University College of London, Royal Free Campus, Division of Medicine, Institute for Liver and Digestive Health, London, United Kingdom; 4University College of London, Royal Free Campus, Research Department of Surgical Biotechnology, Division of Surgery and Interventional Science, LONDON, United Kingdom; 5Nordic Bioscience, Biomarkers and Research A/S, Herley, Denmark; 2Universita' degli Studi di Milano, Fondazione IRCCS Ca’ Granda Ospedale Maggiore Policlinico, Department of Pathophysiology and Transplantation, Milan, Italy; 3University College of London, Queen Square Institute of Neurology, Department of Clinical and Movement Neurosciences, London, United Kingdom; 3University of Bari “Aldo Moro”, Clinica Medica “Frugoni”, Interdisciplinary Department of Medicine, Bari, Italy; 1University of Gothenburg, Institute of Medicine, Sahlgrenska Academy, Wllenberg Laboratory, Department of Molecular and Clinical Medicine, Gothenburg, Sweden
Email: e.caon@ucl.ac.uk

Background and aims: We established that the I148M variant of the patatin-like phospholipase domain-containing 3 (PNPLA3) protein, a key risk locus for fibrogenic progression of chronic liver disease, is associated with mitochondrial dysfunction and defective antioxidant response. The antifibrotic Nuclear Receptor 4A1 (NR4A1) is a key element in mitochondrial metabolism and antioxidant response. By employing transcriptomic analysis we investigated the impact of PNPLA3 I148M mutation on mitochondrial dysfunction, antioxidant response and NR4A1 expression in human hepatic stellate cells (hHSCs) and in an established cohort of patients with NAFLD. 3D culture models were employed to further validate the results.

Method: RNAseq was performed on primary hHSC genotyped for PNPLA3 (I148M) variants CG/GG and cultured on plastic. Biopsies from livers of 125 obese individuals classified as normal liver/simple steatosis/severe NAFLD were genotyped for PNPLA3 (I148M) variants CG/GG and RNAseq was performed. Cell behaviour of hHSCs CC/CG genotyped. The comparison high-resolution upregulated antifibrotic gene involved in mitochondrial function, antioxidant response and ECM remodelling, the activated upstream regulator TGFB1 and the target gene NR4A1. Analogous pathways were dysregulated in the analysis of a 700 gene panel in hHSCs CC/GG for PNPLA3 variants cultured in a 3D model of healthy and cirrhotic scaffolds. In particular, the “Oxidative stress” pathway was markedly upregulated by cirrhotic ECM compared to healthy ECM, and PRO-C1/PRO-C3 secretion was increased by TGFB1. The 3D model was used for further analysis: COX activity and expression, ROS scavenger CYGB gene expression and NRF2-repressor KEAP1 protein were significantly downregulated in CG–PNPLA3 hHSCs compared to CC–PNPLA3 hHSCs and in cirrhotic scaffolds. NR4A1 gene and protein expression were downregulated in CG–PNPLA3 hHSCs vs CC–PNPLA3 hHSCs in healthy scaffolds and by TGFB1 in cirrhotic scaffolds.

Conclusion: The PNPLA3 I148M variant in hHSCs is linked to disrupted mitochondrial function and antioxidant response. NR4A1, a TGFB1-regulated antifibrotic gene involved in mitochondrial...
metabolism, is downregulated in CG-PNPLA3 hHSCs. Importantly, these defects were maximized in a 3D model recapitulating the ECM microenvironment of cirrhotic human liver.

SAT009
HTD1801 (berberine ursodeoxycholate), a unique single molecule with multiple beneficial effects in metabolic and liver diseases
Meng Yu¹, Ru Bai¹, Xinxiang Fu¹, Zhaobin Chen¹, Weijian Liu¹, Leigh MacConell¹, ²HighTide Therapeutics USA, LLC, United States
Email: lmacconell@hightidetx.com

Background and aims: A number of chronic liver diseases remain without adequate therapy and may require treatment with multiple mechanisms of action. Ursodeoxycholic acid (UDCA) has been shown to have beneficial effects in some liver diseases primarily through choleretic and anti-inflammatory effects. Berberine (BBR) has a long history of use in traditional medicine, emerging as a novel therapeutic with metabolic, antimicrobial, and anti-inflammatory effects. HTD1801 is a new molecular entity consisting of a salt of UDCA and BBR (1:1 stoichiometry), offering the benefits of its parent compounds and novel effects derived from its unique molecular structure. It has been shown to be beneficial in human studies of hyperlipidemia, NASH and PSC.

Method: The physico-chemical properties of HTD1801, BBR and UDCA were compared via x-ray diffraction, Fourier transform infrared spectroscopy, melting point analysis, LogD evaluation, and solubility analysis using fasted and fed state simulated intestinal fluid (FaSSIF and FeSSIF). Efficacy was evaluated in a preclinical NASH model (golden hamsters fed a high fat diet, 8/group) after 6 weeks of daily treatment of HTD1801, UDCA, or BBR-chloride (BBR-CI).

Results: The crystal form of HTD1801 is a hemi-nonahydrate with a honeycomb-like 3-D structure distinct from BBR-CI and UDCA. HTD1801 has a lower melting point (∼120 °C) compared to BBR-CI (204–206 °C) and UDCA (200–205 °C). LogD profiles were substantially enhanced for HTD1801 across the pH range for BBR and at pH 6.5 for UDCA vs BBR-CI or UDCA alone. Dissolution in FaSSIF showed peak concentrations of BBR and UDCA from HTD1801 of ∼0.6–0.7 mg/ml in contrast to <0.2 mg/ml for BBR-CI and UDCA alone. Dissolution in FeSSIF showed peak concentrations of BBR and UDCA from HTD1801 of ∼0.3–0.35 mg/ml in contrast to <0.15 mg/ml for BBR-CI and UDCA alone. Studies in the NASH hamster model showed that HTD1801 at 200 mg/kg for 6 weeks significantly reduced ALT, AST, bilirubin, LDL-c and triglycerides (Table 1). Furthermore, significant histologic improvements were observed in Fibrosis and the NAS with HTD1801. In contrast, UDCA or BBR alone generally resulted in minimal changes in biochemical or histological parameters.

Table 1: Biochemical and Histologic Changes in Hamster Model of NASH After 6 Weeks of Treatment

<table>
<thead>
<tr>
<th>Group</th>
<th>ALT (IU/L)</th>
<th>AST (IU/L)</th>
<th>Total Bilirubin (μmol/L)</th>
<th>ALB (g/L)</th>
<th>Triglycerides (mmol/L)</th>
<th>Fibrosis Score</th>
<th>NAS Score</th>
</tr>
</thead>
<tbody>
<tr>
<td>Normal Control Group</td>
<td>39.4 ±13.4</td>
<td>60.0 ±24.9</td>
<td>0.80 ±0.1</td>
<td>1.44 ±0.2</td>
<td>1.4 ±0.2</td>
<td>0.1 ±0.1</td>
<td>0.5 ±0.5</td>
</tr>
<tr>
<td>Model Control Group</td>
<td>133.7 ±2153.0</td>
<td>278.8 ±425.3</td>
<td>3.26 ±0.9</td>
<td>1.9 ±0.9</td>
<td>3.8 ±0.2</td>
<td>2.0 ±0.0</td>
<td>1.1 ±0.6</td>
</tr>
<tr>
<td>HTD1801 210 mg/kg</td>
<td>44.0 ±34.7</td>
<td>1133.0 ±2153.0</td>
<td>0.08 ±0.03</td>
<td>1.1 ±0.02</td>
<td>2.13 ±0.04</td>
<td>1.3 ±0.05</td>
<td>0.7 ±0.05</td>
</tr>
<tr>
<td>UDCA 150mg/kg</td>
<td>92.1 ±431.3</td>
<td>28.5 ±47.3</td>
<td>1.7 ±0.6</td>
<td>3.8 ±0.5</td>
<td>2.2 ±0.2</td>
<td>1.8 ±0.2</td>
<td>3.9 ±0.6</td>
</tr>
<tr>
<td>BBR-CI 51.2mg/kg</td>
<td>595.5 ±580.7</td>
<td>250 ±238.6</td>
<td>2.25 ±0.5</td>
<td>6.5 ±1.2</td>
<td>3.7 ±0.4</td>
<td>2.3 ±0.1</td>
<td>8.3 ±0.3</td>
</tr>
</tbody>
</table>

Conclusion: These data show that HTD1801 has physico-chemical properties distinct from UDCA or BBR that provide improved dissolution and lipophilicity characteristics which may result in the beneficial effects seen in fibroinflammatory liver diseases.

SAT010
Metabolic, biochemical, histopathological and transcriptomic effects of long-acting FGF21 analogue in the GAN diet-induced obese and biopsy-confirmed mouse model of NASH
Malte H. Nielsen¹, ², Denise Oró¹, Henrik B. Hansen¹, Matthew Gillum², Michael Feigh¹, ³Gubra, Hørsholm, Denmark; ²University of Copenhagen, CBMR, Kbh N, Denmark
Email: mni@gubra.dk

Background and aims: Fibrolast growth factor 21 (FGF21) plays a central role in energy, lipid and glucose metabolism and has been demonstrated to reduce hepatic steatosis, inflammation and fibrosis in rodent models of NASH. The long-acting FGF21 analogue efruxifermin has in a recent phase 2 clinical trial (BALANCED) demonstrated promising efficacy for both NASH resolution and improvement in fibrosis stage as compared to placebo controls (Harrison et al. Nature Medicine, 2021). The present study aimed to evaluate the metabolic, biochemical and histopathological effects of the long-acting FGF21 analogue PF-05231023 in the GAN (Gubra-Amylin NASH) diet-induced obese (DIO) mouse model of NASH with hepatic fibrosis.

Method: Male C57BL/6j mice were fed the GAN diet high in fat, fructose and cholesterol for 34 weeks prior to study start. Only animals with liver biopsy-confirmed NAFLD Activity Score (NAS) ≥5 and fibrosis (stage ≥F1) were included and stratified into treatment groups. DIO-NASH mice received (SC, BIW) vehicle (n = 14) or PF-05231023 (10 mg/kg, n = 14) for 12 weeks. Vehicle-dosed chow-fed C57BL/6j mice (n = 6) served as lean healthy controls. Pre-to-post liver biopsy histopathological scoring was performed for within-subject evaluation of NAS and Fibrosis Stage. Terminal quantitative liver histology, liver whole-transcriptome analysis, blood and liver biochemistry were assessed.

Results: The long-acting FGF21 analogue induced a body weight loss of approx. 8% from baseline and reduced hepatomegaly, plasma transaminases as well as plasma/liver lipids (total cholesterol, triglycerides) as compared to vehicle-treated animals. Notably, PF-05231023 treatment demonstrated ≥2 point significant improvement in NAS and 1-point significant improvement in Fibrosis Stage. Therapeutic effects of PF-05231023 were supported by reduced quantitative histological markers of steatosis (lipsid, hepatocytes with lipid droplets) and inflammation (number of inflammatory foci, galectin-3). FGF21 did not improve histomorphometry markers of fibrosis (PSR, collagen 1α1), albeit a marker for activated stellate cells (α-SMA) was significantly reduced, suggesting attenuation of fibrogenesis activity. Finally, PF-05231023 improved NASH-associated transcriptome signatures, including lowered expression of hepatic genes associated with inflammation and fibrogenesis.

Conclusion: Long-acting FGF21 analogue PF-05231023 improved metabolic, biochemical and liver histological markers of steatosis, inflammation and fibrogenesis in biopsy-confirmed DIO-NASH mice. Consistent with clinical findings, PF-05231023 improved NAS and Fibrosis Stage. These findings further validate clinical translatability of the GAN DIO-NASH mouse model.
SAT011
NAFLD-induced encephalopathy is associated with low-grade brain tissue hypoxia and inflammation, as well as cerebrovascular, glial, metabolic and behavioural alterations
Anna Hadjihambi1,2,3, Christos Konstantinou2,3, Jan Klohs4,5, Patrick Hosford6, Adrien Le Guennec7, I. Jane Cox2,3, Rajiv Jalan8, Salvatore Lecca9, Chris Donnelly1,10, Luc Pellerin1,11.
Department of Biomedical Sciences, Lausanne, Switzerland; 2Foundation For Liver Research, The Roger Williams Institute of Hepatology, London, United Kingdom; 3KCL, Faculty of Life Sciences and Medicine, United Kingdom; 4University of Zurich and ETH Zurich, Institute for Biomedical Engineering, Switzerland; 5University of Zurich and ETH Zurich, Neuroscience Centre Zurich, Switzerland; 6University College London, Neuroscience, Physiology and Pharmacology, United Kingdom; 7KCL, NMR Facility, United Kingdom; 8UCL, Institute for Liver and Digestive Health, United Kingdom; 9UNIL, The Department of Fundamental Neuroscience, Switzerland; 10UNIL, Institute of Sports Science, Switzerland; 11Université et CHU de Poitiers, Inserm U1082, France
Email: ucbthad@ucl.ac.uk

Background and aims: Over the last decade, non-alcoholic fatty liver disease (NAFLD) has become increasingly known as a multisystem disease, with its clinical burden not only confined to liver-related morbidity and mortality. Indeed, the most common liver-related complication of NAFLD over a long period of follow-up is encephalopathy. To confirm this, using a mouse model of NAFLD, we investigated alterations in cerebral physiology, metabolism and behaviour.

Method: Behavioural tests were performed in mice (C57BL/6) following 16 weeks of control diet or high fat diet+high fructose/glucose in water (HFDHF/HG). Cerebral blood volume (CBV; indicator of vascular density), brain tissue oxygenation at baseline and in response to systemic hypercapnia (10% CO2) were monitored under anaesthesia by optoacoustic tomography and optical fluorescence. Cerebral blood flow (CBF) was measured via arterial spin labelling MRI and blood pressure [BP] was monitored via a catheter under anaesthesia. Neuronal activity was assessed by in vivo electrophysiology. Cortical mitochondrial respiratory capacities (via oxygen consumption) and brain metabolite and lipid concentrations were measured by high-resolution respirometry and NMR spectroscopy respectively. Meso scale discovery and qPCR were used to evaluate plasma and cortical cytokines. Brain inflammation was further assessed by microglial (Iba-1) and astrocyte (GFAP) immunofluorescence. Liver steatosis was confirmed by histology.

Results: Mice with NAFLD exhibited: an anxiety and depression-related behaviour, but preserved learning and memory lower brain oxygenation attributed to the decreased CBV, brain inflammation, and cortical microglial and astrocytic alterations (increased number, % area covered and volume of cells), which led to elevated oxygen consumption increased lipid concentrations, but a decrease in some metabolites preserved cerebrovascular reactivity, neuronal activity and CBF compensated by the elevated BP.

Conclusion: This study provides evidence indicating a key role of NAFLD in inducing brain dysfunction likely due to the development of low-grade brain tissue hypoxia and inflammation, as well as cerebrovascular, glial, metabolic and behavioural alterations. Such chronic effects are expected to worsen with disease progression, leading to a NAFLD-induced encephalopathy, while increasing patients’ risk for neurodegenerative conditions, such as Alzheimer’s disease, that share the above pathophysiological mechanisms.

SAT013
Targeted metabolomics reveals alterations in one-carbon metabolism in NAFLD patients
Mikkel Werge1, Adrian McCann2, Elisabeth Galsgaard3, Dorte Holst3, Anne Bugge2, Lise Lotte Gluud1, 1Copenhagen University Hospital Hvidovre, Gastro Unit, Denmark; 2Bevital AS, Norway; 3Novo Nordisk A/S-site Måløv, Måløv, Denmark
Email: mikkel.parsberg.werge@regionh.dk

Background and aims: One-Carbon Metabolism (OCM), represents the convergence of numerous metabolic pathways including homocysteine metabolism, glutathione biosynthesis, folate and methionine cycles, transsulphuration pathway, and the choline oxidation pathway. Several mechanisms such as hepatic lipid homeostasis and oxidative stress may link OCM to non-alcoholic fatty liver disease (NAFLD). We aimed to investigate biomarkers and related B-vitamin cofactors coupled to OCM in NAFLD.
Method: This prospective study included 100 patients with histologically verified NAFLD and 50 age and sex matched healthy controls. Targeted metabolomic analyses were performed on fasting plasma samples using tandem mass spectrometry paired with gas or liquid chromatography, or microbiological assay to measure B-vitamin cofactors and metabolites relevant to OCM and glutathione production. RNA-sequencing was performed on 18 NAFLD liver biopsies with F0 to F4 fibrosis and 6 controls to measure expression levels of cystathionine β-synthase (CBS) and cystathionine γ-lyase (CSE).

Results: The included patients (50% with type 2 diabetes) had NAFLD with fibrosis score of F0 (n = 26), F1 (n = 25), F2 (n = 20), F3 (n = 12), and F4 (n = 17). Patients with NAFLD had higher BMI than controls (mean: 34.7 vs 26.6, p <0.0001). Cystathionine was increased in patients with advanced fibrosis (p = 0.006) and the GSG index (glutamate/(serine+glycine)), a proxy measure of glutathione synthesis, was increased in patients with NASH compared to those without NASH (p = 0.0003). Plasma concentrations of betaine and pyridoxal 5′-phosphate, the active form of vitamin B6, were lower in NAFLD patients compared to controls. Expression of CSE decreased with increasing fibrosis score (p = 0.0021).

Background and aims: We previously identified subsets of non-alcoholic fatty liver disease (NAFLD) patients with different metabolic phenotypes. Here we align metabolomic signatures with cardiovascular (CV) and genetic risk factors, and lipid lowering medication.

Method: We analyzed serum from an international cohort of 1143 individuals with biopsy-proven NAFLD using mass spectrometry and NMR based metabolomics. We further analyzed the metabolomes of four mouse models with impaired VLDL-triglyceride (TG) secretion (Mat1a-KO, 0.1MCD, Mttp-LKO, Tm6sf2-LKO), and one (Ldlr−/−.Leiden/high fat fed) with normal VLDL-TG secretion. We identified three metabolic subtypes (A, B, and C; 47%, 27%, and 26% respectively). Subtype A phenocopied the metabolome of mice with impaired VLDL-TG secretion; subtype C phenocopied Ldlr−/−.Leiden mice; subtype B showed an intermediate signature. Percentage of patients with NASH and fibrosis were comparably distributed among subtypes, although subtypes B and C exhibited higher ALT, AST, and GGT levels than subtype A. Serum VLDL-TG levels and secretion were lower among subtype A compared to the subtypes B and C. Subtype A VLDL-TG was independent of steatosis, whereas subtypes B and C showed a curvilinear relationship. Serum TG, cholesterol (Chol), VLDL, small dense LDL, and remnant lipoprotein Chol were lower among subtype A compared to subtypes B and C, while LDL-Chol-to-HDL-Chol ratio was similar. Subtype A associated with the TM6SF2 NAFLD risk allele, lower percent of patients with intermediate/high CV disease risk (Framingham risk score ≥10% at 10 years), and higher percent of patients with lipid lowering medication.
SAT015
Deletion of ATR in hepatocytes improves NAFLD features by increasing mitochondrial function
Maeva Saroul1, Pierre Cordier1, Christelle Kabore1, Romain Donné2, Ivan Nemazenny3, Fabienne Foufelle4, Pascale Bossard2, Chantal Deslouet3, 1Team Proliferation Stress and Liver Physiopathology, Centre de Recherche des Cordeliers, INSERM, Sorbonne Université, Université de Paris, Paris, France; 2ICahn School of Medicine at Mount Sinai, The Lujambio Lab, Oncological sciences, New York, United States; 3Platform for Metabolic Analyses, Structure Fédérative de Recherche Necker, INSERM US24/CNRS UMS 3633, Paris, France; 4Team Metabolic Diseases, Diabetes and Co-morbidities, Sorbonne Université, Université de Paris, Paris, France; 5Université de Paris, Institut Cochin, INSERM, CNRS, Paris, France
Email: maeva.saroul@inserm.fr

Background and aims: Chronic diseases such as obesity and diabetes are now considered as a social and economic burden. The liver is a central organ affected by these conditions resulting in a high level of fat accumulation, defined as Non-Alcoholic Fatty Liver Disease (NAFLD). Alarmingly NAFLD (steatosis) progresses pejoratively to Non-Alcoholic Steatohepatitis (NASH). NASH has the potential to progress to more severe stages as cirrhosis and hepatocellular carcinoma (HCC). The biological mechanisms underlying NAFL/NASH are not entirely understood. In various chronic liver diseases, aberrant DNA Damage Response (DDR) is a hallmark of disease aggravation. In NAFLD, DNA damage are present in human fatty livers and increase with disease progression. We previously showed that fatty hepatocytes division is associated with the activation of the DDR mediated by the kinase ATR. Whether ATR, per se, participates to Non-Alcoholic Fatty Liver Disease remains largely unknown.

Method: We used a hepatic- specific in vivo CRISPR/Cas9 approach using AAV vector, to generate ATRDeltap mice. C57BL/6J ATRDeltap and control (CTR) mice were fed a Choline-Deficient High-Fat Diet (CD-HFD) for 16 and 24 weeks. RNAseq analyses combined with molecular and cellular approaches have been performed on ATRDeltap and CTR NAFLD livers. Metabolic parameters have been investigated using Liquid Chromatography associated to Mass-Spectrometry. We also collected data on primary hepatocytes cultures isolated from our NAFLD models.

Results: Unexpectedly, silencing of hepatocyte ATR in murine models of NASH reduced hepatocyte proliferation and cell death. We show, in particular, a decrease in Caspase 8 and cleaved Caspase 3 activities that parallels with a marked increase in BCL2 expression. We also provide evidence that deletion of hepatic ATR improves fatty acid metabolism by regulating lipogenesis (e.g. Fas, ACC SREBP1C) and anti-oxidative response (e.g. NQO1, GSTM3, HO1). To go further, we isolated primary hepatocytes from our NAFLD mice models to assess the mitochondrial function. ATR deletion led to activation of mitochondrial respiration in steatotic hepatocytes with a partial restoration of mitochondrial capacities, an improvement of basal/maximal respiration, ATP production and attenuation of proton leak. Flux analyses demonstrated also that ATRDeltap hepatocytes increase their glycolysis capacities. Finally, we observe in NAFLD primary hepatocytes that ATR deletion increases the anti-oxidative defense against paraquat-induced oxidative stress.

Conclusion: Inhibition of ATR improves NASH features in CD-HFD fed mice, particularly by acting on mitochondrial function. This suggest that ATR might be a potential marker of mitochondrial dysfunction in NAFLD.
SAT017
Human Liver Organoids with myeloid lineages model the multicellular crosstalk in Non-Alcoholic Steatohepatitis
Milad Rezvani1,2, Kyle Lewis1, Kentaro Iwasawa2, Yuqi Cai1, Yuko Milfon1, Masaki Kimura4, Ranran Zhang2, Praneet Chaturvedi3, Takanori Takebe2,3,4,5,6,1 Charité Campus Virchow Clinic, Department of Pediatrics, Division of Gastroenterology, Nephrology and Metabolic Medicine, Berlin, Germany; 2Cincinnati Children’s Hospital Medical Center, Department of Pediatrics, Division of Gastroenterology, Hepatology and Nutrition, Cincinnati, United States; 3Cincinnati Children’s Hospital Medical Center, Division for Stem Cell and Organoid Medicine (CuSTOM), Cincinnati, United States; 4Cincinnati Children’s Hospital Medical Center, Division of Developmental Biology, Cincinnati, United States; 5Yokohama City University Graduate School of Medicine, Department of Regenerative Medicine, Yokohama, Japan; 6Tokyo Medical and Dental University, Institute of Research, Bunkyo City, Japan

Email: milad.rezvani@charite.de

Background and aims: Non-alcoholic Steatohepatitis (NASH) is characterized by hepatocyte injury due to lipotoxicity and inflammatory responses elicited by granulocytes and other myeloid immune cells. Developing therapies against NASH requires platforms modeling both processes. We previously described human liver organoids (HLOs) from induced pluripotent stem cells (iPSCs) recapitulating human hepatogenesis. In turn, studies demonstrated myelopoiesis in human fetal livers. We hypothesized that HLOs may recreate the complex fetal liver microenvironment to co-differentiate hepatocytes and myeloid lineages from iPSCs.

Method: We differentiated human iPSCs into gut spheroids via endoderm induction using activin A and Matrigel embedding. We analyzed HLOs via qRT-PCR, immunostaining, single-cell RNA sequencing (scRNAseq) and FACS. To generate HLOs with myeloid lineages (MyHLOs), we incorporated combinations of cytokines relevant to the differentiation of neutrophils, monocytes, macrophages, and Kupffer Cells.

Results: scRNAseq data from day 14 cultures revealed mesoderm, ectoderm and an immature hepatocyte population. We also identified a hemogenic endothelial population as putative source of myelopoiesis. We trialed basic myeloid differentiation, added IL-3, followed by GM-CSF and M-CSF, and found abundant macrophages by Giemsa stain. We diversified the myeloid cell subsets using defined cytokine and small molecular cocktails and completed the differentiation protocol with G-CSF. On day 30, we identified via Giemsa stain neutrophils, macrophages and their progenitors. We singularized MyHLOs and isolated CD45+CD14-CD16+CD66b+ Neutrophils that phagocytosed at similar levels but migrated faster than primary adult neutrophils, macrophages and their progenitors. We singularized MyHLOs and isolated CD45+CD14-CD16+CD66b+ Neutrophils that phagocytosed at similar levels but migrated faster than primary adult neutrophils. We transferred these MyHLOs into bone marrow-depleted mice modeling sinusoidal obstruction syndrome using Busulfan and Monocrotaline, respectively. Transplanted mice suffered from exacerbated liver injury with neutrophil-infiltrated necrotic foci. Next, we isolated from MyHLOs monocytes that predominantly expressed CD45+CD14+CD16+ with a CD163+ macrophage subset (12%).

Hepatocytes in MyHLOs were immature relative to HLOs by Albumin secretion and CYP3A4 activity. To develop an appropriate NASH model, we defined a hybrid media restoring mature secretary and metabolic function and allowing continued myelopoiesis. We added Palmitic Acid to MyHLOs and detected neutrophil-extracellular traps and reactive oxygen species. This stress response could be alleviated by adding neutrophil or macrophage activation inhibitors, demonstrating cellular crosstalk.

Conclusion: We developed MyHLOs as a novel human liver organoid platform consisting of hepatocytes and syngeneic neutrophils, monocytes and macrophages, which allows to interrogate inter-lineage crosstalk in a human NASH model.

SAT018
Senescence, hand in hand with hepatic iron overload during the progression of NAFLD
Miren Bravo1, Jorge Simón1, Naroa Goikoetxea1, Sofía Lachiondo-Ortega1, Leire Egia-Mendikute2, Mate Maus3, Serena Pelusi1,4,5, Josep Amengual4, Ester Gonzalez-Sanchez2, Javier Vaquero3, Ruben Nogueiras3, Asís Palazón2, Luca Valentì3, Isabel Fabregat1, Manuel Serrano3,4,5, María Luz Martínez-Chantar5, CIC bioGUNE-Centro de Investigación Cooperativa en Biocicncias, CIBERehd, Liver Disease Lab, Dermo, Spain; CIC bioGUNE-Centro de Investigación Cooperativa en Biocicncias, Cancer Immunology and Immunotherapy Lab, Dermo, Spain; IRB Barcelona-Institute for Research in Biomedicine, Barcelona, Spain; Magiagalli Clinic IRCCS Cà Granda Foundation Ospedale Maggiore Policlinico, Department of Transfusion Medicine and Hematology-Translational Medicine, Milano, Italy; University of Milan, Department of Pathophysiology and Transplantation, Milano, Italy; IDIBELL Institut d’Investigació Biomèdica de Bellvitge, CIBERehd, TGF-β and Cancer Group, L’Hospitalet de Llobregat, Spain; CIMUS, University of Santiago de Compostela-Instituto de Investigación Sanitaria, CIBERObn, Department of Physiology, Santiago de Compostela, Spain; Catalan Institution for Research and Advanced Studies (ICREA); CIC bioGUNE-Centro de Investigación Cooperativa en Biocicncias, Liver Disease Lab, Dermo, Spain

Background and aims: Increased hepatic iron stores are observed in non-alcoholic fatty liver disease (NAFLD) patients. Its disturbed homeostasis may potentiate the onset and progression of the disease, increasing oxidative stress and altering lipid metabolism. Moreover, iron dyshomeostasis has been related to senescence, which in turn is involved in the development of chronic metabolic and inflammatory disorders. In this work, we aimed to study the implication of hepatic iron burden and its interrelationship with senescence in the context of NAFLD.

Method: First, a transcriptomic analysis in obese individuals was corroborated in three different diet-induced NAFLD mice models (high fat diet; choline-deficient high fat diet, and 0.1% methionine and choline-deficient diet, 0.1%MCD). In primary hepatocytes treated with methionine and choline-deficient medium (MCDM). Second, male C57BL/6 mice fed with 0.1%MCD were treated with deferiprone (1 mg/ml), an iron chelator, in drinking water.

Results: In 125 obese individuals (transcriptomic cohort), we found a direct correlation between histological NASH and both circulating and liver mRNA levels of ferritin (Ft). Moreover, tissue damage as well as Ft increase, positively correlated with the senescence marker p21 overexpression. In accordance, 0.1% MCDD fed mice, showed significantly increased iron levels both in...
liver and serum. Oral treatment with deferiprone significantly improved liver histopathology (steatosis, inflammation, fibrosis and ROS) and normalized liver-to-body weight ratio. A decrease in hepatic CD45 infiltrating cells was also observed by FACS, where B-cell, granulocyte and macrophage counts were diminished; and serum transaminase (ALT and AST) and iron levels were decreased. Primary hepatocytes isolated from treated mice showed reduced mitochondrial ROS generation (MitoSOX) and increased ATP production. Accordingly, succinate dehydrogenase (SDH) activity and fatty acid oxidation (FAO) were increased. In vitro, deferiprone avoided lipid accumulation in MCDM treated primary hepatocytes, also increasing FAO and SDH activity, and prevented mitochondrial membrane potential decrease. Finally, iron chelation decreased the expression of p21 both in vivo and in vitro. In the latter approach, moreover, senescence-associated beta-galactosidase activity was suppressed.

**Conclusion:** Our results demonstrate that cellular senescence goes hand in hand with hepatic iron accumulation during the progression of NAFLD. We prove that mitochondrial function recovery by deferiprone plays an essential role in ameliorating lipid metabolism, but also modulating immune response. This points out iron chelation as a potential drug for the treatment of NAFLD, a chronic disease with an increasing prevalence worldwide.

**SAT020**

Factors associated with increased gut permeability and severity of liver disease in diabetic patients with NAFLD

Robertta Forlano1, Benjamin H. Mullish1, Laura Martinez-Gil1, Jesus Miguens Blanco1, Tong Liu1, Evangelos Triantafyllyou1, Charlotte Skinner1, Mark Thursz1, Julian Marchesi1, Pinelopi Manousou1, Imperial College London, Department of Metabolism, Digestion and Reproduction, United Kingdom

Email: r.forlano@imperial.ac.uk

**Background and aims:** The disruption of the gut-liver axis represents a crucial step towards the development and progression of non-alcoholic fatty liver disease (NAFLD). We investigated gut permeability and factors associated with it in patients with type-2 diabetes mellitus (T2DM) screened for NAFLD in primary care.

**Method:** Consecutive patients with T2DM were screened for liver disease by bloods, ultrasound and liver stiffness measurement (LSM). Elevated LSM was defined as LSM>8.1 kPa. Faecal metabolites were measured by liquid chromatography-mass spectrometry. Microbiota composition was analysed by 16s rRNA gene sequencing, faecal cytokines by immunoassay. To assess gut-permeability, we set up an *in-vitro* model with monolayers of Madin-Darby canine kidney cells, whose permeability was estimated by trans-epithelial electric resistance (TEER) on epithelial volt/ohm meter. Faecal water (FW) was added to the model and TEER was measured across the monolayers at different time points. Experiments were replicated pre-treating FW with a cocktail of protease inhibitors. *E. faecalis* spent medium and phosphate-buffered saline (PBS) were used as positive and negative controls respectively.

**Results:** Three hundred patients were enrolled: 287 were included; 13 withdrew. Overall, 184 (73%) had NAFLD, 28 (10%) other causes of liver disease and 75 (26%) no liver disease. *Proteobacteria* were higher in those with normal liver, while *Firmicutes* and *Bacteroidetes* were less abundant in those with NAFLD and elevated LSM (n=17) compared to those with normal liver (n=17). An *Anaeroplasma ASV* was less abundant in NAFLD vs normal liver, while *Monoglobus ASV* was less abundant in NAFLD and elevated LSM vs NAFLD and normal LSM. Moreover, those with NAFLD and elevated LSM showed significantly lower levels of faecal IFN-gamma (p=0.02).

Stool samples were used in the model of gut permeability. Overall, FW from patients with NAFLD and elevated LSM caused the greatest change in the TEER vs those with normal liver. When inhibitors of bacterial proteases were added, the effect of FW on TEER was significantly weaker, suggesting a component of bacterial protease activity. In this sub-group of samples, faecal valerate was significantly lower in those with NAFLD and elevated LSM compared to normal liver (0.28 vs 0.47, p=0.007). Clinically, TEER correlated inversely with BMI (p=0.029) and waist circumference (p=0.019) and positively with LSM (p=0.009) and AST (p=0.036). No association was found with HbA1 or HOMA-index.
IRF3 is a transcription factor involved in the induction of inflammatory response. The aim was to validate these data and examine the role of IRF3 across the NAFLD spectrum.

**Method:** IRF3 rs141490768 C>T was genotyped in an independent Validation cohort of 241 patients with severe NAFLD, vs. 32, 537 controls from the GnomAD-NFE database without ExAC. In the overall cohort, we tested the enrichment in IRF3 rare variants (allelic frequency, AF <0.01) by ProxECAT (Proxy External Controls Association Test, accounting for differences in genotyping platforms) between 443 severe NAFLD cases compared to GnomAD-NFE (n = 64, 603). IRF3/pIRF3 immunohistochemistry (IHC) was performed in 16 NAFLD patients stratified by disease severity.

IRF3 transcriptional activity was assessed in 125 obese individuals severe NAFLD (transcriptomic cohort) by using virtual inference of protein activity by enriched regulon analysis.

**Results:** We confirmed an enrichment of rs141490768 in the validation (OR 5.84, 95%CI 1.4–24.1; p = 0.044) and in the overall cohort (OR 13.6, 95%CI 6.3–29.5; p = 1.5 × 10^-7). Furthermore, we detected an enrichment in IRF3 rare variants in patients with severe NAFLD vs. controls (ratio of functional mutations to proxies 7.0 in cases vs 0.3 in controls; p = 1.2 × 10^-7).

IHC showed a progressive increase in nuclear pIRF3 staining in both hepatocytes and non-parenchymal cells with NAFLD severity (from normal liver to steatosis to NASH). Consistently, we observed increased expression of transcriptional targets (beta = 0.022 across disease severity; p = 0.013).

By using CRISPR/Cas9 genome editing in human HepG2 hepatoma cells, we generated IRF3-/-, IRF3-CL-, and rs141490768 knock-in clones to study the functional impact of IRF3 variation on inflammation and fibrogenesis in 3D multilineage spheroids with hepatocytes and stellate cells.

**Conclusion:** We found an enrichment of IRF3 rare variants in patients with severe NAFLD vs. controls. IRF3 activity was upregulated across the spectrum of NAFLD. Additional studies are required to uncover the mechanism underpinning predisposition to disease progression in carriers of IRF3 variants.

**SAT022**

Sex-dependent hepatoprotective role of IL-22 in NAFLD-related fibrosis

Mohamed Noureldin Hassan Ali Abdelanbi1, Manuel Flores Molina1, Genevieve Soucy1, Vincent Quoc-Huy Trinh1, Nathalie Bédard1, Sabrina Mazouez1, Jessica Dion1, Sarah Tran1, Marc Bilodeau1, Naglaa Shoukry2, Centre de Recherche du Centre hospitalier de l’Université de Montréal (CRCHUM), microbiologie, infectiologie et immunologie, Montreal, Canada; 3Centre de Recherche du Centre hospitalier de l’Université de Montréal (CRCHUM), pathologie et biologie cellulaire, Montreal, Canada; 4Centre de Recherche du Centre hospitalier de l’Université de Montréal (CRCHUM), Département de médecine, Montreal, Canada

**Background and aims:** Non-alcoholic fatty liver disease (NAFLD) is a major health problem with complex pathogenesis. The incidence and severity of NAFLD is higher in males than females but the mechanisms underlying this sex difference are not well understood. IL-22 is a pleiotropic cytokine that can be both protective and/or pathogenic during liver injury and inflammation. IL-22 was shown to be hepatoprotective in NAFLD-related liver injury. However, these studies relied primarily on exogenous administration of IL-22 and did not examine the sex-dependent effect of IL-22. Here, we sought to characterize the role of endogenous IL-22 signaling during NAFLD-induced liver injury in males and females.

**Method:** We used immunofluorescence (IF), flow cytometry, histopathological assessment and gene expression analysis to examine IL-22 production and characterize the intrahepatic immune landscape in human subjects with NAFLD (n = 20; 11 males and 9 females) and...
in an in vivo western high fat diet-induced NAFLD model in IL-22RA knock out (IL-22RA KO) mice and their wild type (WT) littermates.

**Results:** Examination of publicly available datasets from two cohorts with NAFLD demonstrated increased hepatic IL-22 gene expression in females as compared to males (p = 0.0327 and p = 0.0279, respectively). Furthermore, our IF analysis of liver sections from NAFLD subjects (n = 20) demonstrated increased infiltration of IL-22 producing cells in females (p = 0.0002). We validated the same observation in WT female mice with NAFLD (p = 0.0002). The lack of endogenous IL-22 signalling (IL-22RA KO) led to exacerbated liver damage, inflammation, apoptosis and liver fibrosis in female but not male mice with NAFLD.

**Conclusion:** Our data suggest a sex-dependent hepatoprotective antiapoptotic effect of IL-22 during NAFLD-related liver injury in females.

**SAT023**

Identification of novel targets in adipose tissue involved in non-alcoholic fatty liver disease progression

Marta Lopez-Yus1, Silvia Lorente-Cebrian2, Carlos Hörndler3, Almudena Sobrino-Prados3, Carmen Casamayor3, Alejandro Sanz Paris3, Vanesa Bernal Monterde3, Jose M Arbones Mainar1, 1Instituto Aragonés de Ciencias de la Salud, Zaragoza, Spain; 2University of Zaragoza, Zaragoza, Spain; 3Hospital Universitario Miguel Servet, Zaragoza, Spain

Email: jmarbones.iaacs@aragon.es

**Background and aims:** Obesity is a major risk factor for the development of non-alcoholic fatty liver disease (NAFLD) as dysfunction of subcutaneous adipose tissue (scWAT) may lead to fat accumulation in other organs. It is therefore essential to identify the molecular mechanisms underlying progression of the disease and the role played by the adipose tissue. Our main objectives were: 1) to identify new dysregulated genes in scWAT potentially involved in the development of NAFLD, 2) to establish an in vitro model of hMSC-derived adipocytes (hMSC) that could reflect the different stages of NAFLD, and 3) to validate the expression of selected genes in our in vitro model.

**Method:** Biopsies from the abdominal scWAT from 45 patients were obtained and their respective transcriptomes sequenced (RNAseq). Using a computational analysis, we obtained a set of genes upregulated in patients with elevated fatty liver index (FLI). The expression of those genes of interest were validated by qPCR in a different cohort of 50 patients. In this case, the expression in scWAT levels of the genes of interest were correlated with the NAFLD Activity Score (NAS) of liver biopsies. Lastly, hMSC were also isolated from scWAT of patients of this cohort and differentiated into adipocytes to establish an in vitro model that could reflect the different stages of NAFLD. Differentiation capacity of these hMSC was compared and expression of selected genes was measured by qPCR in hMSC-derived adipocytes.

**Results:** We observed reduced expression of the adipocyte differentiation marker FABP4 mRNA, as well as an impaired lipid accumulation, measured by oil red O stain, in hMSC-derived adipocytes of NAFLD patients (Figure 1A). Four genes, first identified in the RNAseq cohort and then confirmed by qPCR in the validation cohort, also showed a differential regulation pattern in hMSC-derived adipocytes, increasing their mRNA expression accordingly to the degree of hepatic steatosis: SOCS3, DUSP1, SIK1, and GADD45B (Figure 1B).

**Conclusion:** Our results constitute a proof-of-concept of the great importance of adipose-liver crosstalk and suggest that impaired adipogenic capacity of hMSC is a critical event in promoting the development of NAFLD. We propose four genes as key players in NAFLD progression.

**SAT024**

Isoleucine and valine correct hepatic lipid processing, reduce liver steatosis and suppress inflammation in obese mice with manifest NASH

Eveline Gart1,2, Wim van Duyvenvoorde1, Jaap Keijer2, Kanita Salic1, Martine C. Morrison1, Robert Kleemann1, 1TNO-Locatie Leiden-Gaubiusgebouw, Leiden, Netherlands; 2Wageningen University and Research, Wageningen, Netherlands

Email: Eveline.gart@tno.nl

**Background and aims:** Non-alcoholic steatohepatitis (NASH) is associated with disturbed liver lipid handling and excessive accumulation of hepatic fat. Branched-chain amino acids (BCAAs) may beneficially modulate hepatic lipids, however it remains unclear whether individual BCAAs can attenuate already established NASH.

**Method:** After 26 weeks of obesogenic diet (FFD) run-in, mice were treated with individual BCAA, valine or isoleucine (3% of FFD), for another 12 weeks and were then compared to FFD controls.

**Results:** Valine and isoleucine did not affect obesity and dyslipidemia compared to FFD, but significantly reduced hyperinsulinemia. Valine and isoleucine significantly reduced ALT, CK-18m30, and total liver steatosis. Microvesicular steatosis was strongly decreased, by 61% (valine) and 71% (isoleucine). Hepatic 4-hydroxynonenal (4-HNE), a marker for oxidative stress induced lipid peroxidation, immunoreactivity was significantly decreased with valine and isoleucine. Functional transcriptome analysis demonstrated an upregulation of BCAA metabolism genes (e.g. BCAT, PP1MK, BCKDHA), deactivation of lipid synthesis regulators (SREBF1, AGT, IGF1) and activation of regulators involved in lipid oxidation (AMPK, ACOX1, EHHADH) and mitochondrial biogenesis (PPARGC1a, CLUH). This correction of critical metabolic pathways by valine and isoleucine was accompanied by significantly decreased lobular inflammation, and suppression of FFD-stimulated inflammatory pathways controlled by IL-1b and TNFa.

**Conclusion:** The intervention with either valine or isoleucine corrected multiple lipid metabolism processes and reduced NASH-associated steatosis and inflammation which was substantiated by suppression of critical inflammatory pathways.
SAT025
Butyrate protects against diet-induced NASH and liver fibrosis and suppresses specific non-canonical TGFβ signaling in human hepatic stellate cells

Eveline Gart1,2, Wim van Duyvenvoorde1, Karin Toert1, Martien P.M. Caspers1, Lars Verschuren1, Aswin L Menke1, Roeland Hanemaaijer1, Jaap Keijer2, Kanita Salic3, Robert Kleemann1, Martine C. Morrison1. 1NO-locatie Leiden-Gaibusgebouw, Leiden, Netherlands; 2Wageningen University and Research, Wageningen, Netherlands

Email: Eveline.gart@tno.nl

Background and aims: In obesity-associated non-alcoholic steatohepatitis (NASH), persistent hepatocellular damage and inflammation are key drivers of fibrosis, which is the main determinant of NASH-associated mortality. The short-chain fatty acid butyrate can exert metabolic improvements and anti-inflammatory activities in NASH. However, its effects on NASH-associated liver fibrosis remain unclear.

Method: Putative antifibrotic effects of butyrate were studied in Ldlr-/-Leiden mice fed an obesogenic diet (HFD) containing 2.5% (w/w) butyrate for 38 weeks and compared to a HFD-control group. Antifibrotic mechanisms of butyrate were further investigated in TGF-β-stimulated primary human hepatic stellate cells (HSC).

Results: HFD-fed mice developed obesity, insulin resistance, increased plasma leptin levels, adipose tissue inflammation, gut permeability, dysbiosis and NASH-associated fibrosis. Butyrate corrected hyperinsulinemia, lowered plasma leptin levels and attenuated adipose tissue inflammation, without affecting gut permeability or microbiota composition. Butyrate lowered plasma ALT and CK-18M30 levels and attenuated hepatic steatosis and inflammation. Butyrate inhibited fibrosis development as demonstrated by decreased hepatic collagen content, αSMA and Sirius-red-positive area. In TGF-β-stimulated HSC, butyrate dose-dependently reduced collagen deposition and decreased procollagen1 stimulated primary human hepatic stellate cells (HSC).

Conclusion: Metabolic function of the hepatic tissue was compromised by NASH. The deficit was related to replacement of liver tissue with fat and in the more advanced disease of late NASH also to other structural changes. Total liver function was preserved, in the late NASH rats by the marked growth of fat-free liver mass. The mechanism behind this functionally compensatory liver growth is not known.

SAT026
Experimental non-alcoholic fatty liver disease causes regional liver functional deficits while total metabolic liver function is preserved

Peter Lykke Eriksen1, Karen Louise Thomsen1, Stephen Hamilton-Dutoit2, Hendrik Vlister1, Michael Soerenesen1,2,3,4. 1Aarhus University Hospital, Department of Hepatology and Gastroenterology, Aarhus, Denmark; 2Aarhus University Hospital, Institute of Pathology, Aarhus, Denmark; 3Viborg Regional Hospital, Department of Internal Medicine, Viborg, Denmark; 4Aarhus University Hospital, Department of Nuclear Medicine and PET, Aarhus, Denmark

Email: ple@clin.au.dk

Background and aims: The increasing incidence of non-alcoholic fatty liver disease (NAFLD) has imposed a need for understanding how the disease affects metabolic liver function. The aim of this study was to investigate in vivo effects of the structural liver changes on hepatic metabolic function assessed by the regional and total capacity for galactose elimination in a rodent model of diet-induced NAFLD of different stages.

Method: Sprague Dawley rats were fed a standard chow (control) or a high-fat, high-cholesterol diet for 1 (n = 8) or 12 weeks (n = 8), resulting in development of early and late NAFLD, respectively. In vivo liver metabolic function was assessed directly in the liver tissue by 2-[18F]fluoro-2-deoxy-D-galactose positron emission tomography. Post mortem liver tissue was used for autoradiography, histology and fat quantification.

Results: Early NAFLD livers had steatosis with 18 volume % fat. Late NAFLD livers had 32 volume % fat and showed features of non-alcoholic steatohepatitis (NASH) (inflammation, ballooning and fibrosis). Regional galactose metabolism was reduced in both early and late NAFLD with a median hepatic standard uptake value (SUV) of 9.8 and 7.4 (p = 0.02), respectively, compared to ~12.5 in controls. Results were confirmed by the autoradiography measurements. In early NAFLD the decreased SUV was explainable by the degree of fat infiltration. In late NAFLD, SUV was decreased beyond that attributable to fat, likely related to the structural NASH features mentioned. Still, in both groups total capacity for galactose elimination remained intact. In late NAFLD, there was an increase in fat-free liver mass to 21 g vs. 15 g in early NAFLD and control rats (p ≤0.002).

Conclusion: Metabolic function of the hepatic tissue was compromised by NASH. The deficit was related to replacement of liver tissue with fat and in the more advanced disease of late NAFLD probably also to other structural changes. Total liver function was preserved, in the late NAFLD rats by the marked growth of fat-free liver mass. The mechanism behind this functionally compensatory liver growth is not known.

SAT027
Hepatic lipid fingerprint reveals sex-dependent lipid droplet composition in metabolic associated fatty liver disease

Elisabet Rodriguez-Tomàs1, Gerard Baiges Gaya2, Helena Castañé2, Andrea Jiménez Franco3, Jordi Camps Andreu4, Jorge Joven Maitelli1, 1Universitat Rovira i Virgili, Medicine and Surgery, Reus, Spain; 2Institut d’Investigació Sanitària Pere i Virgili, Medicine and Surgery, Reus, Spain; 3Hospital Universitari Sant Joan de Reus, Reus, Spain

Email: elisabet.rodriguez@urv.cat

Background and aims: Metabolic Associated Fatty Liver Disease (MAFLD) is a spectrum of heterogeneous fatty-liver disorders that affects a quarter of the population. Despite new findings, there is no effective drug treatment and lifestyle interventions to address this disease in a long term. Nevertheless, lipid droplet accumulation is the onset of the natural course of MAFLD being lipid composition a necessary field to approach. In this context, phospholipids are the main constituents of the plasma membrane and changes in its composition are linked with the progression of this disease. How these changes affect women and men is an unsolved question. Thus, the purpose of the study was to identify changes in the lipid signature and phospholipid metabolism during liver disease progression as well as to observe the influence of the liver in the plasma lipidome of morbidly obese women and men.
Method: Liquid Chromatography coupled with Mass Spectrometry was used to perform a semi-targeted lipidomic in plasma and liver tissue from morbidly obese patients with non-alcoholic steatohepatitis (NASH) (men = 18; women = 34) and non-alcoholic fatty liver (NAFL) (men = 13; women = 38) who underwent bariatric surgery.

Results: Different lipome profiles between women and men were observed using linear discriminant analysis in plasma and liver tissue (A). Nevertheless, when the liver disease progress to NASH these sex differences disappear. In addition, we found changes in the lipides associated with hepatic lipid droplet. Concretely, we observed an impairment of triglycerides (TG) and an increase of cholesterol ester levels in both sexes (B). In opposite to liver findings, the plasma TG levels increased in women but not in men. Interestingly, women showed changes in the lipid droplet composition with a loss of polyunsaturated fatty acid (PUFA)-containing TG. In addition, we also observed a decrease in the phospholipid levels in both plasma and liver. Hepatic phosphatidylcholine/phosphatidylethanolamine (PC/PE) and ether-linked PC/PE molar ratio decreased, and fatty acid composition of phospholipids was less polyunsaturated in PC and sphingomyelin (SM) in women between NASH and NAFL. Instead, men did not show any significant difference.

Conclusion: Phospholipid metabolism and hepatic lipid droplet composition seem to be influenced by sex and plasma lipome seem to mimic the hepatic alterations.

SAT028
Lipidomics and proteomics reveal mitochondrial dysfunction in liver and visceral adipose tissue from patients with non-alcoholic steatohepatitis
Helena Castañé1, Andrea Jiménez Franco2, Elisabet Rodriguez-Tomàs2, Gerard Baiges Gaya1, Jordi Camps3, Jorge Joven2,3.1Institut d’Investigació Sanitària Pere Virgili, Unitat de Recerca Biomèdica, Reus, Spain; 2Universitat Rovira i Virgili, Medicina i Cirurgia, Reus, Spain; 3Hospital Universitari Sant Joan, Unitat de Recerca Biomèdica, Reus, Spain
Email: helena.castanev@gmail.com

Background and aims: The association of chronic liver disease with obesity and diabetes is clinically important in the context of silent pandemics and there are no pharmacotherapeutic interventions. The initial step of the disease spectrum appears to be a simple accumulation of lipids, steatosis, but can progress to more severe forms initiated by non-alcoholic steatohepatitis (NASH). The pathogenic mechanisms leading to progression are not completely understood but growing evidence likely suggests metabolic dysfunction in multiple and related organs. Lipidomics and proteomics from liver and adipose tissue, with the help of machine learning algorithms, could explain clinical traits and shed light on interorgan crosstalk in patients with NASH. Also, alterations in circulating lipids in patients with NASH have not been previously explored in association with tissue-specific lipid signatures in obesity. We sought to distinguish obese patients with and without NASH identifying the lipome in plasma, liver, and subcutaneous and visceral adipose tissue.

Method: Patients with extreme obesity (n = 118; n = 58 with NASH diagnostic, and n = 60 were non-NASH) that underwent metabolic surgery donated a liver and a visceral adipose tissue (VAT) biopsy, and blood sample, from which we extracted the lipome and proteome.
Results: Liver and VAT shared a relatively common lipidome and proteome signature. Regarding lipidomics, mostly all lipid species were altered: glycerophospholipids were diminished in both tissues and tri and diglycerides were increased in liver and decreased in VAT. Volcano plots found more differences between NASH and non-NASH patients in their VAT than in their liver proteome, though both tissues had proteins located in mitochondria and with essential roles in energy metabolism altered in NASH. Quantitative enrichment set analysis pointed to impaired mitochondrial beta-oxidation. On the other hand, plasma lipidome and proteome was different enough between NASH and non-NASH patients, thus machine learning algorithms were applied to build a predictive model which had high diagnostic ability.

Conclusion: Lipidomic and proteomic signature not only affects hepatic tissue, but also visceral adipose tissue. The alterations can also be observed in plasma, and the optimal combination of these variables could be a new biomarker of liver severity.

SAT029 Targeting liver glutaminase 1 modulates hepatic ammonia in experimental Non-Alcoholic Steatohepatitis

Maria Mercado-Gómez1, Nara Goikoteeta1, Marina Serrano-Macia1, Sofía Lachiondo-Ortega2, Rubén Rodríguez Agudo1, Petar Petrov3, Miren Bravo1, Claudia Gil-Pitarch1, Irene González-Reco1, Jorge Simón Espinosa1, María Luz Martínez-Chantar1, Teresa Cardoso Delgado3. 1CIC bioGUNE-Centro de Investigación Cooperativa en Biociencias, Derio, Spain; 2La Fe University and Polytechnic Hospital, Valencia, Spain

Background and aims: Hepatic ammonia, a key nitrogen-containing compound, is augmented in NAFLD, specifically in more advanced stages of the disease such as NASH with potential implications in its treatment. Whereas both gut-derived ammonia and decreased hepatic ureagenesis have been shown to contribute to increased hepatic ammonia content under these conditions, the contribution of hepatic ureagenesis have been shown to contribute to increased ammonia metabolism altered in NASH. Quantitative enrichment set analysis pointed to impaired mitochondrial beta-oxidation. On the other hand, plasma lipidome and proteome was different enough between NASH and non-NASH patients, thus machine learning algorithms were applied to build a predictive model which had high diagnostic ability.

Conclusion: Lipidomic and proteomic signature not only affects hepatic tissue, but also visceral adipose tissue. The alterations can also be observed in plasma, and the optimal combination of these variables could be a new biomarker of liver severity.

SAT030 Clinical relevance of an animal model of non-alcoholic steatohepatitis (NASH) and digital pathology with artificial intelligence (DP-AI) analyses of hepatic fibrosis

Yishuang Wei1, Mengnan Zhang1, Jiliang Zhang1, Xiao Teng2, Qiang Yang3, Alvin Leong2, Gideon Ho2, Henry Lu1, Deming Xu1, WuXi AppTec, Discovery Biology Unit, WuXi Biology, Shanghai, China; 1WuXi AppTec, Discovery Biology Unit, WuXi Biology, Shanghai, China; 2Histolindex Pte Ltd, Singapore, Singapore; 3Hangzhou Chouyi Technology Co., Ltd., Hangzhou, China

Background and aims: Clinical relevance of animal models for NASH is crucial for assessment of in vivo efficacy of compounds in development. The validity of efficacy assessment rests on histopathology of not only steatosis, ballooning and inflammation but also fibrosis. However, hepatic fibrosis varies from model to model. In the current study, we applied an automated quantitative DP-AI system to a mouse model of NASH to evaluate the hepatic fibrosis and the antifibrotic activity of obeticholic acid (OCA), in particular the fibrous septa that are typical in the late-stage of the NASH patients.

Method: In the mouse NASH model, after animals develop steatosis on feeding of high-fat diet (HFD), they are treated with carbon tetrachloride (CCL4) to induce hepatic fibrosis. Test compounds are administered during the CCL4 induction. The liver histopathology is analyzed by the standard means. For DP-AI analyses, second-harmonic generation (SHG)/two-photon excitation fluorescent (TPEF) microscopy is used for imaging of unstained liver sections. Collagen fibers are identified and quantified by an AI-based algorithm that recognizes the portal tract (PT) and the central vein (CV), and examines collagen bundles therebetween, with reference to septa diagnosed in the human NASH livers.

Results: Our previous studies indicated that the combination of HFD and CCL4 induces an extra level of fibrosis that is the target of antifibrotic activity of OCA. DP-AI analyses confirmed this observation. While CCL4 alone induced significant fibrosis, an extra level of fibrosis was induced by the combination, as determined by SHG% (of total area). With the treatment of OCA, the extra fibrosis was suppressed (Fig. 1-B). Although a basal level of fibrosis was observed in both the healthy control and the HFD induction by SHG% (Fig. 1-B), no or minimal septa were present in either (Fig. 1-C). The induction of septa was greatly increased when HFD and CCL4 were combined (septa% vs. SHG% in Fig. 1-B and -C). The OCA treatment reduced septa in the HFD+CCL4 model by ~50%, quantitatively much greater than that determined by SHG% (Fig. 1-B and 1-C). We then tested compounds that are in the NASH clinical trials, including agents targeting FXR, ASK1, PPAR-alpha/delta, pan-PPAR, CCR2/CCR5, THR-beta, ACC1/2, SAAO/VAP-1, and GLP1. Their efficacies were largely consistent with the respective clinical outcomes.
Conclusion: Our results demonstrate that the septa identified by the DP-AI system in the HFD+CCL4 model are NASH related, and they are the target of antifibrotic activities of NASH compounds with demonstrated clinical efficacies. Such septa could represent the bridging fibrosis as observed the NASH patients. The HFD+CCL4 model is therefore clinically relevant in terms of histopathological presentation and targets of NASH compounds.

**SAT031**
Small changes in the metabolism of bile acids by the gut microbiota are associated to NASH pathogenesis
Justine Gillard1,2, Morgane Thibaut2, Martin Roumain3, Giulio C. Muccioli3, Anne Tailleux4, Bart Staels5, Laure Bindels6, Isabelle Leclercq1.1 UCLouvain, Laboratory of Hepato-Gastroenterology, Institute of Experimental and Clinical Research, Belgium; 2UCLouvain, Metabolism and Nutrition Research Group, Louvain Drug Research Institut, Belgium; 3UCLouvain, Bioanalysis and Pharmacology of Bioactive Lipids, Louvain Drug Research Institut, Belgium; 4University of Lille, Inserm, CHU Lille, Institut Pasteur de Lille, U1011-EGID, France.
Email: justine.gillard@uclouvain.be

Background and aims: Primary bile acids (BAs) synthesized by the hepatocytes are secreted, modified and reabsorbed in the gut. Specifically, gut bacteria deconjugate BAs through bile salt hydrolase (BSH) activity and transform primary to secondary BAs through 7alpha-dehydroxylation. We showed that BAs contribute to NASH pathogenesis and that the enterohepatic BA pool is altered and secondary BAs lowered in experimental NASH, suggesting impaired bacterial biotransformation. However, here, our aim is to study the gut microbiota and its BA-metabolizing activities in a NASH experimental model.

Method: We co-housed and fed with HFD for 12 weeks foz/foz (NAS≥6) and WT (NAS≤1) mice and harvested samples after 12 h fasting/4 h refeeding. We analyzed microbial composition of the caecal content using 16S rRNA gene sequencing, BAs by LC-MS/MS and measured BSH activity.

Results: Alpha-diversity (measured by the Shannon and the observed amplicon sequence variant (ASV) indexes) and beta-diversity (reported by the Morisita Horn index) within and among caecal samples were similar in foz/foz and WT mice. The proportion of the variance explained by the genotype was low (9.2%, p = 0.32). The relative abundances of bacterial phyla and families were not significantly different, except for the Bacteroidaceae family more abundant in the caecal content of foz/foz mice (3.13% vs 1.27% in WT, p = 0.007).

The BSH activity in caecal content was similar in both groups, matching the similar overall microbial composition. Nevertheless, the low secondary to primary BAs ratio and the low secondary BAs concentration suggested a lower 7alpha-dehydroxylation activity in foz/foz mice. One specific ASV was detected only in 38% of the foz/foz while present in 100% of the WT mice at low abundance. The relative abundance of this ASV correlated significantly with the secondary to primary BAs ratio (Fig A), with the concentration of the secondary deoxycholic acid (r = 0.8478, p = 0.0006) and with the NAFLD activity score (Fig B). We hypothesized that this ASV exhibits a 7alpha-dehydroxylase activity, which could explain that its lower prevalence leads to a reduced production of secondary BA, thereby contributing to NASH pathogenesis.

**SAT032**
Unravelling the landscape of adipose tissue macrophages in human non-alcoholic fatty liver disease
Markus Boesch1, Hannelie Korf2, Rita Furtado Feio de Azevedo1, Ellen Deleus1, Matthias Lannoo2, Lena Snets3, Lukas Van Melkebeke1,2,3, Marie Wallays4, Tania Roskams4, Pierre Bedossa4, Andreas Lindhorst5,6, Jeff Verbeek2,3, Thierry Voet8,9, Alejandro Sifrim8,9, Martin Gericke8,9, Schalk van der Merwe1,3,1 KU Leuven, Laboratory of Hepatology, CHROMETA department, Belgium; 2KU Leuven, Department of Abdominal Surgery, Belgium; 3UZ Leuven, Department of Gastroenterology and Hepatology, Belgium; 4KU Leuven and University Hospital Leuven, Department of Imaging and Pathology, Belgium; 5Beaujon Hospital Paris Diderot University, Department of Pathology, Physiology and Imaging, France; 6Martin-Luther-University Halle-Wittenberg, Institute of Anatomy and Cell Biology, Germany; 7Leipzig University, Institute of Anatomy, Germany; 8Wellcome Trust Sanger Institute, Cancer Genome Project, United Kingdom; 9KU Leuven, Department of Human Genetics, Belgium; 10Wellcome Trust Sanger Institute, Sanger Institute-EBI Single-Cell Genomics Centre, United Kingdom.
Email: markus.boesch@kuleuven.be

Background and aims: Non-alcoholic fatty liver disease (NAFLD) is the most common cause of chronic liver disease, thereby affecting 25% of the world population. Patients with non-alcoholic fatty liver (NAFL) can progress further to non-alcoholic steatohepatitis (NASH), characterized by steatosis and hepatic inflammation. It has been postulated that ongoing inflammation in the adipose tissue compartment, potentially driven by macrophages, accounts for this disease transition. Previous studies already showed a significant heterogeneity within the macrophage pool in obese adipose tissue. Here, we aim to unravel the human visceral adipose tissue macrophage population on a single cell level in a well-defined human NAFLD population.

Method: Visceral adipose tissue (VAT) biopsies were collected from obese patients undergoing bariatric surgery (UZ Leuven, Belgium). Liver biopsies were performed and assessed by expert liver pathologists based on the fatty liver inhibition of progression (FLIP) algorithm and steatosis, activity, and fibrosis (SAF) score to distinct patient groups. Adipose tissue macrophages were freshly dissociated and single cell RNA-seq was performed using 10X Genomics 3′ v3 on samples of 2 obese controls without NAFLD, 3 NAFL and 4 NASH patients.
Results: The VAT contains multiple macrophage and monocyte subtypes with distinct transcriptional profiles. Among these, we observed an increased influx of pro-inflammatory macrophages and pro-inflammatory monocytes in patients with NASH compared to their obese counterparts. Additionally, anti-inflammatory/angiogenic macrophages were almost completely absent in tissue from NASH patients as compared to obese controls. Velocity and pseudotime analysis also revealed that these macrophages are no longer replenished in NASH patients.

Conclusion: Our study characterized the landscape of human adipose tissue macrophages that points towards a NASH-related loss of anti-inflammatory/angiogenic macrophages. Further studies unraveling their tissue localization and function are ongoing.

SAT032
Atorvastatin attenuates diet-induced non-alcoholic steatohepatitis in ApoE<sup>−</sup>3-Leiden mice by reducing hepatic inflammation
José A. Inía<sup>1,2,3</sup>, Anita M. van den Hoek<sup>1</sup>, Geurt Stokman<sup>1</sup>, Martine C. Morrison<sup>1</sup>, Elisabeth Pieterman<sup>1</sup>, J. Wouter Jukema<sup>2,3</sup>, Hans Princen<sup>1</sup>, <sup>1</sup>The Netherlands organization for applied scientific research (TNO), Metabolic health research, Leiden, Netherlands; <sup>2</sup>Leiden university medical center (LUMC), Eindhoven laboratory for experimental vascular medicine, Leiden, Netherlands; <sup>3</sup>Leiden university medical center (LUMC), Cardiology, Leiden, Netherlands
Email: jose.inia@tno.nl

Background and aims: Non-alcoholic fatty liver disease (NAFLD) is considered the hepatic manifestation of the metabolic syndrome, and due to the worldwide obesity epidemic, the prevalence of both NAFLD and the more severe form non-alcoholic steatohepatitis (NASH) is rapidly rising. Patients with metabolic syndrome are often prescribed statins to prevent development of cardiovascular disease as a result of a disturbed lipoprotein metabolism. Although the effects of statins on cardiovascular disease are relatively well described, data on their effects on NASH are lacking. Here, we evaluated the effects of atorvastatin on NASH and liver fibrosis development and inflammatory parameters.

Method: ApoE<sup>−</sup>3-Leiden mice were fed a Westernized diet (WTD) with or without atorvastatin admixture for 32 weeks. Plasma parameters and inflammatory markers were evaluated and hearts and livers were histologically and biochemically examined at study end point.

Results: Atorvastatin significantly reduced the WTD-induced increase in plasma cholesterol levels (−43%, p < 0.01) and thereby significantly attenuated the development of atherosclerosis (lesion area −47%, p < 0.01 compared to WTD). Atorvastatin significantly reduced hepatic steatosis (−22%, p < 0.01) and resulted in a robust decrease of hepatic inflammation (−80%, p < 0.01) and fibrosis (−92%, p < 0.001) compared to mice that received the WTD only. Interestingly, atorvastatin almost fully blunted the accumulation and formation of hepatic cholesterol crystals (−78%, p < 0.05), structures that drive inflammation via inflammasome activation. Analyses on inflammatory markers substantiated this effect and revealed a significant reduction in infiltration of hepatic macrophages, neutrophils and monocytes as well as lower levels of pro-inflammatory cytokines.

Conclusion: Atorvastatin attenuates the development of NASH by reducing intrahepatic cholesterol crystals and cholesterol ester levels, hepatic steatosis, inflammation and fibrosis.

SAT034
Carnitine signature in liver correlates with non-alcoholic fatty liver disease progression
Andrea Jiménez Franco<sup>1</sup>, Helena Castañé<sup>2</sup>, Gerard Baiges Gaya<sup>2</sup>, Elisabet Rodríguez-Tomás<sup>1</sup>, Jordi Camps Andreu<sup>1</sup>, Jorge Joven Mariéd<sup>3</sup>; <sup>1</sup>Universitat Rovira i Virgili, Medicine and surgery, Reus, Spain; <sup>2</sup>Hospital universitari Sant Joan de Reus, Medicine and surgery, Reus, Spain
Email: andreajfranco99@gmail.com

Background and aims: NAFLD is a global silent pandemic that increases in parallel with obesity, that is unknown for most of the population. NAFLD begins with simple inflammation, steatosis, and can become a severer stage known as NASH (Non-alcoholic steatohepatitis), which can only be diagnosed by liver biopsy. In the livers of NASH patients there is mitochondrial dysfunction, which impairs metabolism of the cell, impacting in its global health. Mitochondria is closely related to lipid metabolism: carnitines support the transport of fatty acids into mitochondria for beta-oxidation, thus their concentration may be affected in the development of NAFLD and its progression to NASH.

We sought to distinguish patients with NASH from patients without NASH by measuring carnitine concentrations in both plasma and liver, and to evaluate whether there may be an association between these species and mitochondrial dysfunction.

Method: The study includes 110 morbidly obese participants from the Hospital Sant Joan de Reus who have undergone bariatric surgery. From the liver biopsy we characterized NASH by using NAFLD Activity Score (NAS). 51 patients were classified as Non-NASH, 49 patients as NASH and 10 patients as Uncertain NASH diagnostic. We performed semi-targeted lipidomics to quantify carnitine species from liver and plasma samples, and we use Western blot to semi-quantify proteins of lipid metabolism and mitophagy in liver samples.

Results: Using multivariate analysis, we have been able to determine that in the liver there was a specific profile of the lipids. By comparing the concentrations in liver of NASH patients with Non-NASH patients revealed that most carnitine concentrations were found to be decreased in NASH. Western blot results determined that both beta-oxidation and autophagy of mitochondria is highly correlated with carnitines and NAFLD. Slight differences were observed between the plasma carnitine concentrations of the different patients. Carnitines could not be used as markers for this disease because were not specific enough.

Conclusion: Beta-oxidation and proteins associated to mitochondrial dynamics and mitophagy were found to be altered as the disease progressed. Mitophagy was activated, and fatty acid beta-oxidation was suppressed. On the other hand, as the liver severity increased, carnitine decreased with a specific signature.
**SAT035**

**Type 2 diabetes and religious fasting: effects on metabolism and liver steatosis**

Svenja Sydor1, Ender Engin 1, Mustafa Özçürümė1, Anja Figge1, Josef Pospišil 1, Andreas Jähnert1, Jan Best1, Wing-Kin Syn2, Ali Canbay1, Lars Bechmann1, Paul Manka1,1 University Hospital Knappschaftskrankenhaus Bochum, Department of Internal Medicine, Bochum, Germany; 2 Medical University of South Carolin, Division of Gastroenterology and Hepatology, Department of Medicine

Email: svenja.sydor@rub.de

**Background and aims:** Religious fasting during the holy month of Ramadan requires abstaining from food and liquids during the day. After sunset, it is allowed to consume food and drinks in defined periods. Fasting results in a reduced and timed calorie intake and can be regarded as a form of intermittent fasting. Type 2 diabetes (T2D) is a significant risk factor for the development of non-alcoholic steatohepatitis (NASH), the progressive form of non-alcoholic fatty liver disease (NAFLD). Recently several studies suggested some benefits of interval fasting for patients with T2D and NASH. Here, we aimed to characterize the impact of a one-month interval fasting period on liver health, glucose and lipid metabolism in a cohort of T2D patients.

**Method:** 20 muslim patients from a German metropolitan region were included. The status of the liver was assessed by Fibroscan®, including the measurement of the controlled attenuation parameter (CAP). Additionally to anthropometric measurements, patients’ blood samples were collected at the beginning and end of the four-week fasting period to quantify key parameters of liver injury, lipid and glucose metabolism.

**Results:** Following the fasting period transient elastography measurements (8.0 ± 1.2 vs. 8.6 ± 1.6 before/after fasting) and CAP values (311.4 ± 9.6 vs. 302.6 ± 10.4 before/after fasting) showed modest changes. In contrast, LFTs, apoptosis marker (M30), and adiponectin significantly decreased after the fasting period. Serum levels of triglycerides were lower following the fasting period. Glucose levels did not change significantly, but serum levels of C-peptide and insulin increased following the fasting period. In addition, the patients experienced a significant weight loss at the end of the fasting month.

**Conclusion:** In this cohort of T2D patients, we demonstrated that a 4-week intermittent fasting period resulted in an improvement in different serum parameters associated with glucose, liver, and lipid metabolism.

**SAT036**

**The I48M PNPLA3 variant mitigates Niacin beneficial effects: how the genetic screening in non-alcoholic fatty liver disease (NAFLD) patients gains value**

Erika Paolini1,2, Miriam Longo1,3, Marica Meroni1, Roberto Picotti1,3, Annalisa Cespiati1,4, Rosa Lombardi1,4, Anna Ludovica Francazani1,4, Paola Dongiovanni1, 1 General medicine and metabolic diseases, Fondazione IRCCS Cà Granda Ospedale maggiore Policlinico, Milan; 2 Università degli Studi di Milano, Milan, Italy, Department of Pharmacological and Biomolecular Sciences, Milan; 3 Department of Clinical Sciences and Community Health; 4 Università degli Studi di Milano, Fondazione IRCCS Cà Granda Ospedale Maggiori Policlinico, Milan, Italy, Department of Pathophysiology and Transplantation

Email: paola.dongiovanni@policlinico.mi.it

**Background and aims:** The PNPLA3 p.I148M variant is the main genetic predictor of NAFLD and its impact on fat accumulation can be modulated by nutrients. Niacin (NIA) reduces triglycerides (TGs) synthesis and ROS production in NAFLD patients. However, the interplay between NIA and p.I148M polymorphism has not been explored yet. This study aims to: 1) assess the dietary and circulating NIA levels in NAFLD patients stratified according to the presence of the p.I148M variant; 2) examine the efficacy of NIA in Hep3B and HepG2 cells, which are wild-type and homozygous for the p.I148M mutation, respectively.

**Method:** We enrolled 172 patients (Discovery cohort) with non-invasively assessed NAFLD. Dietary NIA was collected from food diary, while serum NIA was quantified by ELISA. Hepatic expression of genes related to NAD metabolism was evaluated by RNAseq in bariatric NAFLD patients (n = 125). HepG2 and Hep3B cells were transfected with a siRNA targeting PNPLA3 and treated with palmitic acid (PA) 0.25 mM alone/plus NIA 0.5 mM for 24 hrs.

**Results:** At bivariate analysis NAFLD patients showed reduced dietary NIA (p = 0.01). The p.I148M variant was correlated with lower levels of alimentary and circulating NIA (p = 0.01, p = 0.03 vs non-carriers). At multivariate analysis, adjusted for sex, BMI, and alimentary NIA, the p.I148M mutation was associated with reduced serum NIA (β = − 18.01; CI: −35.6−0.57; p = 0.04), suggesting that it may independently modulate NIA systemic availability. The expression of enzymes related to NAD biosynthesis was impaired in p.I148M carriers (p = 0.006). NIA supplementation reduced TG synthesis alongside oxidative injury and ER stress in hepatoma cells (p < 0.001, p < 0.05 vs PA). The efficacy of NIA was hidden by the p.I148M variant in HepG2 cells, suggesting that the loss of lipase activity blunted the NIA protective role. Consistently, PNPLA3 silencing masked the beneficial effect of NIA on TG overload in Hep3B cells, whereas it didn’t affect fat accumulation in HepG2 ones (p < 0.001, p < 0.05 vs PA). The effectiveness of NIA on oxidative/ER stress was maintained in both cell lines silenced for PNPLA3 (p < 0.001, p < 0.05 vs PA), thus suggesting that it might mitigate the protective role of NIA in lipid handling but not in hepatocellular damage.

**Conclusion:** NIA levels were reduced in NAFLD patients who carry the p.I148M variant. PNPLA3 silencing compromised the efficacy of NIA in hepatoma cells, thus suggesting its supplementation in NAFLD patients should be preceded by genetic screening.

**SAT037**

**The co-presence of PNPLA3, MBOAT7 and TM6SF2 loss-of-functions impairs mitochondrial morphology and number in severe NAFLD patients**

Miriam Longo1,2, Erika Paolini1,3, Marica Meroni1, Michela Ripolone4, Laura Napolì5, Roberto Picotti1,2, Marco Maggioni5, Maurizio Moggio5, Anna Ludovica Francazani1,6, Paola Dongiovanni1, 1 Fondazione IRCCS Cà Granda Ospedale Maggiori Policlinico, Milan, Italy, Department of Clinical Sciences and Community Health; 2 University of Milan, Department of Pharmacological and Biomolecular Sciences; 3 Fondazione IRCCS Cà Granda Ospedale Maggiori Policlinico, Milan, Italy, Department of Pathophysiology and Transplantation

Email: paola.dongiovanni@policlinico.mi.it

**Background and aims:** Mitochondrial (mt-) dysfunction is a key event occurring in the progressive forms of non-alcoholic fatty liver...
disease (NAFLD) up to hepatocellular carcinoma (HCC). We previously demonstrated that human HepG2 cells, homozygous for the I148M PNPLA3 variant and silenced for MBOAT7 and TM6SF2 genes (MBOAT7<sup>−/−</sup>TM6SF2<sup>−/−</sup>) by CRISPR/Cas9, enriched mt-mass and accumulated damaged mitochondria with loss of cristae paralleled by functional defects in the oxidative phosphorylation. In the attempt to translate in vitro results in human NAFLD, we aimed to: 1) assess whether mt-morphology, circulating D-loop copy number and expression, which reflect mt-mass, correlated with disease severity and number of the 3 at-risk variants (NRV = 3) in biopsied NAFLD subjects (n = 26, Discovery cohort); 2) evaluate circulating D-loop levels in a larger cohort of biopsied NAFLD patients (n = 773, Validation cohort), including n = 101 NAFLD-HCC. Hepatic D-loop levels were evaluated in intra- and extra-tumoral tissues of 3 NAFLD-HCC individuals.

**Method:** NAFLD patients were stratified according to NRV and to NAFLD activity score (NAS). Mt-morphology was assessed by transmission electron microscopy (TEM).

**Results:** In the Discovery cohort, NAFLD patients with NRV = 3 showed NAS = 5–7 along with the highest D-loop content compared to patients with 1–2 or no variants (p < 0.01), reflecting what was observed in vitro. At TEM, patients carrying NRV = 3 showed an enrichment of mt-mass and an elevated pattern of mt-morphological alterations as swollen shapes with loss of internal matrix, rupture of double membranes or giant/elongated mitochondria. In the Validation cohort, the NRV = 3 associated with NAS and HCC risk (p < 0.05) at multivariate analysis adjusted for age, sex, BMI and diabetes. At ordinal regression analysis adjusted as above plus the presence of NRV = 3, the D-loop levels were independently associated with steatosis, necroinflammation, ballooning, fibrosis, and NAS (p < 0.001) and were significantly increased in NAFLD patients with NRV = 3 (p = 0.03). Finally, in 3 NAFLD-HCC patients D-loop copies were higher in the intra-tumoral tissues compared to extra-tumoral ones, showing the highest number in one patient carrying all 3 at-risk variants.

**Conclusion:** PNPLA3, MBOAT7 and TM6SF2 loss-of-functions impair mt-functionality and mass in vitro and NAFLD patients. The assessment of D-loop copies may be a useful biomarker for the evaluation of disease course in genetically predisposed subjects.

**SAT028**

The association of spleen volume with sex, age, type 2-diabetes, and non-alcoholic fatty liver disease—initial results from more than 35,000 UK Biobank participants

Samuel Helgesson<sup>1</sup>, Sambit Tarai<sup>2</sup>, Taro Langner<sup>2</sup>, Häkan Ahlström<sup>1,2</sup>, Lars Johansson<sup>2</sup>, Joel Kullberg<sup>1,2</sup>, Elin Lundström<sup>1,2</sup>, <sup>1</sup>Uppsala University, Department of Surgical Sciences, Radiology, Sweden; <sup>2</sup>Antaros Medical AB, BioVenture Hub, Mölndal, Sweden

Email: samuel.helgesson@gmail.com

**Background and aims:** Non-alcoholic fatty liver disease (NAFLD) is defined as excessive hepatic fat infiltration not related to alcohol/drug abuse. When estimating liver fat with magnetic resonance imaging (MRI), a threshold of 5.56% is typically used for NAFLD (Szczepaniak et al. 2004). The contemporary pandemics of obesity and type 2-diabetes (T2D) drive a global increase in NAFLD, with a substantial risk of sequential progression to non-alcoholic steatohepatitis, fibrosis, and cirrhosis. As interconnected to the liver via the hepatic portal vein, the spleen can be enlarged due to increased portal venous pressure as a result of hepatic fibrosis. However, the current knowledge of the spleen volume (SV) distribution in a normal aging cohort, and its association with T2D and early stages of NAFLD, is limited and therefore the subject of investigation in this work.

**Method:** A deep-learning method for spleen segmentation and SV estimation was developed and validated (training data = 85 manual segmentations, Dice score = 93%, symmetric mean absolute percentage error = 7.88%) on neck-to-knee MRI images from the UK Biobank (UKBB). In total, 37,019 subjects were included in the study after exclusion of 1,800 subjects with potential failure segmentations, Dice score = 93%, symmetric mean absolute percentage error = 7.88% on neck-to-knee MRI images from the UK Biobank (UKBB). In total, 37,019 subjects were included in the study after exclusion of 1,800 subjects with potential failure segmentations, Dice score = 93%, symmetric mean absolute percentage error = 7.88%. The cohort was grouped into Controls (unlikely diabetic, n = 33,970) and T2D subjects (n = 1,558), using an algorithm developed on UKBB clinical data (Eastwood et al. 2016) and by discarding intermediate/possible diabetic subjects.

**Results:** Moving average curves of SV vs age, in controls and subjects with T2D, are presented in Fig 1A, with 95% confidence intervals (CI) of the weighted arithmetic average SV displayed. Similar curves of SV vs liver PDFF are presented in Fig 1B. The SV was larger in males than in females and in T2D compared to controls, for both sexes, within the approximate age range 55–77 years. There was a similar pattern of age-related decrease in SV in male and female controls. Within certain age intervals, SV appeared to decrease faster with age in T2D subjects compared to in controls. Increasing SV with increasing liver PDFF was observed for both sexes already at low liver PDFF values. For liver PDFF >25%, the measurement uncertainty (CI) was relatively large, as influenced by the low sample size.

**Conclusion:** Clear patterns demonstrated men, younger subjects, and individuals with T2D and NAFLD to have larger spleens compared to...
Targeting adipose tissue macrophages ameliorates hepatic injury in a murine model of NAFLD

Celia Martínez Sánchez1,2, Mar Coll1, Delia Blaya1, Octavi Bassegoda1,2, Muhammad Fayyaz3, Raquel A. Martinez Garcia de la Torre1, Kelly Swanson4, Andrew Smith4, Pere Ginès1,2,3, Isabel Graupera1,3, Laia Aguilar1,1Institut d’Investigacions Biomèdiques August Pi i Sunyer (IDIBAPS), Liver Unit, Barcelona, Spain; 2Centro de Investigación Biomédica en Red de Enfermedades Hepáticas y Digestivas (CIBEREHID), Spain; 3Hospital Clínic de Barcelona, Spain; 4University of Illinois at Urbana-Champaign, United States; 5University of Illinois at Urbana-Champaign

Email: celiamartinezsa@gmail.com

**Background and aims:** Adipose tissue dysfunction with infiltration of pro-inflammatory macrophages is a hallmark in obesity leading to an impairment of metabolic homeostasis. Non-alcoholic fatty liver disease (NAFLD) is intimately associated with obesity and it has been shown that pro-inflammatory adipose tissue macrophages (ATMs) induce hepatic inflammation although their role in fibrogenesis is still unknown. The aim of the present study is to assess the role of ATMs in hepatic fibrogenesis by modulating the pro-inflammatory phenotype of ATMs.

**Method:** Dextran (500 kDa) nanocarriers conjugated with dexamethasone (dexa) were used to modulate ATMs’ phenotype in a NAFLD models based on high-fat (HFHD) and high fat high cholesterol (HFHC) diets. After feeding animals for 5 months, dextran conjugates were administered i.p. twice per week for 5 additional weeks. In order to study dextran uptake, i.p. administration of dextran-FITC was evaluated by flow cytometry and immunofluorescence. Hepatic and AT macrophages’ phenotype switch was assessed by flow cytometry and gene expression analysis. The anti-inflammatory effect of dextran conjugates in liver and adipose tissue was evaluated by assessing key inflammatory markers expression by qPCR and immunostaining. Changes in hepatic fibrosis and NAS score were explored by histopathological analysis. In-vitro phenotypic modulation of human ATMs incubated with dextran conjugates were evaluated by qPCR. The effect of human ATMs on hepatic stellate cells (HSCs) activation was assessed by culturing HSCs with ATMs conditioned media.

**Results:** Animals fed with HFHC diet displayed increased liver and adipose tissue macrophage infiltration with an enhanced pro-inflammatory phenotype compared to animals receiving HFH. Compared to HFD, liver tissue from HFHC model showed higher NAS score and fibrosis degree. Dextran-dexa conjugates were predominantly engulfed by macrophages from the AT. Conjugated nanocarriers administration significantly switched the pro-inflammatory phenotype of ATMs without significant differences in liver macrophages. Dextran-dexa treatment caused a significant reduction of hepatic inflammation, NAS score, and hepatic fibrosis in the HFHC model. Human ATMs treated with dextran-dexa attenuated their pro-inflammatory phenotype and reduced HSCs activation.

**Conclusion:** Dextran-dexamethasone conjugated administrated i.p. are predominantly uptaken by adipose tissue macrophages inducing a switch of their pro-inflammatory phenotype which in turns attenuates liver inflammation and fibrosis. In vitro modulation of human ATMs by dextran nanocarriers reduce activated phenotype of HSCs. These results demonstrate that modulating the pro-inflammatory phenotype of ATMs might be a good strategy to reduce hepatic fibrosis and inflammation in NAFLD.
SAT041
Phospholipid fingerprints reveal sex differences in the adipose tissue phospholipid composition from morbidly obese patients
Gerard Baiges1,2, Elisabet Rodríguez-Tomàs3, Helena Casteñé1,2, Andрейa Jimenez Franco2, Jordi Camps4, Jorge Joven1,2,3 1Fundación Instituto de Investigación Sanitaria Pere Virgili, Tarragona, Spain; 2Rovira i Virgili University, Tarragona, Spain; 3Hospital Universitari Sant Joan de Reus, Reus, Spain
Email: gerardbaiges93@gmail.com

Background and aims: Obesity is a metabolic disease that requires adipose tissue mechanisms of hyperplasia and hypertrophy to ensure energy storage. Nevertheless, men show a higher risk to have insulin resistance, diabetes mellitus and liver disease at a lower weight than women. Phospholipid metabolism plays an important role in the development of adipocytes as well as in determining their size. Concretely an enrichment of phosphatidylcholine (PC) in the plasma membrane of adipocytes increases their fluidity and size too. Thus, the purpose of the study was to explore the phospholipid metabolism in both subcutaneous and visceral adipose tissue to observe if their regulation is influenced by sex and the liver disease severity.

Method: Semi-targeted lipidomic was carried out from abdominal-subcutaneous (SAT) and omental-visceral adipose tissue (VAT) morbidly obese patients candidates to undergoing bariatric surgery. The patients were classified based on pathology severity: non-alcoholic fatty liver (NAFL)-NAFLD activity score (NAS) between 0 and 2 (38 women and 13 men); non-alcoholic steatohepatitis (NASH)-NAS ≥5 (34 women and 18 men).

Results: We observed the phospholipid levels were not influenced in both tissues by the liver disease progression. Nevertheless, we found that women showed a higher PC/PE molar ratio than men, independently of the disease severity. In addition, we found a less content of polyunsaturated fatty acids in the sn2-position of lysophosphatidylcholines (sn2LPC) between women and men, evidencing different responses in the lipid remodelling. This lipid remodelling in women was associated with an increase of fatty acids (C22) as well as in determining their size.

Conclusion: These results demonstrate that women and men have a different phospholipid fingerprint, conferring different biological properties to adipocytes. Thus, the higher PC/PE molar ratio observed in women could explain the intrinsic capability to get more fat in SAT regions than men.

SAT042
Ubiquitination of GSDMD regulated by NEDD4 is involved in hepatocyte pyroptosis of non-alcoholic steatohepatitis
Rui Jin1, Xiaoxiao Wang2, Feng Liu2, Huiying Rao1, 1Peking University People’s Hospital, Peking University Hepatology Institute, Beijing, China; 2Peking University People’s Hospital, Peking University Hepatology Institute, Beijing, China
Email: rao.huiying@163.com

Background and aims: Hepatic injury and death are significant histological features of non-alcoholic steatohepatitis (NASH). Previous studies have shown that gasdermin D (GSDMD)-mediated pyroptosis is involved in the progression of NASH, but its specific mechanism is still unclear. This study intends to clarify further the signaling pathway of GSDMD involved in pyroptosis of liver cells in NASH and further explore the role of ubiquitin enzymes regulating GSDMD in the pathogenesis of NASH.

Method: Methionine-choline deficient (MCD) diet fed male wildtype C57BL/6 mice aged 6–8-week mice to induce NASH mouse model. CRISPR technique (AAVD-TJB-GSDMD-SaCas9 system) was used to target and knock down hepatocellular GSDMD in mice. Immunoprecipitation combined with multi-dimensional mass spectrometry was used to identify the ubiquitin-regulating GSDMD. Normal human cell line L02 were also used to investigate the effect of pyroptosis in hepatocytes on liver inflammation and injury.

Results: Compared with control mice, the expression level of GSDMD mRNA in the liver of NASH mice was downregulated, however, the GSDMD protein levels were upregulated, suggesting that GSDMD protein might undergo post-translational modifications. By detecting the expression and cellular localization of GSDMD in the liver by immunohistochemical staining, we found that the GSDMD positive cells in the liver of NASH mice were mainly hepatocytes, suggesting that GSDMD mediated pyroptosis mainly occurred in hepatocytes. We also tried to identify the exact pathway that induced pyroptosis in NASH and found that Caspase1 protein levels and cleavage were increased in NASH mice compared with control ones, whereas Caspase11 protein levels were not significantly changed, suggesting that pyroptosis in the liver is mainly induced by the activation of classical pathway. Further detection found that the ubiquitination level of GSDMD was increased in Caspase1 knockdown mice, suggesting that the decrease of the ubiquitination level of GSDMD during the progression of NASH depends on caspase1. By analyzing immunoprecipitation combined with multi-dimensional mass spectrometry, compared with control mice, the expression level of E3 ubiquitin ligase NEDD4 downregulated in NASH mouse model. We further verified that NEDD4 was an interacting protein of GSDMD.

Conclusion: NEDD4 might be involved in the ubiquitination of GSDMD to promote hepatocyte pyroptosis which depended on caspase1 in NASH development.

SAT043
Unraveling the transcriptional dynamics of NASH pathogenesis affecting atherosclerosis development
Anita M. van den Hoek1, Serdar Özerse2, Martien P. M. Caspers2, Geurt Stokman1, Arianne van Koppens1, Roeland Hanemaaijer3, Lars Verschuren4, 1The Netherlands Organization for Applied Scientific Research (TNO), Department of Metabolic Health Research, Leiden, Netherlands; 2The Netherlands Organization for Applied Scientific Research (TNO), Department of Microbiology and Systems Biology, Zeist, Netherlands
Email: a.vandenhoek@tno.nl

Background and aims: The prevalence of non-alcoholic steatohepatitis (NASH) is rapidly increasing and is associated with an increased incidence of cardiovascular disease (CVD). In fact, CVD remains the major overall cause of mortality in patients with NASH. Although NASH and CVD share common risk factors, the mechanisms by which NASH may directly contribute to the development to CVD remain poorly understood. The aim of this study was to gain insight

Conclusion: These results demonstrate that women and men have a different phospholipid fingerprint, conferring different biological properties to adipocytes. Thus, the higher PC/PE molar ratio observed in women could explain the intrinsic capability to get more fat in SAT regions than men.
POSTER PRESENTATIONS

into the dynamics of key molecular processes of NASH that drive atherosclerosis development.

Method: A time-course study was performed in Ldlr−/−.Leiden mice, a well-established model for hyperlipidemia that develop NASH with advanced fibrosis and atherosclerosis when fed a high fat diet. NASH and atherosclerosis development in the aortic root were histologically analyzed. Comprehensive transcriptome analysis of liver and aorta was used to identify the temporal dynamics of key processes in both tissues. Dynamical GENIE3 (dynGENIE3) was used for gene regulatory network (GRN) inference using the differentially expressed genes (DEGs) from time series. In this way liver regulators were identified for each aorta target gene by extracting dynamics in the liver that precede dynamics in the aorta and were linked to atherosclerosis development.

Results: The Ldlr−/−.Leiden mice developed obesity, hyperlipidemia, insulin resistance in a time-dependent manner with hepatic steatosis and development of hepatic inflammation preceding the athero- sclerosis development. Transcriptome analysis of liver and aorta revealed a time-dependent increase of pathways related to NASH and fibrosis followed by an increase in proatherogenic processes the aorta. DynaGENIE3 identified specific liver regulators related to lipid metabolism (SC5D and TM7SF2), inflammation (IL1A) and fibrosis (PDGF) linked to a set of aorta target genes related to vascular inflammation (VCAM1 and CCL2).

Conclusion: Time-resolved analyses of NASH and atherosclerosis in Ldlr−/−.Leiden reveal pathogenic liver processes precede atherosclerosis development in the aorta. Gene regulatory network analysis identified hepatic key regulators and gene modules driving the atherogenic pathways and regulators in the aorta.

SAT044
Repeate dl cycling in obese mice improves hepatic inflammation
Jelle C.B.C. de Jong1,2, Nanda Keijzer1, Nicole Worms1, Geurt Stokman1, Nikki van Trigt1, Aswin L. Menke1, Anita M. van den Hoek1, 1The Netherlands Organization for Applied Scientific Research (TNO), 2Wageningen University, Human and Animal Physiology, Wageningen, Netherlands

Background and aims: Lifestyle interventions aimed to reduce body weight remain the current treatment of choice for non-alcoholic steatohepatitis (NASH), but are difficult to maintain and often lead to cycles of weight loss and regain (weight cycling). Although pertaining literature on weight cycling remains controversial, numerous studies indicate that weight cycling leads to an increased risk of developing Type 2 Diabetes or cardiovascular disease. Relative few studies investigated the association between weight cycling and NASH and atherosclerosis development.

Method: Ldlr−/−.Leiden mice received a high fat diet (HFD) for 20 weeks to induce obesity and NASH. Mice were then maintained for 16 weeks on the HFD (control group) or were subjected to 4 weight cycling episodes (using diet change). In addition, a group of mice on HFD were added with a similar body weight as the weight cycling group upon sacrifice (weight matched HFD reference group). The effects on body composition, plasma and liver biochemical variable and liver and fat histology were assessed.

Results: Weight cycling tended to slightly decrease body weight and total fat mass as compared to the HFD control group, but adipocyte size and fat inflammation were similar. Weight cycling did not result in a significant change in blood glucose or plasma insulin levels as compared to HFD control group, while plasma alanine transferase (ALT) levels were significantly reduced (with −40%, p = 0.010) and tended to be reduced as well as compared to weight matched HFD reference group (with −16%, p = 0.051). Hepatic macrovesicular steatosis was similar in the weight cycling and HFD control group (28% and 29%, respectively). Microvesicular steatosis tended to be increased upon weight cycling (from 17% in HFD control to 24% in weight cycling group, p = 0.077), but not as compared to the weight matched HFD reference group (20% microvesicular steatosis). Weight cycling resulted in a robust decrease in hepatic inflammation as compared to both HFD control group (with −67%, p = 0.004) and weight matched HFD reference group (with −60%, p = 0.014). Hepatic fibrosis was not affected by weight cycling.

Conclusion: The results of our weight cycling experiment argue against the postulate that weight cycling leads to unfavorable metabolic effects and in fact revealed a beneficial effect on hepatic inflammation.

SAT045
The functional roles of BMP10 in the pathogenesis of non-alcoholic fatty liver disease
Wenjun Zhang1, Hanying Chen2, Ying Liu3, Zachary Rokop1, Weimian Shou1, Chandreshkumar Kuhal1, 1Indiana University School of Medicine, Department of Surgery, Indianapolis, United States; 2Indiana University School of Medicine, Genome Editing Center, Indianapolis, United States; 3Indiana University School of Medicine, Department of Pediatrics, Indianapolis, United States

Email: sakubal@iupui.edu

Background and aims: BMP10 belongs to the Transforming Growth Factor (TGF)-beta superfamily that comprises of more than 45 cytokines based on amino acid sequence homology. Unlike most of other BMP proteins that only function locally at the site of expression (autocrine/paracrine function), BMP10 can act on remote tissue as a circulating cytokine (endocrine function). Recently, BMP10 expression was detected in hepatic stellate cells in human liver. Here we investigated the roles of BMP10 in the regulation of homeostasis of liver metabolism and pathogenesis of non-alcoholic fatty liver disease (NAFLD).

Method: We generated Bmp10−/− mice and crossed with the Rosa26-CreERT2 mice to create BMP10 postnatal conditional knockout mice (named as Bmp10cKO), which Bmp10 can be efficiently ablated via activated Cre recombinase activity in all adult tissues/cell types following estrogen agonist-tamoxifen induction in the postnatal mouse. Bmp10cKO mice (male, 8-week-old) and controls (Bmp10+/−/lox), were subjected to high fat high sucrose diet (HFSD) feeding for 20 weeks. A normal chow diet (ND) was used as feeding control. At the end of the diet exposure, we evaluated: (i) liver histology (ii) liver fibrosis by fast green/Sirius red staining; (iii) liver functional tests; (iii) immunoreactivity of selected inflammatory cell markers by IHC and (v) circulating BMP10 levels are significantly elevated prior to transplantation (4 with non-alcoholic steatohepatitis (NASH)) transplantation with Gene Ontology (GO) analysis revealed that leukocyte cell adhesion, fatty acid metabolism, and lipid localization process were among the most altered Biological Process (BP) (Fig. 1C). In cirrhotic patients undergoing liver transplantation, we found that circulating BMP10 levels are significantly elevated prior to transplantation as compared to the post-transplant levels and normal controls, reaching to an average value of 2.89 ± 1.46 ng/ml (p < 0.001) (Fig. 1D).
CONCLUSION: These data suggest that BMP10 plays a pivotal role in the regulation of liver metabolism and pathogenesis of NAFLD/NASH.

SAT046 Pharmacokinetics, safety, and tolerability of BMS-986263, a lipid nanoparticle containing HSP47 siRNA, in participants with severe hepatic impairment

Giridhar Tirucherai1, Eric Lawitz2, Claudia De Oliveira1, Hisham Qosa1, Edgar Charles1, 1Bristol Myers Squibb; 2The Texas Liver Institute, University of Texas Health San Antonio, San Antonio, United States

Email: giridhar.tirucherai@bms.com

BACKGROUND AND AIMS: BMS-986263 is a retinoid-conjugated lipid nanoparticle delivering siRNA designed to degrade heat shock protein 47 (HSP47) mRNA and prevent synthesis of HSP47 protein, a collagen-specific chaperone involved in fibrosis development. Evaluation of BMS-986263 in patients with non-alcoholic steatohepatitis and compensated cirrhosis (NCT04225936) is ongoing. In part 1 of the hepatic impairment (HI) phase 1 study (NCT04225936), significant changes in pharmacokinetics (PK) and safety were not observed in participants (pts) with mild or moderate HI compared with healthy pts. Here, part 2 results (severe HI) are presented.

METHOD: Pts with severe HI (Child-Pugh score 10–14) were matched by age and body mass index (BMI) to a cohort of pts with normal hepatic function. All received a single intravenous 90 mg BMS-986263 infusion; serial blood samples were collected for PK analyses. The primary end point was PK of BMS-986263 components including siRNA (active ingredient), DPD (retinoid-conjugated targeting agent), and S104 (ionizable lipid). Secondary and exploratory end points were safety and PK of HEDC (cationic lipid component), respectively.

RESULTS: The mean (SD) age and BMI for severe HI pts (n = 8) were 55.5 (3.7) years and 34.3 (12.0) kg/m², respectively, compared with 56.1 (4.1) years and 30.6 (8.3) kg/m², respectively, for normal-matched pts (n = 8). Relative to normal-matched pts, siRNA geometric mean exposure (AUC (0–7)) was 163% greater in pts with severe HI and C_max was higher by 58% (figure). DPD exposure was 31% higher in pts with severe HI compared with normal-matched pts and C_max was 6% higher. The severe HI cohort also had a 452% increase in S104 exposure (88% higher C_max), and a 44% increase in HEDC exposure (23% higher C_max) compared with normal-matched pts. In total, 3/8 pts had 4 adverse events (AEs) in the severe HI cohort (infusion-related reaction [IRR; n = 2], nausea [n = 1], and dysuria [n = 1]); no normal-matched pts had AEs. Two pts experienced treatment-related AEs that were IRRs of severe back pain/chest tightness that resolved in less than 30 minutes without requiring treatment or study discontinuation.

SAT047 Amino acid glycine suppresses steatohepatitis and tumorigenesis in hepatocyte-specific phosphatase and tensin homolog knockout mice

Kazuyoshi Kon1, Kumiko Arai1, Akira Uchiyama1, Hiroo Fukada1, Toshifumi Sato2, Maki Morinaga1, Kyoko Fukuhara1, Reiko Yaginuma1, Shunhei Yamashina1, Kenichi Ikejima1, 1Juntendo University School of Medicine, Department of Gastroenterology, Tokyo, Japan

Email: kazukon@juntendo.ac.jp

BACKGROUND AND AIMS: Establishing a preventive treatment for hepatocellular carcinoma (HCC) following non-alcoholic steatohepatitis (NASH) is an urgent issue. The Aim in the present study was to investigate the effect of the amino acid glycine on NASH-related HCC using hepatocyte-specific phosphatase and tensin homolog (PTEN)-deficient mice.

METHOD: Male Alb-Cre TG (+) PTENflox/flox mice aged 11–17 weeks were fed a normal diet or a diet containing 5% glycine for 2 or 24 weeks. Wild-type or TG (-) mice fed a normal diet were used as control. The expression of 4-hydroxynonenal (4HNE) and CD8 was evaluated by immunohistochemical staining. Total glutathione level was measured using enzymatic method. The number of liver tumors with a diameter of 2 mm or more was counted. The expression of mRNA in liver tissue was measured by RT-PCR.

RESULTS: PTENflox/flox mice developed severe steatohepatitis with lobular inflammation and ballooning hepatocytes after 2 weeks, and serum ALT levels significantly increased to 163 ± 30 IU/L compared to 41 ± 4 IU/L in control, whereas the glycine-containing diet clearly improved steatohepatitis and significantly reduced serum ALT levels to 23 ± 10 IU/L. The expression of 4HNE was enhanced in the liver of PTENflox/flox mice as compared with control, and was suppressed by glycine administration. Total glutathione in the liver tissue of PTENflox/flox mice was significantly decreased from 2.2 ± 0.2 micro mol/g in the control to 1.4 ± 0.1 micro mol/g, and significantly increased to 1.8 ± 0.1 micro mol/g by glycine administration. After 24 weeks of experiment, the liver of PTENflox/flox developed a tumor of 2.6 ± 1.0, but glycine-containing diet completely suppressed tumor formation to 0 ± 0. The expression of IL12B mRNA was slightly increased in PTENflox/flox mice compared to the control, and glycine administration further increased the expression to 4 times or more of the normal diet. In liver tissue, the expression of CD8-positive...
Conclusion: Glycine markedly improved steatohepatitis and inhibited hepatic tumorigenesis in hepatocyte-specific PTEN knockout mice. Our findings indicate that glycine acts as an anti-oxidative stress to improve steatohepatitis in the early stages, and contributes to the activation of antitumor immunity and suppresses tumor formation in the carcinogenic stage. It was demonstrated that glycine has the potential to prevent NASH-related carcinogenesis.

SAT048
Advanced quantitative phenotypic fibrosis and steatosis scoring is more superior to histology-based conventional staging in NASH animal models

Li Chen 1,2, Dipankar Bhattacharya 3, Scott Friedman 3, Mathieu Petitjean 1. 1PharmaNest, Princeton, United States; 2PharmaNest Inc, Princeton, United States; 3Icahn School of Medicine at Mount Sinai, New York, United States

Background and aims: The defining pathologic elements of non-alcoholic steatohepatitis (NASH) are fat accumulation, inflammation, and fibrosis. While conventional histopathology remains the gold standard for diagnosis and staging, this method has limitations, as it uses a narrow range for scoring, qualitative evaluation, and it is prone to inter-observer variability. The Phenotypic Fibrosis Composite Score (Ph-FCS) calculated by the FibroNest image analysis platform is a novel continuous phenotypic scoring and quantifier of fibrosis and steatosis. Here, we compared Ph-FCS to the conventional scoring in the FAT-NASH model, whose features closely align with human NASH (Tsuchida et al, J. Hepatology 2018; doi: 10:1016/j.jhep.2018.03.011).

Method: Mice (n = 5 per group) were fed a normal diet or the FAT-NASH regimen (high fat, high fructose, high cholesterol, very low dose CCl4) for 12 or 24 weeks to induce NASH. In other groups, NASH mice (n = 8) were treated with vehicle or with the clinical-stage drug obeticholic acid (OCA, 30 mg/kg, by gavage) for 24 weeks. Liver histological sections were stained with picrosirus red for collagens and imaged at 40X in white light with an Aperio Digital Pathology platform. FibroNest®, a cloud-based image analysis platform, was used to quantify the fibrosis phenotype including 32 traits for collagen system. FibroNest®, a cloud-based image analysis platform, was used to quantify the fibrosis phenotype including 32 traits for collagen system.

Results: For Healthy vs NASH at 12 wks and 24 wks, FibroNest Ph-FCS FIBROSIS scores (averages) 2.21, 3.08 (p = 0.01), and 6.21 (p = 0.0001) respectively, while the conventional method scores 0, 2.2 (p = 0.0003), and 3 (p = 0.0006). For Vehicle vs OCA, FibroNest Ph-FCS FIBROSIS scores were 6.27 and 4.47 (p = 0.03) respectively, while the conventional method scores were 3.3 and 2.5 (p = 0.09). For Healthy vs NASH at 12 wks and 24 wks, FibroNest STEATOSIS scores (averages) were 0.08, 14.71 (p = 0.001), and 22.43 (p = 0.003) respectively, while the conventional scores were 0.08, 14.71 (p = 0.001), and 22.43 (p = 0.003) respectively.

Conclusion: FibroNest shows a markedly wider dynamic range of difference between the groups in the FAT-NASH study. This allows greater detection and sensitivity for subtle changes. FibroNest® provides a more sensitive and reliable evaluation of fibrosis severity and progression in NASH and for the evaluation of therapeutic drug efficacy.

SAT049
Chemical suppression of adipose triglyceride lipase improves non-alcoholic steatohepatitis in a diabetic and hyperlipidemic mouse model

Emmanuel Dauda Dixon 1, Alexander D Nardo 1, Thierry Claudel 1, Claudia Fuchs 2, Veronika Mlitz 1, Tatjana Stojakovic 2, Hubert Scharnagl 1, Gernot Grabner 1, Robert Zimmermann 1, Michael Trauner 1. 1Medical University of Vienna, Hans Popper Laboratory of Molecular Hepatology, Division of Gastroenterology and Hepatology, Department of Internal Medicine III, Wien, Austria; 2University Hospital Graz, Clinical Institute of Medical and Chemical Laboratory Diagnostics, Graz, Austria; 3Medical University of Graz, Clinical Institute of Medical and Chemical Laboratory Diagnostics, Graz, Austria; 4University of Graz, Institute of Molecular Biosciences, Graz, Austria

Background and aims: Metabolic comorbidity such as diabetes, obesity and metabolic syndrome plays a key role in the pathogenesis and progression of non-alcoholic fatty liver disease (NAFLD). Increased adipocyte triglyceride lipase (ATGL/PNPLA2) activity, because of insulin resistance, may result in enhanced release of fatty acids from white adipose tissue to the liver, where it precipitates the development and progression of NAFLD. Therefore, ATGL is an attractive target to avert metabolic liver injury. We tested whether the pharmacological ATGL inhibitor Atglistatin hinders metabolic syndrome and improves liver injury in STAM mice as a model of non-alcoholic steatohepatitis (NASH).

Method: Two-days-old C57BL/6j male mice received a single subcutaneous streptozotocin (STZ) injection (100 mg/kg body weight). HFD intervention in the STZ-injected mice representing metabolic syndrome and improves liver injury in STAM mice as a model of non-alcoholic steatohepatitis (NASH).

Results: Atglistatin reduced body weight (−2.54 g), despite a comparable consumption of food between the STAM and Atglistatin groups. The bodyweight reduction was due to a decrease in fat (−40%) and liver mass (−23%). Atglistatin treatment significantly improved fasting blood sugar (−12%). Interestingly, the intestinal length was longer (+50%) in the Atglistatin mice in comparison to the STAM mice.

Conclusion: Atglistatin reduced body weight (−2.54 g), despite a comparable consumption of food between the STAM and Atglistatin groups. The bodyweight reduction was due to a decrease in fat (−40%) and liver mass (−23%). Atglistatin treatment significantly improved fasting blood sugar (−12%). Interestingly, the intestinal length was longer (+50%) in the Atglistatin mice in comparison to the STAM mice.
In line with a trend for reduced ALT, there was a significant improvement in histological liver injury assessed by H&E staining and NAFLD score (−45%). The NAFLD score revealed improvement of steatosis (−60%) and inflammation (−35%) but not ballooning in the Atglistatin group. Immunohistochemistry showed that Atglistatin treatment significantly reduces Mac2 positive cells in the liver (−50%) and gonadal white adipose tissues (gWAT) (−60%) compared to the untreated STAM group, indicating a reduced infiltration of immune cells into the liver and gWAT.

**Conclusion:** Atglistatin improved metabolic features and liver injury in the STAM mice by reducing inflammation and fat accumulation in key metabolic tissues such as the liver, the adipose tissue, and the intestine.

**SAT050**

Methionine adenosyltransferase 1a antisense oligonucleotides induce the fibroblast growth factor 21-driven recovery from obesity and associated hepatoestenosis

Xabier Buque1, Diego Saenz de Urturi1, Begoña Porteiro2,3, Cintia Folgueira4, Alfonso Mora4, Teresa Cardoso Delgado5,6, Endika Prieto-Fernández7, Paula Olazola4,8,9, Beatriz Gómez Santos1, Maider Apodaka-Biguri1, Francisco González-Romero1, Ane Nieva-Zuluaga1, Mikel Ruiz de Gauna1, Naroa Goikoetxea8,6, Juan Luis García Rodríguez1, Virginia Gutiérrez de Juan5,6, Ikerbasque Basque Country University, Physiology, Leioa, Spain; 2Department of Physiology, CIMUS, University of Santiago de Compostela-Instituto de Investigación Sanitaria, Spain; 3CIBER Fisiopatología de la Obesidad y Nutrición (CIBERobn), Spain; 4Myocardial Pathophysiology, Centro Nacional de Investigaciones Cardiovasculares (CNIC), Spain; 5Liver Disease Laboratory, CIC bioGUNE-BRTA (Basque Research and Technology Alliance), Spain; 6Centro de Investigación Biomédica en Red de Enfermedades Hepáticas y Digestivas (CIBERehd), Spain; 7Department of Genetics, Physical Anthropology and Animal Physiology, Faculty of Science and Technology and Faculty of Medicine and Nursing, University of the Basque Country UPV/EHU, Spain; 8Department of Liver and Gastrointestinal Diseases, Biodonostia Health Research Institute-Donostia University Hospital, University of the Basque Country (UPV/ EHU), Spain; 9Ikerbasque, Basque Foundation for Science, Spain; 10Gene regulatory Control in Disease, CIMUS, University of Santiago de Compostela- Instituto de Investigación Sanitaria, Spain; 11IONIS Pharmaceuticals, Inc., United States; 12Department of Biochemistry and Genetics, School of Sciences, University of Navarra, Spain; 13Division of Gastroenterology and Hepatology, Medical University of South Carolina, United States; 14Section of Gastroenterology, Ralph H Johnson, V AMC, United States; 15Division of Gastroenterology and Hepatology, Medical University of South Carolina, United States; 16Ikerbasque Basque Research Institute, Spain.

**Background and aims:** High methionine and S-adenosylmethionine (SAMe) serum levels are related with obesity and both high and low liver SAMe levels promote non-alcoholic fatty liver disease with age. Dietary methionine restriction and deficiency in some enzymes of the methionine cycle confer resistance to obesity development. Here we investigated: i) if the pharmacological knockdown (KD) of methionine adenosyltransferase (Mat1a) gene, expressed exclusively in liver and which product synthesizes SAMe, provides beneficial outcomes in obesity and comorbidities. ii) The mechanism and molecular agents implicated in these outcomes.

**Method:** Liver Mat1a was silenced in high-fat diet (HFD)-fed and in genetically obese mice using antisense oligonucleotides (ASO). Liver specific fibroblast growth factor (Fgf21) knockout (KO) mice were used and KD of brown adipose tissue (BAT) β-klotho and Ucp-1 was performed. Changes in body weight, glucose and fat metabolism and energy expenditure were analyzed together with liver and BAT histologies and metabolic fluxes. Primary cultures of hepatocytes from HFD-fed Mat1a or control ASO-treated mice were also used.

**Results:** In HFD-fed and in genetically obese mice, Mat1a silencing induced thermogenesis leading to a pronounced weight loss and reversal of insulin resistance and hypertriglyceridemia. Mat1a ASO
background aims: The PNPLA3 I148M variant explains >10% of the risk of cirrhosis but the underlying pathophysiology remains unknown. We studied the effect of this variant on hepatic metabolism in vivo under multiple physiological conditions by combining a recruit-by-genotype approach with state-of-the-art stable isotope techniques.

Method: We recruited a total of 93 healthy participants (mean age 53 ± 1 yrs, BMI 30 ± 1 kg/m², 19% men; 37 homozygous carriers [148MM] and 56 non-carriers [148II]). Hepatic de novo lipogenesis (DNL) was assessed in 48 participants after an overnight fast using D_2O (148MM, n = 19; 148II, n = 36). Hepatic fate of exogenous fatty acids (FA) was determined in 26 participants using a mixed meal enriched in [13C]-labeled FA (148MM, n = 12; 148II, n = 14). Rates of endogenous glucose production, ketogenesis and hepatic mitochondrial citrate synthase flux were assessed in 12 participants before and after a 6-day ketogenic diet by Positional Isotopomer NMR Tracer Analysis (PINTA) by infusing [3-13C]-lactate, [13C4]-beta-hydroxybutyrate (BOHB) and [2H7]-glucose (148MM, n = 6; 148II, n = 6). Intrahepatic triglycerides (IHTG) were assessed by 1H magnetic resonance spectroscopy and hepatic mitochondrial redox state was assessed by the ratio of plasma [BOHB] and [acetoacetate].

Results: After an overnight fast, the 148MM group had higher plasma BOHB concentrations (+104%, p < 0.05) and lower DNL (-47%, p < 0.01) than the 148II group, independent of plasma FA and insulin concentrations. After a mixed meal, exogenous [13C]-labeled FAs in the 148MM group were channeled more towards ketogenesis (+265%, p < 0.05), increased plasma BOHB (+90%, p < 0.05), 2) increased mitochondrial redox state and 3) decreased rates of hepatic mitochondrial citrate synthase flux (-31%, p < 0.01). Plasma concentrations of GDF-15, a mitochondrial stress marker, were also increased by 40% (p < 0.01) in the 148MM group compared to the 148II group.

Conclusion: Homozygous PNPLA3 I148M carriers have alterations in both intrahepatic anabolic/catabolic processes and mitochondrial function as reflected by increased rates of hepatic lipolysis, decreased rates of DNL and increased hepatic mitochondrial beta oxidation/ketogenesis. These changes in turn were associated with an increased mitochondrial redox state and reductions in hepatic mitochondrial citrate synthase flux. Taken together these results

Background and aims: Targeting Mat1a reverses obesity, dyslipidemia, insulin resistance and hepatosteatosis through the hepatocyte secretion of FGF21 in a mechanism driven by NRF2.

SATO51
NLRP3 inflammasome dependent cell death in myeloid cells drives liver inflammation and fibrosis in murine steatohepatitis
Benedikt Kaufmann1,2, Agustina Reca3, Aleksandra Leszczynska1, André D. Kim1, Laela M. Booshehri1, Helmut Fries2, Daniel Hartmann2, Lori Broderick1, Hal M. Hoffman1, Ariel Feldstein1.
1Department of Pediatrics, University of California San Diego, La Jolla; 2Department of Surgery, TUM School of Medicine, Klinikum rechts der Isar, Technical University of Munich
Email: benedikt.kaufmann@hotmail.com

Background and aims: Non-alcoholic fatty liver disease (NAFLD) is the leading cause of chronic liver disease worldwide showing a rapidly rising prevalence among all age groups. Cellular death is crucial in the pathogenesis of NAFLD and driving liver inflammation as well as fibrosis. The NLRP3 inflammasome, a multiprotein complex promoting activation of caspase-1 as well as interleukin 1β (IL-1β) release, is recognized to promote programmed cell death in the form of pyroptosis. The cell-specific contribution of the activation of the NLRP3 inflammasome in myeloid cells in NAFLD remains unknown.

Method: A conditional Nlrp3 knock-out mouse was generated and bred to mice expressing Cre under the control of Lysozyme to recruit myeloid cells. Liver inflammation and fibrosis of pyroptosis. The cell-specific contribution of the activation of the NLRP3 inflammasome. The NLRP3 inflammasome, a multiprotein complex, is recognized to promote programmed cell death in the form of pyroptosis. The cell-specific contribution of the activation of the NLRP3 inflammasome in myeloid cells in NAFLD remains unknown.

Results: Myeloid-specific Nlrp3 knock-out resulted in a systemic and hepatic decrease of IL-1β release compared to control mice induced by LPS/ATP injection. NASH-associated cell death and hepatic inflammation was ameliorated in myeloid-specific Nlrp3 knock-out mice in the CDAA-HFAT model. In addition, fibrosis and hepatic stellate cell activation were decreased in myeloid-specific Nlrp3 knock-out mice.

Conclusion: This study provides new insights in the role of NLRP3 activation in myeloid cells in the pathogenesis of NAFLD and identifies myeloid specific NLRP3 inflammasome activation as crucial for the progression of NAFLD to fibrotic-NASH.

SATO52
The PNPLA3 I148M variant increases intrahepatic lipolysis and beta oxidation and decreases de novo lipogenesis and hepatic mitochondrial function in humans
Panu Luukkonen1,2,3,4, Kimmo Porthan1,3, Noora Ahlholm1,3, Fredrik Rosqvist5,6, Sylvie Dufour7,2, Xian-Man Zhang2,7, Juhani Dabek1,3, Tiina Lehtimäki8, Wenla Seppänen9, Marijo Orlo-Melander8, Leanne Hodson5, Kit Falk Petersen7, 2

1Department of Surgery, TUM School of Medicine, Klinikum rechts der Isar, Technical University of Munich; 2Minerva Foundation Institute for Medical Research, Helsinki, Finland; 3Yale School of Medicine, Department of Medicine, New Haven, United States; 4University of Helsinki, Department of Medicine, Helsinki, Finland; 5University of Oxford, Oxford Center for Diabetes, Endocrinology and Metabolism, Oxford, United Kingdom; 6Uppsala University, Department of Public Health and Caring Sciences, Clinical Nutrition and Metabolism, Uppsala, Sweden; 7Yale School of Medicine, Yale Diabetes Research Center, New Haven, United States; 8University of Helsinki and Helsinki University Hospital, Department of Radiology, HUS Medical Imaging Center, Helsinki, Finland; 9Lund University, Department of Clinical Sciences, Diabetes and Endocrinology, Malmö, Sweden; 10Yale School of Medicine, Department of Cellular and Molecular Physiology, New Haven, United States
Email: panu.luukkonen@finnnet.fi
provide new insights in the mechanisms by which the PNPLA3 I148M variant promotes liver disease (Figure).

SAT053
Two diseases, one model-assessing the suitability of FOZ mice to examine CVD in NAFLD
Sebastian Bott¹, Laurent Dumas², Dessy Chanta², Isabelle Leclercq³, Evangelos-Panagiotis Daskalopoulos⁴, Hrag Esfahani⁴. ¹Institute of Experimental and Clinical Research (IREC), Laboratory for Hepato-gastroenterology (GAEN), Brussels, Belgium; ²Institute of Experimental and Clinical Research (IREC), Pole of Pharmacology and Therapeutics (PATH), Université catholique de Louvain (UCL), Belgium; ³Institute of Experimental and Clinical Research (IREC), Pole of Pharmacology and Therapeutics (PATH), Université catholique de Louvain (UCL), Belgium; ⁴Institute of Experimental and Clinical Research (IREC), Laboratory for Hepato-gastroenterology (GAEN), Brussels, Belgium. Email: sebastian.bott@uclouvain.be

Background and aims: Non-alcoholic fatty liver disease (NAFLD) is an umbrella term which describes different states of liver disease, ranging from simple steatosis to non-alcoholic steatohepatitis (NASH), cirrhosis and finally hepatocellular carcinoma. NAFLD case numbers are constantly rising for three decades with around one quarter of the global population being affected today. Patients with NAFLD are at higher risk of developing cardiovascular disease (CVD), whereby most fatalities in CVD relate to atherosclerosis. Actually, CVD-dependent mortality is more frequent in patients with NAFLD in comparison to liver-related mortality. This association is related to the common metabolic risk factors such as obesity, dyslipidemia, diabetes, and hypertension shared by both NAFLD and CVD. Even more, NAFLD itself is considered as an independent risk factor for CVD (the leading cause of death globally), the link for this latter association is however still unknown. Established pre-clinical animal models only focus on one of the two diseases, yet. Therefore, the aim of this study was to assess the opportunity of using a single mouse model to examine NASH and cardiovascular disease concurrently to facilitate analysis of potential mechanistic links between both diseases.

Method: Male fat aussie mice (FOZ) and their age-matched wildtype (WT) controls were fed regular chow and high fat diet (60% kcal fat) for 24 weeks. Animals were then sacrificed, liver samples were gathered for histological assessment of the hepatic conditions, blood was sampled for determination of nitrosylated hemoglobin (HbNO) levels via electron paramagnetic resonance spectroscopy (EPR), the aorta was searched for atherosclerotic plaques and rings of first order mesenteric arteries were isolated and utilized in a wire myograph to assess carbachol (10^-8M to 10^-5M)-triggered nitric oxide (NO)-dependent relaxation to search for endothelial dysfunction, an early hallmark of atherosclerosis.

Results: FOZ mice on high fat diet (FH) featured all hepatic characteristics of progressive NASH (steatosis, ballooning, inflammation, fibrosis; NAFLD activity score = 8). Although no plaques in the aorta were found, a significant reduction in their mesenteric arterial NO-dependent relaxation at a carbachol-concentration of 10^-5M compared with wildtype mice on high-fat diet (WH) was detected; [p <0.05]; (A). In addition, EPR showed the lowest HbNO-level in FOZ mice fed a high-fat diet (B).

Conclusion: These results demonstrate suitability of the FOZ mouse model for studies to examine CVD in NAFLD since it develops all key characteristics of progressive liver disease and endothelial dysfunction, an essential hallmark in the development of atherosclerosis which represents the main cause of death in CVD.

SAT054
Oleic acid-induced acute lung injury in Ob/Ob mice fed with high-fat-diet exacerbate bile acid uptake and liver injury that was reversed by antagonizing their entry
Johnny Amer¹, Ahmed Salhab¹, Rifaat Safadi¹. ¹Hadassah Hebrew University Hospital, Liver Unit, Jerusalem, Israel. Email: johnnymamer@hotmail.com

Background and aims: Acute respiratory distress syndrome (ARDS) is a serious complication of COVID-19 and present in a large percentage of COVID-19 deaths. Many studies suggest that people with obesity are at increased risk of severe COVID-19, however, mechanism on liver-lung axis remains unknown. We aimed to evaluate whether bile acid (BAs) trafficking interfere with acute lung injury (ALI) in animal model with obesity.

Method: Leptin deficient (ob/ob) mice fed with high-fat-diet (Ob/Ob HFD) were i.p injected with oleic acid (OA) to induce ALI. To modulate BAs uptake, mice were i.p treated with neutralizing antibody for sodium taurocholate co-transporting polypeptide (NTCP; BAs-transporter). Broncho-alveolar lavage fluid (BALF), lungs, livers and serum were obtained from mice and assessed for inflammatory (HandE staining, ALT and pro-inflammatory panel of cytokines), fibrosis (Sirius red staining, a-smooth muscle actin, collagen and fibronectin) and metabolic (BAs, cholesterol, triglyceride, glucose tolerance test (GTT) and fasting blood sugar (FBS)) profiles. In addition, alveolar-capillary membrane injury of surfactant D (SP-D) and the receptor for advanced glycation end-products (RAGE). BAs trafficking were assessed in primary lung cells and their impact on proliferation and apoptosis were evaluated.

Results: Compared to WT-littermates, OA-induced lung injury and was worsened in the in the Ob/Ob HFD in the histopathology outcome. In addition, BALF of the Ob/Ob HFD showed elevated levels of BAs (3-fold; P = 0.002) associated with increased GM-CSF, INF-g, IL-1, IL-6 and IL-8 (p <0.01). Moreover, Ob/Ob HFD with OA showed elevated serum levels in liver enzymes, lipids, glucose and metabolic markers (p <0.01). In addition, Ob/Ob HFD livers showed an exacerbated fibrosis profile. NTCP neutralizing antibody in Ob/Ob HFD while inhibited BAs uptake/trafficking in both primary alveolar type II (BALF showed 4-fold increase in BAs) and primary hepatocytes livers showed 3-fold increase in BAs). SP-D, RAGE and serum metabolic
SAT055
The ubiquitin-like modifier FAT10 is upregulated during NASH and impairs PPAR-alpha activity

Ludivine Clavreul1, Alexia Coutte1, Lucie Bernard1, Joel Haas1, Nathalie Hennuyer1, An Verrijken2,3, Luc Van Gaal2,3, Sven Francque1,4, Guillaume Lassailly1, Bart Staels1, Réjane Paumelle1.
1University of Lille, EGID, Inserm, CHU Lille, Institut Pasteur de Lille, U1011, Lille, France, UMR 1011, LILLE, France; 2Faculty of Medicine and Health Sciences, University of Antwerp, Laboratory of Experimental Medicine and Paediatrics, Antwerp, Belgium; 3Antwerp University Hospital, University of Antwerp, Department of Endocrinology, Diabetology and Metabolism, Antwerp, Belgium; 4Antwerp University Hospital, Department of Gastroenterology and Hepatology, Antwerp, Belgium; 5CHU of Lille, University of Lille, Department of digestive system diseases, U995, LIRIC, Lille, France
Email: ludivine.clavreul.etu@univ-lille.fr

Background and aims: PPAR-alpha is a nuclear receptor involved in the regulation of lipid metabolism and inflammation in the liver. This transcriptional factor is known to prevent Non-alcoholic Steatohepatitis (NASH), a liver disease characterized by steatosis, inflammation, and ballooning. Indeed, PPAR-alpha is a promising target for the cure of this disease but its gene expression is decreased during NASH development. We show that FAT10, an ubiquitin-like protein known to be involved in proteasomal degradation, is overexpressed in NASH patient’s livers and is inversely correlated to PPAR-alpha expression suggesting a role for FAT10 on PPAR-alpha modulation in hepatocytes during NASH progression.

Method: FAT10 and PPAR-alpha hepatic expressions during NASH development were characterized in mice fed two or five weeks with a choline-deficient (CDAA) diet inducing NASH by transcriptomic analysis and immunofluorescence and correlated to histological grade of NASH. The impact of FAT10 modulation on PPAR-alpha expression was then investigated in vitro in HepG2 cell line using either a stable overexpression and cytokine treatment inducing FAT10, or siRNA inhibiting FAT10. QPCR and western-blot were performed to assess FAT10 and PPAR-alpha expressions and functional effects on lipid metabolism were quantified by BODIPY staining and Seahorse. Finally, the interaction between FAT10 and PPAR-alpha was observed with co-immunoprecipitation and Proximity Ligation Assay (PLA).

Results: In vivo, FAT10 expression is increased in murine NASH livers and associated to a decreased PPAR-alpha expression. In vitro, FAT10 overexpression reduces the expression of PPAR-alpha target genes while FAT10 down-regulation increases them. Moreover, FAT10 overexpressing cells accumulate more lipid droplets and have an impaired fatty acid beta-oxidation. Finally, PPAR-alpha and FAT10 co-immunoprecipitate in human hepatocytes, and this interaction was confirmed by PLA in vitro and in vivo.

Conclusion: These observations show that FAT10 is overexpressed during NASH and correlates negatively with PPAR-alpha expression. Furthermore, FAT10 overexpression is associated with an impaired PPAR-alpha transcriptional activity leading to an inhibition of lipid metabolism in hepatocytes. The interaction observed between FAT10 and PPAR-alpha suggests that FAT10 could be a new modulator of PPAR-alpha activity in hepatocytes during NASH progression.

SAT056
TNF-alpha knockout mice are protected from diet-induced NAFLD in a model of non-obese NAFLD

Katharina Burger1, Finn Jung1, Anja Baumann1, Annette Brandt1, Raphaela Stalfer1, Victor Sanchez1, Ina Berghelm1, 1University of Vienna, Department of Nutritional Sciences, Wien
Email: ina.bergheim@univie.ac.at

Background and aims: By now, non-alcoholic fatty liver disease (NAFLD) is the most common liver disease worldwide being strongly associated with obesity and insulin resistance but also with dietary pattern. The pro-inflammatory cytokine tumor necrosis factor alpha (TNF-alpha) is thought to be a critical factor in many overweight associated diseases including NAFLD; however, the impact of dietary pattern herein has not yet been fully understood. In the present study we determined the effect of a fat-, sucrose- and cholesterol rich diet in the development of NAFLD in the absence of obesity in TNF-alpha knock out mice (KO) and wild-type animals.

Method: Male TNF-alpha KO and wild-type C57BL/6j mice (6–8 weeks old, n = 8) were pair-fed either a liquid control diet (C) or a liquid fat-, sucrose-, and cholesterol-rich diet (FSC) for 9 weeks. A glucose tolerance test (GTT) was performed in week 8. Markers of liver damage and inflammation as well as insulin signaling were determined in liver tissue. TLR 2 and TLR 4 ligands e.g. lipoteichoic acid and endotoxin were determined using a SEAP reporter activity cell assay in portal plasma.

Results: Despite similar body weight FSC-fed wild-type mice developed liver steatosis with beginning inflammation and insulin resistance when compared to C-fed wildtype mice, whereas FSC-fed TNF-alpha KO mice were significantly protected from inflammatory alterations in liver and impaired glucose tolerance. In line with these findings, mRNA expression of interleukin 1 beta (IL-1ß) and interleukin 6 (IL-6), as well as levels of NOx were also significantly higher in livers of FSC-fed wild-type mice while being almost at level of control in FSC-fed TNF-alpha KO mice. Expression of insulin receptor substrate 1 (Irs1) in liver tissue was also significantly higher in livers of FSC-fed mice compared to all other groups, whereas expression in liver of FSC-fed TNF-alpha KO mice was at the level of controls. Levels of TLR 2 and TLR 4 ligands in portal plasma of both FSC-fed groups were higher than in C-fed groups.

Conclusion: Taken together results of the present study suggest that a lack of TNF-alpha may attenuate the development of diet-induced insulin resistance and NAFLD in mice also in settings of non-obesity induced NAFLD. (This project was funded in part by the Austrian Science Fund)

SAT057
Low dose thyroid hormone improves hepatic mitochondrial fatty acid oxidation and rescues non-alcoholic fatty liver disease in mice

Raghu Ramanathan1,2, Saraha Johnson3,4, Jamal Ibdah2,3,5, 1University of Missouri-Columbia, Department of Medicine-Gastroenterology and Hepatology, Columbia, United States; 2Harry S. Truman Memorial Veterans’ Hospital (VA), Columbia, United States; 3University of Missouri-Columbia, Department of Medicine-Gastroenterology and Hepatology, Columbia, United States; 4University of Missouri-Columbia, Department of Medicine-Physiology and Pharmacology, Columbia, United States; 5University of Missouri-Columbia, Department of Medical Pharmacology and Physiology, Columbia, United States
Email: ibdahj@health.missouri.edu

Background and aims: Non-alcoholic fatty liver disease (NAFLD) is the most common chronic liver disease in the world, with limited therapeutic options. Mitochondrial dysfunction and decreased hepatic mitochondrial fatty acid oxidation (FAO) have been linked to its etiology. Thyroid hormone (TH) is an important regulator of lipid metabolism and may have the potential to treat NAFLD but its use is associated with adverse systemic effects. We hypothesized that
low dose thyroid hormone, which has the advantage of reduced potential for systemic effects, is effective in improving hepatic FAO and rescue of NAFLD. To test this hypothesis, we compared the effects of TH dose on hepatic FAO, mitochondrial quality, and NAFLD histological features in mice.

**Method:** Six-month-old wild-type male mice with a C57BL/6 background maintained on chow diet were used to compare the effects of TH dose on hepatic FAO. Phosphate buffered saline (PBS) was given intraperitoneally (ip) to control mice (n = 8) for 7 days; treatment groups (n = 8 per group) received low doses of triiodothyronine (T3) at 1 and 5 mcg/100 g weight and a higher dose of 25 mcg/100 g weight ip for 7 days. Complete FAO levels in fresh liver lysate were determined after sacrifice. Mitochondrial trifunctional protein (MTP), the main enzyme complex that catalyzes the last three steps of mitochondrial FAO, and key genes regulating mitochondrial biogenesis and mitophagy were also evaluated. In addition, two-month-old male mice were fed western diet (Research Diets Inc, D12451 Rodent Diet, 45 kcal percent fat, 1 percent cholesterol) for 16 weeks to induce NAFLD, then injected with either PBS (n = 6) or 1 and 25 mcg T3/100 g weight ip for 7 days (n = 6 per group). Effects on hepatic FAO, mitochondrial quality markers, and liver histology were assessed.

**Results:** As shown in Figure 1, T3 at various doses resulted in a 4-fold increase in total hepatic CO2 production in mice fed chow diet (p < 0.001) and a 2-fold increase in mice fed a western diet (p < 0.05). There was no statistical difference between effects of lower and higher doses of T3 on FAO. Hepatic MTP protein and RNA expression levels remained unchanged in mice injected with T3 compared to control mice suggesting that T3-induced FAO is not due to increased FAO enzyme expression. RNA expression studies suggest that T3 improves mitochondrial mitophagy and biogenesis. Both lower and higher doses of T3 were effective in rescue of NAFLD in western diet-fed mice with significant histological improvement of steatosis and inflammation, and reduction of ALT levels (p < 0.05) compared to control mice.

**Conclusion:** TH at low dose improves hepatic FAO and rescues NAFLD in mice. This study suggests that low dose thyroid hormone is a potential treatment modality for NAFLD.

![Figure 1. TH dose and hepatic FAO.](image-url)
**Conclusion:** We report for the first time the 3D imaging of liver fibrosis pathology using an in-house developed light-sheet fluorescence microscopy system. Through the imaging of slide-free whole core liver biopsies, we showed that fibrosis variability occurs even in the different optical sections of the biopsy sample. Comprehensive mapping of hepatic extracellular matrix proteins and imaging of slide-free biopsy samples can improve the accuracy of histological assessment and stratification of NASH patients.

**SAT059**

### In vivo functional genetic screen with a pooled-shRNA library for therapeutic targets of non-alcoholic fatty liver disease

Yong-An Lee1, Chee Chong Lek1, Amanpreet Kaur1, Rong Gao1, Agnes Bee Leng Ong1, Yee Siang Lim2, Shireen Soh2, Winston Chan3, Yock Young Dan3, Huck Hui Ng4, Torsten Wuestefeld1,5,6, 1Genome Institute of Singapore (GIS), Laboratory of in vivo genetics and gene therapy, Singapore, Singapore; 2Genome Institute of Singapore (GIS), Laboratory of Precision Disease Therapeutics, Singapore, Singapore; 3Guangzhou Regenerative Medicine and Health Guangdong Laboratory, China; 4National University of Singapore, Department of Medicine, Singapore, Singapore; 5National Cancer Centre Singapore, Singapore, Singapore; 6Nanyang Technological University, School of Biological Sciences (SBS), Singapore, Singapore

**Background and aims:** With a rapidly increasing prevalence, non-alcoholic fatty liver disease (NAFLD) is recognized as the most common cause of chronic liver disease worldwide. The massive growth of NAFLD is causing a significant burden in health care with social and economic implications. However, unlike other highly prevalent diseases, it remains an underrepresented disease with social and economic implications. However, unlike other highly prevalent diseases, it remains an underrepresented disease with social and economic implications. Therefore, there is an urgent need to develop innovative therapies. To address this, we are combining patient samples’ transcriptomic profiling with the disease mouse models and in vivo functional genetic screens with the hope of developing therapeutics for this dreaded disease.

**Method:** We sequenced liver tissues from 130 patients covering different stages of NAFLD to determine dysregulated genes in the patients. Based on the transcriptomic data, a pooled transposon-based shRNA library targeting the dysregulated genes was generated for in vivo genetic screening. The library was directly and stably delivered into hepatocytes of two different mouse models by using hydrodynamic injection. Mice were fed with “Western Diet” supplemented with high fructose and Choline deficient L-amino acid defined high-fat diet (CDHFD) for two different models, respectively, to recapitulate human pathology of the NAFLD. As a control, normal chow-fed animals were served. Our approach’s underlying idea is that shRNAs that confer benefits to the hepatocyte in the detrimental environment of the disease will be enriched over time. At the end of diet treatment, livers were harvested, and the abundance of each shRNA was determined by deep sequencing. Highly enriched shRNAs were validated for their potential therapeutic impact by various studies, including in vitro assays for proliferation and in vivo by repopulating FAH-/- mice so that every hepatocyte expresses the shRNA of interest. Repopulated mice were exposed to NAFLD-inducing diets, and histopathology parameters were evaluated.

**Results:** Our screens have identified novel shRNAs highly enriched in the disease models. One of the shRNAs has been validated for reducing liver fibrosis in the CDHFD model, the aggressive NAFLD model. From the various in vitro and in vivo assays, the candidate gene silencing showed promoted regeneration of hepatocytes without tumor developments.

**Conclusion:** We show that combining the study of NAFLD patient liver transcriptome with in vivo functional genetic screening in the disease mice models could discover new candidates as therapeutic targets of the disease. We identified and validated a new target for treating NAFLD through our approach. We are currently investigating the underlying molecular mechanisms. Our study may contribute to new insights into the therapeutic development of the disease.

**SAT060**

### Hepatic insulin resistance is the basis of bile acid dysmetabolism in non-alcoholic fatty liver disease

Sami Qadri1,2, Emilia Vartiainen1,2, Noora Ahlholm1,2, Kimmo Por Thornton1,2, Anne Juutila3, Anne Sammalkorpi1, Johanna Arola1, Taru Tukiainen1, Matej Orešič3,4, Tuulia Hyötyläinen4, Hannele Yki-Järvinen1,2, 1University of Helsinki and Helsinki University Hospital, Department of Medicine, Helsinki, Finland; 2Minerva Foundation Institute for Medical Research, Helsinki, Finland; 3University of Helsinki, Institute for Molecular Medicine Finland, FIMM, Helsinki, Finland; 4University of Helsinki and Helsinki University Hospital, Department of Pathology, Helsinki, Finland; 5Örebro University, School of Medical Sciences, Örebro, Sweden; 6University of Turku and Aboa Akademi University, Turku Bioscience Centre, Turku, Finland; 7Örebro University, School of Science and Technology, Örebro, Sweden

**Background and aims:** Non-alcoholic fatty liver disease (NAFLD) is associated with increased circulating bile acids (BAs). It is unknown whether this reflects altered intrahepatic BA metabolism due to NAFLD or the associated insulin resistance (IR). To dissociate steatosis from IR, we compared BA metabolism in NAFLD associated with either IR or high genetic risk.

**Method:** In 106 patients undergoing a liver biopsy, we analysed serum/liver BAs, the hepatic transcriptome (RNA-seq), and concentrations of plasma FGF-19 (marker of intestinal BA metabolism). Using HOMA-IR and a validated weighted Polygenic Risk Score (PRS) for NAFLD, we divided the patients into matched groups to compare the effects of NAFLD associated with IR (‘High HOMA-IR’ vs. ‘Low HOMA-IR’) or with high genetic risk (‘High PRS’ vs. ‘Low PRS’) on BA metabolism.

**Results:** An untargeted analysis identified distinct clusters of patients with simultaneously increased BAs, HOMA-IR, and liver fat content. Compared to ‘Low HOMA-IR’, patients with ‘High HOMA-IR’ had significantly higher total (+57%, P = 0.011) and especially conjugated (+82%, P = 0.002) serum BAs, but unchanged hepatic BAs. Expression of the primary hepatic BA uptake transporter NTCP was downregulated, while plasma FGF-19 was unchanged. Despite having the same degree of steatosis and NASH compared to the ‘High HOMA-IR’ group, patients with ‘High PRS’ had similar serum/liver BAs
We studied 89 patients with a biopsy-proven NAFLD and 20
understanding of NAFLD pathophysiology.

Conclusion: In NAFLD without advanced fibrosis, serum BAs are
increased due to IR, which may impair hepatocellular BA uptake. Intrahepatic BAs are unchanged in NAFLD.

SAT061
Non-alcoholic fatty liver disease features a reduced reverse
dysfunction and/or with the necro-inflammatory milieu in NASH.
Conclusion: Taken together, these data show that NAFLD is
associated with a reduced absolute content of polyunsaturated FFA
and phospholipids within HDL. We, therefore, speculate that an
impaired PUFAs transport from peripheral tissues to the liver (via FFA
and HDL) might be a contributing factor in NAFLD pathophysiology
(Fig. 1E).

Background and aims: Non-alcoholic steatohepatitis (NASH) is
associated with the dysregulation of lipid metabolism and hepatic
inflammation. The mechanism underlying NASH is unclear. We aim to
investigate the role of X-box binding protein-1 (XBP1) in the
progression of NASH.

Method: Human liver tissues obtained from patients with NASH and
control group were used to assess XBP1 expression. NASH models
were developed in hepatocyte-specific Xbp1 knockout (Xbp1–/–), macrophage-specific Xbp1 deletion (Xbp1â–), macrophage-
specific Nlrp3 knockout, and wild-type (Xbp1â–/â– or Nlrp3â–/â–) mice fed with high-fat diet for 26 weeks or methionine/choline
deficient diet for 6 weeks.

Results: The expression of XBP1 was significantly upregulated in the
liver samples from NASH patients. Hepatocyte-specific Xbp1 defi-
cency inhibited the development of steatohepatitis in the mice fed
with the high-fat or methionine/choline deficient diets. Meanwhile,
macrophage specific Xbp1 knockout mice developed less severe
steatohepatitis and fibrosis than wild-type Xbp1â–/â– mice in response to the high-fat or methionine/choline deficient diets.

Macrophage-specific Xbp1 knockout mouse showed M2 anti-inflam-
matory polarization. Xbp1 deleted macrophages reduced steato-
hepatitis less severe in macrophage-specific Nlrp3 knockout mice than in wild-type Nlrp3â–/â– mice. Xbp1 deleted macrophages prevented the
hepatic stellate cells activation through decreased expression of TGF-
β1. Less fibrotic changes were observed in macrophage-specific Xbp1
knockout mice than in the wild-type Xbp1â–/â– mice. Inhibition of
XBP1 suppressed the development of NASH.

Conclusion: XBP1 regulates the development of NASH. XBP1
inhibitors protect against steatohepatitis. XBP1 thus is a potential
target for the treatment of NASH.
SAT063 FXR binding and transcription in the liver is significantly altered in obese patients with NAFLD

Martin Wagner1, Emilian Jungwirth 1, 2, Katrin Panzitt 1, David Moore3, Tobias Madl4, Gerhard Thallinger 2, Hanns-Ulrich Marschall 5.

1Division of Gastroenterology and Hepatology, Medical University Graz, Graz, Austria; 2Institute of Biomedical Informatics, Graz University of Technology, Graz, Austria; 3Nutritional Sciences and Toxicology, University of California, Berkeley, Berkeley, United States; 4Division of Molecular Biology and Biochemistry, Medical University Graz, Graz, Austria; 5Department of Molecular and Clinical Medicine/Wallenberg Laboratory, Sahlgrenska Academy, University of Gothenburg, Gothenburg, Sweden

Email: martin.wagner@medunigraz.at

Background and aims: FXR binds to distinct hormone response elements on the chromatin to dictate gene regulation. In mice, these genomic FXR binding profiles are distinct in normal and obese mice, suggesting that FXR activation may produce different outcomes in a different metabolic background. We studied FXR binding profiles and transcriptional outputs in the livers from normal weight and morbidly obese patients with NAFLD, who were treated with either placebo or the FXR ligand obeticholic acid (OCA).

Method: We tested the hepatic FXR cistrome by FXR ChIP-seq and the transcriptome by RNA-seq in liver biopsies of normal and morbidly obese human subjects who had been enrolled in a clinical trial for the treatment with the FXR agonist OCA (NCT0162502). We matched the outcomes of these genomic studies with metabolic profiles of those patients.

Results: In ChIP-seq, a method to determine transcription factor binding on a genome-wide scale, FXR binding sites are inherently different between obese and non-obese patients. In obese patients, FXR bound 26605 sites and only 10270 in non-obese patients. Interestingly, while OCA could recruit additional binding sites in non-obese patients, OCA did not affect FXR binding in obese patients. To explore, which gene sets are selectively targeted by OCA-driven FXR activation in obese patients we integrated the FXR ChIP-seq data with their respective RNA-seq data. In contrast to FXR binding, which remained unaffected by OCA treatment, OCA significantly altered the transcriptome in RNA-seq (1456 genes were up- and 1674 genes downregulated by OCA) in obese patients. Integration of FXR cistromics with transcriptomics revealed activation of “classical” FXR targeted pathways such as bile acid or fatty acid metabolism, however, the top ranked differentially regulated pathways belonged to mitochondrial function. In line with the obese-specific “mitochondrial fingerprint,” PGC-1α, a transcriptional master-regulator of mitochondrial biogenesis, appears to be a direct hepatic FXR target.
Background and aims: Non-alcoholic fatty liver disease (NAFLD) is notoriously heterogeneous in both its pathophysiology and clinical progression phenotypes. Endoplasmic reticulum stress and the coping response through the Unfolded Protein Response (UPR) have shown to play a significant role in NAFLD-related lipotoxicity. Nevertheless, the dissection of the UPR activation in human and mouse NAFLD progression is poorly understood. The aim of this study was to gain a better understanding of the UPR activation in NAFLD progression.

Method: A total of six main regulators were identified as indicators of activation of different UPR-related pathways. The selected components belonged to the three arms of the UPR, named PERK/ATF4, IRE1A/XBP1 and ATF6. SIRT3 was considered the main regulator of the mitochondrial UPR. An exhaustive compilation of gene expression data was carried out from existing literature and Molecular Signature Database (MSigDB) curated collections and using unpublished RNA-sequencing data of the ATF6-null HCC cell line. Gene signatures were filtered and fine-tuned using controlled in vitro experimentation using tunicamycin-treated HCC cell lines. Mus musculus gene symbols were replaced by their human orthologs. Gene set variation analysis (GSVA) and single sample Gene Set Enrichment Analysis (ssGSEA) were used to analyze the enrichment of the UPR signatures in human and mouse expression datasets. Statistical analysis was performed using t-test for comparing means of normally distributed continuous variables and Chi-Square was used for comparing categorical variables.

Results: Forty-seven preliminary signatures in both Homo sapiens and Mus Musculus were defined. After fine-tuning and filtering using controlled ER-stress cell model, a final set of sixteen bona fide UPR signatures were derived, which included 358 genes, distributed along 2 ATF4, 2 ATF6, 3 IRE1A, 7 XBP1, 1 PERK and 1 SIRT3 signatures. Using GSVA and ssGSEA these signatures were applied to two NAFLD progression (n = 304 patients, different stage of NAFLD progression F0–4) and two NASH–Hepatocellular Carcinoma (NASH–HCC) (n = 180 samples, including Normal, Cirrhosis, NASH and NASH–HCC and their peritumoral liver counterparts), human data sets. As NAFLD progresses to NASH and NASH–HCC, the expression of UPR branches is generally decreased. Patients can be split into distinctive groups regarding specific UPR profiles.

Conclusion: NAFLD progresses to NASH and NASH–HCC showing specific patterns of ER stress responses. The application of bona fide UPR signatures to human NAFLD gene expression data sets, allows for a UPR-based classification that could have potential prognostic and/or predictive value.
Background and aims: Non-alcoholic steatohapatitis (NASH), the inflammatory subtype of non-alcoholic fatty liver disease (NAFLD) associated with obesity and type 2 diabetes mellitus (T2DM), can lead to advanced liver disease. There are limited data evaluating T cell subsets in multiple tissue compartments or following weight loss in NAFLD. We hypothesised that circulating and tissue T cells changed in advanced versus mild NASH.

Method: Prospective samples were collected under ethically-approved protocols; peripheral blood from 37 NAFLD patients and 7 controls, with primary comparisons between advanced (elastography ≥9.7 kPa or ≥F3) and mild (elastography <8.2 kPa or ≤F2) NAFLD. A subset undergoing bariatric surgery (n = 21) underwent additional simultaneous sampling of liver, visceral (VAT) and subcutaneous adipose tissue (SAT) for flow cytometry immuno-profiling, with further blood samples after weight loss.

Results: Peripheral blood MAIT cells were significantly reduced with greater activation in patients with advanced versus mild NAFLD or controls (0.8% vs 3.1%, 3.2% p < 0.05) although IFN gamma and TNF alpha expression was higher in all NAFLD MAIT cells (IL-17 in advanced) compared to control.

In bariatric patients, Th1 (CD4⁺CXCR3⁺) cells were more abundant in NASH vs no-NASH (33% vs 21% p < 0.05), particularly among patients with diabetes in whom pro-inflammatory Th1 and Th17 cells (CD4⁺CD161⁺) expressed higher levels of liver homing CXCR6.

After weight loss, the proportion of Th1, Th17 cells and activated (CD69⁺) CD8⁺ T cells reduced. The proportion of CXCR6⁺ Th1 and Th17 cells reduced, as did IFN gamma expressing CXCR6⁺Th17 cells.

In patients with T2DM NASH, intrahepatic Th17 cell numbers were higher and MAIT cells lower compared to other patient groups, with a similar reduction of MAIT cells in SAT. Conversely, SAT total T cell CXCR6 expression was higher in T2DM NASH than in other patient groups. In T2DM NASH, expression of tissue-retaining CD69 expression on Th1 cells was higher in the liver and lower in VAT.

Conclusion: A peripheral and adipose tissue pro-inflammatory, liver-homing T cell phenotype is evident in patients with T2DM and NASH with improvement in this after weight loss.

SAT067
Therapeutic inhibition of complement component 5 does not reduce NASH progression but does attenuate atherosclerosis development in Ldlr⁻/⁻-Leiden mice
Florence Seidel¹,², Robert Kleemann¹, Wim van Duyvenvoorde¹, Nikki van Triet¹, Sandra van der Kooij³, Cees van Kooten¹, Lars Verschuren³, Aswin L. Menke¹, Lars Verschuren³, Aswin L. Menke¹, Johnathan Winter³, Timothy Hughes³, Paul Morgan⁵, Frank Baas⁵, Kees Fluiter⁴, Martine C. Morrison¹, Amanda Kiliaan², the Netherlands Organisation for Applied Scientific Research (TNO), Metabolic Health Research, Leiden, Netherlands; Radboud University Medical Center, Medical Imaging (Anatomy), Nijmegen, Netherlands; Leiden University Medical Center (LUMC), Internal Medicine (Nephrology), Leiden, Netherlands; the Netherlands Organisation for Applied Scientific Research (TNO), Systems Biology, Zeist, Netherlands; Cardiff University, Systems Immunity Research Institute and UK Dementia Research Institute Cardiff, School of Medicine, United Kingdom; Leiden University Medical Center (LUMC), Clinical Genetics, Leiden, Netherlands

Email: florine.seidel@tno.nl

Background and aims: With the increased mortality that is associated with the obesity-related comorbidities non-alcoholic steatohepatitis (NASH) and atherosclerosis, there is a great need for therapeutic interventions to treat advanced stages of these diseases. Chronic inflammation has been shown to be an important driver in progression of both NASH and atherosclerosis. The complement system, one of the first lines of defence in innate immunity, is thought to play an important role in this chronic inflammatory response. However, the therapeutic value of complement system inhibition in already established disease has not been studied to date. In this study we investigated the potential health effects of therapeutic inhibition of the terminal complement system (via inhibition of complement component 5 (C5)) simultaneously on established NASH and atherosclerosis in a translational model of obesity-related disease.

Method: After 20 weeks of high-fat diet (HFD)-feeding, obese Ldlr⁻/⁻-Leiden mice were treated bi-weekly with an established anti-C5 antibody (BB5.1) or vehicle control, and a separate group of mice was kept on a chow diet as a healthy reference. To confirm adequate inhibition of C5, the complement system activity in plasma as well as the membrane-attack complex (MAC) deposition in the liver were quantified. After 12 weeks of treatment, NASH was analysed histopathologically and genome-wide hepatic gene expression was analysed by next-generation sequencing followed by pathway analysis. Atherosclerotic lesion area and severity were quantified histopathologically in the aortic roots.

Results: Anti-C5 treatment considerably reduced complement system activity in plasma and MAC deposition in liver. The histological examination of livers revealed that systemic anti-C5 treatment did not affect NASH progression, showing no effect on steatosis, inflammation or fibrosis. However, on the gene expression level, anti-C5 treatment did affect the pathways Oxidative phosphorylation and Mitochondrial dysfunction. Anti-C5 treatment was also revealed to be beneficial against atherosclerosis, limiting the total lesion size independently of an effect on plasma cholesterol. In addition, C5 inhibition reduced lesion severity, increasing the area of mild type I-III lesions and lowering the area of severe type IV and V lesions.

Conclusion: We show for the first time that targeting the complement system via C5 inhibition in advanced stages of NASH is not sufficient to reduce disease development, while therapeutic intervention against moderately-advanced atherosclerosis is beneficial to limit further progression of the lesions.

SAT068
The overexpression of TM6SF2 and/or MBOAI7 wild-type genes re-establishes the mitochondrial dynamics in an in vitro NAFLD model.
Erika Paolini¹,², Miriam Longo¹,³, Marica Meroni¹, Giada Trias¹, Chiara Macchi¹, Roberto Picciotto¹,², Adèle Agrèsta¹, Massimiliano Ruscia², Anna Ludovica Fracanzani¹,³, Paola Dongiovanni¹,³, General medicine and metabolic diseases. Fondazione IRCCS Cà Granda ospedale maggiore Policlinico; Università degli Studi di Milano, Milan, Italy, Department of Pharmacological and Biomolecular Sciences; Università degli Studi di Milano, Milan, Italy, Department of clinical sciences and community health, Università degli studi di Milano; Università degli Studi di Milano, Milan, Italy, Department of Pathophysiology and Transplantation
Email: paola.dongiovanni@policlinico.mi.it

Background and aims: Mitochondria adaptability is hampered in the progression from NASH up to HCC. Recently, we demonstrated that HepG2 cells, homoygous for the PNPLA3 I148M variant, and silenced
for MBOAT7 and/or TM6SF2 genes by CRISPR/Cas9 spontaneously developed fat accumulation, exhibited an enrichment of damaged mitochondria, an imbalance in their turnover and finally a higher proliferation rate together with reduced apoptosis. In the attempt to deepen the impact of PNPLA3/MBOAT7/TM6SF2 loss-of-function on mitochondrial abnormalities, we aim to assess whether the overexpression of MBOAT7 and/or TM6SF2 wild-type forms restores the mitochondrial dynamics which was lost in knock-out (KO) models.

**Method:** MBOAT7 and/or TM6SF2 were overexpressed through lentiviral vectors. Mitochondrial morphology and number were assessed by confocal microscopy and D-loop TaqMan Copy Number Assay whereas the function was evaluated by qRT-PCR, Western Blot, Seahorse assay and immunohistochemistry.

**Results:** At Oil Red O staining, the overexpressed cells exhibited a reduction of lipids compared to KO models. The upregulation of MBOAT7 and/or TM6SF2 lowered D-loop levels and increased spaghetti-like globular shape ratio of mitochondria, enhancing the number of normo-shaped ones. The overexpressed models reduced the mRNA levels of PGC1α, master regulator of mitobiogenesis, which was activated in KO cells in response to fusion-fission unbalance, prompted the expression of Mfn1 and Mfn2 (mitochondrial outer membranes proteins involved in fusion) and decreased FIS1 (fission protein) levels, thus re-establishing the mitochondrial turnover. The increased COX-I/SOD2 ratio paralleled the oxygen consumption rate after the overexpression of MBOAT7 and/or TM6SF2, recovering the OXPHOS activity which was impaired in KO cells. Consistently, ROS content, lipid peroxidization and ER/Golgi stress (OXPHOS activity which was impaired in KO cells). Transcriptome analysis showed that IL6-JAK1-STAT3 signaling pathway was significantly enriched in CD1d−/− HFD group compared with WT HFD group. The gene expression level in CD1d−/− HFD group was significantly increased compared with WT HFD group. In vitro studies showed that CD1d gene knockout aggravated FFA-induced NAFL lipid droplet formation and lipid deposition. AG490 inhibition of IL6-JAK1-STAT3 signaling pathway alleviates liver steatosis and down-regulates the gene expression level of lipid metabolism in THE CD1d knockout NAFL group. The expression level of liver immune cells in CD1d−/− HFD group was lower than that in WT HFD group. Compared with WT NCD group, the expression level of immune cells and inflammatory factors was increased in WT MCD group. The expression levels of liver immune cells and inflammatory factors in CD1d−/− MCD group were lower than those in WT MCD group. The expression level of M2-polarized surface markers in macrophages in CD1d−/− MCD group was higher than that in WT MCD group, while the expression level of M1-polarized surface markers in macrophages was lower. CD1d gene knockout aggravated FFA-induced lipid accumulation in mouse laparoscopic macrophages, inhibited M1 polarization of peritoneal macrophages, and promoted M2 polarization of peritoneal macrophages. CD1d gene knockout aggravated fatty acid induced lipid accumulation in mouse BMDM cells, inhibited M1-type polarization of BMDM cells, and promoted the M2-type polarization.

**Conclusion:** Genetics may be involved in the mitochondrial maladaptation during NAFLD and the overexpression of MBOAT7 and/or TM6SF2 in KO HepG2 cells re-established the mitochondrial dynamics and reduced the proliferation rate.

**SAT069**

CD1d knockdown promotes NAFL lipid synthesis by activating the IL6-JAK1-STAT3 signal pathway and reduces inflammatory factors in NASH by decreasing macrophage polarization towards M1 and increasing polarization towards M2

Dandan Shan1,2, Qiuxian Zheng1, Zhi Chen1. Hangzhou, Diagnosis and Treatment of Infectious Diseases, Hangzhou, China; 1The First Affiliated Hospital, Zhejiang University School of Medicine, Hangzhou, China Email: zjuchenzhi@zju.edu.cn

**Background and aims:** Non-alcoholic fatty liver disease (NAFLD) is a chronic progressive liver disease. NAFLD involves multiple complex biological effects that help activate innate and adaptive immunity and exacerbate NAFLD development. CD1d proteins mediate the delivery of self or microbial lipid and glycolipid antigens to activate immune cells, rapidly produce large amounts of cytokines, and trigger innate and adaptive immune responses. Here, we explored the role for CD1d in NAFLD.

**Method:** Flow cytometry and Cytometry by Time of Flight (CyTOF) was used to measure and analyze the expression level of markers on the surface of immune cells in liver tissues of NAFL mice, and the distribution map of immune cells was established. M1 and M2 macrophages in liver tissues was also detected.

**Results:** Compared with the WT HFD group, the CD1d−/− HFD group mice showed a significant increase in liver index, a significant increase in liver steatosis (p < 0.05), ALT level (p < 0.01), AST level (p < 0.05) and a significant increase in serum LDL level (p < 0.01). Transcriptome analysis showed that IL6-JAK1-STAT3 signaling pathway was significantly enriched in CD1d−/− HFD group compared with WT HFD group. The gene expression level in CD1d−/− HFD group was significantly increased compared with WT HFD group. In vitro studies showed that CD1d gene knockout aggravated FFA-induced NAFL lipid droplet formation and lipid deposition. AG490 inhibition of IL6-JAK1-STAT3 signaling pathway alleviates liver steatosis and down-regulates the gene expression level of lipid metabolism in THE CD1d knockout NAFL group. The expression level of liver immune cells in CD1d−/− HFD group was lower than that in WT HFD group. Compared with WT NCD group, the expression level of immune cells and inflammatory factors was increased in WT MCD group. The expression levels of liver immune cells and inflammatory factors in CD1d−/− MCD group were lower than those in WT MCD group. The expression level of M2-polarized surface markers in macrophages in CD1d−/− MCD group was higher than that in WT MCD group, while the expression level of M1-polarized surface markers in macrophages was lower. CD1d gene knockout aggravated FFA-induced lipid accumulation in mouse laparoscopic macrophages, inhibited M1 polarization of peritoneal macrophages, and promoted M2 polarization of peritoneal macrophages. CD1d gene knockout aggravated fatty acid induced lipid accumulation in mouse BMDM cells, inhibited M1-type polarization of BMDM cells, and promoted the M2-type polarization.

**Conclusion:** CD1d plays a protective role in the process of NAFL steatosis, and CD1d deficiency can increase hepatic lipid accumulation and hepatic steatosis by activating il6-JAK1-STAT3 signaling pathway. In NASH stage, CD1d deficiency can promote M2-type polarization of macrophages by inhibiting M1-type polarization of macrophages, thus reducing the level of liver inflammation.
SAT070
The role of immune semaphorins in NAFLD-a pilot study
Ivana Knezevic Stromar1, Maja Mijic2, Lara Samadan3, Slavko Gasparov2, Adriana Vince1,4, Neven Papic1,4, 1University hospital centre Zagreb, Zagreb, Croatia; 2University hospital Merkur, Zagreb, Croatia; 3School of medicine, University of Zagreb, Zagreb, Croatia; 4University hospital for infectious diseases Zagreb, Zagreb, Croatia.

Background and aims: Non-alcoholic fatty liver disease (NAFLD) is associated with chronic low-grade inflammation, impaired immune response and microvascular endothelial dysfunction. Semaphorins, a large family of biological response modifiers, were recently recognized as one of the key regulators of immune response, possibly also associated with chronic liver diseases. However, their role in NAFLD has not been described. The aim of this study was to identify semaphorins associated with NAFLD and to investigate relationship with steatosis and fibrosis stages.

Method: This was a prospective, multicentric, case-control study. The degree of steatosis was estimated using the controlled attenuation parameter (CAP) and transient elastography (TE) was used to measure fibrosis stage. A routine clinical, demographic, anthropometric and laboratory data were collected and serum semaphorin concentrations (SEMA3A, −3C, −4A, −4D, −5A and −7A) were measured by ELISA. Immunohistochemical staining of liver tissue was performed. The correlation between serum semaphorin concentrations and steatosis and fibrosis grade was analyzed.

Results: Ninety-five patients with NAFLD (51.6% males; median age of 54, IQR 44-56 years) and 35 controls (40% males, 41, IQR 31–52 years) were included. Patients with NAFLD more frequently had diabetes mellitus (30.5% vs 8.6%), arterial hypertension (49.5% vs 8.6%), dyslipidemia (28.4% vs 11.4%) and obesity (BMI 31 kg/m2 vs 24 kg/m2). 39 patients with NAFLD had no fibrosis (F0), and in 27, 15, 6 and 8 patients F1 to F4 was detected, respectively. A significantly higher serum concentrations of SEMA3A, −3C and −4D, and lower of SEAMA5A and −7A were found in NAFLD group compared to the healthy controls. There was no difference in semaphorin concentrations according to steatosis grade, but there was significant difference according to fibrosis stage, SEMA3A being lower and SEAMA3C and −4D higher in advanced fibrosis. Immunohistochemistry confirmed the higher expression of SEMA3C and SEMA4D in advanced fibrosis.

Conclusion: We provide the first evidence that immune semaphorins are novel markers of liver fibrosis in patients with NAFLD. Due to their immunomodulatory role, they could be useful in predicting liver capacity to answer challenges of infection, but also potential diagnostic and therapeutic targets in NAFLD.

Figure: SEMA3A, −3C, −4A, −4D, −5A and −7A sera concentrations according to the steatosis and fibrosis stage in patients with NAFLD.

SAT071
Machine learning-enabled continuous scoring of histologic features facilitates prediction of clinical disease progression in patients with non-alcoholic steatohepatitis
Janani Iyer1, Charles Biddle-Snead1, Quang Le1, Pratik Mistry1, Isaac Pinberg1, Victoria Mountain1, Rob Myers2, Chuhan Chung3, Andrew Billin1, Tim Watkins3, Ian Wapinski3, Michael Montalto1, Andrew Beck1, Murray Resnick1, Katy Wack1, 1PathAI, Boston, United States; 2The Liver Company, Palo Alto, United States; 3Gilead Sciences, Inc., Foster City, United States.

Background and aims: Histologic grading and staging of disease severity are typically performed using ordinal scoring systems, which often lack sufficient sensitivity to characterize changes in histology over short periods of time or in response to treatment during clinical trials. Here we demonstrate the prognostic utility of machine learning-facilitated continuous scoring of histologic features.

Method: Liver biopsies and central pathologist (CP) Ishak and Clinical Research Network (CRN) disease severity scores were collected from subjects enrolled in the Ph3, placebo-controlled STELLAR (ST) trials of selonsertib (NCT03053050, NCT03053063). All subjects had CRN fibrosis stage 3 or 4 at baseline (BL) and were assessed for progression to either cirrhosis or liver-related events (LREs). Treatment arms were combined due to lack of measured drug efficacy. PathAI AI-based measurement of NASH histology (AIM-NASH) models were deployed to generate ML-derived predictions for ordinal and continuous CRN grades/stages for steatosis, hepatocellular ballooning, lobular inflammation, and fibrosis (Figure 1A). Cox proportional-hazards, receiver operating characteristic, and Kaplan-Meier (KM) analyses were employed to assess associations between ML-derived disease severity metrics and patient outcomes.

Results: During a median follow-up of 16.5 or 15.8 months, 14.9% (N = 108/725) of F3 subjects progressed to cirrhosis, and 2.5% (N = 20/794) of F4 subjects had liver-related events (LREs) respectively. Progression to cirrhosis in subjects with F3 fibrosis at BL was associated with higher ML continuous and ordinal fibrosis stage and higher manual (Ishak) scoring at BL. Lower ML-derived ordinal but not manual steatosis grade was also associated with progression to cirrhosis. In subjects with F4 fibrosis at BL, lower BL continuous
steatosis grade and ordinal Ishak fibrosis stage were predictive of progression to a LRE. BL continuous fibrosis stage cutoffs of 3.6 and 4.6 stratified subjects into slow vs. rapid progressors to cirrhosis or LREs, respectively (Figures 1B and 1C). ML-derived continuous scoring showed higher discriminatory accuracy to predict progression to cirrhosis and to LREs than ML-derived ordinal scoring (AUROC [90% CI] = 0.66 [0.61, 0.71] vs. 0.59 [0.55, 0.63] and 0.61 [0.52, 0.7] vs. 0.54 [0.47, 0.59] in ST3 and ST4, respectively.

**Conclusion:** AIM-NASH analysis of biopsies from two completed Ph3 NASH clinical trials demonstrates the prognostic potential of continuous histologic scoring methods. These results support further investigation into the value of ML-based continuous histologic scoring methods for measuring clinically meaningful therapeutic effects in NASH clinical trials.

**SAT072**

Increasing plasma concentration of aldol-keto reductase family 1 member B10 and its significance in the progression of non-alcoholic fatty liver disease

Hye Eun Lee¹, Dae Ho Lee¹, ¹Gachon University College of Medicine, Gil Medical Center, Incheon, Republic of Korea, Department of Internal Medicine, Incheon, Korea, Rep. of South

Email: esthe00513@gmail.com

**Background and aims:** Understanding of hepatic gene expression during non-alcoholic fatty liver disease (NAFLD) progression may help to find traceable therapeutic targets. Although efforts to examine the transcriptomic changes that occur as NAFLD progresses have largely used, studies have been limited independent validation. We investigated the feasibility of secretory protein for diagnosis of NAFLD and evaluated the diagnostic accuracy of biomarkers.

**Method:** We incorporated transcriptomic data on healthy subject and NAFLD patient biopsy-proven samples, representing the full histological range from normal liver tissue to steatohepatitis–cirrhosis–hepato cellular carcinoma in both publicly available data base (n = 853) and a separate replication cohort (n = 102). To validate the finding form the transcriptomic data analysis, we confirmed protein level in serum, blood, and liver tissue form patient. In addition, supporting the biological plausibility of these data, we assessed its expression in primary hepatocytes from mice under various metabolic stresses and other stresses, which caused AKR10B expression.

**Results:** We discovered tentative secretory proteins that reflect the progression of NAFLD with a consistent and stepwise increasing pattern for the diagnosis of NASH. We found 4 secretory proteins (AKR1B10, annexin A2P2, ZNF468, and CD24) and we showed through our own cohort study that plasma AKR1B10 could be a clinically applicable biomarker for NAFLD (AUROC 0.834) and for advanced fibrosis (AUROC 0.914) at a cutoff level (≥1078.2 pg/ml). We applied our protocol to monitor NAFLD in patients undergoing bariatric surgery, showing that plasma AKR1B10 levels decreased markedly after surgery. Translating these findings to the protein level, we optimized in vitro cell model using primary mouse hepatocytes treated with free fatty acid and high glucose.

**Conclusion:** In the present study, the circulating concentrations of proteins AKR1B10 were strongly associated with disease activity and fibrosis stage. Plasma AKR1B10 could be a useful non-invasive biomarker for the diagnosis of NAFLD as progression of disease. Further validation studies in the future as a biomarker and a probable therapeutic target for NAFLD will be warranted.

**SAT073**

Validation of the ADAPT score for the diagnosis of clinically significant fibrosis in patients with non-alcoholic fatty liver disease (NAFLD)

Arun Sanjaly, Sudha Shankar², Katherine Yates³, Clayton Deho⁴, James Bolognese⁵, Brent Tetri⁶, Kris Kowdley⁷, Raj Vuppulanchi⁸, Mohammad Siddiqui⁹, Cynthia Behling⁹, James Tonascia¹⁰, Anthony Samir¹¹, Claude Sirlin¹², Sarah Sherlock¹³, Kathryn Fowler¹⁴, Helen Heymann¹⁵, Tania Kamphaus¹⁶, Rohit Loomba¹⁷, Roberto Calle¹¹.

¹Virginia Commonwealth University, Department of Internal Medicine, Division of Gastroenterology, Richmond, United States; ²AstraZeneca, Gaithersburg, MD, United States; ³Virginia Commonwealth University, Richmond, VA, United States; ⁴Virginia Commonwealth University, Richmond, VA 23298, United States; ⁵Virginia Commonwealth University, Richmond, United States; ⁶Harvard Medical School/ Massachusetts General Hospital, Boston, MA; ⁷University of California San Diego, La Jolla, CA, United States; ⁸Pfizer Inc, 610 Main Street, Cambridge, MA, United States; ⁹Foundation for NIH, North Bethesda, MD, United States; ¹⁰Nafld research center, San Diego, CA, United States; ¹¹Regeneron Pharmaceuticals Inc, Tarrytown, NY, United States

Email: arun.sanyal@vcuhealth.org

**Background and aims:** There is an unmet need for validation of diagnostic tools to identify patients with NAFLD who have stage 2 or greater fibrosis that meet regulatory standards for qualification. The ADAPT score is anchored on PROC3, a collagen fragment released during fibrogenesis and being developed for this purpose. PROC3 is measured either with ELISA or on the COBAS platform. The aims of this secondary analysis of the NIMBLE circulating work stream stage 1 dataset were to: (1) evaluate the utility of the ADAPT score (Proc-C3-based fibrosis algorithm that includes Age, Diabetes, Pro-C3 and Platelet count) for the diagnosis of clinically significant fibrosis (≥ stage 2), advanced fibrosis (≥ stage 3) or cirrhosis (stage 4) in patients with NAFLD, and (2) determine if ADAPT performance varies based on whether PROC3 is measured by ELISA or COBAS.

**Method:** A retrospective analysis of a sample set from the NIDDK NASH CRN DB2 adult cohort curated to avoid spectrum bias by balanced representation of fibrosis stages (0–4) was performed. Histology was independently read by the NASH CRN pathology committee using validated protocols. All samples were obtained within 90 days of a liver biopsy demonstrating NAFLD; a FIB4 score was computed from the same sample as the PROC3. Both ELISA and COBAS based PROC3 results were obtained on each sample. The primary hypothesis was that the ADAPT score would diagnose the fibrosis strata noted above with an AUROC >0.7 with confidence limits that do not intersect 0.5 at the Youden index. The secondary hypothesis was that the AUROC at Youden index would be superior to FIB4 for the same fibrosis strata.

**Results:** A total of 1070 patients, each providing a single set of the readouts, were studied. The distribution of fibrosis stages was: 0 = 222, 1 = 114, 2 = 262, 3 = 277, 4 = 198. Those with stages 0–1 had more NAFL and had a lower NAFLD activity score compared to those ≥ stage 2. Comparison of PROC3 results from ELISA and COBAS methodologies did not show appreciable differences in performance. Data using ELISA are presented below (* primary hypothesis validated, ** secondary hypothesis validated).

<table>
<thead>
<tr>
<th>Sensitivity</th>
<th>Specificity</th>
<th>AUROC</th>
<th>FIB4 AUROC</th>
</tr>
</thead>
<tbody>
<tr>
<td>7.1</td>
<td>85.9</td>
<td>68.1</td>
<td>0.824**</td>
</tr>
<tr>
<td>6.9</td>
<td>74.9</td>
<td>78.7</td>
<td>0.832**</td>
</tr>
<tr>
<td>6.2</td>
<td>76.4</td>
<td>76.8</td>
<td>0.849*</td>
</tr>
</tbody>
</table>

**Conclusion:** The ADAPT score was validated to diagnose clinically significant and advanced fibrosis in those with NAFLD and was superior to FIB4 for both purposes.
SAT074
Obeticholic acid reduces hepatic matrix metalloproteinase activity in a diet-induced ob/ob mouse model of NASH
Marta Cagna1, Giuseppina Palladini1,2, Laura Giuseppina Di Pasqua1, Anna Ciera Cocco1, Luciano Adorini1, Andrea Ferrigno1, Mariapia Vairetti1, University of Pavia, Dept of Internal Medicine and Therapeutics, Pavia, Italy; 2Fondazione IRCCS Policlinico San Matteo, Pavia, Italy; 3Institute of Molecular Genetics, Italian National Research Council (CNR), Pavia, Italy; 4Intercept Pharmaceuticals, San Diego, California, USA
Email: marta.cagna02@universitadipavia.it

Background and aims: Hepatic matrix metalloproteinases (MMPs) play a role in fibrogenesis of NASH contributing not only to the balance between formation and degradation of connective tissue components, but also to signal transduction for tissue repair. We have previously shown that the FXR agonist obeticholic acid (OCA) reduces hepatic MMP activity by restoring RECK, an MMP regulator tissue reversion-inducing cysteine rich protein with Kazal motifs, after ischemia/reperfusion injury (Ferrigno et al, 2020). Here, the effects of OCA on hepatic MMP activity and RECK content were evaluated in a diet-induced NASH model in ob/ob mice.

Method: Lepob/ob (ob/ob) NASH mice fed high fat (HF) diet (AMLN-1, D09100301, with trans-fat, cholesterol and fructose) or control diet were used. After 9 weeks on diet, mice were treated with OCA dosed via dietary admixture 0.05% (30 mg/kg/d) or HF diet for 12 weeks. Liver weight, serum transaminase, alkaline phosphatase, bilirubin, cholesterol, triglycerides, MMP-2 and MMP-9 activity as well as RECK levels were quantified at the end of the study.

Results: HF diet induced a significant increase in liver MMP-9 when compared with mice treated with control diet; OCA administration reduced MMP-9 to levels observed in control diet animals. Although not significant, the same trend occurred for MMP-2. A down-regulation of tissue RECK observed in HF group was recovered by OCA to values comparable to control diet group. A significant increase in liver weight was found in HF diet mice compared to control diet group. OCA treatment reduced liver weight to values comparable with those observed in the control diet group. Serum bilirubin and cholesterol increased in HF diet-treated mice and OCA administration markedly counteracted these increases. OCA did not affect serum transaminase, alkaline phosphatase and triglyceride levels compared to HF diet mice.

Conclusion: Thus, OCA confers protection in a model of NASH, as shown by reduced serum bilirubin and cholesterol levels. This is the first study showing the positive effect of OCA on hepatic MMP-9 via restoration of RECK levels in a NASH model. These are intriguing findings considering a) the crucial role of MMPs in extracellular matrix homeostasis due to stellate cell activation into a profibrogenic phenotype occurring during inflammation and b) the emerging role of RECK in regulating inflammatory and fibrogenic processes. Further studies are necessary to better understand the implications of OCA-induced decrease in hepatic MMPs, and its role in the therapy of NASH.

SAT075
Evaluation of semisynthetic high-fat diets in development of a 4-week mouse NASH model
Ozren Majstorović1, Maja Antolić1, Snježana Ćužić1, Lucija Mušak1, Matea Cedilak2, Hrvoje Brzica1, Martina Bosnar2, Ines Glojnaric1,1, Fidelta Ltd, In vitro pharmacology and toxicology, Zagreb, Croatia; 2Fidelta Ltd, In vitro pharmacology, Zagreb, Croatia
Email: ozren.majstorovic@fidelta.eu

Background and aims: Non-alcoholic fatty liver disease (NAFLD) represents the most common chronic liver condition worldwide. Non-alcoholic steatohepatitis (NASH) is characterized by hepatic steatosis, inflammation, hepatocellular damage, and further, fibrosis. At present, no pharmacological NASH therapy was approved by the FDA, creating a necessity for a reliable preclinical model reflecting disease characteristics seen in humans. Most widely used animal models of NASH are set on nutritional basis, however, their long duration counteracts the need for rapid efficacy testing. In this study, two semisynthetic high-fat diets that act as disease inducers alone, or in combination with 2-hydroxypropyl-ß-cyclodextrin (CDX) or fructose, were evaluated with the aim to develop a shorter but reliable mouse NASH model for screening of potential drug candidates.

Method: C57BL/6 male mice were fed with choline-deficient, L-amino acid-defined, high-fat (60 kcal%) diet (CHAHFD) consisting of 0.1% methionine or high-fat (60 kcal%), cholesterol (1.25%), and cholic acid (0.5%) (HFDCC). In addition, both dietary regimens were supplemented with either 2% CDX, a cyclic oligosaccharide with high affinity to sterols, or 30% fructose in drinking water. After four weeks of feeding, sera were analysed for biomarkers of liver damage (ALT, AST), cholesterol (CHOL), and fasting glucose levels. Livers were weighed and analysed for triglyceride (TG) content and expression of inflammatory (Tnf-alpha, IL-10, and Ccl2) and fibrosis related genes (Col1a1, Timp1, Paa1, Ctgf, Tgf-beta, and Acta2). Histopathological evaluation was conducted using modified NAS score and immunohistochemistry (IHC) for Collagen 1A1 (COL1A1) and macrophage population (F4/80).

Results: Addition of CDX to HFDCC diet resulted in a significant increase in inflammation and fibrosis, as confirmed by NAS, F4/80, and COL1A1 positive area as well as higher expression of both gene panels. In contrast, addition of fructose resulted in a significant increase in steatosis score. CDX addition to CHAHFD resulted in increase of liver damage biomarkers, while inflammation score, COL1A1 surface, and consequently total NAS, where most affected by addition of fructose. When comparing two diets, significantly higher serum CHOL levels were observed in all HFDCC groups, while significant increase in liver TG content was achieved in CHAHFD combinations. Disease progression to perisinusoidal/peripoportal fibrosis was observed with significantly higher intensity of overall parameters when using CHAHFD, however, accompanied by a transient body weight loss.

Conclusion: This study provides the successful recapitulation of main clinical features of NASH in a 4-week dietary induced mouse model, while favoring use of CHAHFD and emphasizing a need for tailored approach in testing pharmacological candidates based on their targets and mode of action.

SAT076
Tyrosinase mutations, a novel predisposing genetic factor for enhanced non-alcoholic steatohepatitis susceptibility
Kaushalya Kulathunga1, Arata Wakimoto2, Michito Hamada2, Satoru Takahashi3, Faculty of Medicine-University of Sabangamuwa Sri Lanka, Department of Physiology, Ratnapura, Sri Lanka; 2University of Tsukuba, department of anatomy and embryology, Tsukuba, Japan
Email: kkulathunga@med.sab.ac.lk

Background and aims: Non-alcoholic fatty liver disease (NAFLD) is an alarmingly rising metabolic disorder. Non-alcoholic steatohepatitis (NASH) is the progressive liver damage with inflammation leading to fibrosis and carcinogenesis. Interestingly, enhanced susceptibility for NASH was observed in B6 albino mice (albino) with high cholesterol diet (HCD), compared to wild type B6 black mice (black), a phenotype not reported before. This study was led to understand the underline mechanism of elevated NASH susceptibility of albino mice.

Method: B6 albino mice carry G291 T point mutation in tyrosinase (Try) gene and this is the only genetic difference compared to B6 black mice. Albino and black mice were fed with HCD for 10 weeks. Normal diet fed mice used as controls. Body weights, blood indices and liver damage related serum parameters were monitored. Liver samples were histologically analyzed. Small intestinal lipid absorption and the expression of intestinal cholesterol transporters were investigated. This study provides the successful recapitulation of main clinical features of NASH in a 4-week dietary induced mouse model, while favoring use of CHAHFD and emphasizing a need for tailored approach in testing pharmacological candidates based on their targets and mode of action.
CRISPR/Cas9 technology and employed to confirm that the observed phenotype is resulted from that specific mutation.

Results: Liver injury with elevated ALT, AST levels were observed in albino mice from post day 1 HCD feeding. 2 weeks of HCD induced NASH in albino mice, but no symptom was observed in black mice even after 10 weeks of diet. Histological analysis of albino mice livers revealed significant inflammatory cells and lipid infiltration, and severe fibrosis. Increased serum chylomicron and very low density lipoprotein levels were observed in albino mice partly because of the low serum lipoprotein lipase levels and partly as the expression changes in small intestinal cholesterol transporters. Similar to B6 albino, CRISPR generated mice exhibited the same liver damage phenotype, confirming the contribution of G291T mutation.

Conclusion: To validate our data in human context, in-silico analysis was carried out to investigate the allele frequencies of two main Try single nucleotide polymorphisms (SNPs). Interestingly, it was revealed that Hispanic populations with highest prevalence of NAFLD/NASH exhibit relatively high allele frequencies with two main Try SNPs, G140Aand G316C. This work uncovered a novel possible genetic factor for NASH development. Further studies are carried out to uncover the contribution of human Try SNPs in the development of NAFLD/NASH.

SAT074
Recapitulating insulin resistance in a 3D human liver model for efficacy testing of drug candidates
Radina Kostadinova1, Lisa Hoeting1, Simon Hutter1, Arianna Menghini2, Anna Zehnder3, Wolfgang Moritz3, Francesco Verdeguer4, Olivier Frey5, InSphero, Schlieren, Switzerland
Email: radina.kostadinova@insphero.com

Background and aims: There is a close link between metabolic liver diseases, type 2 diabetes, and obesity resulting in a severe dysregulation of glucose and lipid metabolism. Understanding the mechanism of inter-cellular and tissue crosstalk and how it relates to metabolic homeostasis offers a great potential to identify novel therapeutic opportunities. Conventional cell culture models lack complex multi-cellular interactions found in the human body and are unable for accurate disease modeling and predictive drug efficacy testing in vitro. Here, we modeled de novo lipogenesis (DNL) and steatosis conditions by the recapitulation of glucose metabolism in 3D human liver co-culture and for efficacy testing of anti-steatotic and anti-diabetic compounds.

Method: We have cultured 3D human liver tissues (hLiMTs) consisting of primary hepatocytes, Kupffer cells and liver endothelial cells in a 96-well format under pathophysiological insulin and glucose conditions in absence (DNL model) or presence of free fatty acids (FFA, OA:PA, steatosis model). After incubation of the tissues with disease stimuli, -the insulin and glucagon sensitivity of hLiMTs was assessed by measurement of the tissue triglyceride levels as well as quantifying glycogen content and gluconeogenesis (GNG) upon hormonal stimulation.

Results: Glucagon induced glycogen storage depletion in hLiMTs. Additional, assay conditions were optimized to quantify GNG by measuring glucose release from fasted hLiMTs. The amount of glucose produced through GNG increased in the presence of increasing concentrations of glucagon. In contrast, increasing concentrations of insulin resulted in reduced glucose release from hLiMTs, indicating an inhibition of GNG. Importantly, insulin resistance was observed in hLiMTs incubated in high glucose and high insulin with and without FFA. Triglyceride levels were increased by about 10-fold in the DNL model and 20-fold in the steatosis model as compared to the healthy control. Treatment with 0.5 μM Fircoscatat, an ACC1 inhibitor, decreased significantly the triglyceride levels in the DNL model.

Conclusion: The presented 3D human liver model replicates the features of glucose and lipid handling in a highly scalable format and its application for efficacy testing of anti-steatotic and anti-diabetic compounds. It constitutes one of the three central elements for building a multi-tissue MPS besides pancreatic islets and adipose microtissues to study human glucose and lipid homeostasis.

SAT079
Novel endosomal trafficking adaptor for the regulation of NAFLD to NASH progression
Karsten Motzler1, Karsten Nalbach2, Revathi Sekar3, Ana Alfaro4, Martin Harbe de Angelis5, Matthias Blüher6, Michael Roden7, Stephan Herzig5, Natalie Kramer5, Christian Behrends5, Anja Zeigerer3, 1Institute for Diabetes and Cancer, Helmholtz Center Munich, 2Institute of Neurochemistry, 3giS (Helmholtz Institute for Metabolic, Obesity and Vascular Research, 4Helmholtz Institute for Metabolic, Obesity and Vascular Research, 5Institute of Clinical Diabetology, 6German Diabetes Center, 7Institute of Experimental Genetics, 8Helmholtz Center Munich; 9Institute of Experimental Genetics, 10Helmholtz Center Munich; 11Helmholtz Institute for Metabolic, Obesity and Vascular Research; 12Institute for Clinical Diabetology, German Diabetes Center; 13Institute for Diabetes and Obesity, Helmholtz Center Munich
Email: karsten.motzler@helmholtz-muenchen.de

Background and aims: Membrane trafficking through the endosomal transport system has gained increased attention for metabolic regulation in recent years. Cells within organs sensitive to metabolic cues, such as the liver, need to reorganize e.g. transporters and hormone receptors upon alterations in nutrient availability. This
reorganization is achieved by the endosomal trafficking machinery and is especially important in highly polarized hepatocytes for the secretion or delivery of certain proteins to apical (biliary) membranes while other proteins must be transported to basolateral (sinusoidal) membranes. Part of the needed specificity is given by different adaptor proteins (APs), aiding cargo recognition and coat protein recruitment during vesicle formation. Here, we are reporting on a novel role of the epsilon subunit of the AP-4 complex (AP4E1) in metabolism and implications for NASH progression. Connecting the two fields of endocytosis and metabolism offers a more thorough understanding of NAFLD and NASH and might help to identify new drug targets.

**Method:** Using mice with hepatocyte-specific knockout (KO) of Ap4e1 and different models of diet-induced NASH together with proteomic and RNA sequencing approaches, we aim to dissect the crosstalk of hepatocytes with other cell-entities within the liver. By assessing the membrane and secretome of primary hepatocytes, we try to identify novel cargo proteins of Ap-4 and how this transport is affecting the transition of NAFLD to NASH.

**Results:** Here, we identify a thus far unknown role for an endocytic membrane trafficking adaptor protein, Ap4e1, in NASH development and progression. Interestingly, we find Ap4e1 to be upregulated both in livers of human NASH patients, and in livers of multiple mouse models of NASH. This is associated with a positive correlation of Ap4e1 protein levels with hepatic fibrosis in mice, suggesting a potential connection between Ap4e1 and NASH progression. Indeed, reduction of Ap4e1 exacerabtes the development of fibrosis, indicating a regulatory role of Ap4e1 in NASH. Membrane and secretome assessment of primary hepatocytes depleted of Ap4e1 reveal interesting hits on novel cargo proteins of this adaptor that are connected to fibrosis development and are currently investiganted further. In addition, ongoing scRNAseq analysis of KO NASH livers are conducted to provide insights into the crosstalk between hepatocytes and other cell types within fibrotic mouse livers to shed light onto the potential connection between Ap4e1 and NASH progression. Indeed, we find upregulation of Ap4e1 to be upregulated both in livers of human NASH patients, and in livers of multiple mouse models of NASH. This is associated with a positive correlation of Ap4e1 protein levels with hepatic fibrosis in mice, suggesting a potential connection between Ap4e1 and NASH progression. Indeed, reduction of Ap4e1 exacerbates the development of fibrosis, indicating a regulatory role of Ap4e1 in NASH.

**Conclusion:** Taken together, our data reveal a novel role of Ap4e1 in the regulation of NAFLD to NASH transition. As Ap4e1 depletion exacerbates disease outcome, we aim to identify the responsible cargo proteins that could reveal a new mechanism to understand NASH development and potentially serve as targets for therapeutic applications.

**SAT080**

**Enzymatic activity dysfunction of the mitochondrial respiratory chain, in the full spectrum of the metabolic associated fatty liver disease**

Alberto García Picazo1, Pilar Gómez Rodríguez2, Pilar del Hoyo Gordillo2, Carolina Ibarrola de Andrés3, Javier Salamanca Santamaría3, Elías Rodríguez Cuéllar3, Cristina Martín-Arriscado4, Jennifer Villa5, Ana Martin Algibez6, Inmaculada Fernández Vázquez7, Miguel Ángel Martín Casanueva7, Mercedes Pérez-Carreras7, 12th October University Hospital, General Surgery, Madrid, Spain; 212th October University Hospital, Endocrinology, Madrid, Spain; 312th October University Hospital, Pathology, Madrid, Spain; 412th October University Hospital, Pathology, Madrid, Spain; 512th October University Hospital, Microbiology, Madrid, Spain; 612th October University Hospital, Gastroenterology, Spain

**Background and aims:** Patients with morbid obesity (MO) develop a huge range of histological injuries related to the metabolic associated fatty liver disease (MAFLD). Those lesions could be a trustful model to study their relation with the mitochondrial dysfunction, which appears in this disease. The main objective is to determine the existence of mitochondrial liver dysfunction in patients with MO and MAFLD.

**Method:** A prospective case-control study was designed, the case group was composed of MO patients having received bariatric surgery, whereas the control group was non-hepatopathy patients. In both groups surgical liver biopsy was performed between 2019 and 2021. Demographic, anthropometric, metabolic, blood test and histological (SAF classification) variables were measured. All patients were divided according to their histological injury grade and the dysfunction of the mitochondrial breath chain, and compared to the control group. Liver mitochondrial respiratory chain (MRC) activity was measured by spectrophotometry. The variables were analysed with Stata version 16 software, statistically significance was set at p <0.05.

**Results:** Case group (n = 53): 66% women, 48 ± 11 years, BMI 45 ± 6; Control group (n = 10): 50% women, 54 ± 13 years, BMI 24 ± 2. MRC activity in case group vs control group: Complex I, 39.8 vs 53.9 (p = 0.01), II- 190.3 vs 275.2 (p <0.001), III-87.6 vs 119 (p = 0.04), IV- 92.6 vs 115 (p = 0.02) and V- 82.8 vs 155.8 (p <0.001). Figure 1: decreased percentage in the MRC activity related with the histological damage: No steatosis (10/53), simple steatosis (7/53), steatosis + inflammation (7/53), steatohepatitis (17/53), Fibrosis (12/53). A relation between HOMA-IR and high levels of insulin with the activity in the complexes I and II (p <0.05) was identified.

**Conclusion:** The enzymatic activity of the 5 complexes of the liver MRC are decreased in patients with MO and MAFLD. This alteration affects the synthesis of ATP (complex V). Insulin resistance and insulinemic index are associated with defects in complexes I and II. Mitochondrial dysfunction already appears in subjects with MO without liver injury and is different according to histological severity. There is less enzymatic activity in early and advanced stages of MAFLD, while it increases with MAFLD inflammatory activity. These enzymatic changes could be due to adaptive disorders of the mitochondria in MAFLD.

**SAT081**

**Lipid-induced phenotypic differences in human non-alcoholic fatty liver disease models determined by matrix-assisted laser desorption/ionization mass spectrometry**

Ruth Walker1, Michalina Zatorska2, Jose Luis Marin-Rubio1, Matthias Trost1, Maria Emilia Dueñas3, Olivier Govaere1, Biosciences Institute, Faculty of Medical Sciences, Newcastle upon Tyne, United Kingdom; 2Translational and Clinical Research Institute, Faculty of Medical Sciences, Newcastle upon Tyne, United Kingdom; Email: olivier.govaere@newcastle.ac.uk

**Background and aims:** Accumulation of lipids is a key part of the pathogenesis of non-alcoholic fatty liver disease (NAFLD) and has recently been associated with endoplasmic reticulum (ER) stress. In vitro lipid loading is often used as an experimental model for NAFLD, though a high-throughput screening platform to understand metabolic changes and lipotoxicity is still lacking. Matrix-assisted laser desorption/ionisation-time-of-flight mass spectrometry (MALDI-TOF MS) is a fast, reproducible, and label-free technology, used for assays in pharmaceutical research and development, drug discovery and
Method: Human hepatoma HepG2 cells were treated with saturated and unsaturated fatty acids including linoleic, oleic and palmitic acid at concentrations of 200 μM and 400 μM, or with the ER stress inducer thapsigargin (1 mM). Cells were mixed one-to-one with 2, 5-dihydroxyacetophenone matrix and analysed by MALDI-TOF MS to determine differences in the phenotypic profiles of metabolites and high molecular weight (HMW) biomolecules. Principal component, hierarchical clustering and multivariate analysis were carried out to identify differences.

Results: Overall, 1372 metabolite and 753 protein unique features were identified by MALDI-TOF MS. Distinctive metabolite profiles were established for each condition, allowing multiplexing and identification of biomarkers. A dose-dependent effect is evident for all lipids and whilst linoleic and oleic acid are often used interchangeably in the field, they induce significant differences in cellular metabolic profiles, having 243 and 76 unique metabolites respectively. Moreover, although thapsigargin and high concentrations of palmitic acid induces ER stress and cellular cytotoxicity respectively, they present substantial differences, indicating that mechanistic differences between these two conditions. Of the lipid treatments, only 400 μM palmitic acid has a significant effect on the profiles of HMW biomolecules, having 605 unique biomolecules, and 47 common proteins.

Conclusion: Taken together, we have developed a fast MALDI-TOF MS comparative screening technique for determining metabolite and HMW biomolecule changes in a human in vitro NAFLD models. Moreover, our data provides distinctive metabolic and stress fingerprints that are relevant during the progression of NAFLD. Biomarkers from these fingerprints may be used as a screening method for therapeutic interventions.
histological change. Statin (5 mg/kg) and ezetimibe (10 mg/kg) were administered during last 4 weeks.

Results: Ezetimibe, statin monotherapy and combination therapy were improved hepatic steatosis. We got liver tissue showing histologically NASH-related change from high fat diet for 12 weeks and administration of TAA for 8 weeks. The improvement of steatosis and inflammation was more pronounced in the statin group, ezetimibe group and combination group. In particularly, ezetimibe shows lower fat contents and statin shows improvement of inflammation.

Simvastatin mono treatment and combination with ezetimibe treatment suppress hepatic fibrosis

The improvement of fibrosis was more pronounced in the statin and ezetimibe group. These results were confirmed as decreased a-SMA and collagen protein level by Western analysing. In PCR transcription, there was lower transcription level of collagen type I and PDGF-d, suggesting there is lowering fibrosis in statin, ezetimibe treated group. There was elevation of collagen type I and a-SMA, PDGF-d in ezetimibe monotherapy group, but it was not correlated a histological finding.

Simvastatin and ezetimibe combination treatment suppresses hepatic inflammation.

The effects about IL-6, IL-1b, and TNF-a were evaluated by quantitative real-time PCR. And it is suggesting that simvastatin mono-treatment and simvastatin, ezetimibe combination therapy exhibits anti-inflammatory effects. IL-6, TNF-a, IL-1b and INOS was decreased in statin and combination group. In this study, Ezetimibe mono-treatment group shows elevation of IL-6, TNF-a. Simvastatin and ezetimibe combination therapy inhibits macrophage migration via downregulating CCR 5 and macrophage activation.

In vitro, Statin and ezetimibe downregulate of expression of CCR5. Many macrophages were also observed in HFD-TAA histology and the number of macrophages was decreased in simvastatin, simvastatin + ezetimibe combination treatment group.

Conclusion: In the NASH-cirrhosis mouse model, ezetimibe showed the improvement of steatosis and statin showed anti inflammatory effect. And the combination therapy showed improvement of fibrosis through macrophage migration and suppression, resulting in TNF-a inhibition. Ezetimibe mono-treatment in NASH-cirrhosis need to be evaluated because of potential side effects.

SAT084
The different modulation of KLB expression impacts on liver damage in NAFLD patients and in an in vitro model: a novel druggable target?

Marica Meroni, Nadia Panera, Giada Tria, Roberto Picciotti, Miriam Longo, Erika Paolini, Antonella Mosca, Annalisa Crudele, Ludgero Tavares, Paula Macedo, John Jones, University of Coimbra, Center for Neuroscience and Cell Biology, Coimbra, Portugal; Addis Ababa Science and Technology University, Biotechnology, Addis Ababa, Ethiopia; CEDOC-Chronic Diseases Research Center, NOVA Medical School, Nova University of Lisbon, Lisbon, Portugal

Background and aims: We previously shown that the rs17618244 variant in β-Klotho (KLB) gene, encoding the hepatic co-receptor of fibroblast growth factor receptor 4 (FGFR4), increases the risk of developing severe NAFLD, NASH and fibrosis both in adults and children, due to lower KLB hepatic/plasma levels. Aim of this study was to investigate the impact of another variant in KLB, the rs12152703, on liver damage in NAFLD patients and to evaluate the effect of KLB in vitro genetic ablation on fat accumulation, oxidative/ER stress, inflammation and cell proliferation.

Method: We evaluated the effect of the rs12152703 variant in 1311 biopsied NAFLD patients of whom 261 were children. Hepatic and circulating KLB levels were measured in a subset of patients (n = 125 and n = 290, respectively). Next, we generated a full knock-out model of KLB gene in HepG2 cells (KLB−/−) by CRISPR/Cas9.

Results: At multivariate analysis, the rs12152703 KLB variant was associated with reduced transaminase levels and with protection against NASH and advanced NAFLD activity score (NAS) (p < 0.05).

Conclusion: Simvastatin and ezetimibe combination therapy suppress hepatic fibrosis.

KLB−/− cells displayed a reduced intra-cellular triglyceride (TG) content (p < 0.05), related to the suppression of genes involved in lipogenesis and TG synthesis (p < 0.05). KLB deletion strongly induced oxidative and ER stress, increasing ROS/RNS production, aldehyde derivate concentrations and ROS-induced DNA damage (p < 0.05). These events triggered the release of pro-inflammatory cytokines into the KLB−/− cultured media (p < 0.05), resembling severe NAFLD. Finally, KLB−/− cells also showed an elevated proliferative rate and invasiveness (p < 0.05).

Conclusion: In sum, the rs12152703 KLB variant protected against severe NASH, whereby enhancing KLB levels differently from the rs17618244 at-risk variation.

Our in vitro results outlined that KLB shutdown may be causally involved in the switching towards progressive forms of liver damage, by inducing ER/oxidative stress, inflammation, and enhanced proliferation, even in the absence of excessive fat accumulation. Thus, KLB may constitute a novel druggable target for the prevention of severe NAFLD.

SAT085
Utilization of gluconeogenic glucose-6-phosphate via pentose phosphate pathway is increased in mice fed a high fat/high sugar diet compared to a high sugar diet alone

Getachew Debas Belete, Ana Costa, Maria Joao Meneses, Ludgero Tavares, Paula Macedo, John Jones, University of Coimbra, Center for Neuroscience and Cell Biology, Coimbra, Portugal; Addis Ababa Science and Technology University, Biotechnology, Addis Ababa, Ethiopia; CEDOC-Chronic Diseases Research Center, NOVA Medical School, Nova University of Lisbon, Lisbon, Portugal

Background and aims: In hepatocytes, the pentose phosphate pathway (PPP) is an important generator of NADPH for de novo lipogenesis (DNL) and for the maintenance of reduced glutathione in antioxidant defense. The development of non-alcoholic fatty liver disease (NAFLD) secondary to high sugar and/or high fat intake is characterized by elevated DNL rates and increased oxidative stress. It is not known whether PPP fluxes are modified in these settings. We developed a double tracer method that provides information on both
DNL and PPP fluxes in feeding mice. We applied this to compare DNL and PPP fluxes in mice fed a normal chow diet supplemented with high-fructose corn syrup (HFCS-55) with a more obesogenic diet composed of high fat chow supplemented with HFCS-55.

**Method:** Twelve C57BL/6 mice were provided with standard chow (SC) with the drinking water supplemented with 30% (w/v) of HFCS-55 (55/45 mixture of fructose and glucose) for 18 weeks. Eleven mice were placed on high-fat chow (HFC) with the same HFCS-55 supplement over the same period. At the beginning of the final evening, all mice were administered with 99% deuterated water containing and the HFCS-55 fructose component was enriched to 20% with [U-13C6]fructose. On the following morning, mice were deeply anesthetized with ketamine/xylazine and sacrificed by cardiac puncture. Arterial blood was collected and centrifuged to isolate plasma, livers were freeze-clamped, and the samples were stored at −80°C until further processing. Liver triglyceride and glycogen were purified and analyzed for 1H and 13C-enrichments by NMR. DNL rates were quantified from lipid 2H-enrichment and adjusted for liver phosphate (G6P) utilized by the PPP was quantified from glycogen 13C-isotopomer analysis.

**Results:** Mice fed HFC + HFCS-55 has greater body weight (50 ± 1 vs 37 ± 1 g, p < 0.0001), higher whole-body adiposity (29 ± 1 vs 16 ± 2%, p < 0.0001), and higher liver triglyceride levels (15 ± 2 vs 8 ± 2 g/100 g liver, p < 0.025) compared to those fed SC + HFCS-55. DNL rates were not significantly different between the two groups although the high-fat chow mice had a tendency for higher rates (1.02 ± 0.1 vs 0.75 ± 0.1 g/100 g liver, p = 0.2109). However, the fraction of gluconeogenic G6P utilized by the PPP was significantly higher for the high-fat chow mice (17.0% versus 13.8%, p = 0.034).

**Conclusion:** A diet high in both fat and sugar is more obesogenic than a diet high in sugar alone. In the presence of high fat, DNL rates were sustained while PPP utilization of G6P derived from gluconeogenesis was significantly increased. This may be explained by additional demand for NADPH above and beyond that consumed by DNL, possibly in response to increased oxidative stress.

**SAT086**

A novel microwell platform to analyse single-cell secretion dynamics and cell communication in NAFLD progression

Richell Booijink1,2, Ruchi Bansal1,2, Leon Terstappen1. University of Twente, Medical Cell Biophysics, Science and Technology, Netherlands; University of Twente, Translational Liver Research, Medical Cell Biophysics

Email: r.s.booijink@utwente.nl

**Background and aims:** Liver inflammation and fibrosis are the hallmarks of non-alcoholic steatohepatitis (NASH). Here, activated and differentiated hepatic stellate cells (HSCs) together with infiltrating and activated immune cells maintain a continuous cycle of cellular activation, inflammation and fibrogenesis. To do this, these non-parenchymal cell populations in the liver microenvironment secrete factors including cytokines and proteins to communicate with their surroundings. Many studies confirmed heterogeneity within these cells on a genomic level. However, how this heterogeneity translates to cellular secretion and communication, and its influence on NAFLD progression remains unclear.

We propose a novel model that enables simultaneous analysis and correlation of single-cell secretion, phenotype, genome and transcriptome, using a self-sorting microwell platform.

**Method:** The self-sorting microwell chip is developed containing 6400 microwells with a diameter of 70 μm, volume of 1.4 nl and 5 μm single pore at the bottom of each well. While placing a cell suspension on the chip, single cells are distributed over the wells, and identified by fluorescent microscopy. The chip is brought into contact with a PVDF membrane, which collects secreted molecules from the single cells. Upon removing the membrane, the concentration of secreted molecules can be determined and correlated to the individual cell that produced them. Therefore, cells of interest can be isolated from the chip and used for further molecular (DNA and RNA) analysis, by punching out the bottom of the microwell into a PCR tube.

**Results:** To validate the model, human HSCs (LX2) and PMA-differentiated human macrophages (THP1) are used to measure collagen-I and TNF-alpha secretion respectively. Upon TGF-β activation, we observed an increase in the number of HSC-secreted collagen-I spots with increased spot intensity and area, which varied greatly per individual cell, confirming the cellular heterogeneity in collagen-I secretion in non-activated and activated cells. Interestingly, treatment with Src kinase inhibitor, KX2-391, led to an average decrease-again with large variety-in the amount of collagen-I secretion.

Furthermore, upregulation of TNF-alpha secretion was observed in pro-inflammatory LPS-stimulated M1 macrophages, seen by an increased number of cells that produced detectable TNF-alpha spots. Again, we saw a heterogeneous distribution in TNF-alpha secretion, and treatment with KX2-391 led to a reduction in the amount of TNF-alpha secreted per cell.

**Conclusion:** We established a method to determine the phenotype and secretome, that can be integrated with genome and transcriptome, of single cells in the NASH microenvironment. Building upon this model by multiplexing cell populations and multiple secreted molecules allows us to map the NASH secretome, exploring novel avenues for NASH treatment.
SAT087
Dysregulation of the urea cycle enzymes determines a more severe NAFLD phenotype in a DIAMOND preclinical model
Rocio Gallego-Durán1,2, María del Rosario García-Lozano1,2, Douglas Maya3,4, Lucia López-Bermudo1,2, Roico Montero-Vallejo1,2, Sheila Gato Zambrano1,2, Antonio Cárdenas-García3,4, Vanessa García Fernández1,2, Blanca Escudero-López1,4, Roico Munoz Hernandez1,2, Antonio Gil-Gomez1,2, Angela Rojas Alvarez-Ossorio1,2, Helena Pastor1,2, Franz Martin-Bermudo3,4, Manuel Romero Gomez1,2,5.
1Instituto de Biomedicina de Sevilla/CSIC/Universidad de Sevilla, SeLiver Group, Spain; 2Hepatic and Digestive Diseases Networking Biomedical Research Centre (CIBERehd); 3Andalusian Center of Molecular Biology and Regenerative Medicine (CABIMER)-CABIMER, University Pablo Olavide–University of Sevilla-CSIC, Spain; 4Biomedical Research Network on Diabetes and Related Metabolic Diseases (CIBERDEM); 5Hospital Universitario Virgen del Rocío, Digestive Diseases Unit
Email: jmpuero-lib@us.es

Background and aims: Non-alcoholic fatty liver disease (NAFLD) is one of the most prevalent liver diseases worldwide, showing a plethora of different pathogenic factors. In this scenario, previous studies have shown an association between the urea cycle dysregulation and different stages of hepatic injury in both patients and preclinical models of NAFLD. The main aim was to evaluate changes in urea cycle enzymes (UCEs) in a DIAMOND preclinical animal model of NAFLD under different dietary interventions.

Method: DIAMOND mice (n = 28) were randomized to three dietary regimens: high-fat diet supplemented with fructose/glucose in drinking water (HF-HFD), choline-deficient high-fat diet model supplemented with 0.1% methionine (CDA-HFD) or standard diet, which was used as a control. HF-HFD and control animals were sacrificed after 21 or 30 weeks of diet intake. CDA-HFD animals were sacrificed after 12 weeks to avoid weight loss along with other adverse outcomes linked to more prolonged exposure to this type of diet intervention. Liver damage characterization includes well-established markers for fibrosis (collagen deposition and COL3A1, and α-SMA expression levels) and inflammation (TNF-α and IL-6 expression), together with body weight and standard biochemical measurements recorded each week or month, respectively. UCEs and glutaminase (GLS) expression levels were evaluated by qRT-PCR.

Results: HF-HFD animals displayed signs of dyslipidemia (hypercholesterolemia), insulin resistance (higher glucose levels), and liver damage (raised AST and ALT levels) together with a 25% and 300% increase in body and liver weight, respectively. CDA-HFD animals displayed similar AST levels, higher ALT levels, and a 200% increase in liver weight but did not show any of the other metabolic disturbances observed in HF-HFD animals. Both diet interventions promoted a general upregulation of fibrotic markers (COL3A1, COL1A1, and α-SMA, and collagen deposition) along with a significant upregulation of the pro-inflammatory marker TNF–α. Transcriptomic evaluation of UCEs revealed a significant mRNA downregulation in carbamoyl phosphate synthetase-1 (CPS1) and ornithine transcarbamylase (OTC1) in both CDA-HFD and HF-HFD animals versus controls, together with an increase in GLS1 expression in all groups of animals.

Conclusion: DIAMOND mice, a preclinical model that mimics NAFLD, showed urea cycle dysregulation under different dietary interventions. These enzymes could play a key role in the development and progression of NAFLD.

SAT088
Quantitative multimodal anisotropy imaging enables automated fibrosis assessment of HandE-stained tissue
Yibo Zhang1, Jun Zhang1, Michael Drage1, Janani Iyer1, Brian Gosink1, Tan Nguyen1, Waleed Tahir1, Victoria Mountain1, Murray Resnick1, Michael Montalto1, Aditya Khosla1, Andrew Beck1, Justin Lee1.
1PathAI, Boston, United States
Email: justin.lee@pathai.com

Background and aims: Clinical Research Network (CRN) histologic scoring of non-alcoholic steatohepatitis (NASH) requires staining two tissue sections per FFPE block: one with HandE (for grading steatosis, inflammation, and ballooning) and one with Masson’s Trichrome (MT; for staging fibrosis). This multi-stain procedure is cumbersome, costly, and inconsistent, introducing interpretability challenges due to variability in staining and intra-biopsy sample heterogeneity. In this study, we develop and evaluate a tool for automated fibrosis assessment based on quantitative multimodal anisotropy imaging (QMAI) of HandE-stained NASH tissue sections. We demonstrate that quantifying HandE-derived fibrosis proportionate area (FPA) using QMAI yields results that correlate strongly with MT-stain color-based fibrosis quantification.

Method: 24 liver core needle biopsies from NASH patients with paired HandE and MT sections (48 slides, CRN fibrosis stages 0–4) were used in this study. HandE sections were imaged using a custom-built multimodal microscope, and MT sections were imaged using a Leica Aperio AT2 scanner. Whole-slide images were reviewed by a board-certified expert NASH pathologist and regions of tissue artifact were excluded from analysis. A pixel-intensity threshold was applied to QMAI images of HandE sections to locate fibrotic regions and compute FPA. For MT sections, color-based segmentation was employed to obtain a binarized fibrosis heatmap from which FPA was quantified. For all sections, a background/foreground algorithm generated the denominator for fibrosis proportion measurements. Concordance between HandE and MT-derived FPA was evaluated via Lin’s Concordance.

Results: Slide-level FPA quantification from paired HandE and MT sections showed strong correlation (Lin’s CCC = 0.950). Visual examination of detected fibrosis on HandE and MT sections corroborates this result and explains discrepancies between QMAI vs. MT fibrosis quantification (Fig. 1).

Conclusion: Quantitative multimodal anisotropy imaging enables fibrosis quantification from HandE-stained NASH biopsy samples that is consistent with conventional fibrosis quantification from MT-stained tissue. By eliminating the need for MT-stained slides, automated fibrosis quantification and staging from HandE sections may simplify and reduce the cost of NASH studies as well as lessen the impact of MT stain-variability and intra-sample heterogeneity on subject screening and end point assessment. Additionally, detecting fibrosis from HandE sections may enable improved interrogation of spatial relationships between fibrosis and various NASH features commonly assessed on HandE (e.g., steatosis, ballooning, and/or inflammation).

Figure: Hepatic expression of UCEs and GLS1 in DIAMOND mice stratified according to ALT tertiles. A) OTC1 B) CPS1 C) GLS1.
Background and aims: Immunohistochemical stains (IHC) often reveal differences between different zones of the liver lobule in health and disease, including non-alcoholic fatty liver disease (NAFLD). However, evidence from IHC often depends on representative images. In NAFLD, lipid vacuoles from macrovesicular steatosis occupy part of the surface and hamper correct interpretation. We developed an image analysis method to quantify IHC staining area of hypoxia marker pimonidazole (Pimo) within different zones of the liver lobule of steatotic livers.

Method: Male C57BL/6j mice were fed the choline-deficient L-amino acid-defined high-fat diet (CDAHFD) or standard diet (SD) for three weeks and received an intraperitoneal injection of Pimo (100 mg/kg) one hour prior to sacrifice (n = 6). Serial sections of formalin-fixed paraffin-embedded liver tissue were stained with haematoxylin-eosin (HandE) and IHC for glutamine synthetase (GS) and Pimo adducts were visualised with 3, 3′-diaminobenzidine (DAB). Whole slide image (WSI) acquisition was performed with the Zeiss Axioskop 1. A script for Fiji open-source image analysis freeware was developed to measure DAB pixel intensities as a function of the relative location (with respect to the central vein and the boundary) within a liver lobule. The autothreshold algorithm ‘Percentile’ binarised the pixels into positive or negative for Pimo based on the global WSI DAB intensity. Data were processed in R Studio, using the additional package “dplyr” for grouped summary statistics.

Results: CDAHFD induced non-alcoholic steatohepatitis (NASH) with panlobular Pimo positivity, whereas hypoxia was present in the centrolobular area in normal livers in SD group. Liver lobules follow the Voronoi principle wherein each lobule originates from a central vein identified by HandE and centrolobular GS staining. These landmarks were manually annotated for each lobule after which the image analysis script calculated the intensity distribution as a function of the pixel position within the lobule. After exclusion of datapoints belonging to fat vacuoles, the percentage of Pimo positive area was calculated in different parenchymal zones. The Pimo positive area was significantly higher in the periportal zone in NASH livers (p < 0.05, Fig.1). Moreover, the ratio of Pimo positive area in periportal (PP) vs. centrolobular (CV) regions was significantly higher in NASH compared to SD (p < 0.001), demonstrating the panlobular nature of Pimo staining in NASH.

Conclusion: The method described herein accurately quantifies the difference in zonal distribution of hypoxia marker Pimo in WSI images of NASH and normal livers. This image analysis method should allow for objective zonal quantification of other epitopes assessed by IHC, including livers affected by NAFLD.
SAT090
CD161 expressing CD4+ CD25hi T cells accumulate in the liver of obese patients with NASH
Rafael Kaeser1, Emilia Schlaak1, Franziska Engels1, Saskia Kùller1, Katharina Zoldan1, Lukas Sturm1, Lena Mayer1, Gabriel Seifert2, Jodok Matthias Fink2, Goran Marjanovic2, Thomas Longerich3, Agnieszka Kabaë4, Edward Pearce4, Dominik Bettinger1, Maike Hofmann1, Robert Thimme1, Bertram Bengsch1, Tobias Böttler1, 1University Hospital Freiburg, Department of Internal Medicine II, Freiburg im Breisgau, Germany; 2University Hospital Freiburg, Department of General and Visceral Surgery, Freiburg im Breisgau, Germany; 3University Hospital Heidelberg, Department of Pathology, Germany; 4Max Planck Institute of Immunobiology and Epigenetics, Department of Immunometabolism, Freiburg im Breisgau, Germany
Email: rafael.kaeser@uniklinik-freiburg.de

Background and aims: Non-alcoholic fatty liver disease (NAFLD) associated with obesity and metabolic syndrome is emerging as a leading cause of chronic liver disease in western countries. Hepatic steatosis may lead to inflammation resulting in non-alcoholic steatohepatitis (NASH) and progressive liver disease. A role of hepatic T cells in driving inflammation is suspected, however, the immuno-pathogenesis of NASH remains incompletely understood. We therefore set out to characterize the immune landscape in NASH livers and non-inflamed livers in obese patients.

Method: Liver tissue was obtained from heavily obese patients undergoing bariatric surgery. Clinical data and blood samples were collected at baseline and longitudinally after surgery. 52 patients undergoing bariatric surgery. Further studies are required to dissect their function and mechanistic role in driving inflammation in NASH patients.

SAT091
GL0034, a novel long-acting glucagon-like peptide 1 receptor agonist exhibits significant efficacy in aged db/db mouse model of non-alcoholic fatty liver disease (NAFLD)
Rajamannar Thennati1, Vinod Burade1, Adolfo Garcia-Ocana2, Richard E Pratley3, Guy Rutter4, Tina Vilsbøll5, Bernard Thorens6, 1University of Florida, College of Medicine, Gainesville, United States; 2University of Florida, College of Medicine, Jacksonville, United States; 3Department of Internal Medicine, Mayo Clinic, Jacksonville, United States; 4Diabetes and Metabolism Research Group, University of Copenhagen, Copenhagen, Denmark; 5University of Copenhagen, Department of Clinical Science, Copenhagen, Denmark; 6University of Florida, College of Pharmacy, Jacksonville, United States

Email: rajamannar.thennati@sunpharma.com

Background and aims: Obesity and type 2 diabetes are the major risk factors for non-alcoholic fatty liver disease (NAFLD) and advanced liver fibrosis. GL0034 is a novel long-acting human glucagon-like peptide 1 (GLP-1) receptor agonist, which selectively activates the GLP-1 receptor.

Method: db/db mice (age: 22–24 week) were divided into vehicle control; GL0034 (20 nmol/kg) or semaglutide (20 nmol/kg). Animals were treated with vehicle or test item every third day (q3d) up to day 28. On day 28, HbA1c, plasma triglycerides, serum alanine aminotransferase (ALT), aspartate aminotransferase (AST), liver transforming growth factor β (TGF-β) and malondialdehyde (MDA) were quantified. Liver steatosis was evaluated using Oil-Red O staining and HandE (haematoxylin and eosin) staining.

Results: Subcutaneous treatment with GL0034 led to a significant reduction in HbA1c, body weight, plasma triglycerides, ALT/AST and liver TGF-β (Table). Insulin levels increased (4.5-fold). Reduction in steatosis was confirmed using Oil-Red O/HandE staining and liver MDA (2-fold decrease) level.

Conclusion: A distinct hepatic CD161-expressing CD4+ CD25hi T cell population is significantly enriched in NASH patients from NAFLD patients undergoing bariatric surgery. Further studies are required to dissect their function and mechanistic role in driving inflammation in NASH patients.
Development of an ex vivo model for non-alcoholic fatty liver disease using precision-cut liver slices

Mei Li1, Vincent de Meijer2, Peter Olinga1, Anika Nagelkerke3, Yana Geng1. 1University of Groningen, Department of Pharmaceutical Technology and Biopharmacy, Netherlands; 2University Medical Center Groningen, Department of Hepato-, Pancreato-, Biliary Surgery and Liver Transplantation, Netherlands; 3University of Groningen, Department of Pharmacological Analysis, Netherlands

Email: yana.geng@rug.nl

Background and aims: Non-alcoholic fatty liver disease (NAFLD) is an emerging healthcare problem, ranging from non-alcoholic fatty liver (NAFL) to non-alcoholic steatohepatitis (NASH), often progresses to fibrosis, cirrhosis along with hepatocellular carcinoma. Progress in this field depends on the availability of reliable preclinical models. In this respect, precision-cut liver slices (PCLS) could provide the preserved multicellular environment allowing for the interplay of various liver cell types. This study aims to investigate NAFLD development in mouse and human PCLS.

Method: Mouse PCLS (mPCLS), from male C57BL/6J mice liver, and human PCLS (hPCLS), obtained from surgical waste material of donor livers, were used. Slices were cultured in GFIPO (William’s E Medium supplemented with Glucose (36 mM), Fructose (5 mM), Insulin (1 nM), Palmitic acid (0.12 mM for mPCLS/0.24 mM for hPCLS) and Oleic acid (0.24 mM for mPCLS/0.48 mM for hPCLS)) to mimic the NAFLD-inducing conditions, and WEGG (William’s E Medium supplemented with Glucose (25 mM)) as control for up to 96 h. PCLS were collected to assess viability and fat accumulation by measuring ATP levels and triglyceride (TG) content. Inflammation and fibrosis were evaluated by RT-qPCR. Additionally, the conditioned medium of hPCLS were collected for culturing LX2 cells (a human hepatic stellate cell line) at 1:3 (v/v) ratio mixed with LX2 medium. The activation of LX2 cells were evaluated by assessing the protein levels and the mRNA expressions of collagen type 1/Col1a1 and alpha smooth muscle actin/ACTA2.

Results: Slices remained viable for up to 96 hours incubation in both WEGG and GFIPO medium, and TG content was increased 71% (mPCLS) and 92% (hPCLS) in GFIPO compared with WEGG group. In GFIPO, mRNA expression of the inflammatory biomarker interleukin 6 was significantly upregulated compared to WEGG (3-fold in mPCLS, 6-fold in hPCLS), as well as interleukin 1β (3-fold in mPCLS, 42-fold in hPCLS), but no significant differences were observed for tumor necrosis factor a expression. COL1A1 and ACTA2 showed an increased trend in GFIPO in both mPCLS and hPCLS, but only ACTA2 was significantly increased in hPCLS (2-fold). In LX2 cells, the conditioned medium obtained from hPCLS cultured in GFIPO promoted the activation of LX2 cells comparing to that of hPCLS cultured in WEGG, shown as significantly increased protein level of collagen type 1 (2-fold), albeit not at mRNA expression level.

Conclusion: GFIPO increased the TG content as well as gene expression of inflammatory and fibrosis biomarkers in both mPCLS and hPCLS, without impairing viability. GFIPO introduced a pro-fibrotic environment in hPCLS, and its conditioned medium promoted collagen production in LX2 cells.

The neolignan honokiol can improve intestinal barrier dysfunction in fructose-induced liver damage in mice

Anja Baumann1, Verena Freutscheidt1, Julia Jelleschitz1, Raphaela Schäfer1, Annette Brandt1, Verena Dirsch2, Ina Bergheim1

1University of Vienna, Department of Pharmaceutical Sciences, Vienna, Austria; 2University of Vienna, Department of Pharmacognosy, Vienna, Austria

Email: ina.bergheim@univie.ac.at

Background and aims: Several studies indicate that a fructose-rich diet may be a risk factor in the development of non-alcoholic fatty liver disease (NAFLD). Studies have shown that this is associated with intestinal barrier dysfunction, and subsequently, with an increased translocation of bacterial toxins. Honokiol, a neolignan found in Magnolia officinalis and used in traditional Chinese medicine, has a variety of biological activities including protective effects on the development of intestinal barrier dysfunction. The aim was to determine if an oral supplementation of honokiol improves intestinal barrier dysfunction in fructose-induced NAFLD.

Method: Female C57BL/6J mice (n = 7/group) were fed a 30% fructose solution or plain water ± 10 mg honokiol per kg body weight per day for 4 weeks. Markers of liver damage and intestinal permeability and toll-like receptor (TLR) 2 as well as TLR4 ligands in portal plasma were measured. In addition, effects of honokiol on fructose-induced intestinal permeability were assessed ex vivo in an everted sac model.

Results: As expected, fructose-fed mice developed liver steatosis which was significantly attenuated in fructose + honokiol-fed mice (NAFLD activity score: fructose vs. fructose + honokiol, p < 0.05). These protective effects of honokiol were associated with a significant protection against the increased intestinal permeability found in small intestinal tissue in fructose-fed mice. In line with the latter, TLR2 and 4 ligands were only significantly or by trend higher in portal plasma of fructose-fed mice while being at the level of controls in fructose + honokiol-fed animals. In support of the in vivo findings, honokiol also significantly attenuated fructose-induced permeability in the ex vivo model.

Conclusion: The results of the present study suggest that an oral supplementation of honokiol can improve intestinal barrier dysfunction in settings of fructose-induced liver damage being also associated with a lessened development of NAFLD. Funded in part by the Interdisciplinary Network of the Faculty of Life Sciences, University of Vienna: Neolignans: new therapeutics in the prevention of diet-induced intestinal barrier dysfunction?

SAT093 Retrospective AI-based measurement of NASH histology (AIM-NASH) analysis of biopsies from Phase 2 study of Resmetirom confirms significant treatment-induced changes in histologic features of non-alcoholic steatohepatitis

Stephen Harrison1, Janani Iyer2, Charles Biddle-Snead2, Sara Hoffman2, Quang Le2, Victoria Mountain2, Murray Resnick2, Katy Wack2, Jim Hennan2, Rebecca Taub2, 1Pinnacle Clinical Research, San Antonio, United States; 2PathAI, Boston, United States; 3Madrigal Pharmaceuticals, Conshohocken, United States

Email: becky@madrigalpharma.com

Background and aims: Biopsy-based end points are recommended for assessing treatment efficacy in non-alcoholic steatohepatitis (NASH) clinical trials. While manual scoring of NASH histology is subject to intra- and inter-rater variability, AI-powered pathology may enable accurate and reproducible histologic assessment. Here we demonstrate the utility of an AI-based tool (AIM-NASH), for scoring NASH histology in a retrospective analysis of clinical trial liver biopsies.

Method: PathAI AIM-NASH algorithms were deployed on whole slide images of liver biopsies from 104 subjects enrolled in a Phase 2 (Ph2), placebo-controlled, 36-week study of the efficacy of MGL-3196 treatment in patients with NASH and NASH CRN stage 1–3 fibrosis (NCT02912260). Models predicted ordinal and continuous Clinical Research Network (CRN) scores in addition to exploratory features such as portal inflammation. Concordance between clinical pharmacology and AIM-NASH scores and features was evaluated. Differences in end point response rates and in changes in continuous scores and exploratory features between treated and placebo subjects were computed.

Results: All biopsy-based end points that were met via manual histologic scoring were also met by AIM-NASH (Table 1). ML continuous scoring revealed a statistically significant reduction in steatosis and a greater sub-ordinal reduction in fibrosis in treated versus placebo subjects. The measured reduction in continuous
fibrosis score was greater than the reduction in collagen proportionate area (CPA) in treated subjects. Change in ML-derived area proportion of portal inflammation was significantly correlated with change in portal inflammation scores from both central readers (p = 0.009 and p = 0.011, respectively), while concordance between both central readers for portal inflammation scoring was kappa = 0.298.

Table 1: Response rates per end point via manual vs. AI-based scoring

<table>
<thead>
<tr>
<th>End point</th>
<th>Scorer</th>
<th>Response (%)</th>
<th>Response (%)</th>
<th>p value</th>
</tr>
</thead>
<tbody>
<tr>
<td>2-point or greater</td>
<td>AIM-NASH</td>
<td>0.41</td>
<td>0.19</td>
<td>0.0327</td>
</tr>
<tr>
<td>improvement in NASH</td>
<td>Central reader</td>
<td>0.59</td>
<td>0.26</td>
<td>0.0044</td>
</tr>
<tr>
<td></td>
<td>Reader 2</td>
<td>0.42</td>
<td>0.19</td>
<td>0.0252</td>
</tr>
<tr>
<td>NASH resolution without</td>
<td>AIM-NASH</td>
<td>0.26</td>
<td>0.07</td>
<td>0.3501</td>
</tr>
<tr>
<td>worsening of fibrosis</td>
<td>Central reader</td>
<td>0.25</td>
<td>0.06</td>
<td>0.0226</td>
</tr>
<tr>
<td></td>
<td>Reader 2</td>
<td>0.21</td>
<td>0.03</td>
<td>0.0190</td>
</tr>
</tbody>
</table>

Conclusion: This ML approach detected similar proportions of primary end point responders as manual scoring. ML-derived continuous features demonstrated sensitivity to changes in NASH histology and enabled more granular exploration of sub-ordinal treatment effects. Such AI-based tools show promise as assistive devices for NASH pathologists in clinical trial settings.

SATO95
Insights to molecular mechanism of Essentielle: In vitro studies in hepatic cell lines HepaRG and steatotic HepaRG
Dominik Wupperfeld1, Gert Fricker1, Beatrice Bois De Fer2, Branko Popovic3, 4Ruprecht-Karls University of Heidelberg, Heidelberg, Germany; 5Sanofi, Gentilly, France; 3Sanofi, Frankfurt, Germany
Email: branko.popovic@sanofi.com

Background and aims: Non-alcoholic fatty liver disease is the most common liver disease worldwide and treatment options are limited. Essential Phospholipids (EPL, Essentielle®), comprising of multiple unsaturated fatty acids, have shown therapeutic effects but the molecular mechanism remains to be investigated. Here, we report the impact of EPL on hepatocyte function through in vitro studies.

Method: Effects of non-cytotoxic concentrations of EPL (0.1 and 0.25 mg/ml) and its constituents polyenylphosphatidylcholine (PPC) and phosphatidylinositol (PI) (both at 0.1 and 1 mg/ml) on the release of pro-inflammatory cytokines caused by treatment with lipopolysaccharide (LPS) and lipid-metabolizing enzymes were investigated in human hepatocyte cell lines (HepaRG, steatotic HepaRG) using ELISA and Glucose-6-phosphat dehydrogenase (G6PD) activity assay kits. To induce steatosis in HepaRG cells, differentiated cells were treated with stearic acid and oleic acid for two weeks.

Results: Lipopolysaccharide (1, 5 μg/ml) treatment for 24 h induced release of cytokines. In LPS-treated HepaRG cells EPL (0.25 mg/ml; p = 0.0063), PPC (1 mg/ml; p < 0.0001), PI (0.1 mg/ml; p = 0.0396, 1 mg/ml; p = 0.0023) significantly reduced the release of IL-6. Treatment with EPL (0.1 mg/ml; p < 0.0001) and PI (1 mg/ml; p = 0.0029) increased the release of IL-6 in LPS-treated steatotic HepaRG cells. IL-8 secretion increased significantly (p = 0.001) in LPS treated HepaRG and steatotic HepaRG cells in response to all lipid formulations. G6PD activity was unchanged by all treatments in HepaRG and steatotic HepaRG cells. In HepaRG cells human lecithin cholesterol acyltransferase (LCAT) expression was significantly downregulated upon treatment with EPL (0.1 mg/ml; p < 0.0001, 0.25 mg/ml; p = 0.0436), PPC (1 mg/ml; p < 0.0001), PI (1 mg/ml; p < 0.0001) and upregulated by PPC (0.1 mg/ml; p = 0.0009). However, in steatotic HepaRG cells, a significant increase of expression of LCAT was observed upon treatment with PI (1 mg/ml; p = 0.0088). Endogenic expression of human acyl Coenzyme A oxidase 1 (ACOX1) and fatty acid synthase (FAS) was lower in HepaRG cells compared to steatotic HepaRG cells. While in HepaRG cells ACOX1 expression decreased upon treatment with EPL (0.1 mg/ml; p = 0.0126, 0.25 mg/ml; p = 0.0031), PPC (0.1 mg/ml; p = 0.0145, 1 mg/ml; p = 0.0434), PI (1 mg/ml; p = 0.0404), none of the treatments affected ACOX1 expression in steatotic HepaRG cells. FAS expression remained unchanged in HepaRG cells upon treatment with lipid formulations. However, in steatotic HepaRG cells, FAS expression was significantly reduced (p < 0.0001) in response to treatment with all lipid formulations in all concentrations.

Conclusion: In vitro investigations in hepatocyte cell lines provided valuable insights into the impact of EPL on pro-inflammatory cytokine release, lipid-metabolizing enzymes which may improve liver function.

SATO96
Exposure to the SARS-CoV-2 spike protein in an in vitro model of steatosis enhances hepatocyte oxidative stress: implications for COVID-19 and accelerated disease progression
Angus Jacobs1, Katie Morgan1, Steven Morley1, Kay Samuel2, Jonathan Fallowfield3, Peter Hayes1, John Plevris1, 2The University of Edinburgh, Hepatology department, Edinburgh, United Kingdom; 3Scottish National Blood Transfusion Service, Tissues, Cells, and Advanced Therapeutics, Edinburgh, United Kingdom; 4The University of Edinburgh, Centre for Inflammation Research, Edinburgh, United Kingdom
Email: anguskerrjacob@gmail.com

Background and aims: Metabolic dysfunction-associated fatty liver disease (MAFLD) has been identified as a predictor of liver injury in patients hospitalised with coronavirus disease 2019 (COVID-19). The key severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) receptor, angiotensin converting enzyme 2 (ACE2), is suggested to play a protective role in the pathogenesis of MAFLD. Our unpublished data shows that human hepatic ACE2 expression correlates positively with increasing MAFLD progression, from steatosis through steatohepatitis to cirrhosis. The extent to which COVID-19 may accelerate MAFLD progression remains unclear. Here we use an in vitro steatosis model to investigate susceptibility to liver injury following exposure to SARS-CoV-2 spike protein S1 subunit and thus a possible role of COVID-19 in accelerating MAFLD progression.

Method: Following 24 h exposure of fully differentiated (day 14) HepaRG cells were exposed to the SARS-CoV-2 spike protein S1 subunit (0.05 μg/ml, 0.1 μg/ml, and 0.5 μg/ml), changes in cell conformation of the cell layer were measured using electric cell-substrate impedance sensing (ECIS). Cytokine secretion was quantified following exposure to a stenotic stimulus (oleate) ± S1 subunit using a flow cytometry-based cytokine bead array assay and the metabolic effects assessed by measurement of reactive oxygen species (ROS) and ATP by chemiluminescence assays.

Results: Our data show that 24-h exposure to the SARS-CoV-2 spike protein S1 subunit caused a concentration-dependent alteration in HepaRG cell tight-junction integrity and/or basolateral adhesion. However, the S1 subunit had no significant effect on HepaRG cell viability at any of the tested concentrations. Treatment of HepaRG cells with oleate ± S1 significantly increased secretion of proinflammatory cytokine IL-6 (mean ± SEM; oleate alone: 31.3 ± 9.0 pg/ml; oleate + S1: 33.5 ± 2.9 pg/ml) compared to untreated cells (18.7 ± 2.9 pg/ml; both p < 0.05) and cells treated with the S1 subunit alone (16.0 ± 3.2 pg/ml, both p > 0.05). In our in vitro steatosis model, the addition of the S1 subunit appeared to have an additive effect, significantly increasing ROS production (mean ± SEM; 63, 700 ± 3500 relative luminescence units (RLU)) compared to untreated cells (40, 500 ± 2100 RLU, p < 0.05), but there was no effect on ATP production.

Conclusion: Our data indicate that the SARS-CoV-2 spike protein S1 subunit affects tight junction integrity and promotes oxidative stress in oleate-treated HepaRG cells, and that fat-loading increases...
proinflammatory cytokine secretion. This could in turn cause activation of profibrotic signalling pathways and accelerate disease progression in MAFLD.

NAFLD: Therapy

SAT101
Efficacy and safety of leronlimab in patients with non-alcoholic steatohepatitis: topline results of NASH01 clinical trial
Mazen Noureddin1, Eric Lawitz2, Angela Ritter3, Tarek Hassanein4, Kelly Bowman5, Scott Kelly6, Eisa Mahyari7, Jonah Sacha8, Scott Hansen9, Christopher Recknor9, 1 Cedars Sinai, Liver Disease and Transplant Center, Los Angeles, United States; 2 The University of Texas Health Science Center San Antonio, Texas Liver Institute, San Antonio, United States; 3 Center for Advanced Research and Education, Gainesville, United States; 4 Southern California GI and Liver Centers, Coronado, United States; 5 Sensible Healthcare, Oceoe, United States; 6 CytoDyn Inc., Vancouver, United States; 7 Oregon Health and Science University, Genetics, Beaverton, United States; 8 Oregon Health and Science University, Vaccine and Gene Therapy Institute, Beaverton, United States

Email: crecknor@cytodyn.com

Background and aims: CCR5 modulates key metabolic, inflammatory, and fibrogenic pathways in the pathogenesis of NASH. NASH01 was conducted to determine efficacy, dose and safety of leronlimab, a known CCR5 binding agent, in patients with NASH.

Method: In this multi-center phase 2a, dose ranging, two-part trial, part 1 was designed as a double-blind, randomized, placebo-controlled trial, patients with NASH phenotype who had MRI proton density fat fraction (PDFF) ≥ 5% and corrected T1 (cT1) ≥ 800 ms were randomly assigned 1:1 weekly SQ leronlimab 700 mg or placebo and part 2 as open label comparing leronlimab 350 mg to part 1 placebo group. Treatment duration was 14 weeks. The primary end point was change from baseline in PDFF and secondary end points were change from baseline in cT1 fibro-inflammatory activity and change in serum CK18 and K18 by M30-M65 ELISA at week 14.

Results: Analyses were conducted on the full analysis set (n = 72) of whom 44% were of Hispanic or Latino ethnicity and 58% with baseline moderate to severe fibro-inflammation (cT1 ≥ 875 ms). Mean percent change from baseline PDFF was significantly reduced in the 350 mg group vs placebo (-5.94% vs +9.85%, p = 0.008) but not in the 700 mg group (+3.75% vs +9.85%, p = 0.135). Mean change cT1 was significantly reduced in the 350 mg group vs placebo (-24.38 ms vs +27.64 ms, p = 0.021) but not in the 700 mg group (-2.73 ms vs +27.64 ms, p = 0.059). Significant reductions were seen in the 350 mg subgroup with baseline cT1 ≥ 875 ms in both PDFF and cT1 vs placebo (-4.37% vs +9.85%, p = 0.020 and -42.00 ms vs +27.64 ms, p = 0.011) respectively. In subjects with cT1 ≥ 950 ms at baseline, PDFF and cT1 were significantly reduced with 350 mg vs placebo (-9.39% vs +9.85%, p = 0.027 and -68.85 ms vs +27.64 ms, p = 0.009) respectively. Mean change in baseline to week 14 for M65 ELISA (CK18 and K18) decreased in the 350 mg group (340.55 to 332.4 U/L, +6.85%) while increased in placebo (301.96 to 411.64 U/L, +36.6%). In post hoc analyses, mean percent PDFF and mean cT1 were significantly reduced in the pooled 350 + 700 mg group compared to placebo (-1.09% vs +9.85%, p = 0.014 and -13.30 ms vs +27.64 ms, p = 0.013) and in the 700 mg group with genetic haplotypes known to over produce CCR5 compared to placebo (-27.8% vs +9.85%, p = 0.014 and -45.4 ms vs +27.64 ms, p = 0.013). There was no grade 3 or higher drug related treatment emergent adverse event. Injection site reaction and mild diarrhea occurred more frequently with leronlimab than placebo but were not associated with discontinuation.

Conclusion: The primary end point (PDFF) and secondary end points (cT1) were met for the 350 mg group and moderate to severe fibro-inflammation by cT1 ≥ 350 mg subgroup at baseline. The pooled 350 + 700 mg group also had significant reductions in PDFF, cT1 vs placebo. Treatment with leronlimab was well tolerated. These results are supportive of further trials with leronlimab for NASH.

SAT102
Reduced triglycerides and LDL cholesterol from once-weekly administration of the well-tolerated novel FGF21 analogue 0499
Kirsten Dahl1, Jakob Schioler Hansen2, Jesper Clausen3, Mads Sundby Palle1, Cassandra Key2, Birgitte Andersen4, 1 Novo Nordisk A/S, Denmark; 2 Novo Nordisk Bio Innovation Hub, United States; 3 ICON Early Phase Services, United States

Email: kdhl@novonordisk.com

Background and aims: Activation of the fibroblast growth factor 21 (FGF21) receptor complex has been associated with several attractive effects in preclinical models, including weight loss and decreased hepatic fat content. This has led to the pursuit of FGF21 for pharmacotherapy within obesity and non-alcoholic steatohepatitis (NASH), which has to date been limited by lack of suitable FGF21 analogues. Here we report an investigation of the safety and tolerability of repeated administration of a new FGF21 analogue 0499 in healthy participants.

Method: In a randomized, blinded, placebo-controlled, multiple ascending dose study, healthy males and females with body mass index ~ 30 kg/m2 received weekly subcutaneous injections of placebo or 0499 for 12 weeks. FGF21 dose levels were 3, 9, 27, 60 and 120 mg. In each dose cohort, 9 participants were randomized to active treatment and 3 to placebo. Participants were followed for safety monitoring and pharmacokinetic sampling until 36 days after last dose. A total of 57 participants were randomized.

Results: There were no serious adverse events related to treatment. Weekly administration of doses from 3 to 60 mg/week were well tolerated. There were no notable findings from hematology, clinical chemistry or vital signs. Adverse events observed at doses from 3 to 60 mg/week were vomiting, increased appetite, nausea and diarrhea. Nausea and diarrhea were also observed with placebo. Statistically significant weight gain of 4.5%-points (%-pt) (placebo adjusted) was observed in the 3 mg group. In the higher dose groups, weight changes of ≥2%-pt were observed (not statistically significant vs placebo). In the 120 mg cohort, all 6 participants who started treatment experienced tolerability issues within the first 3 weeks including moderate gastroesophageal reflux, vomiting, nausea and diarrhea. Further enrolment in the cohort and treatment with 120 mg were stopped. One participant experienced generalized urticaria at 9 mg/week. In total, 25 participants did not complete due to adverse events (n = 5) or other reasons. Withdrawals were distributed (3, 6, 3, 6 and 4 participants in the 3, 9, 27, 80 and 120 mg, and placebo groups, respectively). The plasma half-life of 0499 was 120 hours.

Conclusion: The primary end point (PDFF) and secondary end points (cT1) were met for the 350 mg group and moderate to severe fibro-inflammation by cT1 ≥ 350 mg subgroup at baseline. The pooled 350 + 700 mg group also had significant reductions in PDFF, cT1 vs placebo. Treatment with leronlimab was well tolerated. These results are supportive of further trials with leronlimab for NASH.
Conclusion: The novel FGF21 analogue was well tolerated at doses up to 60 mg/week for 12 weeks. Treatment was associated with beneficial effects on lipid profile including lowering of TG and LDL levels. These results are encouraging for the further development of 0499 for treatment of NASH.

SAT103
Multimodality assessment of hepatic fibrosis: ranked paired reading and artificial intelligence identifies fibrosis improvement with aramchol missed by conventional staging

Vlad Ratziu1, Yusuf Yilmaz2, Don Lazas3, Scott Friedman4, Carolin Lackner5, Cynthia Behling6, Oscar Cummings7, Li Chen8, Mathieu Petitjean9, Yossi Gilgun-Sherki10, Shaul Kadosh10, Arun Sanjay11, Sorbonne Université, Institute for Cardiometabolism and Nutrition (ICAN) and 15 Sorbonne Université, Institute for Cardiometabolism and Nutrition (ICAN) and Hôpital Pitié-, Salpêtrière, INSERM UMR 1138 CRC, Paris, France; 2Liver Research Unit, Institute of Gastroenterology, Marmara University, and Department of Gastroenterology, School of Medicine, Marmara University, Istanbul, Turkey; 3ObjectiveHealth, Inc., United States; 4Division of Liver Diseases, Icahn School of Medicine at Mount Sinai, United States; 5Medical University of Graz, Graz, Austria; 6Department of Pathology, Sharp Health System, United States; 7Department of Pathology and Laboratory Medicine, Indiana University School of Medicine, Indianapolis, United States; 8Pharmanest Ltd., United States; 9Calmed pharmaceuticals, Israel; 10Stateexcellence Ltd., Israel; 11Department of Gastroenterology, Virginia Commonwealth University, United States

Email: vlad.ratziu@inserm.fr

Background and aims: Aramchol is a partial inhibitor of hepatic stearoyl-CoA desaturase with direct anti-fibrotic activity in pre-clinical models and histological improvement in a phase 2b trial. This open-label study explored the speed and extent of fibrosis reduction. We compared different methodologies of fibrosis scoring to optimize the design of a registrational placebo-controlled investigation.

Method: 46 Patients (pts) with NASH and fibrosis (28 F3, 11 F2, 7 F1) documented by biopsy were randomized 1:1:1 to receive Aramchol 300 mg BID and underwent a control biopsy at weeks 24, 48 or 72. Biopsies were read by 3 independent pathologists individually, followed by a consensus reading, which determined the final NASH CRN scoring. Three different assessments of the antifibrotic effect were studied on the same slides: 1) a ≥1 stage reduction by NASH CRN; 2) a ranked assessment (improvement/worsening/stable) of paired (pre and post baseline) biopsies, blinded to sequence; 3) an automated and continuous score of Fibrosis Composite Severity (FCS), using FibroNest™, a quantitative digital pathology image analysis and artificial intelligence (AI) Method: a 0.3 reduction in FCS (4 fold higher than the analytical variability) identified any reduction in fibrosis; a 25% relative decline in FCS, a strong reduction in fibrosis.

Results: Control biopsies were performed for 26, 15 and 5 pts at 24, 48, and 72 weeks, respectively. Mean (sd) baseline FCS was 5.05 (1.05). Table shows greater fibrosis improvement with longer duration of therapy for both conventional histology and digital pathology readings. Mean FCS reduction was −0.62 (p = 0.017) at Wk24 and −1.74 (p < 0.0001) at Wk≥48. AI evaluation was consistent with paired reading in 21/24 (87.5%) of the pts with fibrosis improvement. When analyzed by AI, 17/23 pts with unchanged NASH CRN stages had any fibrosis response, including 7 with a strong response. Similarly, 13/17 pts with stable ranking had a fibrosis response, including 5 with a strong reduction. No pts with worse CRN stages or worsening ranking had a strong AI fibrosis reduction.

SAT104
The effect of glucagon on rates of hepatic mitochondrial oxidation and pyruvate carboxylase flux in man assessed by positional isotopomer tracer analysis (PINTA)

Kitt Falk Petersen1, Gerald I. Shulman1. Yale University, Internal Medicine, New Haven, United States

Email: kitt.petersen@yale.edu

Background and aims: Dual GLP-1/glucagon agonists are now in clinical trials for the treatment of T2D and NASH. In addition to promoting further reduction in food intake on top of GLP-1, the glucagon component of these dual agonists may also promote increased rates of hepatic mitochondrial fat oxidation.

Method: In order to investigate this possibility we assessed the glucagon-specific effects of a dual agonist on rates of hepatic mitochondrial oxidation (VCS) and pyruvate carboxylase flux (VPC) in humans by infusing glucagon to achieve a physiological increase in plasma glucagon concentrations in combination with a novel 13C isotopomer tracer analysis (PINTA). We method to assess rates of hepatic VCS and VPC in 15 healthy volunteers using a paired study design. Following an overnight fast a 2-h IV infusion of [3-13C]lactate (4.3 μmol/Kg-min) and [1, 2, 3, 4, 5, 6, 6-2H7]glucose (0.22 μmol/Kg-min) was begun and during the last 2 hours glucagon (GLG) was co-infused [6 ng/ (Kg-min)] or no GLG (CON).

Results: The GLG infusion resulted in a ~2.4 fold increase in plasma GLG conc. (from 75 ± 11 to 183 ± 20 pg/ml; P < 0.0001), which was associated with an ~20% increase in both plasma C-peptide (from 1.89 ± 0.17 to 2.30 ± 0.26 ng/ml; P = 0.02) and plasma insulin conc. (from 9.9 ± 2.0 to 12.0 ± 2.4 μU/ml; P = 0.06). Plasma glucose conc. increased from 4.90 ± 0.16 to 5.64 ± 0.19 mmol/L (P = 0.0001) which was associated with a tendency for increased rates of glucose production (CON:1042 ± 123 vs. GLG:1148 ± 122 μmol/min; p = 0.086) despite no change in rates of VPC flux (CON: 403 ± 69 vs. GLG: 373 ± 55 μmol/min; p = NS). In contrast, this physiological increase in plasma GLG concentrations caused an 85% increase in rates of hepatic VCS (p < 0.05).

Conclusion: Aramchol resulted in a high proportion of fibrosis improvement using three separate biopsy reading methodologies, with a larger treatment effect with longer duration of therapy. Both ranked assessments and AI evaluations identified more subjects with fibrosis improvement, indicating greater sensitivity to change vs categorical scoring. Digital pathology quantification by AI reveals a high level of fibrosis improvement that would have been missed by conventional histological measurements. AI technologies are promising for the detection of fibrosis changes in future clinical trials.
Conclusion: Taken together these studies demonstrate that a physiological increase in plasma glucagon promotes increased rates of hepatic mitochondrial oxidation in humans, which may provide additional benefits to the anorexic effects of dual GLP-1/glucagon agonists to reduce hepatic steatosis.

SAT105
Identification of biomarkers of histological response in patients with non-cirrhotic NASH treated with Lanifibranor
Jerome Boursier1, Hugo Herve2, Clémence M Canivet2, Marine Roux2, Pierre Broqua1, Michael Cooreman1, Jean-Louis Junien3, Jean Louis Abitbol2, Philippe Huot-Marchand2, Lucile Dzen3, Sanjaykanumar Patel4, 1Angers University, HIFIH Laboratory UFR ES EA3859, Angers; 2Angers University, HIFI Laboratory UFR ES EA3859; 3Inventiva; 4Inventiva, France

Background and aims: Lanifibranor, a pan-PPAR agonist, is a promising investigational compound for treating non-alcoholic steatohepatitis (NASH), as shown by histological efficacy in the phase 2b NATIVE trial (Franque SM et al 2021). We aimed to predict lanifibranor treatment response in NATIVE based on serum biomarkers.

Method: Patients receiving lanifibranor 800 or 1200 mg/d were pooled and those with end-of-treatment (EOT) liver biopsies were selected (n = 142). The histological end points ‘NASH resolution and fibrosis improvement’ (E1) and ‘NASH resolution without worsening of fibrosis’ (E2) according to NASH CRN criteria were assessed. A panel of more than 70 biomarkers related to metabolism, inflammation, tissue injury and fibrosis were evaluated by baseline, absolute and relative changes at EOT. Biomarker selection was done using classical univariate analysis, PCA and sPLS-DA, and combined in scores by logistic regression.

Results: 42 (30%) and 63 (44%) patients were respectively E1 and E2 responders; 4 parameters were independently associated with E1 response: baseline adiponectin and ferritin, and relative changes of fructosamine and ALT were selected (n = 142). The histological end points ‘NASH resolution and fibrosis improvement’ (E1) and ‘NASH resolution without worsening of fibrosis’ (E2) according to NASH CRN criteria were assessed. A panel of more than 70 biomarkers related to metabolism, inflammation, tissue injury and fibrosis were evaluated by baseline, absolute and relative changes at EOT. Biomarker selection was done using classical univariate analysis, PCA and sPLS-DA, and combined in scores by logistic regression.

Results: 42 (30%) and 63 (44%) patients were respectively E1 and E2 responders; 4 parameters were independently associated with E1 response: baseline adiponectin and ferritin, and relative changes of fructosamine and ALT were selected (n = 142). The histological end points ‘NASH resolution and fibrosis improvement’ (E1) and ‘NASH resolution without worsening of fibrosis’ (E2) according to NASH CRN criteria were assessed. A panel of more than 70 biomarkers related to metabolism, inflammation, tissue injury and fibrosis were evaluated by baseline, absolute and relative changes at EOT. Biomarker selection was done using classical univariate analysis, PCA and sPLS-DA, and combined in scores by logistic regression.

Conclusion: Combined biomarker signatures have good positive and negative predictive value for histological response under lanifibranor treatment in NASH.

SAT106
TERN-101, a farnesoid X receptor agonist, demonstrated similar safety and efficacy in non-alcoholic steatohepatitis patients with coronavirus disease of 2019 (COVID-19) exposure compared to those with no COVID-19 exposure in phase 2a LIFT study
Eric Lawitz1, Rohit Loomba2, Douglas Denham2, Diana Chung4, Erin Quirk4, Lois Lee4, Tonya Marmon4, Kris Kowdley5, 1Texas Liver Institute, San Antonio, United States; 2University of California San Diego, La Jolla, United States; 3Clinical Trials of Texas, Inc., San Antonio, United States; 4Terns Pharmaceuticals, Foster City, United States; 5Liver Institute Northwest, Seattle, United States

Background and aims: TERN-101 is a non-steroidal farnesoid X receptor (FXR) agonist with enhanced liver distribution being developed for the treatment of non-alcoholic steatohepatitis (NASH). The phase 2a LIFT study (NCT04328077) was a double-blind, placebo-controlled study in adults with noncirrhotic NASH conducted during the COVID-19 pandemic. TERN-101 (5, 10, and 15 mg) administered for 12 weeks was overall safe and well-tolerated and significantly decreased alanine aminotransferase (ALT) and corrected T1 (cT1) relaxation time. We reviewed COVID-19 exposure in LIFT to explore any potential impact on TERN-101 safety and efficacy.

Method: COVID-19 antibody testing was performed at Screening, and Weeks 0, 6, and 12, and with ad hoc antibody and qualitative virus testing available in the event of COVID-19 symptoms. We evaluated overall safety and key efficacy parameters in patients with COVID-19 exposure, defined as patients with COVID-19 infection as an adverse event (AE) or detectable COVID-19 antibodies during the study.

Results: Of 100 enrolled and treated patients, 96% completed the LIFT study with no discontinuations due to AEs and no deaths; AEs occurred in 38.5% of the placebo and 56.8% of the TERN-101 groups. 97% of the patients had post-baseline COVID-19 antibody results. Of the 24 COVID-19 exposures identified, 4 had documented COVID-19 vaccination during the study (16.7%). COVID-19 infection was reported for 7 patients (7%): 6 who received TERN-101 and had mild to moderate AEs (Grade 1 or 2), and 1 placebo patient who developed a severe AE (Grade 3) that resolved. Among all 24 COVID-19 exposures, non-COVID-19 related treatment-emergent AEs were reported in 7 of 19 (36.8%) patients receiving TERN-101 vs 1 of 5 (20.0%) patients receiving placebo. ALT and cT1 changes at Week 12 among COVID-19 exposures were similar to patients without exposure of COVID-19.

Conclusion: NASH patient recruitment and retention in the LIFT Study was feasible during the COVID-19 pandemic with successful...
SAT107 Favorable lipid and pruritus profile of liver-distributed farnesoid X receptor agonist TERN-101 at clinically efficacious doses in non-alcoholic steatohepatitis phase 2a LIFT study

Kris Kowdley1, Eric Lawitz2, Rohit Loomba3, Erin Quirk4, Daria Crittenden4, Diana Chung5, Tonya Marmon1, 1Liver Institute Northwest, Seattle, United States; 2Texas Liver Institute, San Antonio, United States; 3University of California San Diego, NAFLD Research Center, La Jolla, United States; 4Terns Pharmaceuticals, Foster City, United States; 5University of California San Diego, NAFLD Research Center, La Jolla, United States; 6Enanta Pharmaceuticals, Foster City, United States

Email: email@ternspharma.com

Background and aims: TERN-101 is a potent, non-steroidal farnesoid X receptor (FXR) agonist with enhanced liver distribution under investigation for treatment of non-alcoholic steatohepatitis (NASH). Dose-related pruritus and unfavorable lipid effects have raised concerns about FXR agonists as a treatment for NASH. In the phase 2a LIFT study, TERN-101 was overall safe and well-tolerated at all dose levels, with significant reductions in alanine aminotransferase (ALT) and corrected T1 (cT1) relaxation time at 10 and 15 mg. Here we report additional details on lipids and pruritus from LIFT.

Method: LIFT was a double-blind, placebo-controlled study (NCT04328077) evaluating 5, 10 and 15 mg TERN-101 for 12 weeks in 100 adults with non-cirrhotic NASH. Low-density lipoprotein (LDL) and high-density lipoprotein (HDL) cholesterol were assessed at baseline and every 4 weeks. Pruritus was captured as part of routine adverse event (AE) reporting.

Results: No difference in LDL percent change from baseline was observed for 5 and 10 mg TERN-101 vs placebo at any timepoint; 15 mg had significant differences at all timepoints (+15.9% at Week 12). HDL was not different from placebo at Week 12 for 5 and 10 mg TERN-101. Changes in LDL and HDL by thresholds were assessed post-hoc (Table). Pruritus AEs (including pruritic rash) were reported in 11 of 74 (14.8%) patients receiving TERN-101 and none receiving placebo. Onset of pruritus ranged from Day 2 to Day 73. Pruritus resolved with ongoing TERN-101 treatment for 8 of 11 patients. All events were mild or moderate (Grade 1–2), with incidence overall balanced across TERN-101 groups. Grade 2 pruritus occurred in two 10 mg patients (generalized pruritus) and one 15 mg patient (pruritus localized to bilateral forearms). No patient discontinued TERN-101 due to pruritus.

Table: Lipid changes by threshold at Week 12

<table>
<thead>
<tr>
<th>n (%)</th>
<th>Placebo</th>
<th>5 mg</th>
<th>10 mg</th>
<th>15 mg</th>
</tr>
</thead>
<tbody>
<tr>
<td>n = 23</td>
<td>n = 24</td>
<td>n = 25</td>
<td>n = 21</td>
<td></td>
</tr>
<tr>
<td>LDL increase ≥25 mg/dL</td>
<td>4 (17)</td>
<td>4 (17)</td>
<td>2 (8)</td>
<td>4 (19)</td>
</tr>
<tr>
<td>HDL decrease ≥10 mg/dL</td>
<td>1 (4)</td>
<td>1 (4)</td>
<td>2 (8)</td>
<td>5 (24)</td>
</tr>
</tbody>
</table>

Conclusion: LDL and HDL mean changes, and proportion of patients with lipid changes by specified thresholds, were similar for 5 and 10 mg TERN-101 and placebo at Week 12. Pruritus AEs were not dose-dependent and did not lead to treatment discontinuation. These data support an overall differentiated and favorable safety and tolerability profile for TERN-101 at potentially efficacious dose levels.

SAT108 Liver-distributed farnesoid X receptor agonist TERN-101 demonstrates potent target engagement with a favorable exposure-response profile in non-alcoholic steatohepatitis patients

Cara H. Nelson1, Christopher Jones1, Kevin Klucher1, Feng Jin2, Tonya Marmon1, Diana Chung3, Erin Quirk4, Daria Crittenden1, 1Terns Pharmaceuticals, Foster City, United States; 2Polaris Consulting, Foster City, CA, United States

Email: cnelson@ternspharma.com

Background and aims: TERN-101 is a potent, non-steroidal farnesoid X receptor (FXR) agonist with enhanced liver distribution being developed for treatment of non-alcoholic steatohepatitis (NASH). In the dose-ranging phase 2a LIFT study (NCT04328077), TERN-101 demonstrated significant decreases in alanine aminotransferase (ALT) and corrected T1 (cT1) relaxation time in NASH patients, and was overall safe and well-tolerated with no discontinuations due to adverse events. We present the pharmacokinetic (PK) and pharmacodynamic (PD) results from the LIFT study.

Method: LIFT was a double-blind, placebo-controlled study in adults with noncirrhotic NASH. Patients (N = 100) were randomized and treated with placebo or TERN-101 (5, 10 or 15 mg) for 12 weeks. All patients had PK and PD samples collected at Week 0 (predose) and at trough timepoints (~24 hours post-dose) on Weeks 2, 4, 6, 8 and 12. Additionally, a subset of patients (N = 26) participated in an intensive PK/PD substudy at Weeks 0 and 12. PD markers of FXR agonism included 7-alpha-hydroxy-4-cholesten-3-one (C4) and fibroblast growth factor 19 (FGF19). A preliminary population PK model was used to estimate exposures in all patients.

Results: Sustained decreases in C4 were noted with levels significantly lower in the 10 and 15 mg groups vs placebo at most trough timepoints. In the PK/PD substudy, the maximal percent change in C4 and FGF19 occurred at 6 hours postdose. At Week 12, peak C4 decreases were dose-dependent and reached significance in the 10 and 15 mg groups (~56% and ~96%, respectively); peak FGF19 change increased with dose and was significant in the 15 mg group (777%). FGF19 returned towards baseline levels at 24 hours postdose in all groups. TERN-101 exposures in the LIFT study were approximately dose proportional with some overlap in exposures between the 10 and 15 mg groups. An exposure-response analysis demonstrated a trend of greater decreases in change of cT1 with increasing exposures of TERN-101.

Conclusion: TERN-101 resulted in significant FXR target engagement in the liver relative to the intestine, as evidenced by sustained decreases in C4 at the 10 and 15 mg doses and transient increases in FGF19. Higher exposures of TERN-101 were associated with greater decreases in cT1, a marker of fibroinflammation improvement in NASH patients. These analyses support further development of TERN-101 for the treatment of NASH, either alone or in combination with other agents.

SAT109 EDP-297: a novel, highly potent, farnesoid X receptor agonist, results of a phase 1 study in healthy subjects

Alaa Ahmad1, Christine Marotta1, Ed Luo1, Jart Oosterhaven2, Sjoerd van Marle2, Nathalie Adda1, 1Enanta Pharmaceuticals Inc, United States; 2PRA, Netherlands

Email: aahmad@enant.com

Background and aims: EDP-297 is a potent FXR agonist under development for the treatment of non-alcoholic steatohepatitis (NASH). EDP-297 attenuates NASH-relevant pathways of steatosis, liver injury, inflammation, and apoptosis both in vitro and in vivo. Here, we present pharmacokinetic (PK), and pharmacodynamic (PD), food effect (FE), and safety results of a single ascending dose (SAD) and multiple ascending dose (MAD) phase 1 study in healthy subjects (HS).

Table: Lipid changes by threshold at Week 12

<table>
<thead>
<tr>
<th>n (%)</th>
<th>Placebo</th>
<th>5 mg</th>
<th>10 mg</th>
<th>15 mg</th>
</tr>
</thead>
<tbody>
<tr>
<td>n = 23</td>
<td>n = 24</td>
<td>n = 25</td>
<td>n = 21</td>
<td></td>
</tr>
<tr>
<td>LDL increase ≥25 mg/dL</td>
<td>4 (17)</td>
<td>4 (17)</td>
<td>2 (8)</td>
<td>4 (19)</td>
</tr>
<tr>
<td>HDL decrease ≥10 mg/dL</td>
<td>1 (4)</td>
<td>1 (4)</td>
<td>2 (8)</td>
<td>5 (24)</td>
</tr>
</tbody>
</table>

Conclusion: LDL and HDL mean changes, and proportion of patients with lipid changes by specified thresholds, were similar for 5 and 10 mg EDP-297 and placebo at Week 12. Pruritus AEs were not dose-dependent and did not lead to treatment discontinuation. These data support an overall differentiated and favorable safety and tolerability profile for EDP-297 at potentially efficacious dose levels.
Method: A randomized, double-blind, placebo-controlled (PBO) study was conducted to evaluate the safety, tolerability, PK/FE, and PD of single and multiple doses of EDP-297 in HS. Subjects received EDP-297 as a single dose (SAD, 5 cohorts, 20–600 μg) or once daily (QD) for 14 days (MAD, 5 cohorts, 5–90 μg). (6 active: 2 PBO/cohort), except in the SAD food effect cohort (8 active: 2 PBO). PD measurements included fibroblast growth factor 19 (FGF-19) and 7α-hydroxy-4-cholesten-3-one (C4).

Results: A total of 82 subjects (n = 42 in SAD; n = 40 in MAD) received at least one dose of EDP-297 or PBO. EDP-297 was generally well tolerated. No severe adverse events or discontinuations due to adverse events (AEs) in SAD and MAD (up to 60 μg) were observed. Most AEs were mild and not related/unlikely related to study drug. In the SAD part, pruritus was observed in 300 μg (n = 2), 600 μg (n = 2), PBO (n = 1); during the MAD part, pruritus was reported in 30 μg (n = 1), 60 μg (n = 2), and 90 μg (n = 4), PBO (n = 2); the majority were mild or moderate, except for n = 4 severe cases at 90 μg MAD, with n = 1 that led to drug discontinuation. There were no clinically significant abnormal laboratory or abnormal ECG findings, except for n = 1 Grade 2 ALT elevation (MAD 90μg) that was not associated with other liver enzyme abnormalities. There were no clinically meaningful changes in the lipid profile, except for a trend towards decrease in HDL and increase in LDL at MAD 90μg; and mean lipids values were within normal range during the entire study. Plasma exposures increased with increasing single and multiple doses, with mean t1/2 following multiple doses of ~9–12.5 hours. No food effect was observed. Strong FXR target engagement was demonstrated, with increase in FGF-19 and decrease in C4 up to 95% and 92%, respectively.

Conclusion: Overall, EDP-297, a potent and selective FXR agonist, was safe and well tolerated with PK suitable for once daily oral dosing, a strong target engagement and no food effect.

SAT110
Weight loss with semaglutide treatment or time-restricted feeding differentially improves non-alcoholic steatohepatitis in diet-induced obese insulin resistant mice
Francois Briand1, Estelle Grasset1, Natalia Breyner1, Thierry Sulpice1.
1Physiogenex, Escalquens, France
Email: f.briand@physiogenex.com

Background and aims: Due to its positive correlation with obesity/type 2 diabetes, the prevalence of non-alcoholic steatohepatitis (NASH) is increasing worldwide. Weight loss represents a promising therapeutic strategy for NASH and liver fibrosis. Here we compared the weight loss benefits of the glucagon-like peptide-1 (GLP-1) receptor agonist semaglutide (SEMA) or time-restricted feeding (TRF) in diet-induced obese insulin resistant mice.

Method: Male C57BL6/J mice were fed a 60% high fat/2% cholesterol diet with 10% fructose supplemented drinking water (HFCF diet) for 25 weeks to induce obesity and NASH/liver fibrosis. After the 25-week diet-induction period, mice were kept on HFCF diet and treated with vehicle (control) or SEMA 0.06 mg/kg s.c. QD or placed on TRF from the last 3 hours of the dark cycle till the end of the light cycle, without access to food, but free access to normal drinking water (i.e., without fructose) every day, for 6 weeks. After 6 weeks, blood and liver were collected for biochemistry and histology analysis.

Results: SEMA treatment for 6 weeks induced a 20% lower caloric intake, which led to a 21% lower body weight (p < 0.001 vs. control). TRF had a weaker effect on caloric intake (-9%), but also reduced body weight (~11%, p < 0.05 vs. control). Both SEMA and TRF reduced the HOMA-IR index of insulin resistance and significantly reduced plasma ALT and AST levels, but these effects were more pronounced with SEMA. TRF, and to a greater extent SEMA, significantly reduced liver weight (SEMA: ~37%, TRF: ~27%), hepatic fatty acids (SEMA: ~61%, TRF: ~41%), triglycerides (SEMA: ~67%, TRF: ~36%, p < 0.05) and total cholesterol (SEMA: ~48%, TRF: ~30%) levels. Accordingly, SEMA showed a stronger reduction in steatosis score than TRF, but both led to significantly lower NAFLD activity score. SEMA and TRF significantly reduced the hepatic gene expression of MCP-1 (inflammation), alpha-SMA, TGF-beta, Collalpha1 and TIMP1 (fibrosis). However, SEMA did not alter liver fibrosis (as shown by Sirius Red staining), while TRF showed a clear anti-fibrotic effect in the liver, with significantly lower % Sirius Red labelling (p < 0.05 vs. control).

Conclusion: SEMA markedly reduced body weight and liver steatosis but did not improve hepatic fibrosis. Although its weight loss effect was less pronounced, TRF improved both NASH and liver fibrosis. These TRF benefits should be further investigated in the clinical setting.

SAT111
ECC4703, a full thyroid hormone receptor beta (THRβ) agonist, demonstrated excellent selectivity and liver targeting properties and improvement of plasma lipid, NAFLD activity score and fibrosis in NASH animal model
Jianfeng Xu1, Zhao Yongliang1, Julie Zhu1, Jianfeng Xu1, Jingye Zhou1.
1Eccogene (Shanghai) Co., Ltd., Shanghai, China
Email: jfxu@eccogene.com

Background and aims: Non-alcoholic steatohepatitis (NASH) is a metabolic liver disease featuring ectopic fat accumulation, hepatocellular damage, chronic inflammation, and progressive fibrosis. Resmetirion (MGL3196) as THRβ agonist has demonstrated THR β selectivity and liver targeting, which translate to plasma lipid lowering, potential of fibrosis improvement and thus NASH resolution in humans. However, MGL3196 is a partial agonist compared to the natural ligand T3 in ligand binding and liver gene expression. A full agonist may provide superior efficacy for NASH and dyslipidaemia.

Method: Ligand binding to human THRβ and THRα was measured based on recruitment of a coactivating activator peptide to the receptors. Liver targeting was determined in PTU-induced rat hypothryroïdism model with induction of THR target gene in liver and heart. Activities in rat and human primary hepatocyte were measured with a reporter gene driven by thyroid response elements. A diet-induced obesity with CCH4 in mice (DIO-CCH4) was applied to evaluate the effect of ECC4703 on plasma lipid and liver pathology.

Results: In a ligand bind assay, ECC4703 is a potent THRβ agonist with relative β vs α selectivity of 49. In PTU rat, ECC4703 elicited robust induction of liver gene DIO1 but no effects on heart gene α-MHC at up to 50 mpk, indicating superior liver targeting. It’s noteworthy in both in ligand binding and liver gene expression, ECC4703 showed Emax equivocal to T3 which suggested full agonism. In rat and human hepatocytes, ECC4703 led to potent reporter gene expression, ensuring species translation. In DIO-CCH4 NASH model, ECC4703 treatment resulted in significant decrease in plasma lipid, improvement of liver NAS score and fibrosis, but no effects on heart weight.
Conclusion: In summary, ECC4703 is a novel full THRβ agonist with excellent in vitro and in vivo profile, and potentially best-in-class compound for NASH and dyslipidemia treatment.

SAT112 LIVRQNac increases fatty acid oxidation in a primary human hepatocyte model of non-alcoholic steatohepatitis
Matthew Russell1, Christopher Newgard2,3, Guofang Zhang4, Arianna Nitzel5, Michael Hamill6, Karim Azer1, Axcella Therapeutics; 2Duke Molecular Physiology Institute; 3Department of Medicine, Duke University Medical Center; 4Flagship Pioneering
Email: mrussell@axcellatx.com

Background and aims: Endogenous metabolic modulators (EMM) are naturally occurring compounds with signaling and regulatory properties. When selectively combined, in unique stoichiometric ratios, EMMS can treat complex diseases with system-wide dysregulation of metabolic pathways. LIVRQNac, an EMM composition of 5 amino acids (AA) and n-acyl cysteine (Nac), decreased liver fat accumulation (in vivo and in vitro) by reducing triglyceride accumulation. AXA1125, the clinical formulation of these same EMMS, decreased liver fat content in subjects with non-alcoholic fatty liver disease by magnetic resonance imaging measurement of liver proton density fat fraction, MRI-PDFF. The present study investigated the in vitro dose-dependent effects of LIVRQNac on fatty acid oxidation (FAO), the putative mechanism of these effects, in a primary human hepatocyte (PHH) NASH model.

Method: PHHs were plated on collagen coated wells and incubated with 5% CO₂. On day 3, cells were incubated in custom media containing 500 μM carnitine, 10 μg/ml insulin, EGF 1 μM dexamethasone, and custom AA concentrations (as in healthy human plasma) with and without LIVRQNac (10X and 30X) and with lipotoxic insult with 5% CO₂. On day 3, cells were incubated in custom media containing 500 μM carnitine, 10 μg/ml insulin, EGF 1 μM dexamethasone, and custom AA concentrations (as in healthy human plasma) with and without LIVRQNac (10X and 30X) and with lipotoxic insult with [U-13C] palmitate replacing palmitate and then analyzed for 13C-labeled BHB, the ketone body, β-hydroxybutyrate; FAO, fatty acid oxidation; M2, mass isotopomers where number represents the number of heavy atoms in the molecule.

Results: 13C labeling of fatty acid-derived metabolites (%) was significantly increased by LIVRQNac treatment vs control. Increases were observed in labeled palmitoylcarnitine (p < 0.001), acetylcarnitine (p < 0.05), and acetyl-CoA (p < 0.05) in LIVRQNac- 10X, and 30X treated cells vs control. M2 labeled β-hydroxybutyric acid (terminal FAO product) increased 102% in LIVRQNac-treated cells (0.108 nmol, 10X; 0.133 nmol, 30X) vs control (0.066 nmol; p < 0.0001; Fig.).

Conclusion: Increases in labeled palmitoylcarnitine, acetylcarnitine and acetyl-coA reflected an increase in FAO in PHHS treated with LIVRQNac. Consistently, there was an increase in total and labelled β-hydroxybutyric acid in LIVRQNac-treated cells indicating an increase in ketogenesis. These data support a mechanism for AXA1125’s clinical effect of decreasing liver fat, by increasing ketogenesis and increasing FAO.

SAT113 Assessment of therapeutic effect of liraglutide in newly established cell culture model of non-alcoholic and drug-induced fatty liver disease
Tea Omanovic Kolaric1,2, Vjera Nincevic3, Tomislav Kizivat2, Milorad Zjalic2, Lucija Kuna2, Ines Bilic-Curcic2,3, Martina Smolic1,2, 1Faculty of Medicine Osijek, Department of Pharmacology, Osijek, Croatia; 2Faculty of Dental Medicine and Health Osijek, Department of Pharmacology and Biochemistry, Osijek, Croatia; 3University Hospital Centre Osijek, Clinical Department of Nuclear Medicine and Radiation Protection, Osijek, Croatia; 2Faculty of Medicine Osijek, Department of Medical Biology and Genetics, Osijek, Croatia; 3University Hospital Centre Osijek, Clinical Department of Diabetes, Endocrinology and Metabolism Disorders, Osijek, Croatia
Email: msmolic@mefsos.hr

Background and aims: The impact of non-alcoholic fatty liver disease (NAFLD) on global health is becoming more significant with the growing incidence of obesity and drugs consumption. Therefore, more research is necessary in order to enlighten underlying pathophysiologic mechanisms for these conditions and possible therapeutic approaches. Aims of our study were to establish reliable in vitro models of non-alcoholic and drug-induced fatty liver disease (DIFLD) and also to investigate possible therapeutic solutions in these in vitro models.

Method: Huh7 cell culture models of NAFLD and DIFLD were established by incubation of Huh7 cells with 0, 5 mM oleic acid (OA), 5 μM to 20 μM of amiodarone, 1 μM to 10 μM of tamoxifen for various time periods (24 h, 48 h), respectively. Cells where cotreated with 1 nM to 100 nM of liraglutide in order to assess its potential beneficial effect in fatty liver models. Cell viability was measured by MTT (3-(4, 5-dimethylthiazol-2-yl)-2, 5-diphenyltetrazolium bromide) assay. Changes in cell shape and the extent of hepatosteatosis were assessed by fluorescent microscopy as shown in Figure. Cell nuclei were stained with Hoechst, and fat droplets were stained with Oil-Red-O. Triglyceride (TG) accumulation was measured by TGO-PAP method and the results were read on the microplate reader.

Figure: Effects of tamoxifen, amiodarone and OA on the fat accumulation in Huh7 cell culture after 24 h of treatment with: A- control, B- 10 μM tamoxifen, C- 20 μM tamoxifen, D- 20 μM amiodarone, E- 40 μM amiodarone, F- 0, 5 mM OA.
Results: Tamoxifen significantly reduced cell viability in a dose-dependent manner after just 24 h treatment, compared to amiodarone and OA. Liraglutide co-treatment improved cell viability and the effect was greater after a longer period of treatment, especially in tamoxifen-treated cells for almost 30% (p < 0.05). Microscopic observations demonstrated microsteatosis as the predominant form of liver cell injury in this time period, with the greatest accumulation of fat in OA model. Accordingly, TG accumulation was highest in OA model, while liraglutide diminished TG accumulation in all three models.

Conclusion: This newly established cellular Huh7 model of NAFLD and DIFLD could provide a new tool for further studies on these conditions. Nevertheless, further research is needed to better understand the onset of fatty liver changes, drug toxicity, and the possible role of liraglutide in their treatment.

SAT114

Efx treatment improved histopathology and non-invasive markers of liver injury and fibrogenesis to a similar extent in NASH patients with high-risk PNPLA3 genotypes, compared to those with lowest genetic risk: a post-hoc analysis of balanced study

Erik Tillman1, Reshma Shringarpure2, Guy Neff3, Rashmeer Patil4, Peter Ruane2, Bradley Freilich5, Cynthia Behling6, Erica Fong8, Brittany de Temple7, Kitty Yale8, Stephen Harrison10, Tim Rolph8.

1Akero Therapeutics, South San Francisco, United States; 2Akero Therapeutics, South San Francisco, United States; 3Covenant Research and Clinics, Fort Meyers, United States; 4South Texas Research Institute; 5Ruane Clinical Research Group Inc; 6Kansas City Research Institute; 7Pacific Rim Pathology; 8Akero Therapeutics, South San Francisco, United States; 9Akero Therapeutics, South San Francisco, United States; 10Pinnacle Clinical Research

Background and aims: The PNPLA3 I148M genetic variant confers increased risk of progressive NAFLD, cirrhosis, and HCC. Concurrent insulin resistance further increases the risk associated with I148M. 1

The aim of this analysis was to evaluate whether I148M presence influenced patients’ baseline characteristics and/or response to the long-acting FGF21 analog efruxifermin (EFX) in the BALANCED Main Study.

Method: 80 NASH patients with F1-F3 fibrosis were randomized in a controlled design comparing EFX treatment for 16 weeks with placebo.2 End-of-treatment liver biopsies were available for patients with ≥30% relative reduction in liver fat content (LFC) by MRI-PDFF after 12 weeks of EFX dosing. All EFX-treated patients with MRI-PDFF met this threshold. The PNPLA3 rs738409 SNP was genotyped in all consenting patients. Baseline characteristics and treatment responses were compared across PNPLA3 genotypes: I/I (lowest risk), I/M (intermediate risk), or M/M (highest risk) for all EFX-treated patients with available genotype, biomarker, and histology data.

Results: Of 42 EFX-treated patients genotyped for PNPLA3, 11 were I/I, 22 were I/M, and 9 were M/M.

At Baseline, carriers of the lowest risk (I/I) genotype were older, with more insulin resistance and hypertriglyceridemia, whereas those carrying the highest risk (M/M) genotype were younger, with less insulin resistance and lower triglyceride levels. Histologic response to EFX was observed across all 3 PNPLA3 genotypes, with larger improvements in histopathology seen in patients with M/M genotype. Although the extent of NASH resolution was similar across all genotypes at 40–56%, all 9 M/M carriers achieved ballooning resolution. The extent of fibrosis regression appeared greater in M/M than I/I patients: in EFX-treated patients with paired biopsies that consented to genotyping, 7/9 (78%) M/M carriers had a ≥1-stage improvement in fibrosis compared to 4/10 (40%) of I/I patients, while 4/5 (80%) M/M patients with F2/F3 fibrosis at baseline improved by 2 stages compared to 3/6 (50%) I/I patients. Improvements in metabolic and liver-related biomarkers were comparable across PNPLA3 genotypes.

Conclusion: EFX significantly improved liver manifestations of metabolic disease including NASH histology across PNPLA3 genotypes, including in patients with highest risk of progression to end-stage liver disease.


SAT115

Oxygen-nutrient mismatch: a novel concept to explain how Obeticholic acid benefits NASH treatment

Gerond Lake-Bakaar1, John Robertson2, Charles Aardema3.

1Presbyterian St. Luke’s Medical Center, Transplant Center, Denver; 2Blacksburg, Bioengineering, Blacksburg, United States; 3Biomedinnovaations LLC, Denver, United States

Background and aims: The oxygen-nutrient mismatch concept, first proposed for alcoholic steatohepatitis, ASH, could also apply to non-alcoholic steatohepatitis, NASH. Both are consequences of the unique dual liver blood supply. The hepatic artery, HA, accounts for 20 percent of liver blood flow. However, it provides over 50 percent of oxygen requirements and has myogenic elements for autoregulation. By contrast, the portal vein, PV, lacks autoregulatory capacity and carries deoxygenated blood, rich in nutrients. Thus, HA oxygen delivery could fail to match excess alcohol (ASH) or nutrient intake (NASH). Furthermore, chronic obstructive sleep apnoea (OSA) and intermittent hypoxia, common in NASH could induce chronic liver damage from tissue hypoxia. Obeticholic acid (OCA), is a highly selective, potent agonist for the farnesoid-X-receptor (FXR). It effectively treats NASH fibrosis. It can impact vasoactive responsiveness; however, the mechanism of action is unclear.
We studied the effects of OCA on HA, PV, and hepatic vein, HV, flow in porcine liver perfused ex vivo with a cardio-emulation pump, the CaVESWave® system to determine whether vascular effects could explain its efficacy in the treatment of NASH.

**Method:** Six fresh porcine livers (two controls) were continuously perfused with phosphate buffered saline (PBS). OCA dosing was delivered in solution with methyl cellulose as carrier, directly into the portal vein catheter. Perfusion was initiated with the HA settings at 120/80 mmHg, PV around 15 mmHg and temperature at 15° C. Flow rates in HA, PV and HV were measured throughout. Carrier only was injected at 30 min intervals in the controls. For the treatment group, 0 mg OCA/kg liver weight, followed by 0.14, 0.28, 0.56 and 1.12 mg/kg, injected at 30 min intervals.

**Results:** The cardio-emulated waveforms showed little variability, either before or after drug treatment was started (figure 1). HA pressure varied between 117 and 122 mmHg (systolic) and 75–84 mmHg (diastolic); perfusate pH between 7.35 and 7.4; DO between 104 and 105 and temperature 15.8 and 17.5° C.

Control livers (n = 2) showed minor changes in flow after treatments with vehicle (figure 2). The maximum percentage increase in HA flow was 3.3 ± 3.5 and HV flow, 4.8 ± 2.8. By contrast, PV flow was reduced by up to −9.1 ± 5.9.

In OCA treated livers (n = 4), there was a clear dose-relationship between OCA and HA, HV and PV. Hepatic venous outflow and HA flow increased progressively to 11 ± 11.8 and 9.9 ± 8.9, respectively. Conversely, PV flow was reduced by up to −19 ± 16%.

**Conclusion:** OCA in dose responsive manner increased HA flow rates and inversely reduced PV flow, consistent with an active hepatic artery buffering response. Thus, increased delivery of oxygen rich HA blood, coupled with reduced nutrient rich PV blood, provides a rational concept for the beneficial effect of chronic OCA in NASH.

---

**SAT116**

**Sustained reduction of triglyceride and LDL cholesterol from single administration of the novel long-acting FGF21 analogue 0499**

Kirsten Dahl1, Martin Friedrichsen1, Rasmus RibeL-Madsen1, Jakob Schieler Hansen2, Jesper Clausen1, Mads Axelsen1, Mads Sundby Palle1, Cassandra Key2, Harumi Murakami2, Birgitte Andersen1. 1Novo Nordisk A/S, Denmark; 2Novo Nordisk Bio Innovation Hub, United States; 3ICON Early Phase Service, San Antonio, TX, United States; 4SOUSEIKAI Sumida Hospital, Tokyo, Japan

**Email:** kdhl@novonordisk.com

**Background and aims:** Activation of the fibroblast growth factor 21 (FGF21) receptor complex has been associated with several attractive effects in preclinical models including weight loss and decreased hepatic fat content. This has led to the pursuit of FGF21 for pharmacotherapy within obesity and NASH, which has to date been limited by lack of suitable FGF21 analogues. Here we report the exploration of a new FGF21 analogue 0499 with the purpose of investigating the safety profile, pharmacokinetic (PK) and pharmacodynamic (PD) potential of the new molecule.

**Method:** In a randomized, blinded, placebo-controlled first human dose (FHD) study, healthy male participants with a BMI around 30 kg/m² received a single subcutaneous administration of either placebo or 0499 at dose level: 2, 6, 12, 24, 48, 96, or 180 mg. In a separate study in Japanese healthy male participants, 3 dose levels: 12, 30, and 96 mg were tested to confirm consistent safety profile and PK characteristics across ethnicity. In both studies, participants were followed for 36 days post-dose while blood samples were obtained for safety evaluation, PK and PD assessments. A total of 78 participants received a single dose of 0499.

**Results:** The safety profile, as well as PK and PD results were comparable for the two studies. The adverse events observed were mainly related to the gastrointestinal tract including nausea, diarrhea, frequent bowel movements and vomiting. Increased appetite was also observed. Treatment was not associated with changes in heart rate, body temperature, clinical laboratory safety parameters, or body weight. Plasma triglyceride and LDL cholesterol levels were decreased in a dose-dependent manner while HDL cholesterol was increased. The changes in the lipid parameters were sustained for up to 28 days after the single administration. The plasma half-life of 0499 was approximately 120 hours.

**Conclusion:** From the two studies of 0499 in healthy participants, it was concluded that the novel FGF21 analogue 0499 has an acceptable safety profile at all tested dose levels, and that the PK profile seems compatible with a once-weekly dose regimen. The remarkable improvement on the plasma lipid profile is encouraging for the further development of 0499 for treatment of NASH.
Background and aims: Inhibition of the acetyl-CoA carboxylase (ACC) isoforms ACC1 and ACC2 reduces lipogenesis, stimulates lipid oxidation, and improves histologic features and fibrosis-related biomarkers in non-alcoholic steatohepatitis (NASH). Obeticholic Acid (OCA), as an FXR agonist, reduces bile acid synthesis and regulates lipid metabolism in the liver. We evaluated the effect of an ACC inhibitor (ACCI) and OCA in combination on lipid and amino acid metabolism in the humanized liver of chimeric PXB mice (PhoenixBio, Japan).

Method: Adult male PXB mice (n = 10, randomized by blood human albumin concentrations) were administered with ACC1 (an analog of firsocostat) and/or OCA (10 mg/kg, QD, PO for both compounds) for 18 days and livers were collected 2 h after the last dose. Untargeted metabolomic profiling of liver tissue was performed at Metabolon, Inc (Morrisville, NC, USA) using a combination of LC-MS methods (1).

Results: Humanized liver mice developed spontaneous steatosis due to the lack of FGF19 signaling in the liver as engulved human hepatocytes did not respond to mouse FGF15. ACC1 and OCA combination showed additive effects to reduce neutral lipids (triglycerides, diacylglycerols) and long chain fatty acids, and increase acyl-carnitines and 3-hydroxybutyrate. Although the combination reduced 7-hydroxylcholesterol, OCA increased cholesterol and cholesterol esters alone or in combination with ACC1. Primary and secondary bile acids were mainly decreased by OCA and further reduction was observed in combination. OCA and combination increased N-acetylated amino acids and combination also increased polyamines and nicotinamide adenine dinucleotide hydride.

Conclusion: Metabolomic analysis revealed that lipid metabolism and energetic profile were rapidly changed by ACC1 or OCA treatment and combination of both agents reduced lipid synthesis and promoted fatty acid oxidation in the liver of humanized mice. These changes are similar to the clinical findings in NASH patients treated with ACC1 and FXR agonist combination, and support the utility of humanized mouse model to elucidate molecular pathways mediated by NASH therapies.

Reference:

SAT118 Identification of a fibrosis endotype in NAFLD patients more prone to interventions aimed at reducing fibrogenesis

Ida Villesen1, Jadine Scragg2,4,5, Diana Leeming3, Olivier Govaere3,6,7

Background and aims: Non-alcoholic fatty liver disease (NAFLD) is associated with inflammation and hepatocellular damage, leading to activation of fibroblasts and fibrosis development. Fibrosis is known to be the single most important factor for predicting liver-related clinical outcomes and is quantifiable by biomarkers of collagens including PRO-C3, PRO-C4 and PRO-C5, measuring formation of type III, IV and V collagen, respectively. However, patient heterogeneity is evident, and it remains largely unknown how to accurately identify patients in most need of treatment. Monitoring fibroblast activity through formation of collagen, may enable identification of fibrosis endotypes; a high or low activity stage of fibrosis formation. This segregation may identify patients more likely to experience anti-fibrotic effect due to therapy or weight loss.

Method: Clinically confirmed NASH patients, weight stable (±3%) since diagnoses, were recruited from hepatology clinics at a tertiary centre in the UK. Patients were prescribed an 8–12-week VLCD (~ 800 kcal/day) intervention. Serum markers were determined at baseline and every second week until end of diet, 4 weeks post-VLCD and at 5 months follow-up. The biomarkers PRO-C3, PRO-C4 and PRO-C5 were quantified by ELISA. For analysis, patients were stratified at baseline into high and low levels of formation of fibrosis, determined by the biomarkers.

Results: 26 patients (mean age 56 and BMI of 42) were included. With a mean weight loss of 9.7% all patients were found to improve liver measures including ALT and AST from baseline to post-VLCD. Yet, patients separated into high and low biomarker levels at baseline, based on the median, were found to differ in response to intervention. Thus, high levels of PRO-C3 (above 11.4 ng/ml) were found to associate with a decrease of 40% from baseline to end of diet while low levels remained unchanged, the same was seen for PRO-C4 (above 263.5 ng/ml) with ~ 55% decrease and PRO-C5 (above 857.4 ng/ml) with ~ 57% in high-level groups, indicating decreased formation of fibrosis following weight loss, while low biomarker levels remained unchanged throughout the course of the study.

Table 1: Patient baseline characteristics

<table>
<thead>
<tr>
<th></th>
<th>High PRO-C3</th>
<th>Low PRO-C3</th>
<th>High PRO-C4</th>
<th>Low PRO-C4</th>
<th>High PRO-C5</th>
<th>Low PRO-C5</th>
</tr>
</thead>
<tbody>
<tr>
<td>BMI (mean ± SD)</td>
<td>42 (± 9)</td>
<td>39 (± 8)</td>
<td>41 (± 8)</td>
<td>40 (± 8)</td>
<td>41 (± 9)</td>
<td>41 (± 7)</td>
</tr>
<tr>
<td>ALT (mean ± SD)</td>
<td>55 (± 41)</td>
<td>41 (± 17)</td>
<td>56 (± 37)</td>
<td>38 (± 23)</td>
<td>55 (± 39)</td>
<td>40 (± 19)</td>
</tr>
<tr>
<td>AST (mean ± SD)</td>
<td>40 (± 21)</td>
<td>29 (± 12)</td>
<td>35 (± 20)</td>
<td>32 (± 16)</td>
<td>33 (± 19)</td>
<td>35 (± 17)</td>
</tr>
<tr>
<td>ELF</td>
<td>10 (± 0.9)</td>
<td>10 (± 0.7)</td>
<td>10 (± 0.8)</td>
<td>10 (± 0.8)</td>
<td>10 (± 0.8)</td>
<td>10 (± 0.8)</td>
</tr>
</tbody>
</table>

p values indicate significant different from high group, calculated using t-test and indicated as *p < 0.05, **p < 0.01

Conclusion: NAFLD patients respond heterogeneously to intervention with regards to their fibrogenesis profile, in which some experience a decrease and other are unchanged, suggesting an endotype of patients more amenable to anti-fibrogenesis intervention.

SAT119 The pan-PPAR agonist lanifibranor improves markers of cardiometabolic health in patients with NASH independent of weight change

Michael Cooreman1, Sven Francque2, Martine Baudin2, Philippe Huot-Marchand1, Lucile Dzen1, Jean-Louis Junien2, Pierre Broqua3, Manal Abdelmalek4, 5Inventiva, United States; 6University Hospital Antwerp, Belgium; 7Inventiva, France; 8Duke University School of Medicine, United States

Background and aims: Lanifibranor therapy resulted in significant efficacy on the histological end point ‘NASH resolution and improvement of fibrosis’ as well as on markers of cardiometabolic health (CMH) in the phase 2b NATIVE study. Modest weight gain was reported as a PPAR effect, which has been ascribed to the maturation of insulin-sensitive, metabolically healthy subcutaneous adipose
tissue. We evaluated markers of CMH by changes in weight in the lanifibranor and placebo arms.

**Method:** NATIVE enrolled 247 patients with SAF activity score 3–4, fibrosis stage F0–F3 in 3 arms: lanifibranor 800, 1200 mg/d and placebo for 24 weeks; 217 (lanifibranor: 144, placebo: 73) patients who completed the trial with weight data at baseline and end of treatment (EOT) were included in the analyses. Mean weight increase at EOT was 2.4 (2.6%) and 2.7 (3.1%) kg for 800 and 1200 mg lanifibranor, respectively; patients were divided in 3 groups according to % weight change: ≤2.5% (n = 73, 51%); 2.5–5% (n = 23, 16%); >5% (n = 48, 33%). Biomarkers of lipid and glucose metabolism, insulin resistance, inflammation, liver tests, diastolic blood pressure (DBP), hepatic steatosis (NASH-CRN grading) and Controlled Attenuation parameter (CAP) were evaluated at screening and EOT, and compared between the weight change groups.

**Results:** Improvement of CMH markers at EOT compared to baseline occurred to the same degree in the 3 weight change groups for the pooled lanifibranor arms: increase in HDL-cholesterol, and decrease in total triglycerides, APO-B, APO-B/APO-A1, APO-C3, fasting glucose and insulin levels, Hba1c, HOMA-IR and hs-CRP, along with decreases in hepatic steatosis, ALT, AST, GGT and DBP. Adiponectin, a PPARγ downstream mediator, increased in all 3 weight change groups, with a higher increase in the >2.5% weight increase groups, compared to the <2.5% weight increase group. With placebo, 12 (16%) patients with weight change ≥2.5% at EOT had no improvement of CMH markers, no change in adiponectin levels, and had increases in steatosis and worsening of liver tests, HOMA-IR and DBP.

**Conclusion:** Biomarkers of CMH improve with lanifibranor therapy, independent of weight change. These beneficial effects occur in parallel with a marked increase of adiponectin, which marks adipose tissue health and improves insulin sensitivity; the data provide further evidence that PPARγ-induced weight gain is metabolically distinct from lifestyle-related weight gain.

**SAT120**

Lanifibranor therapy reduces the FibroScan-aspartate aminotransferase (FAST) score associated with histological ‘NASH resolution and improvement of fibrosis’ and biomarker response


**Background and aims:** Lanifibranor, a pan-PPAR agonist, has shown efficacy on the histological end point ‘NASH resolution and improvement of fibrosis’ in the phase 2b NATIVE trial. We evaluated the effect of lanifibranor on the FAST score, a promising non-invasive test (NIT) for active NASH with significant fibrosis, and its correlation with histological and biomarker response in NATIVE-enrolled patients with F2/F3 fibrosis.

**Method:** Patients with non-cirrhotic NASH and SAF-activity score 3–4 enrolled in NATIVE (n = 247) received lanifibranor 800, 1200 mg/d or placebo for 24 weeks. A total of 112 patients had baseline F2-F3 fibrosis and FAST scores available at baseline and end of treatment (EOT). FAST combines liver stiffness measurement by vibration controlled transient elastography, controlled attenuation parameter and aspartate aminotransferase levels and provides the probability (between 0 and 1) for active NASH with significant fibrosis (NAS≥4 and F≥2): ≥0.65: high-risk, 0.35–0.65: intermediate-risk, ≤0.35 low-risk. FAST scores were compared between lanifibranor and placebo arms using a mixed model adjusted for baseline value; the correlation between changes in FAST scores at EOT and liver histology and biomarkers of metabolism, inflammation and fibrosis was also evaluated.

**Results:** Mean (SD) FAST score at baseline was 0.55 (0.22), similarly distributed in the 3 treatment arms, with 34% at high-risk NASH, 45% at indeterminate risk and 21% at low-risk. At EOT, FAST significantly decreased from baseline, with mean absolute changes of ~0.22 and ~0.23 for lanifibranor 800 and 1200 mg respectively (both p < 0.01), and ~0.09 for placebo. Mean FAST score at EOT was 0.31 for both lanifibranor arms and 0.51 for placebo; 67% in both lanifibranor and 27% in placebo arms had FAST ≤0.35 (low-risk) at EOT. Decreases in FAST scores correlated with histological end point ‘resolution of NASH and improvement of fibrosis’, and with improvement in triglycerides, Apo-C3 and ferritin levels.

**Conclusion:** Treatment of NASH patients with F2/F3 fibrosis with lanifibranor for 24 weeks leads to a significant reduction of the FAST score compared to placebo and this decrease correlates with improvements in liver histology and biologically relevant biomarkers responses. These results not only support the histological efficacy data but also the potential of the FAST score as a NIT to monitor disease progression and response to therapy.
and waist circumference change in each group. When compared to baseline, patients in the intervention group had a significant reduction in weight (−2.4%, p = 0.006) and ALT level (−8.5 U/L, p = 0.004); whereas patients in the control group had a significant decrease in weight (−1.2%, p = 0.034) but not ALT level (−6 U/L, p = 0.19). The intervention group had a greater reduction in percent weight loss and ALT than the control group, but the statistically significant levels were not reached.

Conclusion: In this preliminary result, encouraging LSI and delivering MAFLD information via social media application to patients with MAFLD resulted in a significant reduction in weight and ALT level compared to baseline, and the results appeared to be better than SOC. However, the complete data of all eligible patients as well as change in liver steatosis and fibrosis is yet to be confirmed.

SAT122

Efficacy and mechanism of time-restricted fasting in non-alcoholic liver disease

Jiang Deng1, Dandan Feng1, Ning Gao1, Juanjuan Shi1, Shuangshuo Dang1, 1The Second Affiliated Hospital of Xi’an Jiaotong University, Department of Infectious Disease, Xi’an, China Email: dang212@126.com

Background and aims: Non-alcoholic fatty liver disease (NAFLD) lacks specific treatment drugs. The aims of this study were to analyze the efficacy and mechanism of time-restricted fasting (TRF) in the treatment of NAFLD.

Method: Thirty-two male rats were randomly divided into three groups: Normal group, which was given a standard diet; NAFLD group, which was given a 60% high-fat diet; and TRF group, which was given a 60% high-fat diet, eating was allowed for 6 hours per day. After 15 weeks, the liver lipidomics and other indicators were determined, detected, and compared.

Results: A total of 1062 metabolites were detected. Compared with the Normal group, weight, body fat ratio, aspartate aminotransferase, total cholesterol, low-density cholesterol, fasting blood glucose, uric acid and the levels of 317 lipids in the NAFLD group were higher, whereas 265 lipids were down-regulated (p < 0.05). Compared with the NAFLD group, weight, body fat ratio, daily food intake, and the levels of 253 lipids in the TRF group were lower; 82 lipids were up-regulated (p < 0.05), serum triglyceride level was increased, but there was no statistical significance (p > 0.05). Kyoto Encyclopedia of Genes and Genomes pathway enrichment was conducted according to the results of differential metabolites, and the results showed that the pathways involved mainly included metabolic pathways, regulation of lipolysis in adipocytes, fat digestion and absorption, etc. Reverse transcription polymerase chain reaction proved that TRF improved the abnormal expression of FAS and PPARα genes in the NAFLD group (p < 0.05).

Conclusion: Six hours of time-restricted fasting improves non-alcoholic fatty liver disease by regulating lipid synthesis and metabolism, without an excessive increase in triglyceride levels.

SAT123

Functionalizing novel cancer related genes in liver disease and liver regeneration

Nooshin Nourbakhsh1, Torsten Wuestefeld1, Agnes Bee Leng Ong1, Rong Gao1, 1Genome institute of Singapore, In vivo genetics and gene therapy, Singapore, Singapore; 2Yong Loo Lin School of Medicine, National university of Singapore, Medicine; 3National Cancer Centre Singapore, Singapore; 4Nanyang Technological University, School of Biological Sciences, Singapore Email: nnourbakhsh@gis.a-star.edu.sg

Background and aims: Caloric abuse and an inactive lifestyle have led to a widespread obesity and metabolic syndrome epidemic. Non-alcoholic fatty liver disease (NAFLD) and non-alcoholic steatohepatitis (NASH) are considered to be the hepatic consequence of it. As NAFLD/NASH condition are highly prevalent and drives a growing incidence rate of HCC, it is considered to be an important and alarming health issue. The critical question how the combination of an inflammatory microenvironment, created by NAFLD/NASH, abnormal metabolism and ongoing liver regeneration contributes to DNA instability and as a consequence promotes cancer is still unanswered. By this project we aim to reveal new relevant biomarkers for early and easier detection, treatment stratification and monitoring as well as approaches to therapies for both prevention and treatment in people who are at high risk for presenting fatty liver associated HCC to improve human health border.

Method: We take advantage of in vivo functional genomics screen in a mouse model of progressive fatty liver disease (Choline deficient high fat diet) to address this question. We screened a mir30 based shRNA library targeting 1000 genes, which human orthologs showed dysregulation in cancer. Scoring shRNAs will be validated in vitro as well as in vivo for influencing cell proliferation, survival and transformation and further will investigate the underlying mechanism with the goal for therapeutic intervention in disease progression.

Results: Computational analysis of shRNA abundance comparing CDHFD vs normal chow group shows selective enrichment for a number for targets. In vitro Knockdown of target genes show significant increasing in cell proliferation compared to control group. Short listed targets proceed for in vivo validation in NASH mouse model as well as in vivo liver repopulation and regeneration assay.
Chow feeding (chow-reversal) for 8, 16 or 24 weeks (n = 14–kept on the GAN diet or received dietary intervention by switching to included and stratified into treatment groups. DIO-NASH mice were complete resolution of hepatomegaly, hypercholesterolemia, outcomes and liver histology, as demonstrated by robust weight loss, results: Chow-reversal promoted substantial benefits on metabolic expression signatures. Biochemistry was assessed. Liver senescence markers included p21 quantitative liver histology, RNA sequencing, blood and liver evaluation of NAFLD Activity Score and Fibrosis Stage. Terminal Pre-to-post liver biopsy histology was performed for within-subject group). Chow-fed C57BL/6J mice (n = 10) served as normal controls. Background and aims: Lifestyle change remains the first-line intervention for non-alcoholic steatohepatitis (NASH). This study aimed to evaluate long-term low-caloric dietary intervention on liver disease and markers of hepatocellular senescence in the GAN diet-induced obese mouse model of NASH. Method: Male C57BL/6 mice were fed the GAN diet high in saturated fat, fructose, and cholesterol for 34 weeks prior to study start. A liver biopsy was sampled 4-weeks prior to study start. Only animals with biopsy-confirmed steatosis (score ≥2) and fibrosis (stage ≥F1) were included and stratified into treatment groups. DIO-NASH mice were kept on the GAN diet or received dietary intervention by switching to chow feeding (chow-reversal) for 8, 16 or 24 weeks (n = 14–16 per group). Chow-fed C57BL/6J mice (n = 10) served as normal controls. Pre-to-post liver biopsy histology was performed for within-subject evaluation of NAFLD Activity Score and Fibrosis Stage. Terminal quantitative liver histology, RNA sequencing, blood and liver biochemistry was assessed. Liver senescence markers included p21 histomorphometry, mitochondrial respiratory capacity and gene expression signatures. Results: Chow-reversal promoted substantial benefits on metabolic outcomes and liver histology, as demonstrated by robust weight loss, complete resolution of hepatomegaly, hypercholesterolemia, elevated transaminase levels and hepatic steatosis in addition to attenuation of inflammatory markers. Notably, all DIO-NASH mice demonstrated ≥2 point significant improvement in NAFLD Activity Score following dietary intervention. While not improving fibrosis stage, chow-reversal (≥16 weeks) reduced quantitative fibrosis markers (PSR, collagen 1α1, α-SMA). Notably, these changes were accompanied by improved liver mitochondrial respiration, complete reversal of p21 overexpression and partial reversal of hepatocellular senescence-associated gene expression signatures. Conclusion: Chow-reversal substantially improved metabolic, biochemical, and histological hallmarks of fibrosing NASH. Interestingly, molecular signatures of hepatocellular senescence in GAN DIO-NASH mice were also improved following long-term low-caloric dietary intervention, making the model suitable for profiling emerging senotherapeutics targeting senescent hepatocellular cells for the treatment of NASH.

SAT124 Effect of long-term dietary intervention on liver pathology and markers of hepatocellular senescence in the GAN diet-induced obese mouse model of NASH Kristoffer Voldum-Clausen1, Denise Oró1, Martin Rønn Madsen1, Mathias Flensted-Jensen2, Cecilie Holmegaard Andersen2, Steen Larsen2, Henrik B. Hansen1, Michael Feigh1, 1Gubra, Harsholm, Denmark; 2Xlab, University of Copenhagen, Denmark

Background and aims: Intestinal microbiota (IM) has emerged as a key factor conditioning the development and progression of non-alcoholic fatty liver and although fecal microbiota transplant (FMT) has been proposed as a promising therapeutic strategy, effective colonization of the colon is difficult to achieve. Our group has developed an endoscopic placement hydrogel able to release substances (covergel) that used as a carrier could improve FMT. We aimed to assess the role of IM in the mechanisms leading to steatosis and fibrosis and to compare the efficacy of covergel for FMT delivery with single colonoscopy vs the standard-method, in a rat model of steatohepatitis with fibrosis.

Method: 24 rats were fed with a diet rich in fat/cholesterol/fructose throughout the study (15 weeks) and carbon tetrachloride was injected for 12 weeks (NASH rats). 6 rats (healthy controls) were standard chow fed. At week 12, feces were collected to: 1) assess microbiota phylogenetic profile, and 2) pooled and cryopreserved as "NASH feces" and "healthy feces" for FMT. At week 13, NASH rats were randomized in 3 groups and underwent FMT by single colonoscopy to receive: group 1: 0.5 ml of healthy feces in 3.5 ml of saline (standard method); group 2: 0.5 ml of healthy feces in 3.5 ml covergel (HF-covergel-FMT); group 3: 0.5 ml of NASH feces in 3.5 ml covergel. Rats were euthanized at week 15 and fibrosis (Mason’s Trichromic staining) and steatosis (Oil Red staining) degrees were assessed in liver samples. Plasma biochemical parameters were also quantified.
Results: In comparison to control rats, NASH rats didn’t develop increased significant body weight gain but an increased in liver to body weight ratio was detected in NASH rats but not in HF-covergel-FMT rats. Levels of albumin, bilirubin, glucose, cholesterol and triglycerides were not altered in any group. ALT and phosphatase alkaline were significantly elevated whereas LDL and HDL-cholesterol significantly reduced in NASH rats. No differences were observed in phosphatase alkaline and LDL-cholesterol between HF-covergel-FMT and control rats. Standard-FMT was not effective in reversing liver fibrosis, although a non-significant improvement was observed (group 1 vs group 3, p = 0.084). In contrast, HF-covergel-FMT was effective in reducing liver fibrosis (group 2 vs group 3; p = 0.001). Moreover, HF-covergel-FMT showed a significant improvement on fibrosis compared to standard-FMT (group 1 vs group 2; p = 0.034). FMT had no significant effect on steatosis.

Conclusion: HF-covergel-FMT significantly reduces liver to weight ratio, normalizes phosphatase alkaline and LDL-cholesterol and significantly reduces fibrosis without significant attenuation of the ongoing steatosis. The use of covergel would be an advantage, since the prolonged residence time of the hydrogel adhered to the mucosa would facilitate microorganism colonization with a single colonoscopy.

SAT126
Reversing diet-induced steatohepatitis and CCl4 induced fibrosis with AN1284 treatment
Rinat Abramovitch1,2, Adi Yehezkel2, Nathalie Nachmansson1,2, Marta Weinstock1, 1Hebrew University-Hadassah Medical Center, The Wohl Institute for Translational Medicine, Jerusalem, Israel; 2Hebrew University-Hadassah Medical Center, The Goldyne Savid Institute of Gene Therapy, Jerusalem, Israel; 3Hebrew University, School of Pharmacy, Institute for Drug Research, Jerusalem, Israel

Background and aims: Non-alcoholic fatty liver disease (NAFLD) is the leading cause of chronic liver disease that can progress to more aggressive non-alcoholic steatohepatitis (NASH). The molecular and metabolic changes occurring in the development and progression of NAFLD to NASH include oxidative stress, chronic hepatic inflammation and fibrosis. So far, there are no effective drug treatments for NASH. AN1284 is an indoline derivative that exhibits potent antioxidant and anti-inflammatory activities in mice with LPS-activated acute liver damage. The aim of the current study was to determine whether AN1284 could reverse steatosis and fibrosis in a mouse model of pre-existing NASH.

Method: The effect of chronic treatment with AN1284 (1 mg/kg/day) by mini-pumps on pre-existing hepatic steatosis and fibrosis, was examined in two mouse models: (I) western dietary (WD) induced NASH for 6 month and (II) CCl4 induced liver fibrosis. RNA-Seq was used to assess whether changes in cellular processes that occur in human subjects with NASH exists in these mice, and whether they are reversed by AN1284 treatment.

Results: AN1284 treatment (1 mg/kg/day) significantly attenuated liver damage, reduced liver/body ratio, liver fat content and serum ALT levels in dietary induced NASH, and hepatic fibrosis in both models. RNA sequencing showed that the WD significantly elevated the hepatic pathways of steatosis, fibrosis, inflammation, oxidative stress and liver damage seen in human subjects. AN1284 reduced oxidative stress (iNOS) and fibrosis, in association with a decrease in collagen-4 and TGF-beta. RNA-Seq analysis revealed the altered pathways including FXR/RXR, fatty-acid synthase and inflammation (Fig).

SAT127
Spontaneous and drug-induced histological changes in non-alcoholic steatohepatitis: an assessment by meta-analysis of trials
Grazia Pennisi1, Ciro Celsa1, Marco Enea1, Marco Vaccaro2, Vito Di Marco3, Carlo Ciccioli1, Giuseppe Infantino3, Stefanie Parisi1, Claudia La Mantia1, Antonio Craxi1, Calogero Camma1, Salvatore Pettata1, 1Section of Gastroenterology and Hepatology, Dipartimento Di Promozione Della Salute, Materno Infantile, Medicina Interna e Specialistica Di Eccellenza (PROMISE), Palermo, Italy; 2Dipartimento di Scienze Economiche, Aziendali e Statistiche, University of Palermo, 90133 Palermo, Italy

Background and aims: Non-alcoholic steatohepatitis (NASH) has a variable rate of progression, making the effect of investigational drugs difficult to assess and compare. In this study, we provide by meta-analysis a reference standard for histological progression of untreated NASH (patients receiving placebo), and perform a network meta-analysis to estimate the relative efficacy of investigational drugs for NASH.

Method: A comprehensive search of several databases was conducted to detect phase 2 and 3 randomized controlled-trials (RCTs) comparing pharmacological interventions in patients with non-cirrhotic NASH. Resolution of NASH without worsening of fibrosis or ≥ 1 stage reduction of fibrosis without worsening of NASH were evaluated as composite outcomes validated by Food and Drug Administration (FDA). Meta-analysis and meta-regressions were performed on placebo arms, and a network meta-analysis on interventions arms.

Results: A total of 15 RCTs met the eligibility criteria. The meta-analysis on untreated patients arms showed a pooled estimate rate of 17% (95% C.I. 12%-23%); I2 = 86%; p < 0.01) and of 21% (95% C.I. 13%-31%; I2 = 84%; p < 0.01) for resolution of NASH without worsening of fibrosis and ≥1 stage improvement of fibrosis without worsening of NASH, respectively. Phase 3 RCTs, older age and higher AST levels were associate to a lower rate of spontaneous improvement at univariate meta-regression analysis. By network meta-analysis, semaglutide and pioglitazone, alone or plus Vitamin E, had the highest ranking of effectiveness for NASH resolution without worsening of fibrosis (P-score 0.906, 0.890 and 0.826, respectively). Aldafermin, lanifibranor and obeticholic acid had the highest probability to achieve ≥1 stage of fibrosis improvement without
worsening of NASH (P-score 0.776, 0.773 and 0.711, respectively). When combining the two outcomes, lanifibranor, semaglutide and aldafermin were the most effective drugs.

**Conclusion:** Since semaglutide and pioglitazone appear to be more effective on NASH activity while aldafermin, lanifibranor and obeticholic acid perform better on the evolution of fibrosis, combination therapies should be assessed prospectively in subjects who are less likely to improve spontaneously over time, i.e. older patients with biochemically active disease.

**SAT128**

**Synergistic activity of GLP-1 peptide analog XW003 and the long-lasting GIP receptor agonist XW017 in a diet induced obese mouse model**

Xinle Wu1, Haixia Zou1, Bin Wang1, Rui Zhu1, Yan Li1, Wanjun Guo1, Catherine Jones2, Martinj Fenaux2, 3Sciwind Biosciences, China; 2Sciwind Biosciences, United States

**Email:** catherine.jones@sciwindbio.com

**Background and aims:** Glucagon-like peptide-1 (GLP-1) and glucose-dependent insulinotropic peptide (GIP, also known as gastric inhibitory polypeptide) are small peptide hormones termed incretins. Incretins are produced by the gut following food intake and act to stimulate insulin secretion and lower blood sugar. Incretins have additional effects on the digestive tract, liver, pancreas, and central nervous system to maintain metabolic health. GLP-1 receptor agonists have shown promise for treating obesity, type 2 diabetes, and non-alcoholic steatohepatitis (NASH); GIP receptor agonists have the potential to work synergistically with GLP-1 agonists to enhance efficacy.

**Method:** We investigated GLP-1 peptide analog, XW003 (3 nmol/kg), alone or in combination with a long-lasting GIP peptide analog, XW017 (3, 10, 30, 100 nmol/kg), in the diet induced obese (DIO) mouse model. GLP-1 and GIP peptide analogs were dosed subcutaneously QD for 27 days (n = 6 animals per group). We also evaluated in parallel the activity of a dual GLP-1/GIP receptor agonist, tirzepatide (10 nmol/kg), in this mouse model.

**Results:** Treatment of mice with the GLP-1 analog XW003 alone resulted in mean body weight loss of 15.6% compared to baseline after 27 days of treatment. Treatment of mice with the GIP analog XW017 alone did not result in significant weight loss (0% compared to baseline at day 27). Combination of XW003 (3 nmol/kg) with XW017 showed an enhanced effect in inducing body weight loss compared to either peptide alone, with mean weight reductions of 24.6% (XW003 + 30 nmol/kg XW017) and 28.3% (XW003 + 100 nmol/kg XW017), respectively, at the end of treatment. In comparison to tirzepatide, combination of XW003 and XW017 showed comparable or higher levels of weight loss. At day 14, tirzepatide (10 nmol/kg) treatment resulted in a 25.8% weight reduction compared to baseline, while the animals treated with a combination of XW003 (10 nmol/kg) and XW017 (100 nmol/kg) produced a mean weight loss of 33.9%.

**Conclusion:** In conclusion, combinatorial treatment of GLP-1 and GIP receptor agonists showed a synergistic effect on promoting weight loss in a mouse model of obesity.

**SAT129**

**Preclinical pharmacology of low molecular weight GLP-1 receptor agonist XW014**

Wanjun Guo1, Xinle Wu1, Haixia Zou1, Bin Wang1, Rui Zhu1, Catherine Jones2, Martinj Fenaux2, 3Sciwind Biosciences, China; 2Sciwind Biosciences, United States

**Email:** catherine.jones@sciwindbio.com

**Background and aims:** Glucagon-like peptide-1 (GLP-1) is a peptide hormone produced by the gut in response to food intake and then rapidly degraded. GLP-1 has multiple beneficial effects on metabolism, including delaying gastric emptying and increasing satiety, stimulating insulin secretion and lowering blood sugar, reducing liver fat, and promoting weight loss. GLP-1 peptide analogs have shown promise for treating obesity, type 2 diabetes, and non-alcoholic steatohepatitis (NASH). XW014 is a small molecule GLP-1 receptor agonist with improved oral bioavailability and cardiovascular safety. Here we evaluated XW014 in vitro and in vivo activity.

**Method:** GLP-1 receptor agonism was evaluated in vitro by assessing cAMP production in HEK-293 cells. CAMP production in cells treated for 30 minutes with XW014 or comparator was quantified by HTRF-based assay (Cisbio). C57BL/6 mice expressing humanized GLP-1 receptor were dosed with XW014 (50 mg/kg PO BID) or vehicle (n = 4 animals per group) for 4 days. Weight, cumulative food intake, post-prandial glucose, glucose tolerance, and insulin secretion were measured. Cynomolgus monkeys (n = 5) were given a single dose of XW014 (20 mg/kg PO). Intravenous glucose tolerance test (IVGTT) was performed 2 hours after oral dosing.

**Results:** XW014 showed potent GLP-1 receptor agonist activity in cell culture, with a mean EC50 value of 0.44 ± 0.2 mM. In mice expressing the human GLP-1 receptor, treatment with XW014 (50 mg/kg BID) for 4 days resulted in reduced blood glucose, food intake, and body weight. In cynomolgus monkey, treatment with a single dose of XW014 (20 mg/kg) resulted in improved blood glucose suppression and insulin response during IVGTT compared to baseline.

**Conclusion:** XW014 is a potent small molecule agonist of the GLP-1 receptor in vitro and induces effective target engagement in two preclinical models, humanized GLP-1 mice and cynomolgus monkeys. The results support the continued development of XW014 for the treatment of metabolic disease.

**SAT130**

**Integrated transcriptomics of CRV431 treatment in a Phase 2a NASH trial confirms anti-fibrotic effect of pan-cyclophilin inhibition and identifies CRV431-specific biomarkers**

Patrick Mayo1, Stephen Harrison2, Todd Hobbs1, Daren Ure1, Daniel Trepanier1, Erin Foster1, Caroline Zhao1, Robert Foster1, 1Hepion Pharmaceuticals, Edison, United States; 2Pinnacle Clinical Research, Austin, United States

**Email:** pmayo@hepionpharma.com

**Background and aims:** The progression of liver fibrosis in Non-Alcoholic Steatohepatitis (NASH) has been directly linked to increased mortality and morbidity. To date, numerous drug candidates have failed to show a significant benefit in fibrotic end points for NASH patients enrolled in clinical trials. CRV431, a non-immunosuppressive pan-cyclophilin inhibitor has demonstrated pleotropic effects well-suited for the treatment of NASH and fibrosis. A new transcriptomic analysis was performed to further elucidate the action of CRV431 in subjects with biomarker defined F2/F3 NASH and explore transcriptomic markers for clinical responsivity.

**Methods:** RNA sequencing data was obtained from 27 patients with biomarker confirmed F2/F3 NASH participating in a 28-day, Phase 2a trial of CRV431 (NCT04480710). Subjects were administered CRV431 75 mg, 225 mg, or placebo orally once daily for 28 days. RNA sequencing samples were evaluated using FastQC, with quantification in Salmon v1.4.0. Differential expression analysis (DEA) was performed using edgeR. Co-expression networks were constructed using weighted gene co-expression network analysis (WGCNA). DEA was combined with WGCNA to enhance the discriminating ability of highly related genes as potential biomarkers. Functional enrichment was performed using clusterProfiler and GeneWalk, followed by key hub gene selection.

**Results:** Consistent with pre-clinical models, CRV431 down-regulated several collagen genes including COL6A5 (log2Fold = −2.2, p = 0.04), COL7A1 (log2Fold = −4.7, p = 0.0052), COL8A2 (log2Fold = −4.8, p = 0.00076), COL13A1 (log2Fold = −2.4, p = 0.02), COL18A1 (log2Fold = −3.1, p = 0.03), WGCNA analysis identified separate gene modules where CRV431 regulated C6M (r = 0.72, p < 10−100), ProC3 (r = 0.78, p < 10−100) and ALT (r = 0.59, p = 8.9 × 10−200) production. The ProC3 module demonstrated involvement in collagen
Background and aims: BIO89-100 is a long-acting glycoPEGylated analogue of fibroblast growth factor 21 (FGF21) in development for the treatment of non-alcoholic steatohepatitis (NASH) and severe hypertriglyceridemia. PK/PD of BIO89-100 was previously characterized in a multiple-ascending dose (MAD) study in noncirrhotic NASH patients (fibrosis stage F1-3). This phase 1 study was designed to characterize the PK/PD properties of BIO89-100 in adult patients with compensated cirrhosis from NASH (F4) and evaluate the effect of cirrhosis on BIO89-100 PK/PD.

Method: This Phase 1, open-label, single-center study in the USA enrolled a total of 8 adult patients with diagnosed compensated cirrhosis (F4) due to NASH based on Liver Forum criteria. Patients received a single 30 mg SC dose formulation of BIO89-100 via subcutaneous (SC) injection on Day 1. Blood samples for PK and PD assessments were collected before and at predetermined timepoints after BIO89-100 administration. PK parameters were estimated using a non-compartmental approach. As part of exploratory objectives, PD end points from the lipid panel (i.e., triglycerides [TGs], total cholesterol, low-density lipoprotein cholesterol [LDL-C] and high-density lipoprotein cholesterol [HDL-C]) were evaluated as the absolute change and percent change from baseline to Day 8. PK/PD data were consequently compared to historic findings from the MAD study.

Results: A prespecified interim PK/PD analysis was conducted using data from the first 6 patients for PK and all 8 patients for PD. The majority of patients were female (62.5%); mean age was 53.3 years; mean BMI was 37.4 kg/m²; mean VCTE was 28.9 kPa. Following a single 30 mg SC dose in patients with F4 fibrosis, BIO89-100 serum concentration declined in a monophasic fashion with the mean elimination half-life of 62 hours consistent with previous studies. PK exposure differences in F4 patients in this study vs. F1-3 patients in the MAD study were negligible and within a clinical PK variability. Simulated PK profiles using already developed popPK model based on F1-3 data adequately described the F4 PK (Figure). Moreover, BIO89-100 had a robust effect compared to baseline on serum TGs (up to 44% reduction), HDL-C (up to +55% increase), and LDL-C (up to 29% reduction) on Day 8 in patients with F4 NASH. A favorable safety and tolerability profile was observed in this study.

Conclusion: The interim PK/PD data indicate BIO89-100 elicits a robust PK/PD effect independent of NASH fibrosis stage. These findings highlight the feasibility of achieving favorable treatment outcomes in F4 patients with compensated hepatic function without requiring dose adjustment. Overall, these PK/PD properties warrant further investigation to allow assessments of effectiveness of BIO89-100 in a larger F4 population.
Conclusion: These data on pharmacokinetic properties, efficacy and safety profiles overall indicate that HEC96719 is a promising drug candidate for NASH treatment. Planned clinical studies are warranted to further evaluate these effects.

SAT133
Effect of saroglitazar in reducing liver enzymes and liver stiffness in non-alcoholic fatty liver disease: a single arm prospective study
Avisek Chakravorty1, Swetha Sattanathan2, Krishnasadas Devaladas2.
1Government Medical College Thiruvananthapuram, Medical Gastroenterology, thiruvananthapuram, India; 2Government Medical College Thiruvananthapuram, Medical Gastroenterology, thiruvananthapuram, India
Email: avisek.doc@gmail.com

Background and aims: Non-Alcoholic Fatty Liver Disease (NAFLD) is fast becoming the leading cause of cirrhosis worldwide. But the pharmacotherapy of Non-Alcoholic Steatohepatitis (NASH) remains elusive. This trial was conducted to study the effects of the dual peroxisome proliferator-activated receptor (PPAR) agonist Saroglitazar (approved by Drugs Controller General of India for NASH) on liver fibrosis, transaminases and lipid profile in NAFLD patients.

Method: Investigator initiated single arm prospective observational study. Consecutive patients of NAFLD (2016 EASL Clinical Practice Guidelines) with raised transaminases and liver stiffness (LSM) ≥7 kPa (by Transient Elastography) were started on Tab Saroglitazar 4 mg daily. Patients with pregnancy and lactation were excluded. AST/ALT, Lipid profile and LSM were measured at baseline, 6 months and 1 year

Results: 90 patients were started on Saroglitazar. Data was analysed for all patients at 6 months and for the 57 patients who completed 1 year of therapy. At 6 months and 1 year, there was a significant reduction in transaminases (20.8% and 23.6% reduction for AST, 29.5% and 35.4% reduction for ALT, p = 0.00006). Mean liver stiffness reduced from 11.6 kPa at baseline to 9.4 at 6 months and 8.3 at 12 months (21.5% and 28.7% reduction, respectively, p = 0.00001). For those with advanced liver fibrosis at baseline (TE ≥9.9 kPa), the reduction in LSM was 28.2% and 36% at 6 and 12 months, respectively. Total cholesterol, Low density lipoproteins (LDL) and triglycerides reduced significantly (14.5%, 15.3% and 18.6% respectively at 1 year, p < 0.05). No significant difference in High density lipoproteins (HDL) could be found. Significant weight reduction was noted at 6 and 12 months compared to baseline (3.3% and 3.9% reduction respectively, p = 0.00004). No serious adverse effects were noted in any of the patients while on therapy.

Conclusion: Saroglitazar seems to be a promising option for reduction of liver stiffness and transaminitis in NAFLD. Whether there is similar effect on liver histology has to be proven by biopsy-based studies.

SAT134
Intrahepatic microcirculation disorders and hyperammoniemia and their correction at non-alcoholic and steatohepatitis patients with initial stages of liver fibrosis
Tatiana Ermolova1, 1North-western state medical university named after LLMecников, Internal Medicine and Faculty, St.-Petersburg, Russian Federation
Email: t.v.ermolova@mail.ru

Background and aims: Ammonia is new therapeutic target for chronic liver diseases. Some experimental studies demonstrated, that ammonia increases of activity of hepatic stellate cells, stimulating liver fibrogenesis, impairs liver microcirculation, and these processes are reversible after the using of hyperammoniemic medicines. Aims of our study are to estimate blood level of ammonia, intrahepatic microcirculation and efficacy of ornithine (Hepa-Merz) for correction of such disorders at the chronic liver diseases.

Method: We investigated 56 non-alcoholic steatohepatitis (NASH) and 45 HCV patients with initial fibrosis 0–1 stages. Level of ammonia was estimated by biochemical method (PocketChem BA, Arcray, Japan) in capillary blood at the patients and 37 healthy individuals (control), normal ammonia level is less than 60 umol/L. Intrahepatic hemodinamics are determined by polyhepatography (PHG)-modified hepatic impedansometry, non-invasive method for integral estimation of intrahepatic blood flow by checking of tissue resistance to weak electric current. PHG registers a blood flow in zone of hepatic right, left lobes and spleen, integral body impedansography. For correction of blood flow disorders we used hyperammoniemic drug ornithine (Hepa-Merz) in dosage 3 grams 3 times daily for 4 weeks. Efficacy of LOLA we looked in 2 and 4 weeks via the control PHG and control of ammonia.

Results: Analysis of PHG demonstrated, that at all patients we revealed a liver microcirculation disorders- increased blood resistance, abnormal forms and amplitude of waves in sinusoidal level (out flow zone) at NASH patients and presinusoidal level (inflow zone) at viral patients. Level of ammonia in the NASH patients was 137.2 umol/L, in control group-49.3 umol/L (p <0.01). Hyperammoniemia was higher at the NASH patients, compared with viral patients higher (102.3 umol) (p <0.01). Analysis of efficacy of Hepa-Merz showed, that it was effective for correction of hepatic hemodinamic disorders at all patients, in 2 weeks of the treatment we observed normalization or improvement of the wave form, in 4 weeks-wave amplitude. Level of ammonia was decreased in 2 weeks.

Conclusion: NASH patients with initial stages of liver fibrosis are characterized by hyperammoniemia, which is more pronounced in comparison with viral hepatitis. NASH is accompanied by disorders of intrahepatic microcirculation disorders in out flow zone. LOLA improved liver microcirculation and decreases of blood ammonia level at the NASH and HCV patients.

SAT135
Ticagrelor, but not clopidogrel, attenuated hepatic steatosis in a model of non-alcoholic fatty liver disease
Hyunwoo Oh1, Hyo Young Lee1, Huiyul Park2, Dae Won Jun3, Eileen Youn7, Sang Bong Ahn4, Chul-min Lee5, Mi Mi Kim6, Bo-Kyeong Kang5, Joo Hyun Sohn6.
1Uijeongbu Eulji Medical Center, Department of Medicine, Gyeonggi-do, Korea, Rep. of South; 2Uijeongbu Eulji Medical Center, Department of Family medicine, Gyeonggi-do, Korea, Rep. of South; 3Hanyang University College of Medicine, Department of Medicine, Seoul, Korea, Rep. of South; 4Nowon Eulji Medical Center, Eulji University School of Medicine, Department of Medicine, Seoul, Korea, Rep. of South; 5Hanyang University College of Medicine, Department of Radiology, Seoul, Korea, Rep. of South; 6Hanyang University Curi Hospital, Hanyang University College of Medicine, Department of Medicine, Gyeonggi-do, Korea, Rep. of South
Email: bliss153@hanmail.net

Background and aims: Several studies have suggested that platelets are associated with inflammation and may play an important role in...
hepatic inflammation. We tried to evaluate whether antiplatelet drugs could improve non-alcoholic fatty liver disease (NAFLD).

**Method:** Mice were fed a high-fat diet (HFD) to establish an NAFLD model, which was verified through pre-study liver biopsy at 18 weeks. Animals with an NAFLD activity score (NAS) ≥4 were randomized into HFD-only, clopidogrel (CLO; 35 mg/kg/day), and ticagrelor (TIC; 40 mg/kg/day) groups, which were then treated with the respective drug for an additional 15 weeks. Liver and blood samples were collected from all animals at 33 weeks.

**Results:** The TIC group, but not the CLO group, showed significantly lower degree of steatosis and NAS than the HFD group (HFD: 5.3 ± 0.9, TIC: 3.4 ± 1.2; p = 0.0047). Hepatic de novo lipogenesis markers (SREBP1c, FAS, SCD1, and DGAT2 expression) and mRNA expression of inflammatory markers only decreased significantly in the TIC treatment group. Endoplasmic reticulum (ER) stress markers (CHOP, Xbp1, and GRP78) also decreased significantly in the TIC group, but not in the CLO group. Nile red staining intensity decreased in HepG2 cells following TIC treatment. Hepatic de novo lipogenesis markers were decreased significantly in HepG2 cells after TIC treatment.

**Conclusion:** TIC, but not CLO, attenuated steatosis and NAS via inhibiting de novo synthesis as well as ER stress in the biopsy proven NAFLD animal model.

**SAT136**

**Lemon balm extract ALS-L1023, an angiosgenesis inhibitor, inhibits liver fibrosis in a non-alcoholic fatty liver disease model**

Hyo Young Lee1, Hyunwoo Oh1, Eileen Yoon2, Dae Won Jun3, Sang Bong Ahn3, Huiyl Park4, Bo-Kyeong Kang5, Mi Mi Kim5, Chul-min Lee5, Joo Hyun Sohn6.

**Background and aims:** ALS-L1023 is an ingredient extracted from Melissa officinalis L. (Labiate; lemon balm), which grows wild in Europe and the Mediterranean. ALS-L1023 is also known as a natural medicine that suppresses angiogenesis. Herein, we aimed to determine whether ALS-L1203 could alleviate non-alcoholic fatty liver disease (NAFLD).

**Method:** C57BL/6 wild-type male mice (age, 6-weeks-old) were fed a choline-deficient high-fat diet for 10 weeks to induce NAFLD. Two doses (a low dose, 8 g/kg/day; and a high dose, 12 g/kg/day) of the lemon balm extract, ALS-L1023, were selected and mixed with feed for administration. RNA sequencing was performed for the choline-deficient high-fat diet group, ALS-L1023 responder group, and ALS-L1023 non-responder group.

**Results:** There was no significant difference between the groups in mean final body weight or food intake. Biochemical analysis revealed that the ALS-L1023 low-dose group had significantly decreased alanine transaminase and aspartate transaminase compared to the choline-deficient high-fat diet group. Based on Sirius red staining, the area of fibrosis significantly decreased due to the administration of ALS-L1023, and the anti-fibrotic effect of ALS-L1023 was greater than that of obeticholic acid. RNA sequencing was performed after mice were divided into responder and non-responder groups. The responder group had lower expression of genes related to the hedgehog-signaling pathway than the non-responder group.

**Conclusion:** ALS-L1023 may exert anti-fibrotic effects in the NAFLD model.
cohort, 22 (66.7%) had T2DM, 7 (21.2%) had prediabetes, 5 (15.2%) were overweight, and 24 (72.3%) were obese with BMI >30. All 33 had follow-up labs, 20 with follow-up body composition analysis, and 10 with follow-up transient elastography. Median maximum semaglutide dose was 1.0 mg (IQR 0.5–1.0 mg) with median length of follow-up 281 days (range 92–921 days) after semaglutide initiation. Average weight loss achieved at follow-up was 8.45% (p = 0.001, Figure 1). Other body composition parameters such as visceral fat area (VFA) (-7.64%, p = 0.01), percent body fat (-3.46%, p = 0.03), and truncal segmental fat mass (-7.52%, p = 0.01) also significantly improved. ALT significantly decreased (-17.5 U/L, p = 0.04) along with other metabolic parameters HbA1c (-0.7, p = 0.03). Nausea was the most common adverse event.

**Conclusion:** Our study is consistent with prior findings of semaglutide achieving clinically significant weight loss when used in combination with lifestyle modifications, and overall being well-tolerated. Semaglutide was also associated with improved body fat distribution parameters, including VFA, which is most associated with cardiometabolic risk factors and metabolic syndrome, given its anatomic location around the internal organs and hyperlipolytic activity. Improving VFA with semaglutide may improve the dysmetabolic profile of NAFLD patients. Further investigation is needed to evaluate the impact of these weight and body composition improvements on cardiovascular outcomes and overall morbidity and mortality.

**SAT139**

Peggozafermin improved liver histology, liver-related non-invasive tests (NITs) and metabolic profiles in an open-label cohort of a Phase 1b/2a study in subjects with non-alcoholic steatohepatitis (NASH)

Rohit Loomba1, Naim Alkhouri2, Don Lazas3, Pierre Bedossa4,5, Linda Morrow6, Shibao Feng7, Leo Tsend2, Germaine D. Agoliah7, Will Charlton8, Hank Mansbach9, Maya Margalit10, Stephen Harrison11

1UCSD NAFLD Research Center, La Jolla, CA, United States; 2Arizona Liver Health, Tucson, AZ, United States; 3Digestive Health Research/ObjectiveHealth, Nashville, TN, United States; 4Liverpat, Paris, France; 5Newcastle University, Institute of Translational Research, Newcastle, United Kingdom; 6Proscienzo Inc., San Diego, CA, United States; 789bio Inc., San Francisco, CA, United States; 89bio Inc., Herzliya, Israel; 9Pinnacle Clinical Research, San Antonio, TX, United States

Email: maya.margalit@89bio.com

**Background and aims:** Peggozafermin (PGZ), a long-acting glycoPEGylated recombinant human FGF21 analog, had significant liver-related and cardiometabolic benefits, with favorable safety and tolerability, in a Phase 1b/2a study in NASH.

**Method:** In this open label cohort, 20 subjects with biopsy-proven NASH (NAS ≥4, fibrosis stage F2/F3) received SC PGZ 27 mg QW for 20 weeks. Key end points were histology (≥2-point improvement in NAS with ≥1 point improvement in ballooning or inflammation; NASH resolution without worsening of fibrosis, and ≥1 stage fibrosis improvement without worsening of NASH), and safety and tolerability at week 20 (W20). Change in liver fat and liver and metabolic markers were also assessed. Biopsies were read by one central reader.

**Results:** BL characteristics included (means): Age 58.4 years, BMI 37.0 kg/m², NAS 5.3 points, MRI-PDFF 21.1%, ALT 47.1 U/L, ProC3 19.3 ng/ml and Fibroscan™ VCTE score 14.3 kPa. 75% of subjects were female, 85% had T2DM, and fibrosis stage was F3 in 65% and F2 in 35% of subjects. 19/20 subjects completed treatment and had W20 biopsies. At W20, 74% of subjects had ≥2 pt reduction in NAS (mean absolute change −2.4 pts); 32% and 26% had NASH resolution without fibrosis worsening and improved fibrosis without NASH worsening, respectively. There was a consistent improvement in NITs that assess fibrosis compared to BL [VCTE score −4.6 kPa (−31%; p < 0.001), FAST score −0.47 (−76%; p = 0.001)]. FIB-4 −0.29 (−19%; p < 0.01) and ProC3 −4.3 ng/ml (−20%; p < 0.001). 88% of subjects with BL FAST scores in the ‘rule-in’ or ‘indeterminate’ range had ‘rule-out’ FAST scores (≤0.35) at W20. At W20, mean relative reduction in MRI-PDFF was 65% (p < 0.001), and 100% and 79% of subjects had ≥30% and ≥50% reductions, respectively. ALT decreased by 46% compared to BL (p < 0.001); mean absolute decrease in ALT was −27.8 U/L in subjects with elevated ALT at BL, and ALT decreased ≥17 U/L in 71% of these subjects. At W20, significant improvement in HbA1c and lipids, weight loss and increased adiponectin were observed in PGZ-treated subjects. PGZ was safe and well tolerated. There were no deaths, related SAEs or discontinuations due to AEs. Treatment related AEs reported in ≥10% of subjects included diarrhea, nausea, vomiting, injection site bruising, injection site erythema and decreased appetite; there were no reports of AEs grade ≥3, hypersensitivity, tremor or adverse effects on vital signs.

**Conclusion:** PGZ (27 mg QW for 20 weeks) led to meaningful changes in key histology end points and fibrosis-related NITs, reduction in MRI-PDFF and decreased ALT in a cohort of NASH subjects with advanced fibrosis. In addition to these benefits on liver health, PGZ significantly improved metabolic parameters, with good safety and tolerability. These results extend the growing evidence of PGZ’s potential as treatment for NASH. PGZ is currently being evaluated in NASH in the ongoing Phase 2b ENLIVEN study.

**SAT140**

Identification of new therapeutic targets for hepatic regenerative medicine in Non-Alcoholic Fatty Liver Disease (NAFLD)

Shainan Hora1, Rong Gao1, Viktoria Jakovleva2, Agnes Bee, Leng Ong1, Torsten Wuestefeld1, 1Genome Institute of Singapore, Laboratory of In vivo Genetics and Gene Therapy, Singapore, Singapore

Email: Shainan_Hora@gs.a-star.edu.sg

**Background and aims:** Non-alcoholic fatty liver disease (NAFLD) has emerged as the most common cause of chronic liver disease in the recent years. The massive growth in NAFLD cases is being fueled by an increase in global over-nutrition and obesity. Despite this, NAFLD continues to be an underdiagnosed disease with no current approved treatment and only a handful of drugs in clinical trials. A number of strategies are being employed to reverse this end-stage liver disease, including our unbiased genome wide in-vivo functional genetic screen that aims to identify novel regulators of NAFLD and shed light on hepatic regenerative therapy.

**Method:** Western diet animal model that recapitulates NAFLD in in-vivo dynamic tail vein (HDTV) injections into animal liver. To recapitulate the fatty liver phenotype, mice were fed western diet supplemented with cardiometabolic risk factors and metabolic syndrome, given its anatomic location around the internal organs and hyperlipolytic activity. Improving VFA with semaglutide may improve the dysmetabolic profile of NAFLD patients. Further investigation is needed to evaluate the impact of these weight and body composition improvements on cardiovascular outcomes and overall morbidity and mortality.
with high fructose. Following diet treatment for 8-weeks, doxycycline was added to induce shRNA expression enabling gene knockdown, along-with western diet for another 16 weeks. Animal livers were harvested, primary NGS analysis was performed and abundance of each shRNA was determined using differential expression analysis method. Top enriched shRNAs were down-selected using a stringent criterion (95% confidence interval with a 4-fold change), validated using a series of experiments in-vitro and injected into fumarylacetate hydrolase (FAH)-knockout animals to study liver repopulation following diet treatment.

**Results:** We have identified several shRNAs that confer a negative or positive effect on the regenerative capacity of hepatocytes when subjected to detrimental environment such as high fat diet. Top enriched shRNAs have been validated using various in-vitro assays followed by selection of top scoring shRNAs for their impact on fatty liver disease phenotype using in-vivo animal models. Furthermore, we have identified some of the known markers of NAFLD that further validates the authenticity of our screen.

**Conclusion:** RNAi-based functional genetic screen in combination with high-throughput sequencing will allow the identification of new gene targets and uncover new insights underlying NAFLD development and disease progression.

**SAT141**

**The effects of dietary vitamin E intake on NAFLD and sex differences in serum metabolic profile**

Eleonora Scorletti¹, Kate Townsend Creasy², Marijana Vujkovic², Daniel Rader¹-², Kai Markus Schneider³, Carolin Victoria Schneider¹.

¹University of Pennsylvania, Department of Medicine, Philadelphia, United States; ²University of Pennsylvania, Department of Genetics, Philadelphia, United States; ³University of Pennsylvania, Department of Microbiology, Philadelphia, United States

Email: eleonora.scorletti@pennmedicine.upenn.edu

**Background and aims:** Non-alcoholic fatty liver disease (NAFLD) is characterised by the accumulation of lipid droplets in hepatocytes and affects approximately 20–30% of the general population. Currently, there are no approved pharmacological agents available to treat NAFLD. Growing evidence supports the potential benefits of vitamin E in reducing steatosis and lobular inflammation in non-diabetic patients with NAFLD. Despite previous trials tried to assess the efficacy of vitamin E supplementation in patients with NAFLD, there remains a lack of understanding on the effects of vitamin E. Further, there are reported sex differences in NAFLD etiology and severity, although they have been poorly described.

**Method:** We analyzed the UK Biobank (UKB) dataset and selected our study population based on the availability of nutritional assessment. We investigated the association between dietary vitamin E intake with various disease phenotypes, serum metabolites and NAFLD prevalence.

**Results:** Data from >210,000 participants demonstrate that increased dietary vitamin E intake was associated with a lower prevalence of NAFLD and overall mortality. Each standard deviation (SD = 7 mg) vitamin E increase per kJ energy intake was associated with reduced the risk of NAFLD ICD-10 diagnosis by 12.5% (p < 0.0001) and a reduced risk of MRI diagnosis of NAFLD by 24.3% (p < 0.0001). Additionally, we found sex differences in the effect of dietary vitamin E on metabolic profiles. Analysis of serum metabolites showed a greater reduction in gamma-glutamyl transferase (GGT) (p < 1 × 10⁻²) and urate (p < 1 × 10⁻⁸) in males, and a greater increase in sex hormone binding globulin (SHBG) in females (p < 1 × 10⁻¹⁵) (Figure 1).

**Conclusion:** Our study showed that increased dietary vitamin E intake may be beneficial for preventing NAFLD. Moreover, we found sex differences in the effects of dietary vitamin E on serum metabolic profiles. More randomized clinical trials are needed to identify suitable candidates for vitamin E supplementation in NAFLD patients.

[UKB dataset reference number 71300]

**SAT142**

**Favorable safety profile of TERN-201, a highly selective inhibitor of vascular adhesion protein-1, in the non-alcoholic steatohepatitis phase 1b AVIATION study**

Mazen Nouredden¹, Eric Lawitz², Naim Alkhouri³, Robert Jenders⁴, Douglas Denham⁵, Bal Raj Bhandari⁶, Christopher Jones⁷, Cara H. Nelson⁷, Tonya Marmon⁷, Swapna Shenvi⁷, Hiba Graham⁷, Daria Crittenden⁷, Erin Quirk⁷, Diana Chung⁷.¹ Cedars-Sinai Medical Center, Cedars-, Sinai Fatty Liver Program, Los Angeles, United States; ²Texas Liver Institute, San Antonio, United States; ³Arizona Liver Health, Tucson, United States; ⁴Velocity Clinical Research, La Mesa, United States; ⁵Clinical Trials of Texas, LLC, San Antonio, United States; ⁶Delta Research Partners, Monroe, United States; ⁷Terns Pharmaceuticals, Foster City, United States

Email: equirk@ternspharma.com

**Background and aims:** TERN-201, an irreversible inhibitor of vascular adhesion protein-1 (VAP-1) with >7000-fold selectivity over monoamine oxidase A or B, has demonstrated sustained target engagement in healthy human subjects. VAP-1 levels are elevated in over monoamine oxidase A or B, has demonstrated sustained target engagement in healthy human subjects. VAP-1 levels are elevated in patients with NASH. Here we report results from Part 1 of the TERN-201, Phase 1b AVIATION trial in patients with NASH.

**Method:** Part 1 of the two-part AVIATION trial was a double-blind, placebo-controlled study (NCT04897594) in 30 adults with non-cirrhotic NASH phenotype evaluating 10 mg TERN-201 once daily (QD) for 12 weeks followed by off-treatment evaluation at Week 16. The prespecified Part 1 interim analysis primary end point was safety assessed by adverse events (AEs) and laboratory tests; percent change from baseline (BL) in plasma VAP-1 activity was a secondary end point. Exploratory imaging and blood-based biomarkers of liver inflammation and fibrosis were also assessed.

**Results:** Thirty patients, mean age 49.7 years, 22 (73.3%) women, 4 (13.4%) non-whites, mean (±SD) alanine aminotransferase (ALT)
POSTER PRESENTATIONS

67.25 (±31.25) U/L, liver stiffness (LS) 8.68 (±2.03) kPa by transient elastography, multiparametric magnetic resonance liver imaging (MRI) corrected T1 (CTI) 899.9 (±110.2) msec and proton density fat fraction 17.6% (±7.5%) were randomized 2:1 to receive 10 mg TERN-201 or placebo. Nearly all patients (28/30, 95% of TERN-201 and 90% of placebo) completed Part 1. No patient discontinued due to any AE. 10 mg TERN-201 was well-tolerated with a similar incidence of AEs as placebo. All AEs were mild or moderate with no serious AEs or trends in AEs or laboratory abnormalities reported. 10 mg TERN-201 resulted in >98% inhibition of plasma VAP-1 activity in most subjects by Week 2 and sustained suppression through Week 12. There were no statistically significant differences between placebo and 10 mg TERN-201 in change from BL to T1, liver fat fraction, liver enzymes, or cytochrome P450. At Week 12, tissue inhibitor of metalloproteinase-1 (TIMP1), a marker of hepatic fibrogenesis, decreased by 29.58 (±9.26) ng/ml in the TERN-201 group and increased by a mean (± SE) of 13.56 (±14.22) ng/ml in the placebo group relative to BL (p < 0.05).

Conclusion: TERN-201 was well-tolerated with a safety profile similar to placebo in patients with BL multiparametric MRI and LS values indicating NASH with at least stage 2 fibrosis. While 10 mg TERN-201 led to near complete inhibition of plasma VAP-1 activity and decreased levels of the hepatic fibrogenesis marker TIMP1, no statistically significant differences were observed between TERN-201 and placebo on markers of liver inflammation and injury following 12 weeks of treatment. Overall, these data support further assessment of safety and activity of 20 mg TERN-201 in the ongoing Part 2 of the AVIATION Trial in phenotypic NASH.

SAT143
Pegagozafermin led to significant metabolic benefits, in addition to robust beneficial effects on the liver, in an open-label cohort of a Phase 1b/2a study in subjects with non-alcoholic steatohepatitis (NASH)
Naim Alkhoujia, Rohit Loomba5, Juan P Frías5, Linda Morrow4, Shibao Feng2, Leo Tseng3, Germaine D. Agollahi1, Will Charlton1, Hank Mansbach1, Maya Margalit5, Stephen Harrison2, 1Arizona Liver Health, Tucson, AZ, United States; 2USCD NAFLD Research Center, La Jolla, CA, United States; 3National Research Institute, Los Angeles, CA, United States; 4Prosciento Inc., San Diego, CA, United States; 598Bio Inc., San Francisco, CA, United States; 6National Research Institute, Los Angeles, CA, United States; 7University of Pisa, Department of Pharmacy, Pisa, Italy
Email: maya.margalit@89bio.com

Background and aims: Metabolic derangements are key drivers of NASH and significant risk factors for cardiovascular (CV) morbidity and mortality in NASH patients, that increases with advancing fibrosis. While treatments for NASH would ideally address both liver injury and metabolic derangements in this population, metabolic liabilities have been a drawback in several NASH drug development programs. Pegagozafermin (PGZ), a long-acting glycoPEGylated recombinant human FGF21 analog in development for NASH, significantly improved liver and cardiometabolic parameters, with favorable safety and tolerability, in a Phase 1b/2a study in NASH.

Method: In this open label cohort, 20 subjects with biopsy-proven NASH (NAS ≥4, fibrosis stage F2-F3) received SC PGZ 27 mg QW for 20 weeks. Key end points included histology, safety and tolerability. Change in hemoglobin A1c (HbA1c), body weight (BW), triglycerides (TG), non-HDL cholesterol (non-HDL-C), LDL cholesterol (LDL-C) and adiponectin was assessed at Week 20 (W20).

Results: Baseline (BL) characteristics (means) included age 58.4 years, HbA1c 6.6%, BW 104.6 kg, BMI 37.0 kg/m², TG 170.0 mg/dL, non-HDL-C 125.9 mg/dL, LDL-C 92.0 mg/dL, HDL-C 43.4 mg/dL, and adiponectin 3.55 μg/mL. 75% of subjects were female, and 85% had T2DM. 16/19 (84%) subjects who completed treatment took ≥1 anti-diabetic agent (range 1–4 medications, including 15 on metformin and 5 on GLP-1 receptor agonists). 11/19 subjects were treated with statins. At W20, significant improvement in glycemic control, BW and lipid parameters were observed. HbA1c decreased by −0.5% (p < 0.001) in the overall population. In subjects with BL HbA1c ≥6.5% (N = 10; mean BL HbA1c = 7.3%), who were taking an average of 2 anti-diabetic agents, HbA1c decreased by −0.9%, to a mean of 6.4% (p < 0.01), BW decreased by −3.9% (p < 0.001). Adiponectin increased by 88.1% (p < 0.001). TG decreased by 26% in the overall population, and by 32% in subjects with elevated TG at BL (N = 11, mean BL TG 210 mg/dL; p < 0.001 for both comparisons). Non-HDL-C and LDL-C decreased by 18% (p < 0.001) and 13% (p < 0.05), respectively, and HDL-C increased by 23% (p < 0.001). Mean changes in serum lipids in subjects treated with statins were: TG−29.0%; non-HDL-C−22.1%; LDL−16.2% and HDL-C +35.4%.

Conclusion: PGZ (27 mg QW for 20 weeks) led to meaningful reduction in HbA1c and body weight and significant improvement in serum lipids in a cohort of mostly diabetic NASH subjects with advanced fibrosis and significant metabolic derangements, many of whom were already on treatment for diabetes, hyperlipidemia or both. These benefits were additive to robust beneficial effects on liver histology and favorable safety and tolerability, and suggest a potential of PGZ to protect subjects with NASH not only from liver related outcomes, but also from CV risk. PGZ is currently being evaluated in NASH subjects (NAS ≥4, F2-F3) in the ongoing Phase 2b ENLIVEN study.

SAT144
Novel thyroid hormone receptor-beta agonist TG68 safely induces hepatic fat reduction in a non-alcoholic steatohepatitis rat model
Andrea Marco Caddeo1, Marta Anna Kowalik1, Marina Serra1, Simona Rapposelli1, Amedeo Columbano1, Andrea Perra1, Cagliari, Department of Biomedical Sciences, Monserrato, Cagliari, Italy 1; University of Pisa, Department of Pharmacy, Pisa, Italy
Email: andrea.perra@unica.it

Background and aims: Non-alcoholic fatty liver disease (NAFLD) encompasses a broad spectrum of hepatic pathological conditions ranging from simple steatosis to non-alcoholic steatohepatitis (NASH), in absence of alcohol abuse or hepatic viral infections. Patients affected by NASH can develop fibrosis, cirrhosis and, eventually, hepatocellular carcinoma (HCC). Despite the raising interest in finding a strategy for this condition, no pharmacological approaches have been approved for the treatment of NAFLD. In this respect, thyroid hormones (THs) regulate hepatic lipid metabolism by binding thyroid hormones receptors beta (TRβ) in the liver. Alteration of the hepatic TH signaling takes part of the rise and development of liver-associated diseases, such as NAFLD and HCC. To date, the use of THs as therapeutic approach is hindered by the lack of selectivity and adverse extrahepatic side effects, mainly due to their affinity for extrahepatic TRα receptors.

Method: To selectively activate TRβ, we designed and synthesized a novel TRβ agonist, namely TG68. Rats were fed a high fat diet (HFD) ad libitum for 25 weeks, and then animals received orally TG68 (2.8 mg/kg) for three weeks. Blood serum and tissues, including liver, heart and kidney, were collected and analysed after sacrifice.

Results: Blood analysis showed reduced circulating glucose, triglycerides, and cholesterol. Three week-treatment of TG68 significantly reduced liver weight as well as the liver weight/body weight ratio due to an increased fatty acid beta-oxidation and glycolysis rates highlighted by the overexpression of Cpt1a and Ppala 2, respectively. Furthermore, TG68 strongly reduced hepatic fat accumulation and ameliorates liver injury in the absence of extrahepatic toxic effects.

Conclusion: Rats fed a HFD and treated orally with TG68 for the last three weeks before sacrifice, ameliorated liver weight/body weight ratio and intrahepatic neutral lipid content. This study strongly suggests that TG68 is an innovative hepatospecific TRβ agonist, which might be used as a future therapeutic tool for the treatment of NAFLD.
SAT145
Safety and pharmacokinetics (PK) of single and multiple ascending oral doses of ALG-055009, a thyroid hormone receptor beta agonist for the treatment of non-alcoholic steatohepatitis (NASH), in healthy volunteers and subjects with hyperlipidemia
Hakim Charfi1, Jean-Louis Pinquier1, Benedetta Masetto1, Kha Le2, Christopher Westland2, Kusum Gupta2, Lawrence Blatt2, Sushmita Chanda3, John Fry4, Matt McClure1,1 Biotal, Rennes, France; 2Aligos Therapeutics Inc, South San Francisco, United States; 3Aligos Therapeutics Inc, South San Francisco, United States
Email: bmassetto@aligos.com

Background and aims: Thyroid hormone receptor beta (THR-β) agonists rapidly reduce atherogenic lipids such as low-density lipoprotein cholesterol (LDL-C) and triglycerides in serum and the liver, decrease hepatic fat content and improve liver histology. Therefore, therapeutics targeting THR-β represent a promising mechanism of action to treat patients with NASH. ALG-055009, a novel oral thyroid hormone analogue with high THR-β selectivity and nanomolar potency, is being assessed in a first-in-human study (NCT05090111).

Method: In Part 1 of this multi-part, double blind, randomized, placebo-controlled study, multiple cohorts of 8 healthy volunteers (HV) received single ascending doses of ALG-055009 or placebo (3:1 ratio). In Part 2, multiple cohorts of 10 subjects with mild hyperlipidaemia (LDL-C >110 mg/dL) receive a daily (QD) dose of ALG-055009 or placebo (4:1) for 14 days. Adverse events (AE), vital signs, electrocardiogram (ECG), laboratory parameters, including thyroid stimulating hormones, lipids, sex hormone binding globulin (SHBG), and plasma and urine PK samples are collected. Reported here are the available preliminary blinded safety and PK data in HV from the first five cohorts in Part 1 and the first cohort in Part 2. Pharmacodynamic results and data from additional cohorts will be included at the time of the presentation.

Results: Forty HV and 10 subjects with hyperlipidaemia were enrolled in Part 1 Cohorts 1–5 (0.1 mg, 0.3 mg, 0.9 mg, 2.6 mg, 4 mg) and Part 2 Cohort 1 (0.3 mg), respectively. All HV were male with a mean age of 38 years and a mean BMI of 25 Kg/m². Subjects with hyperlipidaemia were mostly male (90%) with a mean age of 41 years, a mean BMI of 27 Kg/m², and a mean LDL-C of 143.1 mg/dL. All 50 participants completed the study. No serious AE has been reported and no AEs have resulted in premature study drug discontinuation. Seven HV (17.5%) and 3 subjects with hyperlipidaemia (30%) experienced at least one treatment emergent AE (TEAE). All TEAEs were mild or moderate in severity and without dose response. Overall, TEAEs observed in more than one subject were: headache (N = 2); rhinopharyngitis (N = 2); insomnia (N = 2). All treatment emergent lab abnormalities were Grade 1, except for two subjects (N = 1 in Part 1 Cohort 4; N = 1 in Part 2 Cohort 1) who experienced a transient asymptomatic Grade 2 lipase elevation that resolved spontaneously by the following visit. No clinically significant changes in thyroid hormones or SHBG were observed. There were no clinically significant changes in vital signs or ECGs. Plasma ALG-055009 exposures increased dose proportionally between 0.1 and 2.6 mg dose levels (4 mg PK pending), with low variability (CV<36%) and ~1.7-fold accumulation following 14 daily doses.

Conclusion: Single doses of ALG-055009 of up to 4 mg and multiple daily 0.3 mg doses for 14 days were well tolerated with a favourable PK profile.

SAT146
A mediterranean diet intervention has beneficial effects on biomarkers of cardiovascular risk and hepatic fibrosis in non-alcoholic fatty liver disease (NAFLD)
Laura Haigh1,2, Olivier Govaere3, Lorna Brownlee1, Sarah Charman3, Alasdair Blain3, Thomas Wilson4, Morten Karsdal5, Stuart Mcpherson2,3, John Mathers6, Quentin Anstee1,2, 1NIHR Newcastle Biomedical Research Centre, Newcastle upon Tyne, United Kingdom; 1Institute of Translational and Clinical Research, Faculty of Medical Sciences, Newcastle University, Newcastle upon Tyne, United Kingdom; 2Liver Unit, Newcastle Upon Tyne Hospitals NHS Foundation Trust, Newcastle upon Tyne, United Kingdom; 3Institute of Biological, Environmental and Rural Sciences, Aberystwyth University, United Kingdom; 4Nordic Bioscience A/S, Herlev, Denmark; 5Institute of Population Health Sciences, Faculty of Medical Sciences, Newcastle University, Newcastle upon Tyne, United Kingdom
Email: laura.haigh@nhs.net

Background and aims: Lifestyle interventions are the mainstay of non-alcoholic fatty liver disease (NAFLD) management. We assessed the feasibility and effectiveness of a Mediterranean diet (MD) intervention on patients stratified according to PNPLA3 rs738409 1148M carriage.

Method: 49 participants with NAFLD were recruited from a tertiary hepatology centre in the UK. In a cross-over design, participants completed Diet 1 (MD) and Diet 2 (control) for 4 weeks, in random order (1:1 allocation), separated by a 4-week washout period. Participants completed one-to-one diet and lifestyle consultations at baseline, end of diet phase 1, end of washout and end of diet phase 2. Participants were advised to maintain baseline levels of physical activity and body weight. At each of these time points we assessed; anthropometry; biochemistry, markers of cardiovascular risk (CVR) and biomarkers of hepatic fibrosis.

Results: Retention of participants was high (n = 48, 98%). At 4 weeks MD adoption significantly increased from low to moderate (mean increase, 3.3 points; from 5.7 ± 1.9 at baseline to 9.0 ± 2.1) as assessed by MD assessment score. There was no change in physical activity and

Changes in physical, biochemical and dietary intake measures after 4-weeks of a MD intervention (n=48)

<table>
<thead>
<tr>
<th>Participant Characteristics</th>
<th>Baseline</th>
<th>Post-MD Intervention</th>
<th>P-Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age (years)</td>
<td>59.0 (51.3–66.9)</td>
<td>60.0 (53.7–66.9)</td>
<td>0.782</td>
</tr>
<tr>
<td>BMI (kg/m²)</td>
<td>35.3 ± 5.5</td>
<td>34.7 ± 5.4</td>
<td>0.091</td>
</tr>
<tr>
<td>Waist circumference (cm)</td>
<td>114 ± 10.8</td>
<td>112 ± 11.3</td>
<td>0.022</td>
</tr>
<tr>
<td>Body composition (kg): Fat free mass</td>
<td>55.2 (45.6–65.4)</td>
<td>55.0 (45.6–65.1)</td>
<td>0.827</td>
</tr>
</tbody>
</table>

Cardiometabolic measures

| Blood pressure (systolic/diastolic) | 138 ± 14/84 ± 5.6 | 136 ± 14/84 ± 5.6 | 0.013 |
| Glucose (mmol/L)                  | 6.7 (5.7–7.6) | 6.5 (5.7–7.6) | 0.017 |
| Triglycerides (mmol/L)            | 2.5 (1.9–3.9) | 2.5 (1.9–3.9) | 0.787 |
| Total cholesterol (mmol/L)        | 4.5 ± 1.7 | 4.1 ± 1.2 | <0.001 |
| HDL (mmol/L)                      | 1.3 (1.1–1.5) | 1.2 (1.1–1.4) | 0.011 |
| TC/HDL ratio                      | 3.2 (2.7–4.1) | 3.1 (2.6–4.0) | 0.0006 |

Values are mean (SD), median (IQR), or number (percentages)

Liver function

| ALB (g/L) | 40 (36–48) | 40 (44–48) | 0.024 |
| ALP (IU/L) | 90 (77–113) | 90 (77–101) | 0.014 |

Hepatic fibrosis

| FIB-4 (cm²/m²) | 14.5 (12.1–23.5) | 13.6 (10.6–20.5) | 0.002 |

Diary Intake

| MEDIAS (p.134) | 5.7 ± 1.9 | 9.0 ± 2.1 | <0.001 |

Values are mean (SD), medians (IQR), or numbers (percentages)

Journal of Hepatology 2022 vol. 77(S1) | S665–S939
S733
Experimental studies are planned. The I148M variant appears to gain less benefit in terms of CVR factors. The effectiveness of a MD intervention, which rapidly improved CVR, carriers of the I148M variant appear to gain less benefit in terms of CVR factors when prescribed a MD intervention. Further validation in larger experimental studies are planned.

**Conclusion:** We have demonstrated the preliminary feasibility and effectiveness of a MD intervention, which rapidly improved CVR, carriers of the I148M variant appear to gain less benefit in terms of CVR factors when prescribed a MD intervention.

**Liver development, physiology and regeneration**

**SAT151**

**CD44 plays critical role in liver regeneration through enhanced redox balancing**

Wan Seob Shim1, Hyun Young Kim2, Keon Wook Kang1, Sang Kyun Kim2. 1Seoul National University, College of Pharmacy and Research Institute of Pharmaceutical Sciences, Seoul, Korea, Rep. of South; 2Chungnam National University, Daebeok Campus, College of Pharmacy, Daejeon, Korea, Rep. of South

**Background and aims:** Liver regeneration triggered by fulminant liver damage accompanies proliferation of hepatic progenitor cells (HPCs). Thus, there has been considerable interest in identifying specific HPC markers. However, the physiological role of HPC markers during liver regeneration is not fully understood. Herein, we identify the mechanistic roles of cluster differentiation (CD)44, a cell surface marker for hepatic regeneration, in HPC proliferation and redox homeostasis.

**Method:** Liver regeneration was induced by liver resection or injection of 250 mg/kg acetaminophen. The activity of the system xc− antipporter was measured using an extracellular glutamate assay and universal 13C6-cystine isotope tracing. Lentiviral Alb-shCD44 (LV-GFP-Alb-mCD44-shRNA) delivery system (a construct comprising the gene encoding shCD44 from the albumin promoter) was used to produce hepatocyte-specific CD44 knockdown mice.

**Results:** After liver resection or exposure to acetaminophen, the CD44 expression level was elevated in mouse primary hepatocytes isolated from regenerative liver tissues. Flow cytometry data identified HPCs, a subpopulation of hepatocytes with a high CD44 expression level and proliferation rate. To elucidate the role of CD44 in HPC proliferation, we knocked it down in AML12 cells. Knockdown of CD44 decreased the expression of xCT as well as the uptake of extracellular cystine through system xc−. CD44 ablation resulted in a diminished intracellular cysteine, glutathione (GSH), and a decreased proliferation rate. The proliferation of HPC isolated on a hyaluronic acid-coated dish was highly sensitive to inhibition of system xc−. Administration of system xc− inhibitor abrogated liver regeneration after acetaminophen (N-acetyl-p-aminophenol; APAP)-induced liver injury. Moreover, liver regeneration following APAP injection was significantly inhibited in hepatocyte-specific CD44 knockdown mice.

**Conclusion:** The obtained results delineate the central role of CD44 in modulating liver-regenerative capacity. Specifically, CD44 contributes to the intracellular redox balance and cell proliferation by enhancing extracellular cystine uptake through system xc−.

**SAT152**

**Development of ECM mimicking 3D-hydrogel scaffolds for liver tissue engineering**

Nathan Carpentier1, Sara Campinoti2, Luca Urbania, Peter Dubruel1, Sandra Van Vlierberghe1, 1Ghent University-Campus Sterre-S4, Gent, Belgium; 2Institute of Hepatology, King's College Hospital, United Kingdom

**Background and aims:** Annually, millions of people die because of liver failure, while the waiting duration for a donor liver is around 12 months. Herein, we target hybrid 3D-printed scaffolds to serve liver tissue engineering (LTE) applications.

As starting materials gelatin in combination with a polysaccharide was used to develop printable hydrogels. As polysaccharides dextran (Dex) and chondroitin sulphate (CS) were selected as mimics for the liver extracellular matrix (ECM) to explore their effect on the cell response. Methacrylated gelatin (GelMA) served as benchmark. The hydrogel materials were characterized on 2D-as well as on 3D-level. HepG2 cells were used to assess the in vitro biocompatibility of the developed hydrogels.

**Method:** Thiolated gelatin (GelSH) was crosslinked with the norbornene-functionalized polysaccharides DexNB and CSNB. Gelatin was methacrylated using methacrylic anhydride (GelMA) as reference material. The different materials were characterized on both 2D- and 3D-level to assess the physico-chemical properties and the biocompatibility. 3D-hydrogel scaffolds of the materials were developed by indirect 3D-printing.

**Results:** DexNB-GelSH and CSNB-GelSH were superior over GelMA as their crosslinking kinetics were significantly faster and they mimicked natural liver tissue (NLT) to a greater extent with respect to physico-chemical properties. The swelling ratio of GelMA, DexNB-GelSH and CSNB-GelSH were all in line with NLT. Atomic Force Microscopy (AFM) measurements revealed superior microscale mechanical properties of the DexNB-GelSH compared to the other materials that deviated more from NLT. On a 3D-level, DexNB-GelSH scaffolds exhibited a compressive modulus of (4.8 ± 1.6)kPa which is in excellent agreement with that of NLT (i.e. 1–5kPa) as compared to GelMA which resulted in a modulus of (8.5 ± 1.9)kPa and CSNB-GelSH (12.6 ± 1.9)kPa. So far, the biocompatibility of DexNB-GelSH and GelMA were compared. However, the in vitro biocompatibility of both materials was comparable based on the MTS assay. The live-dead staining showed that the cells grew more into clusters on the DexNB-GelSH.
scaffolds compared to the more spread morphology which the cells exhibited on the GelMA material.

Conclusion: DexNB-GelSH and CSNB-GelSH scaffolds are promising hybrid materials to support LTE as they exhibit similar physico-chemical properties compared to NLT (cfr. microscale stiffness, compressive modulus, swelling ratio and chemical composition), while cell viability and proliferation of the hepatocytes were preserved.

In future research, different cell types such as primary hepatocytes and organoids will be included in the biological evaluation. Furthermore decellularized liver ECM will be incorporated into the hydrogel material in order to improve the cell interactivity and proliferation.

SAT153
Three-dimensional conditions in a perfusion bioreactor to support maturation of human amnion epithelial stem cells into functional hepatocyte-like cells
Sara Campinoti1, Negin Goudarzi1,2, Bruna Almeida1, I. Jane Cox1, Roberto Gramignoli3, Luca Urbani1,2, 1The Roger Williams Institute of Hepatology, London, United Kingdom; 2King’s College London, Faculty of Life Sciences and Medicine, United Kingdom; 3Karolinska Institutet, Department of Laboratory Medicine, Sweden
Email: luca.urbani@researchinliver.org.uk

Background and aims: Organ or hepatocyte transplantation are efficient treatments for end stage liver disease, but limited by the shortage of donors. Bioengineered liver transplant is a promising approach, but requires functional liver cells. Perinatal stem cells are promising alternative source of somatic cells. We previously validated epithelial cells isolated from full-term amniotic membranes (AEC) as therapeutic strategy to reverse congenital liver disorders or rescue subjects from hepatic failure. AEC cells can mature into hepatocyte-like cells in vivo, supporting their use in regenerative medicine. Decellularized liver extracellular matrix scaffolds (ECM-scaffolds) maintain matrix components and the 3D architecture and can be used to support hepatic maturation and function in vitro. We combined ECM-scaffold technology with primary human AEC and evaluated cell proliferation and functional maturation into hepatocyte-like cells.

Method: primary human AEC were isolated in accordance with current Good Manufacturing Practice (cGMP) and qualified by flow cytometric and biomolecular analysis. Approx. 30–40 × 10^6 AEC from every donor were seeded into rat ECM-scaffolds generated in our lab. The constructs were cultured in custom-made bioreactors both in continuous perfusion and static conditions for 40 days (10 in expansion and 30 in differentiation media). Metabolites and functional products generated by AEC differentiating into hepatocyte-like cells were quantified by NMR, ELISA and luminescent/fluorescent functional assays validated as release criteria for human hepatocyte in clinical use. Additional biomolecular analysis were performed at the end of experimental set.

Results: AEC maintained epithelial characteristics and developed hepatic markers upon maturation. After 2 weeks of hepatic differentiation, AEC expressed hepatoblast markers (AFP). At the end of differentiation, AEC were positive for hepato-specific markers such as CK18, albumin and CYP3A4, but negative for AFP. Albumin and urea quantifications supported hepatic maturation in bioreactor-cultured scaffolds. Phase 1 and 2 functional assays supported hepatic maturation and comparison with fetal/adult human hepatocytes. NMR analysis highlighted changes in the metabolite in the supernatant of differentiated AEC in ECM-scaffolds.

Conclusion: several groups/companies have proposed stem cells as alternative solution, bounded by genetic and epigenetic instabilities, and limited in hepatic maturation level. Here we show functional differentiation of primary human AEC into hepatocyte-like cells by 3D liver matrix support when maintained in a perfusion bioreactor. We conclude that innovative perfusion ECM-scaffold technology may support maturation for multipotent and eventually pluripotent stem cells, with important repercussion in therapeutic approaches and toxicological studies.

SAT154
Knockdown of Glyoxylate reductase/hydroxypropruvate reductase (GRHPR) accelerates liver regeneration and decreases chronic liver damage
Viktoriai Lakovleva1,2, Anna Potapova1, Agnes Bee, Leng Ong1, Rong Gao1, Yock Young Dan2, Torsten Wuestefeld1,3,4, 1Genome Institute of Singapore (GIS), Laboratory of In vivo Genetics and Gene Therapy, Singapore, Singapore; 2National University of Singapore, Medicine, Singapore, Singapore; 3National Cancer Centre Singapore, Singapore, Singapore; 4Nanyang Technological University, Singapore, Singapore
Email: wuestefeldt@gis.a-star.edu.sg

Background and aims: GRHPR dysfunction in humans causes primary hyperoxaluria type 2 (PH2). Excess oxalate leads to kidney stone formation and kidney damage. However, in an in vivo RNAi screen to identify potential modulators of liver regeneration and disease we recently conducted two independent shRNAs targeting GRHPR scored. In addition, GRHPR expression was described to be decreased or lost in a subset of HCC, associated with proliferation rate (Pan et al., Pathobiology 2013:80: 155–162). Intrigued by this, we went on and validated that knockdown of GRHPR in hepatocytes accelerates liver regeneration and protects against liver fibrosis under chronic liver-damaging conditions.

Method: RNAi screen was performed in C57BL/6jlnv mice. shRNA pool contained 253 shRNAs and was delivered into the livers of C57BL/6jlnv mice by hydrodynamic tail vein injections (HDTV). Thioacetamide (TAA) treatment was applied triweekly for 8 weeks (0.2 mg TAA per g bodyweight) to induce chronic liver damage. The abundance of each mRNA was compared to the starting pool. Only enriched candidates were selected for further validation.

GRHPR was then validated in vitro and in vivo. For in vitro studies, a stable liver cell line with GRHPR knockdown was generated and knockdown efficiency was tested by Western Blot. Wound healing assay was performed to validate cell migration in two dimensions. For in vivo studies, we took advantage of the fumarylacetoacetate knockout mouse model (FAH-/-). We delivered an shRNA-expression construct (shGRHPR or shCTRL, non-targeting) into the livers of FAH-/- mice by HDTV, which leads to specific stable integration in hepatocytes. We investigated liver repopulation speed. Furthermore, liver regeneration upon Partial Hepatectomy (PH), and chronic liver damage (TAA model) was investigated on fully repopulated livers, where every hepatocyte expresses the shRNA of interest.

Results: We observed significantly faster cell migration in wound healing assay in case of the GRHPR knockdown. Furthermore, we observed faster clonal expansion in vivo in case of the GRHPR knockdown compared to a non-targeting control. Also, the PH model showed faster liver regeneration at 38 hours and 48 hours time-points in the experimental group compared to the control group. Chronic liver damage model (TAA model) showed a significant reduction of fibrosis in case of GRHPR knockdown compared to...
control. In addition, we observed that GRHPR knockdown in hepatocytes in vivo does not lead to tumor formation for 1 year.

**Conclusion:** Hepatocyte-specific knockdown of GRHPR improves liver regeneration and attenuates liver fibrosis. GRHPR knockdown in hepatocytes seems to be safe regarding liver cancer. We did not see any macroscopic impact on the kidney and mice survived for more than one year with hepatocyte-specific GRHPR knockdown. Nevertheless, kidney pathology has to be further evaluated.

**SAT155**
Expression and function of axon guidance genes in the developing portal tract
Lila Gannoun1, Catalina De Schrevel1, Sabine Cordi1, Frédéric Lemaigre1.1, De Duve Institute UCLouvain, LPAD, Woluwe-Saint-Lambert, Belgium
Email: frederic.lemaire@uclouvain.be

**Background and aims:** The liver lobules consist of hepatocyte cords and sinusoids that radiate from the portal area to the central vein. The portal area contains a branch of the portal vein, a hepatic artery, a bile duct lined by cholangiocytes, lymphatics, nerves and a heterogeneous mesenchyme. During development, the portal mesenchyme instructs differentiation of cholangiocytes, and normal development of the bile ducts is required for hepatic arteriogenesis (Lemaigre, 2020). Yet, how portal mesenchyme, bile ducts and hepatic artery interact during development remains poorly understood. To address this issue, we hypothesize that the 3D morphogenesis of bile ducts and hepatic artery is guided by signaling interactions with mesenchymal cells in the portal tract.

**Method:** To investigate this hypothesis, we separately FACS-purified cholangiocytes and adjacent mesenchymal cells at various stages of liver development in mouse embryos, and subjected the cells to RNAseq analysis. We identified several ligand-receptor pairs where the ligand is differentially expressed in the mesenchyme and the receptor in the cholangiocytes, or vice versa, during duct morphogenesis. These included axon guidance genes, namely genes coding for Slit/Robo proteins, Eph receptors/Ephrins, Semaphorins/Plexins and Netrins/netrin receptors.

**Results:** We determined the cell-specific and spatial expression of selected genes, and focused our functional analyses on Slit/Robo and Netrin/Netrin receptor pairs due to their preferential location of expression near forming ducts (Fig. 1). Using a Cre-loxP strategy we inactivated selected genes in the developing mesenchyme or cholangiocytes. Functional assays, 2D and 3D imaging identified axon guidance genes required for normal development of bile ducts and hepatic artery.

**SAT156**
Patients with chronic liver diseases are at risk for diabetes even before development of cirrhosis
Georgia Bale1, Frédéric Clarembeau1, Peter Stärkel1,2, Géraldine Dahlqvist1, Yves Horsmans1,2, Nicolas Lanthier1,1,2.1 Cliniques universitaires Saint-Luc, Service d’Hépato-gastroentérologie, Brussels, Belgium; 2 UCLouvain, Laboratory of Gastroenterology and Hepatology, Brussels, Belgium
Email: nicolas.lanthier@saintluc.uclouvain.be

**Background and aims:** The prevalence of insulin resistance (IR) and type 2 diabetes mellitus (T2DM) is higher in patients with cirrhosis, compared to control patients without liver disease. The exact mechanism for this is unknown but could include liver inflammation. In this study, we investigate whether cirrhosis is the principal mover of IR or if impaired insulin sensitivity is already present in non-cirrhotic patients with chronic liver diseases.

**Method:** Patients were recruited and divided into three groups: control (CTL), active chronic liver disease without cirrhosis (CLD) and cirrhosis (CIR). In patients not taking pharmacological treatment for
T2DM, IR was quantified using the homeostasis model assessment of insulin resistance (HOMA-IR). The proportion of patients treated for T2DM was recorded in each group. Additionally, HOMA-IR levels among different disease etiologies were compared. The study was approved by the local ethics committee.

**Results:** 422 patients were included in our study. 16 were controls, 278 had a CLD and 128 were cirrhotic (CIR). The causes of liver disease were as follows: metabolic-dysfunction associated fatty liver disease (MAFLD, n = 206), alcoholic liver disease (ALD, n = 117), active chronic hepatitis C (HCV, n = 59), other causes (n = 24). IR, represented by a HOMA-IR value exceeding 2.5, is already present in patients with non-cirrhotic CLD (median HOMA-IR 4.0). HOMA-IR levels lie between those seen in CTL (median HOMA-IR 1.3) and CIR patients (median HOMA-IR 5.7), with a statistically significant difference between the three groups (p value < 0.001) (Figure). Median glycemia in the CLD and CIR groups is the same (98 mg/dL and 99 mg/dL respectively) but insulinemia is different (101.5 pmol/L and 132.3 pmol/L respectively) resulting in distinct HOMA-IR values in CLD and CIR patients (p = 0.018). Compared to CLD patients, patients in the CIR group are also characterised by a higher age, higher AST levels and a lower platelet count consistent with portal hypertension. The number of patients with T2DM is the same in the CLD and CIR groups (36.7 and 37.5% respectively). Finally, HOMA-IR levels differ according to disease etiology (p value < 0.001): MAFLD and HCV associated liver disease are associated with higher levels of IR compared to ALD and other causes of CLD.

**Conclusion:** Chronic liver disease is already a predisposing factor to T2DM, regardless of the presence of cirrhosis. Certain disease etiologies are associated with more severe IR. Cirrhosis is a factor which in itself elicits additional increase in insulin levels. The increased insulin levels in this group may be related to increased IR in this situation or to decreased insulin clearance due to portal hypertension.

**SAT157**
Characterization of bioengineered liver constructs using hepatoblast organoids (HBOs) and human liver extracellular matrix (ECM) 3D-platforms
Margarita Papatheodoridi1, Katerina Zacharisi2, Carola Maria Morelli3, Elisabetta Caon1, Luca Frenguelli1, Andrew Hall3, Ludovic Valleri2, Krista Rombouts1, Giuseppe Mazza1, Massimo Pinzani1, 1University College of London, Royal Free Hospital, Institute for Liver and Digestive Health, London, United Kingdom; 2University of Cambridge, Jeffrey Cheah Biomedical Centre, Welcome-MRC Cambridge Stem Cell Institute, Cambridge, United Kingdom; 3University College of London, Royal Free Hospital, Academic department of Histopathology, London, United Kingdom
Email: margarita.gpap@gmail.com

**Background and aims:** Primary fetal hepatoblast organoids (HBOs) derived from human fetal livers have self-renewal ability and can be consecutively passaged while retaining capacity to differentiate to both the hepatic and biliary lineages. We hypothesized that the environment provided by the decellularised healthy human liver extracellular matrix (ECM) will offer HBOs the natural acellular cues for growth and enhanced metabolic functionality and maturation. Thus, the aim of this study was to demonstrate proof of concept for survival and growth of HBOs in a bio-compatible healthy human liver 3D-platform and assess their functionality.

**Method:** Healthy human liver unsuitable for transplantation was decellularized. Acellular liver tissue was lyophilized ≥24 hours and comminuted to a particulate form. ECM powder was then solubilised, neutralized, sterilised, and mixed with Nanocellulose (Cellink) 70:30 in the resultant ECMgel. HBO cells that had been cultured and expanded on Matrigel were seeded on ECMgel (25 K cells/30 μL). Standard HBO Matrigel cultures (25 K cells/20 μL) were used as controls. ECMgel (n = 36) and Matrigel (n = 36) samples for RNA extraction/gene expression, live/dead staining or ELISAs were collected up to day 14.

**Results:** HBOs repopulated the Matrigel and ECM gel and remained viable for 14 days in maintenance medium. HBO clusters on ECMgel had similar size but displayed a distinctively round shape compared to Matrigel where organoids have a characteristic budding morphology. Albumin gene expression in ECMgel was significantly higher compared to Matrigel samples and showed a significant increase from day 7 to 14. aPFP gene expression showed a decreasing trend from day 7 to 14 in both materials. SERPINA and OTC gene expression of HBOs in ECMgel vs Matrigel was also higher on day 14, while CYP3A4 was higher in ECMgel on both timepoints. AURK gene expression in ECMgel was significantly higher than in Matrigel on day 14, suggesting higher proliferation. KRT19 expression was lower on ECMgel on day 7 compared to Matrigel and ranged in very low levels in all samples. Secreted albumin/aPFP ratio significantly increased from day 5 to 14 in ECMgel indicating improved maturation but not in Matrigel samples.

**Conclusion:** Primary HBOs can grow in a healthy human liver ECM 3D-platform in vitro for at least 2 weeks and start differentiating towards a hepatocyte phenotype with the signals provided solely by the healthy human liver ECM. Overall, by combining two novel bioengineering technologies we showed the feasibility of constructing in vitro small implantable liver tissues that could be used for in vivo transplantation in future studies.

**SAT158**
Novel avenue towards liver regeneration and treatment of acute and chronic liver diseases: safety and PK profile from a first-in-human (FIH) clinical trial for HRX-0215 as first in class MKK4 inhibitor
Birgit Jung1, Markus Weissbach1, Michael Lutz2, Roland Selig2, Stefan Lauffer2, Lars Zender3, Michael Feigh4, Matthias Berse2, Jette Penski2, Esther Kosmella2, Wolfgang Albrecht1, 1 HepaRegenIX GmbH, Tuebingen, Germany; 2 University of Tuebingen, Department of Pharmaceutical Chemistry, Tuebingen, Germany; 3 Tuebingen Center for Academic Drug Discovery and Development (TüCAD²), Tuebingen, Germany; 4 University Hospital Tuebingen, Department of Medical Oncology and Pneumology, Tuebingen, Germany; 5 University of Tuebingen, IFIT Cluster of Excellence EXC 2180 “Image Guided and Functionally Instructed Tumor Therapies”, Tuebingen, Germany; 6 Gubra, Harsholm, Denmark; 7 Centre for Clinical Research Services Berlin GmbH, Berlin, Germany.
Email: w.albrecht@heparegenix.com

**Background and aims:** Impaired liver regeneration is a hallmark of acute and chronic liver diseases and to date liver transplantation still represents the only ultimate treatment for acute liver failure and end stage chronic liver diseases. Recent reports validated Mitogen Activated Protein (MAP) Kinase 4 (MKK4) as a novel target and demonstrated a role as a master regulator of liver regeneration (Wuestefeld et al., Cell 2013). Particularly striking efficacy results
accelerated liver regeneration and improved survival were recently obtained in 85% hepatectomy pig model upon treatment with the MMK4 inhibitor HRX-0215 (5 mg/kg i.v.) (Klotz et al., Hepatology, 2021). Here, we now report data from a FIH clinical trial for HRX-0215 related to safety, tolerability and pharmacokinetics.

Method: A FIH clinical trial for HRX-0215 was conducted in 48 healthy volunteers to assess safety, tolerability and pharmacokinetics in a single-center, double-blind, randomized, placebo-controlled manner. In the Single Ascending Dose part volunteers were dosed from 5 to 500 mg, the Multiple Ascending dose part used daily doses between 100 and 500 mg. HRX-0215 was well tolerated at all doses, no relevant changes of any clinical or laboratory parameters were observed. Within a given dosing strength, PK analysis revealed a dose-proportional increase of exposure with very low interindividual variability. Concentration vs. time profiles of HRX-0215 supports a once-daily dose regimen during further clinical development.

Results:

In vivo loss-of-function studies unravel protein tyrosine phosphatase delta as a regulator of liver regeneration during metabolic liver disease

Armando Andres Roca Suarez1,2,3,4, Laurent Mailly1,2, Natascha Roehlen1,1, Alessia Virzi1,1, Nicolas Brignon1,2, Frank Jühling1,1, Christel Thuillain1,2, Sarah Durandi1,2, Marine Oudot1,2, Eugénie Schaeffer1,2, Romain Martin1,2, Laura Heydmann1,1, Charlotte Bach1,2, Romain Parent3,4, Marine Oudot1,2, Eugénie Schaeffer1,2, Romain Martin1,2, Laura Heydmann1,1, Charlotte Bach1,2, Romain Parent3,4, Carole Jamey1, Daniel Brumaru1,5,6, Nissim Dali-Voucer1,7, Emanuele Felli1,8,10, Patrick Pexactx1,2,10, Atish Mukherji1,2, Catherine Schuster1,2, Thomas Baumert1,2,11, Joachim Lupberger1,2.

Background and aims: In the liver we aimed to study the impact of PTPRD expression on liver regeneration. Differentiated hepatocyte-like human LPCs express higher PTPRD compared to undifferentiated stem-cell like LPCs. Silencing of PTPRD or induction of STAT3 signalling in regenerating livers. Differentiated hepatocyte-like human LPCs express higher PTPRD compared to undifferentiated stem-cell like LPCs. Silencing of PTPRD or induction of STAT3 signaling in LPCs promoted de-differentiation and a stem-cell-like phenotype. Hepatocytes of the PTPRD-deficient mice exhibit impaired peroxisomal function, elevated STAT3 signalling and fat accumulation with elevated diabetic markers. Translating these observations to the clinic, obese patients with low hepatic PTPRD expression exhibited increased levels of clinical markers associated with metabolic disease.

Conclusion: Our results suggest a novel role of the STAT3 phosphatase PTPRD as regulator of hepatic regeneration in liver progenitor cells and fat metabolism in hepatocytes during metabolic liver disease.

SAT161

Integrated proteomics and metabolomics analysis reveals canonical and novel regulatory pathways linked to liver regeneration in living donor liver transplant (LDLT) Donors

Gaurav Tripathi1, Adil Bhat1,2, Manisha Yadav1, Babu Mathew1, Nupur Sharma1, Vasundhara Bindal1, Vinyendrana Pamecha2, Jaswinder Maras1, Shiv Kumar Sarin3, 1Institute of liver and biliary science, Molecular and cellular medicine, New Delhi, India; 2University of California, Los Angeles, Pathology and Lab Medicine, Los Angeles, United States; 3Institute of liver and biliary science, hepatobiliary surgery, New Delhi, India; 4Institute of liver and biliary sciences, hepatology, New Delhi, India Email: jassi2param@gmail.com

Background and aims: Living donor liver transplant (LDLT) Donors provides a unique opportunity to unravel novel biological networks associated to regenerative response. To explore more about liver regeneration, plasma proteomic, metabolomic and the clinical characteristic of LDLT Donors were integrated using network-based modelling with the final aim of uncovering novel biological processes associated to regeneration.

Method: Plasma proteomics and metabolomics were performed on (n = 10) healthy donors at baseline (pre-operative stage) and post-operative stages at Day 1, Day 3 and Day 7. Proteome and metabolome data were analysed using weighted protein/metabolite correlation network analysis WIP/M/CNA to identify clusters of highly correlated proteins and metabolites modules differently expressed in donors at different days. Proteins and metabolites modules were cross correlated to form Multi-Modular Correlation Network (MMCN). Pathway analysis of MMCN identified regeneration linked proteins metabolite network which correlated with post-operative flare in liver enzymes (AST and ALT; p < 0.05).

Results: In comparison to baseline donor sample; post-operative day 1 sample showed 232 differentially expressed proteins (DEP; Up-113, Down-119; p < 0.05) and 177 differentially expressed metabolites (DEM; Up-105, Down-72; p < 0.05). At day 1 VEGF, Hedgehog
signaling, Cell cycle, Tryptophan, Sphingolipid metabolism, Primary bile acid metabolism were increased and Calcium ion signaling, Apoptosis, Arachidonic acid metabolism were decreased (p < 0.05). At Day3: 264 DEP (Up-157, Down-107; p < 0.05) and 267 DEM (Up-136, Down-131; p < 0.05) associated to ILGF signaling, IL-12, NFK-B, MAP-K, JAK-STAT signaling, alanine aspartate metabolism and butanoate metabolism were increased whereas Rho-GTPases, interferon-gamma, Cytokine signaling, and fat metabolism were decreased (p < 0.05). Day7 showed 232 DEP (Up-97, Down-135; p < 0.05) and 299 DEM (Up-133, Down-166; p < 0.05) associated to autophagy, RHO-GTPases signalling and primary bile acid biosynthesis increased and Folate metabolism, N-glycan biosynthesis, Arachidonic acid metabolism, JAK-STAT, IL-12 signalling were decreased. Temporal integration performed using W [P/M] CNA identified MMCN clusters (r>0.5). Correlation of these MMCN clusters with the clinical indicator of liver regeneration (liver functions) led to identification of day wise specificity of MMCN cluster e.g. (Day1 specific MMCN-direc correlates with AST and ALT levels (r>0.5, p < 0.05)). Pathway enrichment of MMCN cluster identified canonical pathways involving haemostasis and regeneration but also enriched novel pathways linked to regeneration.

**Conclusion:** Multi-modular network analysis not only validates canonical pathways involving haemostasis and regeneration but also highlight novel pathways linked to liver regeneration.

SAT162

**Regulation of extracellular Nicotinamide adenine dinucleotide in patients with liver fibrosis: new insights into conventional hepatobiary parameters**

Can Kamali1, Alexander Arnold2, Philipp Brunnbrauer1, Kaan Kamali1, Karl Hillebrandt1, Moritz Schmelzle1, Johann Pratschke1, Felix Krenzien1,3, 1Charité-Universitätsmedizin Berlin, Department of Surgery, Berlin, Germany; 2Charité-Universitätsmedizin Berlin, Institute of Pathology, Berlin, Germany; 3Berlin Institute of Health, Berlin, Germany

**Email:** can.kamali@charite.de

**Background and aims:** The extension of liver resections represents a challenging surgical decision, depending on many factors, such as the patient’s pre-existing conditions, oncological history and expected surgical outcome. A key limiting factor is the hepatic regenerative capacity, which we examined focusing on extracellular nicotinamide adenine dinucleotide (eNAD+) and its implications.

**Method:** Patients undergoing liver resection were recruited, tissue and blood samples were collected, and postoperative liver insufficiency was graded based on the 50–50 criteria. We utilized an assay that we established in our workgroup to measure concentrations of eNAD+ in the plasma samples. Finally we explored the impact of an eNAD+ treatment on 3D primary murine hepatocyte spheroids.

**Results:** Patients with low (grade 0 and 1 fibrosis, n = 56) and high (grade 2, 3 and 4 fibrosis, n = 39) grade fibrosis showed akin transaminase levels (AST, ALT) prior to surgery, while postoperative peak transaminase levels were significantly higher in the low grade fibrosis group (ALT: p = 0.0008, AST: p = 0.0041). Meanwhile, eNAD+ levels were significantly higher in the low grade fibrosis group (Grade 0 to 4, p <0.05). Conversely, increased expression of catalyzing
enzymes of NAD+ synthesis in liver tissue, nicotinamide mononucleotide adenylyltransferase (NMNAT) and nicotinamide phosphoribosyltransferase (NAMPT), were associated with higher fibrosis grade (p < 0.0001). Next, we tested whether eNAD+ was regulated following liver resection. Indeed, patients revealed a higher postoperative eNAD+ decrease than controls (p < 0.0001). At the same time, patients who developed postoperative liver insufficiency (n = 8), exhibited significantly smaller eNAD+ decline than patients who did not develop liver insufficiency (n = 69, p = 0.0325). Next, 3D primary murine hepatocyte spheroids treated with eNAD+ for 12 days demonstrated the highest viability (p < 0.0001) when compared to negative controls, TNF alpha treated or combined TNF alpha and eNAD+ treated hepatocytes. The eNADT treatment group was followed in superiority of viability in successive order by eNAD+ and TNF alpha treated, negative control and finally TNF alpha (lowest viability) treated cell cultures, respectively.

**Conclusion:**
We demonstrated that low grade fibrosis was associated with higher eNAD+ levels and compensatory downregulation of catalyzing enzymes of NAD+ synthesis in liver tissue. Interestingly, eNAD+ was decreased following liver resection and linked to postoperative liver insufficiency. In conclusion, we provide evidence that eNAD+ is determined by the degree of fibrosis of the liver and is significantly regulated after liver resection with implications for future therapy targets.

---

**SAT163**

**Hyaluronan in the prenatal extrahepatic bile duct increases in response to injury**
Iris de Jong1, Mallory Hunt2, Kapish Gupta3, Yu Du4, Jessica Llewellyn3, Abhishek Dhand5, Robert Porte1, William Gaynor6, Rebecca Wells3. 1University Medical Center Groningen, Department of Surgery, Section Hepato-pancreato-biliary Surgery and Liver Transplantation, Groningen, Netherlands; 2Hospital of the University of Pennsylvania, Department of Surgery, Division of Cardiovascular Surgery, Philadelphia, United States; 3Perelman School of Medicine at the University of Pennsylvania, Division of Gastroenterology, Department of Medicine, Philadelphia, United States; 4Perelman School of Medicine at the University of Pennsylvania, Division of Gastroenterology, Department of Medicine, Philadelphia, United States; 5University of Pennsylvania, Department of Bioengineering, Philadelphia, United States; 6Children’s Hospital of Philadelphia, Division of Cardiothoracic Surgery, Philadelphia, United States

**Email:** i.e.m.de.jong@umcg.nl

**Background and aims:** Biliary atresia (BA) is a fibrosing obstructive cholangiopathy and represents the primary cause of obstructive jaundice in infants. The etiology is uncertain, but compelling evidence points toward a prenatal cause. Existing literature on BA focuses mainly on the post-natal period and the early response of the fetal extrahepatic bile duct (EHBD) to injury remains unknown. The objective of this study was to identify unique features of the fetal and neonatal EHBD injury response that had pathophysiological relevance.

**Method:** Mouse, rat, sheep, and human EHBD samples were studied at different developmental time points. Models included a fetal sheep model of prenatal 14- to 21-day injury, human BA EHBD remnant and liver samples taken at the time of the Kasai procedure, EHBDs isolated from neonatal rats and mice, and spheroids generated from primary neonatal mouse cholangiocytes that were cultured in either collagen, low or high molecular weight hyaluronan. A bile duct-on-a-chip device was used to study swelling of a collagenous matrix with and without hyaluronan.

**Results:** A thick layer of hyaluronan encircling the lumen was identified as a unique feature of the normal perinatal EHBD. This layer, which was surrounded by collagen, was significantly thicker in ducts subject to prenatal injury, in parallel with extensive PBG hyperplasia and mucus production, and increased serum bilirubin levels. BA remnants and liver samples similarly showed increased hyaluronan centered around ductular structures, compared with age-matched controls. High molecular weight hyaluronan has a positive effect on spheroid growth, supporting the pro-regenerative environment seen in vivo. Increased hyaluronan levels in the matrix lead to a decreased lumen diameter.

**Conclusion:** A dense layer of hyaluronan around the lumen that decreases rapidly after birth is a unique feature of the mammalian fetal and neonatal EHBD. Prenatal injury causes an increased thickness of the hyaluronan layer, with extensive PBG hyperplasia and mucus production, possibly leading to increased bilirubin levels and swelling and obstruction of the EHBD.
SAT164
Embryogenesis of human fetal liver at various stages of gestation: a histomorphometric study
Pooja Bhadoria1, Kavita Modi1, Brijendra Singh1.1 All India Institute of Medical Science Rishikesh, Fetal Autopsy Lab Anatomy, Rishikesh, India Email: pooja.ana@aiimssrishikesh.edu.in

Background and aims: Correlation of general fetal morphometric parameters with liver dimensions and observation of microscopic features like kupffer cells, hematopoietic activity, stellate cells, glycogen granules, central vein, portal triad carries immense importance in estimation of fetal gestation age, detection of anatomical variations, and identification of congenital anomalies. Hence, we planned to assess prenatal development of human liver between 12 and 36 wks of gestation by evaluating both macroscopic and microscopic parameters using conventional autopsy and histotechniques.

Method: In 33 normal fetuses (gestation age 12–36 wks) were classified in 5 groups as 12–16, 17–21, 22–26, 27–31 and 32–36 wks. Liver parameters like weight, volume, transversal and sagittal diameter, vertical length, length and width of lobes of liver and general morphometric parameters of fetus like weight, crown- rump length, crown-heel length, bi-parietal diameter, head, chest and abdominal circumference, hand and foot length, inner and outer inter-canthal distance were measured. Hematoxylin and Eosin (H&E) sections were studied using Quasmo ISI microscope and image-pro express analyzer.

Results: Out of 33 fetuses (males 27; females 6) and maximum (n = 7) each were in group 17–21 and 27–31 wks. Correlation between gestational age and all general fetal and liver parameters except bi-parietal diameter were statistically significant (p < 0.05). Similarly, significant increase amongst all fetal and liver parameters was seen with increasing gestational age (p < 0.05). On H&E sections (Fig 1) during 12–16 wks, glisson’s capsule, portal triad surrounded by fibrous capsule, central vein, kupffer cells and hematopoietic activity was observed. During 17–21 wks, hepatocytes were present in anastomosing radiating cords with organized hepatic sinusoids and parenchyma. During 22–26 wks, hematopoietic activity became focal, with clear demarcation of hepatic and portal lobule. During 27–31 wks, hepatic and portal lobule was clearly demarcated, hematopoietic activity reduced, Kupfer cells and capsule thickness increased with gestation age. During 32–36 wks, deposition of glycogen granules was observed. Hematopoietic activity became scanty and focal. Hepatic parenchyma became more structured with radiating cords of hepatocytes arising from distinct central vein.

Conclusion: Change in general fetal morphometric parameters and liver parameters except bi-parietal diameter are directly proportional with change in gestation age. Knowledge of morphological and histological features and normal limits of dimensions of liver with respect to gestation age is a reliable reference. Findings of studies can be used to better understand histology of normal liver and stages of development during fetal life to pick variations and anomalies.

SAT165
Generation of universal low-immunogenic human cholangiocyte organoids for treatment of cholangiopathies
Sandra Petrus-Reurer1, Adrian Baez-Ortega2, Inigo Martincorena2, Kourosh Saeb-Parsy1.1 University of Cambridge, Surgery, United Kingdom; 2Wellcome Trust Sanger Institute, United Kingdom Email: sp2016@cam.ac.uk

Background and aims: Other than complex surgery or transplantation, there are no current curative therapies for cholangiopathies affecting the intra- or extrahepatic biliary tree such as Primary Sclerosing Cholangitis (PSC). We have previously shown that human bile duct epithelial cells can be cultured as 3D organoids to generate an unlimited supply of phenotypically- and functionally-mature primary cholangiocyte organoids (PCOs) for the treatment of bile duct disorders. We have used PCOs to generate bioengineered bile ducts to replace the extra-hepatic bile duct, and to treat intrahepatic cholangiopathy in human livers. Since the generation of autologous PCOs is likely to remain logistically and economically prohibitive for the foreseeable future, immune rejection of allogeneic PCOs remains a key outstanding barrier to their clinical translation. We thus aimed to develop universal low-immunogenic cholangiocyte organoids for regenerative medicine applications.

Method: After systemic testing of numerous conditions, HLA I and II double KO (DKO) ‘edited PCOs’ (ePCOs) were generated using CRISPR/Cas9 by dissociating PCOs into single cells, electroporation with the guide-Cas9 complex and sorting for the specific double negative cells. Assessment comparing to parental wild-type (WT) cells was carried out by flow cytometry, functional readouts (e.g. Gamma-glutamyl Transferase and Alkaline Phosphatase analyses), and co-culture with CD4+ and CD8+ lymphocytes in vitro, as well as by engraftment under kidney capsule of immunodeficient mice. Mutational load and CRISPR-mediated off-target genetic mutations of parental vs ePCOs were quantified using whole genome sequencing and Nano seq techniques.

Results: The HLA I and II DKO ePCOs generated maintain a mature PCO phenotype demonstrated by flow cytometry and functional analyses. Immune characterization in vitro by co-culture with CD4+ and CD8+ T cells experiments are ongoing to show that ePCOs have a reduced immunogenicity (Interferon-γ secretion, IFN-g) compared to WT cells. Moreover, upon engraftment into the kidney capsule of immunodeficient mice, ePCOs survive and engraft expressing cholangiocyte markers (e.g. KRT-7, KRT-19) in a similar manner as WT cells. Finally, pilot data on off-target analysis and mutation burden of parental vs ePCOs do not show CRISPR-mediated off-target sites or excess mutation in ePCOs. Additional experiments are ongoing to assess the immune response in vivo using humanised mouse models.

Conclusion: Human PCOs lacking HLA I and HLA II can be successfully generated using a CRISPR-Cas9 approach. ePCOs retain the phenotypic characteristics of mature PCOs both in vitro and in vivo upon engraftment in kidney capsule, but show reduced immunogenicity in vitro when co-cultured with CD4+ and CD8+ cells compared to
parental cells. Pilot data show no CRISPR-driven off-target mutational burden in ePCOs.

SAT166
Opposite PAR2 roles in liver regeneration from autoimmune or direct damage. Solving the conflict
Gal Reches1, Netta Rose Blondhem Shraga1, Florent Carrette2, Assaf Malka3, Natalia Saleev3, Yehuda Gubbay3, Ofrir Ertracht4, Linda M Bradley5, Fred Levine6, Ron Piran7, 1Bar Ilan University, The Azrieli Faculty of Medicine, Safed, Israel; 2Sanford Burnham Prebys Medical Discovery Institute, Infectious and Inflammatory Disease Center, La Jolla, California, United States; 3Galilee Medical Center, Eliachar Research Laboratory, Nahariya, Israel; 4Sanford Burnham Prebys Medical Discovery Institute, Sanford Children's Health Research Center, La Jolla, California, United States
Email: galreich@gmail.com

Background and aims: Liver inflammation will cause hepatic damage. In other cases, hepatic injury or poisoning will induce inflammation. Both scenarios will be defined as hepatitis. We chose two distinct hepatitis models that are typical for these two underlying causes. By doing so, we aimed to characterize the role of PAR2 in liver regeneration and inflammation, to reconcile PAR2 confusing role in many damage models, which sometimes aggravates the induced damage and sometimes alleviates it.

Method: WT and PAR2 knock out (PAR2KO) mice were injected with concanavalin A (ConA) for the immune-mediated model, or with carbon tetrachloride (CCl4) for the direct hepatic damage. Solving the conflict

Results: ConA injection caused limited damage in PAR2KO mice livers, while in the WT severe damage followed by leukocytes infiltration was evident. Reciprocal BM replacement of WT and PAR2KO mice and repeated the damage models.

WT BM into WT KO BM into WT WT BM into KO

WT BM into WT KO BM into WT WT BM into KO

WT BM into WT KO BM into WT WT BM into KO

WT BM into WT KO BM into WT WT BM into KO

WT BM into WT KO BM into WT WT BM into KO

WT BM into WT KO BM into WT WT BM into KO

Figure: ConA induced hepatitis is controlled by PAR2 activation in the immune system

Conclusion: We conclude that when PAR2 is predominantly activated in the immune system, it aggravates hepatitis and when it is activated in the damaged tissue it promotes liver regeneration. When we incorporate this finding and revisit the literature reports, we were able to reconcile the conflicts surrounding PAR2 role in injury, recovery, and inflammation.

SAT167
Chronic injury induces plasticity between cholangiocytes and hepatocytes in the human liver
Vasileios Galanakis1,2, Christopher Gribben1, Alexander Calderwood1, Ilias Moutsopoulos3, Katarzyna Kania4, Emmanuel Athanasiadis4, Michael Allison2, Irina Mohorianu1, Ludovic Vallier1, 1Wellcome-MRC Cambridge Stem Cell Institute, Cambridge, United Kingdom; 2Addenbrooke's Hospital, Cambridge, United Kingdom; 3Cancer Research UK Cambridge Institute, Cambridge, United Kingdom; 4Greek Genome Center, Biomedical Research Foundation, Academy Of Athens, Computational Biology Unit (CBU), Athens, Greece
Email: vasilisgalan@gmail.com

Background and aims: Liver disease is on the rise, resulting in a huge health care burden. The liver’s ability to regenerate is unique amongst the human organs. Liver regeneration is believed to mainly be driven by hepatocyte proliferation following acute liver injury or parenchymal volume reduction. However, in the presence of chronic liver injury the regeneration process is more complex and could involve several mechanisms. Indeed, animal studies suggest that 1) liver stem cells activation, 2) de-differentiation/redifferentiation of cholangiocytes/hepatocytes, 3) transdifferentiation between cholangiocytes and hepatocytes, could be part of this regeneration process. Importantly evidences of regenerative process in human chronic liver diseases, such as in non-alcoholic fatty liver disease (NAFLD), are mainly indicative by histological observations and the underlying mechanisms remain to be fully uncovered.

Method: To define these mechanisms in vivo, we decided to combine state of the art single-nuclei transcriptional analysis (snRNAseq) with functional validations using cholangiocyte organoids. snRNAseq was performed on liver biopsies obtained from over 50 patients across the spectrum of NAFLD. Detailed computational analyses allowed the identification of factors and signalling pathways relevant for regenerative processes. The interest of these factors was further validated using a combination of cholangiocyte organoid system and multiome technology (single nuclei RNAseq and ATAC-Seq) on NAFLD derived cholangiocyte organoids, which were differentiated to hepatocyte like cells in vitro.

Results: Progression of liver disease towards decompensated cirrhosis is accompanied by transcriptomic changes, loss of liver architecture and zonation as well as expansion of ductular cells. Liver plasticity is also observed as evident by the presence of hepatocyte-cholangiocyte bi-phenotyping cells in the late stages of the disease. Similar bi-phenotyping cells can be observed by using the in vitro organoid system thereby suggesting that potential reciprocal plasticity.

Conclusion: Transcriptional analyses of patient biopsies and in vitro modelling suggest that cell plasticity is present in chronically diseased liver. Studying this plasticity may be key to understand the underlying regenerative mechanisms of the chronically injured human liver.

SAT168
In vivo characterization and functional effects of the NAD+ transporter, SLC2A5A1
Sarmistha Mukherjee1, Beishan Chen1, Caroline E Perry1, Melissa Lieu1, Joseph A Baur1, 1Perelman School of Medicine, IDOM, Physiology, Philadelphia, United States
Email: baur@pennmedicine.upenn.edu

Background and aims: SLC2A5A1 has recently been identified as the NAD+ transporter in mammalian mitochondria1,2. SLC2A5A1 (also known as MCART1) allows mitochondria to take up intact NAD+ from the cytoplasm and has previously been identified as a hit of unknown function in screens for essential genes. Although its function is now well established in cell lines, there is little information on SLC2A5A1
in intact tissues in vivo. Here, we are interested in characterizing and understanding the physiological role of hepatic SLC25A51.

Method: We used AA V vectors expressing SLC25A51 or shRNA targeting under the control of the TBG promoter to overexpress or knock down Slc25a51, respectively, in the livers of mice.

Results: Preliminary data show that the SLC25A51 knockdown mice have significantly higher fasting blood glucose and glucose intolerance, whereas overexpression has no effect. In contrast, overexpression lowers glucose in a pyruvate tolerance test whereas knockdown has no effect. As expected, mitochondrial NAD+ and NADH content and redox ratio are significantly higher in the over-expressors without a major change in total tissue NAD. Overexpression of Slc25a51 increased mitochondrial respiration and increased the rate of NAD+ uptake into isolated mitochondria. Conversely, loss of Slc25a51 impaired mitochondrial function. In addition, overexpression of Slc25a51 enhanced liver regeneration, significantly improved mitochondrial respiration and increased NAD+ uptake in post regenerative isolated mitochondria.

Conclusion: So far, our data suggest a direct enhancement of mitochondrial redox metabolism as the mechanism mediating improved regeneration in the over-expressors. Thus, the role of SLC25A51 appears to be conserved in vivo and impacts liver regeneration.

Reference:

SAT169
The hepatocellular vitamin D receptor regulates liver regeneration after partial hepatectomy

Hari Elangovan1,2, Jeremy Keane1, Sarinder Chahal1,2, Jennifer Chen1, Christopher Liddle3,4,5, Jenny Gunton1,2,4,5.
Westmead Institute of Medical Research, The Centre for Diabetes, Obesity and Endocrinology Research, Westmead, Australia; 4Westmead Hospital, Westmead, Australia; 5The University of Sydney, Faculty of Medicine and Health, Camperdown, Australia

Background and aims: There is growing evidence to suggest a role for the vitamin D receptor (VDR) endocrine axis in the modulation of hepatic pathophysiology. However, normal hepatocytes express very low levels of the receptor, and the current dogma suggests that VDR mediates its hepatic functions through paracrine effects from non-parenchymal support tissue. We explored whether hepatocellular VDR (hVDR) might regulate liver regeneration following 2/3 partial hepatectomy (PHx) in a murine model. We hypothesized that hVDR null mice would experience worse regenerative outcomes after PHx.

Method: Hepatocyte-specific VDR null mice (hVDR null) and their floxed control (FC) littermates were bred via albumin promoter driven Cre-LoxP recombination. Utilizing KI67 immunohistochemistry and polymerase chain reaction of cell cycle and apoptotic regulators, we comparatively analyzed the livers of hVDR null and their controls at 1-, 2- and 14-days post PHx.

Results: hVDR elimination blunted the hepatic regenerative response following PHx ([K167 positivity at 48 h hours, 57±1 ± 3% vs 40 ± 6.5%, p = 0.002]) in hVDR null mice (see figure). This reduced cell proliferation appeared to persist into the 14-day mark with a diminution in gross regenerated liver weight (1.03 ± 0.02 g versus 1.11 ± 0.039 g, p <0.05) and a reduced liver-to-bodyweight ratio (3.6 ± 0.2% vs. 4.0 ± 0.4%, p <0.005) in hVDR null mice. Diminished cell proliferation was associated with reduced mRNA expression of cell cycle drivers Cyclin D (p <0.05), Cyclin E1 (p <0.01) and Cdk2 (p <0.05). We did not identify major differences in the expression of apoptotic regulators at the various time points examined.

Conclusion: hVDR supports liver regeneration following PHx and loss of function appears to stymie this process predominantly through impairment in cell cycle transition, consistent with VDR’s function as a transcription factor. These results add further insight into the panoply of mechanisms by which VDR signaling supports hepatic homeostasis following tissue injury. VDR receptor ligands may have therapeutic utility in optimizing regenerative outcomes in the clinical setting.

S107
Selective induction of macrophage RNF41 stimulates liver regeneration in hepatotomized healthy and fibrotic mice

Alenez Moreno-Lanceta1,2,3,4, Mireia Medrano-Bosch1,3,4,5, William Fundora2,3,4,5, Meritxell Persamon4,5, Jessica Aspas3, Marina Parra-Robert4, Sheila Baena2,3, Constantino Fondevilla2,3, Elazer Edelman5,6, Wladimiro Jiménez1,2,4, Pedro Melgar-Lesmes1,2,5.
1Department of Biomedicine, School of Medicine, University of Barcelona, Barcelona, Spain; 2Institut d’Investigacions Biomèdiques August Pi-Sunyer (IDIBAPS), Centro de Investigación Biomédica en Red de Enfermedades Hepáticas y Digestivas (CIBERehd), Barcelona, Spain; 3Liver Transplant Unit, Institut Clinic de Malalties Digestives i Metaboliques, Hospital Clinic, University of Barcelona, Barcelona, Spain; 4Biochemistry and Molecular Genetics Service, Hospital Clinic Universitari, Barcelona, Barcelona, Spain; 5Massachusetts Institute of Technology, Institute for Medical Engineering and Science, Massachusetts Institute of Technology, Cambridge, United States; 6Cardiovascular Division, Brigham and Women’s Hospital, Harvard Medical School, Boston, Boston, United States

Email: pmelgar@ub.edu

Background and aims: Hepatocellular and liver transplantation are the standard of care in patients with liver tumours and end-stage liver disease, respectively. Macrophage RNF41 is an E3 ubiquitin-protein ligase that has been associated with muscle regeneration but its role in liver repair is unknown. We aimed to evaluate the regenerative effects of macrophage RNF41 induction in mouse models of partial hepatectomy.

Method: Fibrosis was induced with i.p. injections of CCL1 (1/8 in corn oil) in BALB/c mice (n = 12) twice a week for 9 weeks. Partial hepatectomy was carried out in twelve healthy (70% resection, HP70) or fibrotic (40% resection, HP40) mice. Selective macrophage RNF41 induction was achieved with i.v. (50 μg/Kg) injection of a plasmid encoding RNF41 regulated by a CD11b promoter and linked to dendrimer-graphite nanoparticles (pRNF41-DGNP) every 3 days for 9 days. A scrambled pRNF41 composition served as control (pSCR-DGNP). Liver restoration rate, proliferating cell nuclear antigen (PCNA) immunostaining, hepatic function and the expression of growth factors were evaluated. In vitro assays were designed to assess hepatocyte proliferation under stimulation with conditioned media from RAW 264.7 macrophages treated with pRNF41-DGNP or pSCR-DGNP.
**Results:** Induction of macrophage RNF41 promoted higher hepatic restoration rate in HP70 mice treated with pRNF41-DGNP than in mice receiving pSCR-DGNP (6.3 ± 0.1 g/body weight, BW vs. 7.1 ± 0.1 g/BW, p <0.001). This effect was highlighted by the higher number of hepatic PCNA positive cells (3.2 ± 0.3 vs. 15.6 ± 0.9%, p <0.001).

Induction of RNF41 did not affect hepatic function (AST, 511.8 ± 8.1 vs. 562.6 ± 59.2 U/L, ns; ALT, 1173 ± 7.3 vs. 122.2 ± 13.3 U/L, ns).

In contrast to healthy mice with HP70, the selective macrophage RNF41 induction did improve liver function in fibrotic HP40 mice (ALT, 742.1 ± 83.7 vs. 325.1 ± 72 U/L, p <0.01; ALT, 175.9 ± 15.15 vs. 65.17 ± 10.2 U/L, p <0.001). The pro-regenerative effect of RNF41 that we observed in both animal models of partial hepatectomy was associated with an increased expression of liver insulin-like growth factor 1 (IGF-1) (HP70, 1 ± 0.1 vs. 4 ± 1 fold change (fc), p <0.05; HP40, 1 ± 0.1 vs. 2.8 ± 0.6 fc, p <0.05). Conditioned media from macrophages treated with pRNF41-DGNP stimulated hepatocyte proliferation (0.2 vs. 0.3 arbitrary units, ai, p <0.0001). This proliferative effect was reduced by IGF-1 blockade with a specific antibody (0.3 vs. 0.2 ai, p <0.0001).

**Conclusion:** Macrophage RNF41 plays a major role in hepatic regeneration after partial hepatectomy. This work provides a novel therapeutic target for the stimulation of liver regeneration after liver resection.

**SAT171**

**Generation of functional ductal organoid with biliary network in decellularized liver scaffold**

Jiaxian Chen1, Xi Liang2, Heng Yao3, Shiwen Ma1, Hui Yang3, Deying Chen3, Jing Jiang1, Dongyan Shi1, Jiaojiao Xin1, Lei Geng3, Yun Li3, Jun Li1.

**Background and aims:** Developing functional biliary tree organoids is essential for liver regenerative medicine. This study aims to construct a functional ductal organoid (DO) with biliary tree network in decellularized liver scaffold (DLS) with primary cholangiocytes.

**Method:** Primary cholangiocytes isolated from mouse extrahepatic bile ducts were transplanted into the rat DLS to construct a functional DO. The developed DOs were dynamically characterized by bio-functions and the bio-processes with metabolomics.

**Results:** Functional DOs was generated in DLS retaining native structure and bioactive factors with mouse primary cholangiocytes expressing enriched biomarkers. The results of morphology assessment showed that the biliary tree-like structures gradually formed from day 3 to day 14. The cholangiocytes in the DOs maintained high viability and highly expressed 9 specific biomarkers (eg. cytokine 7, cytokine 19, EpCAM, aquaporin 1, prominin 1). The basal-apical polarity was observed at day 14 with immunostaining of E-cadherin and alpha-tubulin. The rhodamine 123 transport assay and active polarity was observed at day 14 with immunostaining of E-cadherin.

**Conclusion:** A functional DO, with biliary tree network and differential expression of serotonin, was generated with primary cholangiocytes in DLS. It provides the feasibility for disease modeling and drug screening, and paves the way for future clinical therapeutic applications.

**SAT172**

**Molecular basis of hepatic differentiation of human bone marrow mesenchymal stem cell in vivo**

Dongyan Shi1, Xi Liang2, Jing Jiang1, Lunzhi Yuan3, Jiaojiao Xin1, Suwan Sun4, Beibei Guo5, Xingping Zhou1, Jiaxian Chen1, Tong Cheng3, Xin Chen3, Ningshao Xia1, Jun Li1.1 The First Affiliated Hospital, Zhejiang University School of Medicine, State Key Laboratory for Diagnosis and Treatment of Infectious Diseases, Hangzhou, China; 2Taizhou Central Hospital (Taizhou University Hospital), Precision Medicine Center, Taizhou, China; 3Xiamen University, State Key laboratory of Molecular Vaccinology and Molecular Diagnostics, National Institute of Diagnostics and Vaccine Development in Infectious Diseases, School of life Sciences and School of Public Health, Xiamen, China; 4Zhejiang University School of Medicine, Institute of Pharmaceutical Biotechnology and the First Affiliated Hospital Department of Radiation Oncology, Hangzhou, China.

**Methods:** Macrophage RNF41 plays a major role in hepatic regeneration after partial hepatectomy. This work provides a novel therapeutic target for the stimulation of liver regeneration after liver resection.

**Results:** Induction of macrophage RNF41 promoted higher hepatic restoration rate in HP70 mice treated with pRNF41-DGNP than in mice receiving pSCR-DGNP (6.3 ± 0.1 g/body weight, BW vs. 7.1 ± 0.1 g/BW, p <0.001). This effect was highlighted by the higher number of hepatic PCNA positive cells (3.2 ± 0.3 vs. 15.6 ± 0.9%, p <0.001).

Induction of RNF41 did not affect hepatic function (AST, 511.8 ± 8.1 vs. 562.6 ± 59.2 U/L, ns; ALT, 1173 ± 7.3 vs. 122.2 ± 13.3 U/L, ns).

In contrast to healthy mice with HP70, the selective macrophage RNF41 induction did improve liver function in fibrotic HP40 mice (ALT, 742.1 ± 83.7 vs. 325.1 ± 72 U/L, p <0.01; ALT, 175.9 ± 15.15 vs. 65.17 ± 10.2 U/L, p <0.001). The pro-regenerative effect of RNF41 that we observed in both animal models of partial hepatectomy was associated with an increased expression of liver insulin-like growth factor 1 (IGF-1) (HP70, 1 ± 0.1 vs. 4 ± 1 fold change (fc), p <0.05; HP40, 1 ± 0.1 vs. 2.8 ± 0.6 fc, p <0.05). Conditioned media from macrophages treated with pRNF41-DGNP stimulated hepatocyte proliferation (0.2 vs. 0.3 arbitrary units, ai, p <0.0001). This proliferative effect was reduced by IGF-1 blockade with a specific antibody (0.3 vs. 0.2 ai, p <0.0001).

**Conclusion:** Macrophage RNF41 plays a major role in hepatic regeneration after partial hepatectomy. This work provides a novel therapeutic target for the stimulation of liver regeneration after liver resection.

**Background and aims:** Developing functional biliary tree organoids is essential for liver regenerative medicine. This study aims to construct a functional ductal organoid (DO) with biliary tree network in decellularized liver scaffold (DLS) with primary cholangiocytes.

**Method:** Primary cholangiocytes isolated from mouse extrahepatic bile ducts were transplanted into the rat DLS to construct a functional DO. The developed DOs were dynamically characterized by bio-functions and the bio-processes with metabolomics.

**Results:** Functional DOs was generated in DLS retaining native structure and bioactive factors with mouse primary cholangiocytes expressing enriched biomarkers. The results of morphology assessment showed that the biliary tree-like structures gradually formed from day 3 to day 14. The cholangiocytes in the DOs maintained high viability and highly expressed 9 specific biomarkers (eg. cytokine 7, cytokine 19, EpCAM, aquaporin 1, prominin 1). The basal-apical polarity was observed at day 14 with immunostaining of E-cadherin and alpha-tubulin. The rhodamine 123 transport assay and active polarity was observed at day 14 with immunostaining of E-cadherin.

**Conclusion:** A functional DO, with biliary tree network and differential expression of serotonin, was generated with primary cholangiocytes in DLS. It provides the feasibility for disease modeling and drug screening, and paves the way for future clinical therapeutic applications.
expressions of top 10 TFs confirmed their regulation during the hepatic differentiation periods.

**Figure:** Process of hepatic differentiation of hBMSCs in vivo.

**Conclusion:** This study clarified the molecular basis of rapidly hepatocytic differentiation and maturation within 14 days in vivo, which may help for the clinical use of hBMSCs-derived hepatocytes in liver regenerative medicine.

**SAT173**

**Dynamic alterations of metabolites revealed the vascularization progression of bioengineered liver**

Qian Zhou1, Beibei Guo1, Deying Chen1, Heng Yao1, Xi Liang2, Jiaojiao Xin1, Dongyan Shi1, Keke Ren1, Hui Yang1, Jing Jiang1, Jun Li1.

1The First Affiliated Hospital, Zhejiang University School of Medicine, State Key Laboratory for Diagnosis and Treatment of Infectious Diseases, Hangzhou, China; 2Taizhou Central Hospital (Taizhou University Hospital), Precision Medicine Center, Taizhou, China

Email: lijun2009@zju.edu.cn

**Background and aims:** Vascularization is a critical but challenging process in developing functional bioengineered liver with the decellularized liver scaffolds (DLSs), in which, the process is accompanied by cell-specific metabolic alterations. The aims of the study were to explore the global change in the metabolic profile of human umbilical vein endothelial cells (HUVECs) during vascularization, and to identify the specific metabolites for evaluating the biological activities and cellular status, thereby providing a foundation for future research on the construction of a functionally vascularized bioengineered liver.

**Method:** Decellularize the whole rat liver with the most commonly used cocktail of detergents phosphate-buffered saline, 1% (v/v) Triton X-100 and 0.1% (w/v) sodium dodecylsulfate at a flow rate of 20 ml/min. The resulted DLSs were vascularized with HUVECs, and a liquid chromatography mass spectrometry-based metabolomics was performed on culture supernatants collected at 0, 1, 3, 7, 14 and 21 days during the 3 weeks of dynamic perfusion. The 309 positive metabolites were analysed with principal component analysis, partial least squares discriminant analysis and orthogonal partial least-squares discriminant analysis. MetaboAnalyst 5.0 database was then used for metabolic pathway and enrichment analysis.

**Results:**
1. A total of 1698 peak pairs were detected from the culture supernatant, with 309 metabolites being positively identified with high confidence using the dansyl library.
2. Principal component analysis showed a good separation of phase D1 (d0-d1), phase D3D7 (d3-d7), and phase D14D21 (d14-d21).
3. The biological processes of phase D1 were associated with alanine, aspartate and glutamate metabolism, D-Glutamine and D-glutamate metabolism. The metabolites that were activated in phase D3D7 mainly participated in ubiquinone and other terpenoid-quinone biosynthesis, taurine and hypotaurine metabolism, and beta-alanine metabolism. Meanwhile, the metabolites in phase D14D21 were more relevant to histidine metabolism, and ubiquinone and other terpenoid-quinone biosynthesis.
4. Beta-Alanine discriminated any two phases with AUCs of 0.9100, 0.9125 and 0.9850. Its high expression on day 14 predicted the patency of vascularized bioengineered livers.

**Conclusion:** In this study, we revealed the metabolic alterations that occur during DLS vascularization and divided the vascularization process into 3 phases from metabolic perspective, including phase D1 (cell proliferation and migration), phase D3D7 (vascular lumen formation) and phase D14D21 (functional endothelial barrier formation). A high level of beta-Alanine on day 14 predicted the patency of vascularized bioengineered livers, which confirmed our previous finding that 14 days of in vitro dynamic culture is required for DLS vascularization.

---

**SAT177**

**Pharmacologic inhibition of HSD17B13 is hepatoprotective in mouse models of liver injury**

Manuel Roqueta-Rivera1, Mary Chau1, Kelsey Garlick1, Anand Balakrishnan1, Archie C. Reyes1, Jonathan Lloyd1, Sourav Ghora1, Jiang Long1, Joe Panarese1, Bin Wang1, Khahn Hoang1, Tim Grei1, Lijuan Jiang1, Guoqiang Wang1, Yat Sun Or1, Bryan Goodwin1, Enanta Pharmaceuticals, Inc., United States

Email: mroqueta@enanta.com

**Background and aims:** Genome wide association studies identified a loss of function variant (rs72613567:TA) in HSD17B13 which confers protection against chronic liver diseases. As a result, HSD17B13 inhibitors may have clinical utility in non-alcoholic steatohepatitis and other liver diseases. Here we describe the identification and characterization of a novel, potent, and selective HSD17B13 inhibitor with hepatoprotective effects in preclinical models of liver injury.
POSTER PRESENTATIONS

Method: Multiple chemical series of HSD17B13 inhibitors were identified and optimized for potency, selectivity, and pharmacokinetic properties. Mass spectrometry was used to monitor HSD17B13 inhibition (HSD17B13i) of dehydrogenase activity in biochemical and cellular assays. In vivo, HSD17B13i was evaluated in a mouse model of acute (adenoviral) and chronic liver injury (choline deficient, L-amino acid defined, high fat diet; CDAHFD; A16092201). Markers of inflammation, injury and fibrosis were measured in plasma and liver. Transcriptomics and lipidomics suggested a potential hepatoprotective mechanism for HSD17B13i. Primary human hepatocytes (PHH) carrying the TA allele were used in gain of function studies. Results: In biochemical assays, a tool compound (EP-036332) inhibited human HSD17B13 with a half-maximal inhibitory concentration (EC50) of 14 nM. In cell based assays, EP-036332 inhibited human and mouse HSD17B13 with EC50s of 47 and 55 nM, respectively. EP-036332 was selective for HSD17B13 over other HSD17 enzymes (>400 fold). In an adenoviral liver injury model, both HSD17B13i and a short hairpin RNA targeting mouse HSD17B13 were hepatoprotective. In addition to reduced plasma ALT and TNF-alpha, pharmacologic and genetic inhibition of HSD17B13i had overlapping transcriptional effects, including modulation of natural killer cell cytotoxicity (Ifng, Gzmb), chemokines (Cxcr6, Cxcl9, Cxcl2), and necroptosis (Tnf, Fasl). A similar gene expression profile was seen in a CDAHFD liver injury model (3 weeks of diet lead-in and 8 weeks of HSD17B13i). Within one week, HSD17B13i dose-dependently decreased ALT and favoring an anti-inflammatory (Nlrp3, St14p), anti-fibrotic (Tgfb2, Tgf) gene profile. After 8 weeks of HSD17B13i, liver hydroxyproline, plasma ALT and AST were significantly decreased. Lipidomics revealed HSD17B13i effects on lipid droplet composition (sphingolipids) and lower liver sphingosine-1-phosphate and cholesterol. Consistent with in vivo observations, rescue of HSD17B13i in PHH carrying the TA allele resulted in sphingolipid alterations. Conclusion: Hepatoprotection by HSD17B13i in rodent injury models is characterized by a favorable bioactive lipid profile with a decrease in markers of cytotoxic immune cell activation, cell death, and fibrosis. Overall, these data provide preclinical pharmacologic validation of HSD17B13i inhibitors for the treatment of liver disease.

SAT178
Inhibition of NLRP3 inflammasome by GPR40 agonists
Jeongwoo Park1, Moo-Yeol Lee2, Yoon-Seok Seo2, Sung-Chul Lim3, Sung-Chul Lim 3

Background and aims: NOD-like receptor pyrin domain-containing protein 3 (NLRP3) inflammasome is a multi-protein intracellular complex that activates pro-inflammatory cytokines including interleukin (IL)-1p and IL-18. The activation of inflammasome is known to be related with metabolic inflammation such as the progression of non-alcoholic steatohepatitis. Fasiglifam (TAK875), a selective G-protein coupled receptor 40 (GPR40) agonist with high affinity, significantly improves glucose-dependent insulin secretion and weight gain without hypoglycemia. In this study, we evaluated the functional role of GPR40 agonists in the activation of NLRP3 inflammasome in bone marrow-derived macrophages (BMDMs), kupffer cells and an acute hepatitis mouse model. Method: Primary BMDMs and kupffer cells were mainly used for cell-based analyses. For NLRP3 inflammasome activation, BMDMs were primed with LPS (100 ng/ml) for 4 h, and then pretreated with GPR40 agonists for 10 min, followed by incubation with ATP (1 mM) for 30 min. To test in vivo effects of TAK875, 9 weeks old C57BL/6j male mice were orally administrated with vehicle or 10 mg/kg TAK875 once a day for 4 days. The mice were intraperitoneally injected with 2.5 mg/kg LPS and 750 mg/kg D-galactosamine (D-GaIN), and sacrificed after anaesthetization and blood and liver tissues were collected 4 h after LP5-D-GaIN injection. Results: TAK875 and AMG1638 suppressed activation of NLRP3 inflammasome in BMDMs. TAK875 inhibited the activation of inflammasome by blocking apoptosis-associated speck-like protein containing a CARD (ASC) formation which is a component of inflammasome. TAK875 also suppressed NLRP3 inflammasome-induced pyroptosis of BMDM. Moreover, nuclear factor-kB (NF-kB)-dependent priming signal of NLRP3 inflammasome was also partially inhibited by TAK875 and AMG1638. It has been known that intracellular Ca2+ increase by ATP, nigericin (pore forming toxin) or endoplasmic reticulum (ER) stress activates NLRP3 inflammasome. Pre-exposure of BMDM to TAK875 suppressed ATP-induced intracellular Ca2+ increase, which was reversed by thapsigargin, a sarco/endoplasmic reticulum Ca2+-ATPase (SERCA) inhibitor. Oral administration of mice with TAK875 decreased serum IL-1p increase in mice treated with lipopolysaccharide/D-galactosamine in vivo. Conclusion: These findings provide an evidence that free fatty acid-sensing GPR40 plays a key role in NLRP3 inflammasome pathway.

SAT179
Role of Monocyte chemoattractant protein-induced protein-1 in liver fibrosis and activation of hepatic stellate cells
Natalia Pydyn1, Anna Ferenc1, Justyna Kadlucka1, Piotr Major2, Edyta Kus3, Tomasz Hutsch4, Andrzej Budzynski3, Jolanta Jura1, Jerzy Kotlinowski1. 1Faculty of Biochemistry, Biophysics and Biotechnology, Jagiellonian University, Department of General Biochemistry, Krakow, Poland; 22nd Department of General Surgery, Jagiellonian University Medical College, Poland; 3Jagiellonian Centre for Experimental Therapeutics, Jagiellonian University, Poland; 4Laboratory of Centre for Preclinical Research, Medical University of Warsaw, Department of Experimental Physiology and Pathophysiology, Poland; 5Veterinary Diagnostic Laboratory ALAB Bioscience, Poland

Background and aims: Monocyte chemoattractant protein-induced protein-1 (MCPIP1) is a negative regulator of inflammation, acting through cleavage of transcripts coding for proinflammatory cytokines and by inhibition of NF-kB activity. It was shown that Mcpip1 is involved in suppression of inflammatory response in liver macro- phages. Moreover, overexpression of Mcpip1 reduces liver injury in septic mice, by inhibition of inflammatory reaction. On the other hand, Mcpip1 deletion in liver epithelial cells in Mcpip1 fl/flAlbCre mice resembles features of primary biliary cholangitis. In this study, we analyzed Mcpip1 level in human fibrotic livers and hepatic cells isolated from CCL4-treated mice. We also investigated Mcpip1 impact on activation status of LX-2 hepatic stellate cell line. Method: We analyzed liver biopsies isolated from 30 patients with fibrosis stage ranging from 0 to 4. To induce liver fibrosis during in vivo experiments, mice were injected with CCL4 dissolved in corn oil (0, 2 mg/g), 3 times a week for 4 weeks. In vitro experiments were performed on LX-2 cells treated with TGF-β (5 or 10 ng/ml) to induce process of their activation. Results: Analysis of patients' liver biopsies revealed that Mcpip1 level in liver tissue correlates with the development of fibrosis. To elucidate in which type of liver cells Mcpip1 level is induced during fibrotic changes, we analyzed its level in hepatocytes, HSCs and Kupffer cells isolated from fibrotic murine livers. We found that treatment with CCI4 induces Mcpip1 expression in hepatocytes and hepatic stellate cells. On the other hand, Mcpip1 level in Kupffer cells from fibrotic livers is decreased. To evaluate role of Mcpip1 in activation of HSCs, we stimulated LX-2 cell line with TGF-β which resulted in increase of Mcpip1 level. Moreover, overexpression of Mcpip1 in LX-2 cells led to decreased mRNA expression of HSCs activation markers e.g. Acta2, Tgfb, Colla1 and α-SMA protein level. Contrary, Mcpip1 silencing in LX-2 cells resulted in their increased activation status.
Figure: (abstract: SAT178)
SAT180

The genomic landscape of IDH1 mutant intrahepatic cholangiocarcinoma: a multicentre comprehensive analysis

Margherita Rimini1, Teresa Mercade Macarulla2, Valentina Burgio1, Sara Lonardi3, Monica Niger4, Mario Scartozi5, Ilario Raposelli6, Giuseppe Aprile6, Francesca Ratti1, Federica Pedica1, Helena Verduguer2, Floriana Nappo3, Federico Nichetti3, Eleonora Lai7, Martina Valgiusti2, Alessandro Cappetta7, Carles Fabregat2, Matteo Fassan2, Filippo De Braud7, Marco Puzzoni3, Giovanni Luca Frassinetti7, Francesca Simionato7, Francesco De Cobelli1, Luca Aldrighetti1, Lorenzo Fornaro8, Stefano Cascini1, Andrea Casadei Gardini1. 1Università Vita-Salute, IRCCS-San Raffaele Hospital; 2Vall d’Hebron Institute of Oncology; 3Veneto Institute of Oncology IOV-IRCCS; 4Istituto Nazionale Tumori di Milano; 5Università Hospital of Cagliari; 6Istituto Romagnolo per lo Studio dei Tumori “Dino Amadori”-IRSC; 7Azienda ULSS8 Berica, Vicenza; 8University Hospital of Pisa

Email: margherita.riminigmail.com

Background and aims: The results obtained with new anti-IDH1 drugs in advanced cholangiocarcinoma (CCA) IDH1-mutant (IDH1m) patients, even if positive, didn’t show durable responses. A better understanding of the biomolecular pathway, which could be involved in mechanisms of resistance to treatments, is an urgent need.

Method: We performed a retrospective analysis on 247 CCA patients (125 IDH1m and 122 IDH1 wilde type (wt)) tested with the FoundationOne platform. The primary end point was to perform a clustering analysis on IDH1m patients.

Results: From the clustering analysis, three main clusters resulted evident. The cluster 1 presented 84 mutated genes, including PIK3 related genes (AKT, EGFR, ERBB2, FGFR2, FLT3, PDGFR, PIK3CA, PIK3R1, PTEN, RET, SDHB, SDHC, SDHD and TSC1), and RAS related genes (BRAF, CIC, EGFR, ERBB2, FGFR2, FLT3, MAP2K1, MAP3K1, PDGFR, PTNIN1, RET, SDHD, SDHC and SDHD). The cluster 2 presented 89 mutated genes, including chromatin modification related genes (ARID1A, ASXL1, CREBBP, DAXX, DNMT3A, KDM5C, ML2, ML3, NCO1, PBRM1 and SETD2), DNA damage control related genes (ATM, BAP1, BRCA2, ERCC4, FANC, MLH1, MSH2, MSH6 and TP53) and cell cycle related genes (ABL1, CASP8, CDK4, CDKN2A, CDKN2B, CDK2, CEP152, RBL1 and TP53). At the univariate analysis for OS from the first line therapy, the inclusion in the cluster 1, 2 or 3 was highlighted to have a prognostic impact. In particular, the IDH1 m patients included in the cluster 1 showed a poorer OS compared with those included in the cluster 2 and 3 (p = 0.0025).

In the entire sample of patients (IDH1m and IDH1wt) the most frequently mutated or altered genes in our sample were: CDKN2A (27%), ARID1A (20%), CDKN2B (17%), PBRM1 (17%), KRAS/NRAS (16%), BRAF (16%), TP53 (15%), FGFR2 (10%), BRCA2 (9%), PIK3CA (8.5%), ATM (7%), MTAP (7%) and MAP3K1 (7%). IDH1m patients showed more frequently alterations in CDKN2B (p = 0.04), and less frequently alterations in TP53, FGFR2, BRCA2, ATM and MAP3K1 (p = 0.0006, p = 0.0013, p = 0.0015, p = 0.0047, p = 0.0053, respectively). In IDH1 m cohort alterations in KRAS/NRAS and TP53 resulted to negatively impact PFS while alterations in TP53 and PIK3CA negatively impacted on OS from I line; in the IDH1 wt patients, MTAP negatively impact PFS while TP53 negatively impact OS from I line.

Conclusion: We identified three genomic clusters with prognostic value in IDH1 m patients. This new insight in IDH1m CCA could help to identify mechanisms of resistance to treatments, including anti-IDH1.
**Conclusion:** The Perfusion Technology allows simple and reliable isolation of primary hepatocytes. Perfuser and appropriate reagents were optimized for parenchymal rodent liver cells but can be adapted to non-parenchymal cells. The semi-automated workflow enabling liver perfusion in a closed system is easy to apply and helps to implement the 3R principle because only one liver lobule is perfused, while others can be used for further experimentation. Nested processing allows simultaneous handling of up to 8 samples. The protocol does not require inconvenient perfusion in living animals avoiding the need of animal ethics approval.

**Conflicts of interest:** Carsten Poggel, Timo Adams, Ronald Janzen, Alexander Hofmann and Olaf Hardt are employees of Miltenyi Biotec B.V. and Co. KG.

**Abstract withdrawn**

---

**SAT183**

Ptpn1 deletion protects oval vells against lipoapotosis by favoring lipid droplet formation and dynamics

Pilar Valdecantos¹², Ines Barahona¹², Silvia Calero¹², Ruben Grillo-Risco³, Laura Pereira⁴, Carmen Soler⁵, Lara LaIglesia⁶, M. Jesús Moreno-Aliaga⁶, Laura Herrero⁵, Dolors Serra⁶, Carmelo Garcia-Monzon³, Águeda González³, Jesús Balsinde⁴, Francisco García-Garcia³, Angela Martinez Valverde¹², Instituto de Investigaciones Biomédicas Alberto Sols (CSIC-UAM), Metabolism and Cell signalling, MADRID, Spain; ²Centro de Investigación Biomédica en Red de Diabetes y Enfermedades Metabólicas Asociadas (CIBERdem), Spain; ³Principe Felipe Research Center, Bioinformatics and Biostatistics Unit, Valencia, Spain; ⁴Instituto de Biología y Genética Molecular (CSIC), Valladolid, Spain; ⁵Institut de Biomedicina de la Universitat de Barcelona (IBUB), Department of Biochemistry and Physiology, School of Pharmacy and Food Sciences, Universitat de Barcelona, Spain; ⁶Center for Nutrition Research, Department of Nutrition, Food Science and Physiology, Spain; ⁷Unidad de Investigación, Hospital Universitario Santa Cristina, Instituto de Investigación Sanitaria del Hospital Universitario de La Princesa, Spain

Email: pvaldecantos@iib.uam.es

**Background and aims:** Activation of oval cells has been related to hepatocyte injury during chronic liver diseases including non-alcoholic fatty liver disease (NAFLD). However, oval cells plasticity can be affected by the pathological environment. We previously found a protection against hepatocyte cell death by inhibiting protein tyrosine phosphatase 1B (PTP1B). Herein, we investigated the molecular and cellular processes involved in the lipoapotic susceptibility in oval cells expressing or not PTP1B.
Method: Palmitic acid (PA) induced apoptotic cell death in wild-type (Ptpn1+/+) oval cells in parallel to oxidative stress and impaired autophagy. This lipotoxic effect was attenuated in oval cells lacking Ptpn1 that showed up-regulated antioxidant defences, increased unfolded protein response (UPR) signaling, higher endoplasmic reticulum (ER) content and elevated stearoyl CoA desaturase (Scd1) expression and activity.

Results: These effects in Ptpn1−/− oval cells concurred with an active autophagy, higher mitochondrial efficiency and a molecular signature of starvation, favoring lipid droplet (LD) formation and dynamics. Autophagy blockade in Ptpn1−/− oval cells reduced Scd1 expression, mitochondrial fitness and LD formation and restored lipopapoptosis, an effect also recapitulated by Scd1 silencing. Importantly, oval cells with LDs were found in livers from Ptpn1−/− mice with NAFLD.

Conclusion: Ptpn1 deficiency restrained lipoapoptosis in oval cells through a metabolic rewiring towards a “starvation-like” fate, favoring autophagy, mitochondrial fitness and LD formation. Dynamic LD-lysosomal interactions likely ensured lipid recycling and, overall, these adaptations protect against lipotoxicity. The identification of LDs in oval cells from Ptpn1−/− mice with NAFLD opens new therapeutic perspectives to ensure oval cells viability and plasticity under lipotoxic liver damage.

SAT184 Accurate detection of HBV splice variant DNA by using long-read sequencing
Sanne Hulspas1, Cornelis Knetsch1, Michiel Weber1, Anne Hout1, Leen-Jan van Doorn1.1Viroclinics-DDL, Rijswijk, Netherlands
Email: sanne.hulspas@ddl.nl

Background and aims: Hepatitis B virus (HBV) RNA splice variants might play an important role in the HBV life cycle and pathogenesis. Although the biological and clinical significance of splice variants remains to be defined, some studies have linked HBV spliced variants to impaired response to interferon-α therapy. In depth HBV genome analysis may help to understand the role of splice variants in disease pathogenesis. With long-read sequencing, a spliced HBV genome can be covered by a single read, in contrast to short reads where the spliced genome is sequenced by multiple fragmented shorter reads. In a mixed population sample with both splice variant and full genomes, these shorter reads may originate either from the spliced template or the original full length genome template. In this study, we report our findings on the accurate detection of HBV splice variant DNAs in plasma (derived from RNA splice variants generated in the liver) with PacBio long-read sequencing.

Method: Starting material for the analysis were plasma sample from HBV-infected patients. Nucleic acid extraction was performed by using the QIAamp MinElute Virus Spin Kit (QIAGEN). The isolated DNA was amplified for HBV full genome by PCR and nested PCR, using the Expand high-fidelity PCR kit (Roche Molecular Systems). Sequencing libraries were prepared using the SMRTbell Express Template Prep Kit 2.0 (Pacific Biosciences). All sequencing reactions were performed on the PacBio Sequel System with the Sequel Sequencing Kit 3.0 chemistry (Pacific Biosciences). Sequencing was performed by using the circular consensus sequencing (CCS) mode, creating HiFi consensus reads. Splice variant analysis was done by using our in-house bioinformatics pipeline Athena.

Results: A first indication of the presence of splice variants is obtained by visualizing the amplification products on gel and looking at the read length distribution after sequencing. In our samples we observed multiple amplicons with varying lengths. After sequencing the read length distribution showed samples with full length HBV genome CCS reads (~3200 bp) and shorter CCS reads of varying size (~1600, ~2000, ~2400 bp). CCS reads were bioinformatically mapped against an HBV reference sequence using minimap2. Consequently, the read mapping was parsed with separate scripting on individual read level, resulting in read counts for each unique start and end splice junction combination. The read counts for potential splice variants were summarized in a table and the most prevalent ones were compared with literature. All identified dominant splice variants were virtually identical to the splice variants described in literature. In the example shown, we specifically identified DNAs, derived from SP1, 3 and 9 (Figure 1).

Conclusion: HBV splice variant DNA can be accurately detected with PacBio long-read sequencing.
SAT185

The identification and characterization of novel bile acid-derived Farnesoid X Receptor agonists

Dannielle Kydd-Sinclair1, Kimberly A. Watson1, Alex Weymouth-Wilson2, Gemma Packer1; University of Reading, United Kingdom; 2ICE Group, Italy; 3NZP UK Ltd., United Kingdom

Email: dannielle.kydd-sinclair@reading.ac.uk

**Background and aims:** Since its deorphanisation in the early 2000s, the farnesoid X receptor (FXR) has attracted significant attention due to its role in regulating genes involved in bile acid, lipid, glucose metabolism and inflammation. With these metabolic pathways underlying the aetiology of various liver diseases, it is unsurprising that pharmaceutical efforts have targeted FXR also for their treatment. While several FXR agonists, such as obeticholic acid, have been studied in clinical trials, they have been associated with adverse effects arising from the promiscuity of systemic FXR activation and efforts to limit or selectively modulate FXR downstream effects are now being investigated.

**Method:** *In silico* molecular modelling was performed using Surflex-dock (SYBYL, Tripos) to screen a library of bile acid-derived compounds. Lead compounds were tested further in Lantha screen coagulator recruitment assays (Invitrogen) and in biolayer interferometry assays (Sartorius) using biotinylated, recombinit FXR ligand binding domain. Compounds were added to cultured HepG2 and HuH7 cells for 6 hours, or given to C57BL/6 mice by oral gavage daily for 5 days. After respective treatment, cells or left lobe liver tissue were harvested and total RNA extracted for gene expression analysis by RT-qPCR.

**Results:** We have identified 2 novel compounds as potent and selective FXR agonists. Docking results, confirmed by the co-crystal structures of FXR LBD complexed with each compound, demonstrates a unique binding mode for each compound, not observed with classic bile acids, including occupancy of a receptor sub-pocket associated with allosteric activation. Both compounds had higher affinities for FXR and were more efficacious than obeticholic acid by up to ten times, and coactivator recruitment assays identified potential differential recruitment dependent on the compound complexed with FXR. In vitro, both compounds were more effective than obeticholic acid at regulating FXR target genes, whereas in vivo, there appeared to be compound-dependent differential regulation of these genes.

**Conclusion:** Work here suggests that novel compounds 1 and 2 may be able to achieve gene-specific FXR regulation due to their proposed differential coactivator usage and thus may be promising candidates worthy of further research.

SAT186

SARS-CoV-2 induces pericyte procoagulant response associated with portal vein microthrombosis and intrapulmonary vascular dilations in fatal COVID-19

Alberto Lasagni1, Massimiliano Cadamuro2, Claudia Maria Radu3,4, Arianna Calistri1, Matteo Pilari1, Clarissa Valle2, Pietro Angelo Bonaffini1, Adriana Vitiello2, Sandro Sironi5, Maria Grazia Alessio6, Previtali Giulia2, Michela Sgrozetti2, Andrea Gianatti1, Mario Strazzabosco1, Alastair J Strain9, Dannielle Kydd-Sinclair1, Kimberly A. Watson1, Alex Weymouth-Wilson2, Gemma Packer1; University of Reading, United Kingdom; 2ICE Group, Italy; 3NZP UK Ltd., United Kingdom

Email: dannielle.kydd-sinclair@reading.ac.uk

**Background and aims:** Alterations in portal microvasculature have been reported in lethal cases of COVID-19, but underlying mechanisms and clinical significance are unclear. Intrapulmonary vascular dilations (IPVD) arising during chronic or acute liver disease may contribute to hypoxemia. We hypothesise a link between portal vein microthrombosis and persistent hypoxia in patients with severe COVID-19.

**Method:** Patients who died from COVID-19 (n = 93) and underwent autopsy, were retrospectively analysed for presence of portal vein microthrombosis and IPVD at the capillary level (histology), and hypoxemia (arterial blood gas analysis). Peripheral IPVD was also evaluated by chest-computed tomography (CT), when performed. Hepatic vascular lesions were phenotyped by endothelial (vWF) and pericyte (αSMA or PDGFR-β) markers, tissue factor (TF) and viral nucleoprotein (NP). In-vitro, pericytes were infected with SARS-CoV-2 to measure TF expression and effects on endothelial cell (EC) phenotype.

**Results:** In 15 patients (12 males), portal vein microthrombosis was associated with diffuse IPVD (tissue involvement >75%). They were younger (62 vs 75 years), had a longer illness (27 vs 14 days) with persistent hypoxemia (median PaO2/FiO2 = 106) needing more mechanical ventilation (67% vs 24%), than patients with absent or focal lung vascular abnormalities (n = 78, all p < 0.01). In 13 patients, a significant enlargement of the peripheral intrapulmonary artery diameter unrelated to pulmonary embolism was confirmed by chest-CT (mean = 5, 1 mm, 95% CI 4, 6–5, 5). The small intrahepatic portal veins showed more extensive thrombosis (median = 85 vs 67, 5%, p < 0, 05), with a thicker wall of αSMA+ pericytes (median = 10, 63 vs 4, 98%, p < 0, 01), expressing NP around an intact endothelium compared with the other group of deceased COVID-19 patients. The αSMA area correlated with percentage of thrombosed portal veins (r = 0, 284, p < 0, 05), whereas TF, the initiator of the coagulation cascade, was expressed by pericytes rather than by portal EC. Infection of pericytes in-vitro with SARS-CoV-2 induced increased expression of TF in pericytes, whose conditioned medium induced a pro-coagulant phenotype in ECs, characterized by overexpression of vWF.

**Conclusion:** SARS-CoV-2 infects liver pericytes, eliciting a prothrombotic response and the subsequent hemodynamic changes result in IPVD contributing to the long-lasting respiratory failure. Liver involvement may therefore play a crucial role in a subset of fatal COVID-19.

SAT187

Dual ileal/renal-liver bile acid transporter inhibitors with different transporter selectivity in vitro differentially increase faecal and urinary bile acid excretion in organic anion transporting polypeptide 1a/1b knockout mice in vivo

Ellen Strangberg1, Per-Goran Gillberg1, Ivana Uzelac1, Ingemar Starke1, Britta Bonn1, Jan Mattsson1, Peter Akerblad1, Runa Pal2, Ashwani Gaur2, Ramesh Kangarajan2, Shivendra Singh2, Santosh Kulkarni2, Paul Dawson3, Erik Lindström1; 1Albireo Pharma, Inc., Boston, MA, United States; 2Syngene International Ltd., Bangalore, Karnataka, India; 3Division of Pediatric Gastroenterology, Hepatology and Nutrition, Emory University School of Medicine, Atlanta, GA, United States

Email: ellen.strangberg@albireopharma.com

**Background and aims:** Bile acids (BAs) play an important role in hepatobiliary injury. The apical sodium-dependent BA transporter (ASBT) and Na+-taurocholate cotransporting polypeptide (NTCP) play key roles in maintaining BA homeostasis, and their selective inhibition has shown efficacy in liver diseases. ASBT inhibitors block intestinal and renal BA reuptake and increase faecal BA
excretion, whereas NTCP inhibitors block hepatocyte BA uptake, thereby increasing serum BA levels and urinary BA excretion. Dual-acting, ASBT/NTCP inhibitors may increase BA excretion via both elimination routes. We aimed to determine the ability of potent dual ASBT/NTCP inhibitors with different transporter selectivity to increase faecal and urinary BA excretion in organic anion transporting polypeptide 1a/1b (OATP) knockout (KO) mice.

Method: Half-maximal inhibitory concentration (IC_{50}) values for inhibition of mouse ASBT and NTCP were determined using transfected cells. Male OATP KO mice (n = 5/group) were dosed orally once daily for 7 days at 30 mg/kg. Serum BAs were measured 1 h post-dosing on days 1 and 7. Measurements of plasma 7α-hydroxy-4-cholesten-3-one (C4), a marker of hepatic BA synthesis, and faecal and urinary BA excretion were performed on day 7.

Results: Systemically bioavailable ASBT/NTCP inhibitors with selective potency toward mouse NTCP (AS0909, AS0918) or ASBT (AS0826, AS0893) were compared (Table). On days 1 and 7, AS0909/AS0918 and AS0826/AS0893 increased serum BAs 20–50-fold and 2–8-fold, respectively, vs vehicle. On day 7, urine BAs increased 2–3-fold in response to AS0909/AS0918 and less than 2-fold with AS0826/AS0893. In contrast, faecal BA excretion was not significantly elevated with AS0909/AS0918 but increased 4–8-fold with AS0826/AS0893. Serum C4 levels were increased 2–3-fold with AS0826/AS0893 and unaffected with AS0909/AS0918.

Conclusion: ASBT-selective dual inhibitors significantly increased hepatic BA synthesis and faecal excretion while modestly increasing serum BA levels and urinary BA excretion. Conversely, NTCP-selective dual inhibitors caused pronounced elevations in serum and urine BAs without significantly affecting BA synthesis or faecal excretion. Dual ASBT/NTCP inhibitors with different selectivity may have a role as part of precision medicine strategy to reduce the BA burden in forms of hepatobiliary disease.

### Table: Mouse potency values (IC_{50} [nM])

<table>
<thead>
<tr>
<th>Compound</th>
<th>NTCP</th>
<th>ASBT</th>
</tr>
</thead>
<tbody>
<tr>
<td>AS0909</td>
<td>22</td>
<td>183</td>
</tr>
<tr>
<td>AS0918</td>
<td>27</td>
<td>438</td>
</tr>
<tr>
<td>AS0826</td>
<td>30</td>
<td>16</td>
</tr>
<tr>
<td>AS0893</td>
<td>30</td>
<td>2</td>
</tr>
</tbody>
</table>

Conclusion: ASBT-selective dual inhibitors significantly increased hepatic BA synthesis and faecal excretion while modestly increasing serum BA levels and urinary BA excretion. Conversely, NTCP-selective dual inhibitors caused pronounced elevations in serum and urine BAs without significantly affecting BA synthesis or faecal excretion. Dual ASBT/NTCP inhibitors with different selectivity may have a role as part of precision medicine strategy to reduce the BA burden in forms of hepatobiliary disease.

**SAT188**

**Integrated bile lipidome and meta-proteome analysis classifies lipid species and microbial peptides predictive of carcinoma of the gall bladder**

Nupur Sharma¹², Manisha Yadav¹, Gaurav Tripathi¹, Babu Mathew¹, Vasundhara Bindal¹, Hamed Hemati¹, Sadam Hussain Bhat¹, Jaswinder Maras¹, ¹Institute of liver and biliary sciences, Molecular and cellular medicine, New Delhi, India; ²Institute of liver and biliary sciences, Molecular and cellular medicine, New delhi, India

Email: jassi2param@gmail.com

**Background and aims:** Histopathological examination is gold standard for detection of gall-stone (GS) or gall bladder carcinoma (CAGB). Bile concentrated in the gall bladder, is expected to recapitulate metagenomics/molecular changes associated to development of CAGB.

**Method:** Bile samples were screened for lipidomics and metaproteome (microbiome) signatures capable of early detection of cancer. Analysis of training cohort (n = 87) showed that meta-stability of bile was reduced in CAGB patients (p < 0.05).

**Results:** Our results showed that CAGB was associated with the alteration of bile lipidome and microbiome as indicated by multivariate PLS-regression analysis and alpha, beta diversity indexes. Significant reduction of lipid species and increase in bacterial taxa were found associated to development of CAGB with gallstone and without Gallstone (p < 0.05, Log FC>1.5). Multimodular correlation network (MMCN) created using weighted lipid/Meta-proteomic correlation network analysis (W [L/MP] CNA) showed striking associations between lipid modules and meta-proteomic functionality. A significant and direct correlation of Meta-proteomic modules/functionality and inversely correlation of lipid modules and species with the clinical parameters and bile acid profile was observed in CAGB patients (p < 0.05). Significant increase in bacterial taxa; Leptospira, Salmonella enterica, Mycoplasma gallisepticum and their functionality showed direct correlation with lipid classes; Lysophosphatidylinositol, Ceramide 1-phosphates, Lysophosphatidylethanolamine, others and development of CAGB (r²>0.85). Lipid/metaproteomic signature based probability for CAGB was>90% whereas probability for gall-stone was>80% (p < 0.05). Finally, we identified 8 lipid species of diagnostic capability for...
CAGB and cross-validated, using 4 machine learning approaches in two separate test cohorts (n = 38; bile T1 and paired plasma T2) cohort, which jointly showed highest accuracy (98%), sensitivity (98%) and specificity (100%) with random forest model for CAGB detection.

**Conclusion:** Deep and integrated analysis of bile lipidome and metaproteome identify a panel of lipid species/meta-proteome capable of segregating patients predisposed to carcinogenesis of the gall bladder.

**SAT189**

The effects of apurinic/apirimidinic endonuclease 1 as a sensitizer to sorafenib in hepatocellular carcinoma

Mahzeiar Samadaei1, Daniel Senfter2, Sibylle Madlener2, Karolina Uranowska3,4, Christine Häfner1,5, Michael Trauner1, Nataliya Rohr-Udilova1, Matthias Pinter1, 1Medical University of Vienna, Internal Medicine III, Gastroenterology and Hepatology, Vienna, Austria; 2Medical University of Vienna, Department of Pediatrics and Adolescent Medicine, Vienna, Austria; 3University Hospital St. Poelten, Department of Dermatology, St. Poelten, Austria; 4Medical University of Vienna, Institute of Pathophysiology and Allergy Research, Center for Pathophysiology, Infectiology and Immunology, Vienna, Austria; 5Karl Landsteiner Gesellschaft, Karl Landsteiner Institute of Dermatological Research, St. Poelten, Austria

**Background and aims:** Sorafenib, an oral multikinase inhibitor, was the first-generation targeted therapy for patients with hepatocellular carcinoma (HCC). Apurinic/apirimidinic endonuclease 1/redox factor-1 (APE1/Ref-1) is a protein with dual function in redox regulation and DNA repair. APE1/Ref-1 plays a role in development and metastasis but is also linked to inflammation, hypoxia, autophagy and oxidative stress. APE1/Ref-1 also interacts with PI3K/Akt pathway which, in turn, induce sorafenib resistance. Here, we aim to decipher the specific contribution of APE1/Ref-1 repair and redox functions to sorafenib sensitivity of human HCC cells.

**Method:** Impact of APEX1 expression on overall survival of HCC patients was evaluated by an in silico approach using Human Protein Atlas dataset. To check the effects of bifunctional APE1/Ref-1 in five human HCC cell lines (Huh7, SNU398, AKH12, AKH13, 3P), we introduced domain-specific mutations and applied selective inhibitors to block either the repair or the redox function of this protein. These treatments were combined with sorafenib. Neutral red assay was used to evaluate cell viability. To evaluate cytotoxicity, we quantified loss of membrane integrity by LDH release. Clonogenic and invasion ability of HCC cells were measured by colony formation assay and hanging drop method, respectively. Cell cycle distributions as well as characterization of apoptosis were performed by flow cytometry.

**Results:** In silico approach revealed that HCC patients with lower expression of APEX1 reveal longer overall survival: 6.0 ± 0.5 years (low) vs 3.8 ± 0.4 years (high), p = 0.01, n = 365. APEX1 knock down by siRNA per se—as well as in combination with sorafenib—reduced HCC tumor effects of sorafenib on colony formation in HCC cell lines.

**Conclusion:** Redox function of APE1/Ref-1 seems to be a promising target in HCC. APE1/Ref-1 redox inhibitor E3330 enhances the anti-tumor effects of sorafenib in vitro.

**SAT191**

Soluble guanylyl cyclase expression and signaling in different types of liver fibrosis

Ksenia Brusilovskaya1,2,3,4, Philipp Königshofer1,2,3,4, Benedikt Hofer1,2,3,4, Oleksandr Petrenko1,2,3,4,5, Kerstin Zinobe1,2,3,4, Martha Seif1,2,3, Stefan Günther Kaushcke6, Larissa Pflister6, Philipp Schwabl1,2,3,4, Thomas Reiberger1,2,3,4, 1Medical University of Vienna, Division of Gastroenterology and Hepatology, Department of Medicine III, Vienna, Austria; 2Medical University of Vienna, Vienna Hepatic Hemodynamic Lab (HEPEX), Division of Gastroenterology and Hepatology, Department of Medicine III, Vienna, Austria; 3Medical University of Vienna, Christian-Doppler laboratory for portal hypertension and liver fibrosis, Vienna, Austria; 4CeMM Research Center for Molecular Medicine of the Austrian Academy of Sciences, Vienna, Austria; 5Ludwig Boltzmann Institute for Rare and Undiagnosed Diseases (LBI-RUD), Vienna, Austria; 6Boehringer Ingelheim Pharma GmbH and Co.KG, Biberach, Germany

**Background and aims:** In cirrhosis, impaired NO-soluble guanylyl cyclase (sGC)-cyclic guanosine monophosphate (cGMP)-protein kinase G (PKG-1) signaling contributes to increased intrahepatic vascular resistance and fibrogenesis. We investigated the expression of sGC subunits and the downstream signaling pathway in healthy and diseased liver tissue.

**Method:** Liver tissue samples of cholestatic (bile duct ligation, BDL-4 weeks), toxic (8 weeks-CCl4 and 12 weeks-TAA), and metabolic (12 weeks-choline-deficient high fat diet, CDHFD) rat fibrosis models were used. Healthy control tissues were derived from sham-operated (SO), vehicle-injected (OO/NaCl), and normal-diet-fed (CHOW) animals. Gene and protein expression of sGC subunits and key downstream molecules were analyzed by RT-PCR and Western blot.

**Results:** All models presented severe fibrosis assessed by collagen proportionate area (CPA): BDL: 13.4%; TAA: 8.0%; CDHFD: 8.5%. The expression of sGC subunits alpha1 and beta1 (sGCα1/b1) increased in all fibrosis models, with the most pronounced upregulation in CDHFD (sGCα1: 1.7 ± 0.3-fold, p < 0.01; sGCh1: 2.0 ± 0.3-fold, p < 0.01). Accordingly, 6.9-fold sGCα1 (p = 0.04) and 1.7-fold sGCh1 (p = 0.04)-higher protein levels were detected in CDHFD group. The expression of PKG-1 was significantly increased in TAA and CDHFD models both on gene (TAA: 1.9 ± 0.2-fold, p < 0.01; CDHFD: 1.7 ± 0.2-fold, p < 0.01) and protein (TAA: 4.1-fold, p = 0.04; CDHFD: 3.6-fold, p = 0.04) levels. Moreover, upregulation of the cGMP degrading phosphodiesterase enzymes PDE5 (BDL: 5.1 ± 0.4-fold, p < 0.01; TAA: 1.9 ± 0.2-fold, p < 0.01; TAA: 5.1 ± 0.3-fold, p < 0.01; CDHFD: 5.3 ± 0.9-fold, p < 0.01), and PDE9 (BDL: 2.1 ± 0.1-fold, p = 0.05; TAA: 1.2 ± 0.2-fold, p = 0.79; CDHFD: 2.9 ± 0.3-fold, p = 0.01; CDHFD: 2.7 ± 0.5-fold, p = 0.03) was observed in cirrhosis. PDE5 protein levels also increased in CCl4 (4.7-fold, p = 0.04), TAA (7.8-fold, p = 0.04), and CDHFD (7.2-fold, p = 0.04) models-but remained similar in BDL (p = 0.23).
Conclusion: Expression of sGC alpha1/beta1 subunits increases in liver cirrhosis in different rat models, paralleled by upregulated cGMP-dependent PKG-1 in toxic and CDHFD cirrhosis. In contrast, overexpression of PDE5/9 across all models may indicate insufficient cGMP-related signaling effects in cirrhosis. The functionality of sGC-cGMP signaling in cirrhosis and the impact of pharmacologic activation requires further mechanistic studies.

SAT192
Impact of maternal obesity on liver disease in the offspring: a comprehensive transcriptomic analysis and validation of results
Beat Moeckli1,2, Vaihere Delaune1,2, Julien Prados3, Matthieu Tihy4, Andrea Peloso5, Graziano Oldani1,2, Thomas Delmi1, Nicolas Goossens6, Laura Rubbia-Brandt4, Stéphanie Lacotte1, Christian Toso1,2. 
1University of Geneva, Faculty of medicine, Geneva, Switzerland; 2Hôpitaux Universitaires de Genève (HUG), Chirurgie, Genève, Switzerland; 3University of Geneva, Bioinformatics Support Platform, Geneva, Switzerland; 4Hôpitaux Universitaires de Genève (HUG), Department of clinical pathology, Genève, Switzerland; 5Hôpitaux Universitaires de Genève (HUG), Hepatology and gastroenterology, Genève, Switzerland Email: beat.moeckli@gmail.com

Background and aims: The global obesity epidemic is a major public health concern and particularly affects women of reproductive age. Offspring of obese mothers suffer from an increased risk of liver disease but the molecular mechanisms involved remain unknown. With this study, we uncover new pathways and genes involved in the transmission of liver disease and validate previously identified targets.

Method: We performed an integrative genomic analysis of datasets that investigated the impact of maternal obesity on the hepatic gene expression profile of the offspring in mice. Furthermore, we developed our own murine model of maternal obesity and validated the top deregulated genes by quantitative real-time polymerase chain reaction (qPCR) in our model. Our data is available for interactive exploration on our companion webpage: https://genebrowser.unige.ch/maternalobesity.

Results: We identified five publicly available datasets pertinent to our research question. Pathways involved in metabolism, the innate immune system, the clotting cascade and the cell cycle were consistently deregulated in offspring of obese dams. Concerning genes potentially involved in the development of liver disease, we found Egfr, Vegfb, Wnt2 and Pparg deregulated in multiple independent datasets (Figure). In our own model, we observed higher tendency towards the development of non-alcoholic liver disease (60 vs 20%) and higher levels of alanine amino transferase (41.0 vs 12.5 IU/l; p = 0.008) in female offspring of obese dams. Male offspring presented higher levels of liver fibrosis (2.8 vs. 0.8% relative surface area, p = 0.045). Of the top deregulated genes deregulated in the integrative genomic analysis, we validated the deregulation of Fgf21, Pparg and Ppard by qPCR in our own model of maternal obesity.

Conclusion: Maternal obesity represents a looming threat for the liver health of future generations. Our comprehensive transcriptomic analysis discovered new pathways and molecular targets. This will help to better understand the mechanisms of the development of liver disease in the offspring of obese mothers.

SAT193
Liver directed in utero AAV gene therapy for maple syrup urine disease in a neonatal lethal murine model
Kate Mullany1,2, Ian Alexander1,3, Susan Siew1. 1Children’s Medical Research Institute, Gene Therapy Research Unit, Westmead, Australia; 2The Children’s Hospital at Westmead, Gastroenterology, Westmead, Australia; 3The Children’s Hospital at Westmead, Westmead, Australia Email: kmullany@cmri.org.au

Background and aims: MSUD is a genetic metabolic autosomal recessive condition caused by a deficiency of the mitochondrial enzyme branched chain keto-acid dehydrogenase. Severely affected individuals present in the neonatal period with elevated branched chain amino acid (BCAA) levels leading to encephalopathy and muscle weakness which if untreated progresses to permanent brain injury and/or death. Dietary protein restriction or liver transplantation are current mainstays of therapy, however neither are curative. Liver directed adeno-associated viral (AAV) gene therapy represents a novel potential treatment for MSUD. Our aim is to determine if liver directed AAV gene therapy can rescue the phenotype of a neonatal lethal murine model of MSUD (DBT−/−).

Method: A murine hepatotrophic gene addition vector rAAV8.hDBT (5 × 10^11 vector genome copies per mouse) was administered on D0 of life in 9 homozgyous knockout pups. Outcome measures included

Conclusion: Expression of sGC alpha1/beta1 subunits increases in liver cirrhosis in different rat models, paralleled by upregulated cGMP-dependent PKG-1 in toxic and CDHFD cirrhosis. In contrast, overexpression of PDE5/9 across all models may indicate insufficient cGMP-related signaling effects in cirrhosis. The functionality of sGC-cGMP signaling in cirrhosis and the impact of pharmacologic activation requires further mechanistic studies.
pup growth, serum BCAA levels through mass spectrometry. DBT protein expression via immunoblotting and vector genome copy via digital droplet PCR. Immunohistochemistry was used to assess presence of DBT protein in liver sections. As neonatal vector administration improved survival but did not rescue all pups, the timing of vector delivery was suspected to be critical, and the same vector was administered in utero to pups on E15. Equivalent studies are being initiated to compare outcomes following in utero treatment. **Results:** Gene addition with a codon optimised DBT human transgene significantly improved survival, growth and BCAA levels ($p < 0.05$) compared to untreated knockout pups when administered on D0 of life. DBT protein in vector treated homozygous knock out pups was expressed at 2.5 times higher than untreated wild type pups. Immunohistochemistry demonstrated presence of DBT protein in vector treated pups (Figure 1). We will also present the results from the in utero vector administration.

**Conclusion:** Neonatal murine liver transduction with a human DBT transgene significantly improves the disease phenotype in a murine neonatal lethal model of MSUD. Liver directed AA V mediated gene therapy represents a potential novel treatment for MSUD.

**SAT195**

**Dissecting A-to-I RNA editome of liver macrophages in non-alcoholic fatty liver disease**

**Achilleas Fardelias,** Myriam Aouadi, Sebastian Nock, Ping Chen, Cecilia Morgantini. **Karolinska Institute, Department of Medicine, Center for Infectious Medicine, Huddinge, Sweden;** **Karolinska Institute, Department of Medicine, Cardu Metabolic Unit (CMU), Huddinge, Sweden**

Email: myriam.aouadi@ki.se

**Background and aims:** RNA editing is an epitranscriptomic process referring to modifications in the chemical structure of RNA molecules. Adenosine-to-Inosine (A-to-I) editing is the most common RNA editing event catalysed by a family of enzymes called ADARs (adenosine deaminases acting on RNA). While aberrant RNA editing profiles have been associated with many diseases including neurological disorders and cancers, it has not been previously studied in the setting of non-alcoholic fatty liver disease (NAFLD).

**Method:** We used RNAseq datasets (GSE135251, GSE126848), which liver biopsies from lean, “healthy” obese and NAFLD patients. Global levels of RNA editing activity were estimated in this cohort using the Alu editing index (AEI), a robust signal with a minimal false-positive rate. Human monocyte-derived macrophages were treated with phRodo-labelled Escherichia. coli bioparticles for 2 hours and analyzed via flow cytometry after a 48hour ADAR1-knockdown.

**Results:** We have recently discovered that IGFBP7 transcripts in liver macrophage (LMs) of insulin resistant patients underwent A-to-I RNA editing at a high frequency leading to the production of a variant isoform with a higher capacity to regulate insulin signalling. Consistently, preliminary results from RNAseq analysis of 266 liver biopsy samples from two independent studies indicate that the RNA editing rate of NAFLD patients is considerably higher compared to lean and “healthy” obese. However, analyses of the overall RNA editome of LMs revealed that the RNA editing rate is unexpectedly decreased in obesity. To investigate the functional relevance of RNA editing in human macrophages, ADAR1, the key RNA editing enzyme, was silenced and an improved phagocytic capacity of particles was found.

**SAT194**

**Patient-derived hepatocellular carcinoma organoids as predictors of Treatment Response**

Jun Yong Park, Kyung Joo Cho, Hye Won Lee, Hye Jung Park, Sang Hoon Ahn, Hee Seung Lee, Chul Hoon Kim. **Yonsei University College of Medicine, Division of Gastroenterology, Seoul, Korea, Rep. of South;** **Yonsei University, Brain Korea 21 PLUS Project for Medical Science, Seoul, Korea, Rep. of South;** **Yonsei University, Division of Gastroenterology, Department of Internal Medicine, Seoul, Korea, Rep. of South;** **Yonsei University College of Medicine, Division of Gastroenterology, Department of Internal Medicine, Seoul, Korea, Rep. of South;** **Severance Hospital, Yonsei Liver Center, Seoul, Korea, Rep. of South;** **Yonsei University College of Medicine, Department of Pharmacology, Seoul, Korea, Rep. of South**

Email: drpjpy@yuhs.ac

**Background and aims:** Organoid models using patient-derived cancer tissues has allowed a better understanding of human cancer as well as development of precision medicine. For advanced HCC treatment, the proper models and the pivotal pathways of cancer stem cells (CSCs) are needed. In this study, we evaluate the sensitivity to anti-cancer drugs using HCC organoids (HCOs) and analyze the relationship between drug resistance group and CSCs-related signal for improving the drug response.

**Method:** Patient-derived tumor tissue was digested at 37 °C and mixed with Matrigel. After polymerization of Matrigel, medium was added and changed twice a week. To evaluate whether HCO exhibit different sensitivity to drugs, we tested its sensitivity and analyzed the sensitivity in HCO lines with the difference in gene expression.

**Results:** We successfully established 10 HCOs obtained from 16 HCC patients among. HCOs exhibited heterogeneous morphological features, forming compact structures with or without thick-layered cyst-like structures. HCOs shared somatic mutations and showed high concordance of somatic mutation between primary tumor and organoids. Through the different gross morphology of HCO showed the differential gene expression. Notably, Wnt pathway was significantly enriched in the compact spherical shape of HCO compared to combined shape ($p < 0.05$). We compared the growth of compact shape of HCOs with and without Wnt pathway-related components, however, they failed to form organoids without Wnt. Also, compact shape of HCOs was resistant to treatment with Lenvatinib in vitro.

**Conclusion:** Our results demonstrated that HCOs with specific structural features provide platform to identify the relationship between drug response and CSC-related signal in HCC.
S756 Journal of Hepatology

POSTER PRESENTATIONS

epitranscriptomic landscape of NAFLD and its role in the disease development may lay the foundation for the development of novel therapeutic strategies and new disease biomarkers.

SAT196 Restoring bone marrow hematopoietic stem cells (BM-HSC) reserve augments regression of fibrosis and regeneration in animal model of cirrhosis

Nidhi Nautiyal1,2, Deepanshu Maheshwari1, Pranshu E Rao3, Sujata Mohanty1, Anupama Parasar1, Chhagan Bhari1, Subhrajiit Biswas2, Rakhi Maivall3, Anupam Kumar1, Shiv Kumar Sarin1, 2, Institute of Liver and Biliary Sciences, Molecular and Cellular Medicine, New Delhi, India; 3Amity University Noida, Amity Institute of Molecular Medicine and Stem Cell Research, Noida, India; All India Institute of Medical Sciences, Center of Excellence for Stem Cell Research, New Delhi, India; 4Institute of Liver and Biliary Sciences, Department of Pathology, New Delhi, India; 5Institute of Liver and Biliary Sciences, Department of Hepatology, New Delhi, India

Email: shivsarin@gmail.com

Background and aims: Bone marrow (BM) is a reservoir for hematological and immune cells, plays a central role in resolution of damage and tissue repair. Exhaustion of BM-HSC reserve has been shown to be associated with increased susceptibility to infection, hematological dysfunction and early graft dysfunction post liver transplant in cirrhosis. Whether the loss of BM stem cell (BMSC) reserve in cirrhosis is the cause or a consequence of liver failure is not known. We aim to understand the relation between BM and liver regeneration, and potential therapeutic effect of restoring BM-HSC reserve in the management of chronic liver injury.

Method: C57BL/6 (J) mice were used to develop chronic liver injury through intraperitoneal administration of carbon tetrachloride for 15 weeks (0.1-0.5 ml/kg). Animals were culled at different time points (N = 10 each group; week 3/6/10/15) to study the changes in liver injury, regeneration, BM-HSC and mesenchymal stem cell (MSC) reserve. To restore the BMSC reserve, approximately 4 million healthy whole BM cells (hBM), isolated from GFP-C57BL/6 mice were infused intraperitoneally (IF) after 12 weeks of chronic liver injury. Control animals were infused with saline. Animals post BM infusion were sacrificed (N = 10 each group; 24 hours/day 11/day 21) to study the changes in liver injury, regeneration and BMSC reserve.

Results: Histological analysis of liver tissue (figure 1A) showed progressive increase in fibrosis and hepatocyte proliferation till week 10 with development of portal fibrosis at week 3, bridging fibrosis at week 6 and nodular fibrosis (cirrhosis) at week 10. From 10–15 weeks, while the fibrosis was comparable, there was a significant increase (p < 0.0001) in TUNEL+ hepatocyte and loss of hepatocyte regeneration with hepatic decompensation (ascites (SAAG 1.4 (1.1–1.7) g/dL), jaundice and rise in ammonia (p < 0.001)), suggesting increased hepatocyte injury without compensatory regeneration in development of decompensated cirrhosis. Interestingly, BM studies showed that during the course of chronic liver injury loss of BM MSC occurs between week 3 to 6 followed by loss of LT-HSC between week 6 to 10 followed by regeneration failure (figure 1B). Infusion of hBM in cirrhosis animals (figure 1C) showed that while donor cells disappear by day 21, there was significant increase in total BM LT-HSC reserve by day 11 (figure 1D). hBM recipients showed significant reduction in fibrosis and increased hepatocyte proliferation (figure 1E).

Conclusion: Loss of BM-HSC reserve precedes hepatic regeneration failure indicating seminal role of BM during chronic hepatic injury. IF infusion of hBM induces repopulation of native LT-HSC, accelerates fibrosis resolution and potentiates hepatocyte regeneration in cirrhosis. Hence, restoring BM-HSC reserve can serve as a novel therapeutic approach to augment resolution of fibrosis and native liver regeneration in cirrhosis.

SAT197 Human resident liver macrophages protect against metabolic stress in obesity

Emelie Barreby1, Benedikt Strunz2, Valerio Azzimato1, Joanne X. Shen3, Léa Naudet1, Isabella Sönnerborg1,1, André Sulen1,4, Sebastian Nock1, Laura Levi1, Cecilia Morgantini1,5, Achilleas Fardellas1, Helene Johansson3, Greg Nowak3, Per Stal6, Ewa Ellis1, Erik Naslund2, Volker Lauschke2,8, Niklas Björkström1, Ping Chen1, Myriam Aouadi1,1, Karolinska Institutet, Center for Infectious Medicine, Huddinge, Sweden; Karolinska Institutet, Section of Pharmacogenetics, Stockholm, Sweden; University of Bergen, KG Jebsen Center for Autoimmune Diseases, Norway; Karolinska Institutet, Cardio metabolic unit, Sweden; Karolinska Institutet, Gastroenterology and Rheumatology Unit, Huddinge, Sweden; University of Bergen, KG Jebsen Center for Autoimmune Diseases, Norway; Karolinska Institutet, Cardio metabolic unit, Sweden; Karolinska Institutet, Gastroenterology and Rheumatology Unit, Huddinge, Sweden; Danderyd Hospital, Karolinska Institutet, Division of Surgery, Department of Clinical Sciences, Stockholm, Sweden; Dr Margaret Fisher-Bosh Institute of Clinical Pharmacology, Germany

Email: myriam.aouadi@ki.se

Background and aims: Non-alcoholic fatty liver disease has become the most common chronic liver disease, being associated with an increasing prevalence of obesity and type 2 diabetes. Macrophages contribute to the development of these metabolic disorders in

Figure 1: Restoring bone marrow hematopoietic stem cells (BM-HSC) reserve augments regression of fibrosis and regeneration in animal model of cirrhosis. (A) Representative micrograph showing Sirius red staining (bottom) and H&E staining of PCNA hepatocyte (top) in liver sections at given time points. (B) Graph showing changes in number of BM-HSC colony forming unit (CFU-L) (left) and percentage of long-term hematopoietic stem cells (LT-HSC) (right) with progression of chronic liver injury. (C) Study layout of without infusion in control animals (C) and肝素 infusions in cirrhosis animals. (D) Representative micrograph (left) and bar graph (right) change in liver fibrosis and hepatocyte regeneration in cirrhosis animals with and without BM infusion

Conclusion: Loss of BM-HSC reserve precedes hepatic regeneration failure indicating seminal role of BM during chronic hepatic injury. IF infusion of hBM induces repopulation of native LT-HSC, accelerates fibrosis resolution and potentiates hepatocyte regeneration in cirrhosis. Hence, restoring BM-HSC reserve can serve as a novel therapeutic approach to augment resolution of fibrosis and native liver regeneration in cirrhosis.
Conclusion: We discovered a liver resident macrophage population with a protective role that could reduce oxidative stress induced by lipid accumulation. Targeting specific LM populations could thus represent a promising therapeutic strategy for both liver and metabolic disease.
SAT199
Unravelling the circadian transcriptome and epigenome of the human liver
Atish Mukherji1, Frank Jühling1, Laurent Mailly1, Carla Eller1, Katharina Hetsch2, Cloé Gadenne1, Clara Ponsolle1, Alexandre Haller2, Philippe Baltzinger2,3, Hiroshi Aikata4, Michel Imamura4, Catherine Schuster1, Xiaodong Zhuang5, Joachim Lupberger1, Thomas Baumert6,7, Université de Strasbourg, Inserm, Institut de Recherche sur les Maladies Vérales et Hépatiques, UMR_S1110, Strasbourg, France; 2Institut de génétique et de biologie moléculaire et cellulaire, Illkirch, France; 3CHU de Strasbourg, Internal Medicine, Endocrinology and Nutrition, Strasbourg, France; 4Institute of Biomedical and Health Sciences, Hiroshima University, Department of Gastroenterology and Metabolism, Applied Life Sciences, Hiroshima, Japan; 5Humanitas clinical and research center IRCCS, Hepatobiliary Institute. BECs and iCCA surnantants were analysed by using mass spectrometry. We employed Seurat and Ionnet to analyze and identify gene regulatory networks. Crucially, many of these rhythmically expressed genes and pathways are well-known to get deregulated in chronic liver disease and HCC. These rhythmic genes show a strong correlation between enhancer activation and gene expression.

Conclusion: We have unraveled the identity of circadian genes and gene regulatory networks in human liver cells. This work represents a milestone in understanding the physiology of human liver. Moreover, our findings provide novel opportunities for understanding the molecular relationship between CC in the normal liver but also serve as a reference to understand the perturbation and role of circadian genes in chronic human liver disease and HCC.

SAT200
Single-cell dynamics of interacting mesenchymal and leukocyte populations in advanced NASH
Sofie Bendixen1, Peter R. Sørensen1, Mike Terkelsø1, Daniel Hansen1, Frederik Adam Bjerre1, Kamilla Hejn1, Emma A.H. Scott1, Atish Mukherji1, Philip Hallenborg1, Blagoy Blagoev1, Kim Ravnskjaer1, Frederik Adam Bjerre1, Kamilla Hejn1, Emma A.H. Scott1, Anne-Britt Marcher1, Janusa Vijayathurai1, Sönke Dettlesfen1, Ravnsvkaer1, Philip Hallenborg1, Blagoy Blagoev1, University of Southern Denmark, Odense, Denmark; Odense University Hospital, Odense, Denmark
Email: ravnskjaer@bmb.sdu.dk

Background and aims: Non-alcoholic steatohepatitis (NASH) is an obesity-related disorder caused by extensive fat accumulation in the liver parenchyma. Our findings provide novel opportunities for understanding the hepatic mesenchymal and infiltrating immune cells.

Method: To better understand the liver plasticity during NASH development, we performed single-cell RNA sequencing on livers from mice fed a Western diet for 52 weeks and age-matched healthy controls. A single-reference dataset was established through Seurat 3-based integration.

Results: Here, we confidently annotated 11 cell populations including hepatocytes, hepatic stellate cells (HSC), mononuclear phagocytes (MP), and B- and T-cells. The MP-composition showed an expansion of the Kupffer cell-like cell population in NASH and infiltration of monocytes leading to an increase in macrophage heterogeneity. This was confirmed by analysis of RNA velocities predicting profoundly altered MP plasticity in NASH. Also activated HSCs were present to a higher degree in NASH livers exhibiting enhanced extracellular matrix production. Using SCENIC, we identified subpopulation-specific transcriptional networks likely to underlie HSC activation. Combining gene expression levels from individual subpopulations of HSCs and MPs using nicheNet predicted ligand-receptor interactions reflecting possible cross-talk in healthy and diseased livers. Ongoing spatial and loss of function studies will map relative cell locations and function to validate these interactions.

Conclusion: Our results expose dynamical cellular interactions at a hitherto unprecedented resolution, and contribute to the elucidation of hepatic tissue plasticity during NASH development.
spectrometry-based untargeted and targeted metabolomic approaches. RNA-seq and Reverse transcriptase-polymerase chain reaction (RT-PCR) analyses were performed to identify altered metabolic pathways in iCCA cells. Moreover, iCCA cell proliferation was assessed at different time points post glutaminase-1 (GLS-1) inhibition (CB-839) and immunofluorescence staining for mitochondria was performed.

**Results:** iCCA cells were characterized by enhanced mitochondrial activity compared to BECs, resulting in an increased glutamine and glucose uptake. RNA-seq analysis revealed several altered metabolic pathways in iCCA cells attributed to the Warburg effect and glutamine metabolism. To explore the importance of glutamine metabolism, we further evaluated the mRNA expression of ASCT1 and ASCT2, two glutamine transporters, and GLS1, resulted to be significantly upregulated in iCCA cells. CB-839 treatment revealed that GLS1-high iCCA cells were more susceptible to GLS-1 inhibition compared to GLS1-low cells, along with changing in mitochondrial morphology.

**Conclusion:** Experimental data suggest an impairment of mitochondrial activity of iCCA cells. Resensitizing iCCA cells to metabolic treatments could make them more susceptible to cytotoxic drugs, opening new possibility to improve the outcomes of the iCCA patients.

**SAT202**
Microfluidic 3-dimensional bioprinting and 2-dimensional micropatterns as tools to bioengineer biliary ducts
Lorena Loarca1, Cyrille El Khassi1, Afshan Iqbal2, Latifa Bouzhir1, Alexandre Fuchs1, Erin Bedford3, Jean-Charles Duclos-Vallée1, Emma Andersson1, Pascale Dupuis-Williams1, 2, 3, 4 Université Paris-Saclay, Physiopathogénèse et traitement des maladies du foie, Villejuif, France; 4 Karolinska Institutet, Cell and Molecular Biology, Solna, Sweden; 5 Université de Paris, INSERM, CEA, U 976 HIP, Paris, France; 6 Aspect Biosystems, Vancouver, Canada; 7 FHU Hepatinov, Centre de la GLS1-low cells, along with changing in mitochondrial morphology.

**Conclusion:** Experimental data suggest an impairment of mitochondrial activity of iCCA cells. Resensitizing iCCA cells to metabolic treatments could make them more susceptible to cytotoxic drugs, opening new possibility to improve the outcomes of the iCCA patients.

**SAT203**
Mcpip1 fl/fl LysM Cre mice as an animal model of TNFα-dependent liver endothelial cell dysfunction in humans with chronic inflammation
Dariusz Zurawek1, Natalia Pydy1, Piotr Majord2, Edyta Kus3, Stefan Chlopicki1, Andrzej Budzynski1, Ewelina Pospiech2, Jolanta Jura1, Jerzy Kottinowski3, Faculty of Biochemistry, Biophysics and Biotechnology, Jagiellonian University, Department of General Biochemistry, Kraków, Poland; 2 2nd Department of General Surgery, Jagiellonian University Medical College, Poland; 3 Jagiellonian Centre for Experimental Therapeutics, Jagiellonian University, Poland; 4 Malopolska Centre of Biotechnology, Jagiellonian University, Human Genome Variation Research Group, Poland
Email: j.kottinowski@uj.edu.pl

**Background and aims:** Mcpip1 is an RNase involved in a negative regulation of inflammation, which is tightly linked to the function of endothelial cells. Under such pathological state, endothelium is characterized by increased expression of adhesion molecules, enhanced permeability, diminished production of NO, or increased extravasation of leukocytes to the surrounding tissue. The aim of this work was to verify whether Mcpip1 deletion leads to endothelial activation.

**Method:** We used C57BL6J mouse strain with a knock-out of Mcpip1 gene in leukocytes of myeloid lineage (Mcpip1 fl/fl LysM cre) as a model of endogenous, sterile inflammation. Multiplex Luminex assay was used to determine serum cytokine profile in these mice. Then, we performed differential expression analysis of genes in CD146⁺ endothelial cells (ECs) isolated from livers of 3 and 6-months-old control (Mcpip1 fl/fl) and Mcpip1 fl/fl LysM cre mice by using next generation sequencing (NGS) and RT-PCR method. NGS was followed by gene ontology enrichment analysis (GO) and signaling pathway impact analysis. Activation of hepatic ECs was analyzed by immunohistochemical (IHC) staining. Finally, results observed in mice were compared to ECs liver histology of a group of 40 patients.

**Conclusion:** Microfluidic 3D bioprinting and 2D micropatterns are two technologies that allow for bioengineering of 3D tubular biliary structures that recapitulate in vivo states of health and disease. These models open up opportunities to study organogenesis and physiological-patological cues. The bioprinted tubes could be connected to microfluidic perfusion systems to investigate questions related to bile flow and detoxification. Self-organogenesis of 3D structures on 2D micropatterns is a promising tool to mimic ALGS.

Figure 1. Biliary structures fabricated via microfluidic 3D bioprinting and 3D self-organogenesis on 2D micropatterns (A) 3D reconstruction of confocal Z-stacks of a bioprinted human tube showing F-actin and nuclei labelling (20X). (B) Branches from Jag1Ndr/Ndr biliary trees grown on 2D micropatterns are thinner (top panel, phase contrast, 10X) and with smaller lumens, (bottom panel, orthogonal views, confocal microscopy (40X)). Yellow arrows pointing at lumens.

**SAT203**
Mcpip1 fl/fl LysM Cre mice as an animal model of TNFα-dependent liver endothelial cell dysfunction in humans with chronic inflammation
Dariusz Zurawek1, Natalia Pydy1, Piotr Majord2, Edyta Kus3, Stefan Chlopicki1, Andrzej Budzynski1, Ewelina Pospiech2, Jolanta Jura1, Jerzy Kottinowski3, Faculty of Biochemistry, Biophysics and Biotechnology, Jagiellonian University, Department of General Biochemistry, Kraków, Poland; 2 2nd Department of General Surgery, Jagiellonian University Medical College, Poland; 3 Jagiellonian Centre for Experimental Therapeutics, Jagiellonian University, Poland; 4 Malopolska Centre of Biotechnology, Jagiellonian University, Human Genome Variation Research Group, Poland
Email: j.kottinowski@uj.edu.pl

**Background and aims:** Mcpip1 is an RNase involved in a negative regulation of inflammation, which is tightly linked to the function of endothelial cells. Under such pathological state, endothelium is characterized by increased expression of adhesion molecules, enhanced permeability, diminished production of NO, or increased extravasation of leukocytes to the surrounding tissue. The aim of this work was to verify whether Mcpip1 deletion leads to endothelial activation.

**Method:** We used C57BL6J mouse strain with a knock-out of Mcpip1 gene in leukocytes of myeloid lineage (Mcpip1 fl/fl LysM cre) as a model of endogenous, sterile inflammation. Multiplex Luminex assay was used to determine serum cytokine profile in these mice. Then, we performed differential expression analysis of genes in CD146⁺ endothelial cells (ECs) isolated from livers of 3 and 6-months-old control (Mcpip1 fl/fl) and Mcpip1 fl/fl LysM cre mice by using next generation sequencing (NGS) and RT-PCR method. NGS was followed by gene ontology enrichment analysis (GO) and signaling pathway impact analysis. Activation of hepatic ECs was analyzed by immunohistochemical (IHC) staining. Finally, results observed in mice were compared to ECs liver histology of a group of 40 patients.
Results: Depletion of Mcpip1 protein in myeloid leukocytes led to development of sterile and endogenous inflammation in 6-month-old Mcpip1fl/flLysMCre animals. Mcpip1fl/flLysMCre mice were characterized by increased serum levels of interleukins (IL-5, IL-6Ra, IL-10), chemokines (MCP-2, MCP-5, MIP-3α, MARC), markers of endothelial damage and TNFa. NGS analysis revealed 1094 differentially expressed genes (fold change >2 or <0.5) in ECs isolated from livers of Mcpip1fl/flLysMCre mice as compared to control Mcpip1fl/fl animals. GO analysis pointed out that 'antigen processing and presentation' and 'cell adhesion molecules' were the mostly affected biological pathways in liver ECs of Mcpip1fl/flLysMCre mice. Further, RT-PCR and immunohistochemical analysis confirmed significant upregulation of P-selectin, Vcam1 and Icam1 in hepatic ECs of Mcpip1fl/flLysMCre mice as compared to control littermates. Moreover, we observed significant reduction of the level of liver glycocalyx what was followed by increased serum TNFs levels observed in Mcpip1fl/flLysMCre mice. Finally, patients with high serum levels of TNFa (>14 pg/ml) showed significant decrease in the levels of glycocalyx in the liver.

Conclusion: Mouse genetic model of endogenous, sterile inflammation (Mcpip1fl/flLysMCre) has good translational potential in studies of liver ECs activation and damage observed in patients with chronic inflammation.

Acknowledgments: This work was supported by research grant from National Science Centre, Poland grant number 2017/27/B/N25/01440 to JK.

SAT204 Peroxisome proliferator activated receptor gamma regulates patatin-like phospholipase domain-containing protein 3 in adipocytes in vitro and in vivo in a mouse model of non-alcoholic steatohepatitis
Emmanuel Dauda Dixon1, Thierry Claudel1, Alexander D Nardo1, Veronika Militz2, Claudia Fuchs1, Michael Trauner1. 1Medical University of Vienna, Hans Popper Laboratory of Molecular Hepatology, Division of Gastroenterology and Hepatology, Department of Internal Medicine III, Wien, Austria
Email: michael.trauner@meduniwien.ac.at

Background and aims: The patatin-like phospholipase domain-containing protein 3 (PNPLA3) is expressed highly in the liver and adipose tissue. Despite its unknown metabolic function, the PNPLA3 mutant I148M is associated with non-alcoholic fatty liver disease development and progression. Hence, there is a growing interest in understanding the role of PNPLA3 in adipose tissue and liver biology, the two main organs/tissues responsible for maintaining metabolic flexibility. Peroxisome proliferator-activated receptor gamma (PPAR gamma) binding activity was shown to be maintained in LX2 cells overexpressing the PNPLA3 I148M variant. Therefore, we explored whether PPAR gamma transcriptionally regulates PNPLA3 in vitro and in vivo in STAM mice as a model of NASH.

Method: A 1 kb DNA fragment of the human PNPLA3 promoter was cloned in front of a luciferase reporter gene and co-transfected into rat liver cell (WR) and HepG2 cells. To explore the direct interactions between PPAR gamma and PNPLA3, to explore the direct interactions between PPAR gamma and PNPLA3, we performed co-immunoprecipitation studies in HepG2 cells. Sox4 function was determined in WT and PNPLA3 KO HepG2 cells using luciferase reporter and ChIP assays. Finally, we verified whether PPAR gamma transcriptional regulation is dependent on PNPLA3 expression in mouse models of NASH.

Results: Rosiglitazone induced PNPLA3 mRNA expression (+88%) and significantly increased the luciferase activity in co-transfected cells (+50%), demonstrating PPAR gamma-mediated induction of PNPLA3 promoter activity. Interestingly, two PPREs at positions 713–707 (+92%) and 790–780 (+93%) were bound by the PPAR gamma nuclear protein in the differentiated adipocytes. The introduction of two base-pair mutations into the identified 707mut (-40%) and 780mut1 (-60%) reduced PPAR gamma binding activity, but not 780mut2. Likewise, incubation with an antibody against PPAR gamma also reduced binding (-40%) to the PNPLA3 enhancer regions. In the STAM mouse, pioglitazone treatment increased markedly the expressions of PNPLA3 (+31%) and PPAR gamma (+50%) mRNA and its downstream target genes such as FABP4 and PGC1 alpha in the gonadal white adipose tissue (gWAT). In the liver (with lower PNPLA3 expression compared to white adipose tissue), however, pioglitazone treatment did not significantly increase PNPLA3 (p = 0.56) and PPAR gamma (p = 0.06) gene expression.

Conclusion: This study demonstrates that in the presence of PPAR gamma, PNPLA3 is up-regulated transcriptionally independent of insulin-SREBP mediated effect. This data suggests that PNPLA3 is a PPAR gamma target gene. However, the pathogenetic and therapeutic relevance of this association with regards to adipose tissue and liver function remains to be determined.

SAT205 Animal variants of sodium-taurocholate co-transporting polypeptide permitting hepatitis B virus infection
Fuwang Chen1, Jochen Wettengel1, Florian Gegenfurtner1, Yi Ni2,3, Stephan Urban2,3, Ulrike Protzer1,4. 1Institute of Virology, Technical University of Munich/Helmholtz Zentrum München, Munich, Germany; 2Department of Infectious Diseases, Molecular Virology, University Hospital Heidelberg, Heidelberg, Germany; 3German Center for Infection Research (DZIF), partner site Heidelberg, Heidelberg, Germany; 4German Center for Infection Research (DZIF), partner site Munich, Munich, Germany
Email: Fuwang.chen@tum.de

Background and aims: Evaluation of new therapies to cure chronic hepatitis B virus (HBV) infection is limited by the lack of suitable animal models. Identification of sodium-taurocholate co-transporting polypeptide (NTCP) as a species-specific key factor for HBV entry and infection may allow expanding the HBV host range. Key objective of this study was to analyse species-specific NTCPs for HBV binding and infection in order to advance our knowledge and to discover potential HBV animal models.

Method: NTCPs from various animal species were selected based on their sequence similarity within the human NTCP binding domain (amino acid 157–165). These NTCPs were expressed in HepG2 cells by DNA-plasmid or mRNA transfection. Subsequently, NTCPs expression, bile acid uptake and moreover their capability to support HBV entry and infection were analyzed by luminescence, radiometry, myrB-attO488 staining and subsequent flow cytometry analysis.

Results: Eighteen animal NTCP variants expressed at comparable levels revealed varying levels of bile acids uptake as physiological function of NTCP. MyrB-attO488 staining and subsequent flow cytometry analysis indicated that all NTCP variants except those from macaque and dolphin were able to bind HBV. Furthermore, HBV infection experiments showed that NTCPs from various species including aardvark, rabbit, whale, big brown bat, cat, rhinoceros and horse support de novo HBV infection when expressed on HepG2 cells. In addition, introducing minimal genetic changes into hamster, cow and goat NTCP at amino acid position 82–87 restored the capability to
mediate HBV infection. Notably, cells expressing horse NTCP were even more susceptible to HBV infection compared to the cells expressing all other NTCP variants including human NTCP. Moreover, horse NTCP localization at the plasma membrane was two-fold increased compared to human NTCP, consequently leading to more HBV particles binding and enhanced HBV infection. In addition, HBcore staining and cccDNA quantification revealed that expression of horse NTCP increased total numbers of HBV infected cells and average viral load.

**Conclusion:** The evaluation of selected NTCP variants highlights the importance of two functional domains at aa 82–87 and aa 157–165 to support HBV infection. In addition, modification of cow and goat NTCPs suggested that additional unknown motifs also play a role to accomplish NTCP function in mediating HBV infection. Through our screening, we identified rabbits, cats, and horses as potential HBV hosts if restriction factors downstream of HBV uptake can be overcome. HBV infection could be increased by expressing horse NTCP instead of human NTCP on HepG2 cells. Thus, horse NTCP is a promising candidate to create new in vitro and in vivo models and help to clarify NTCPs mode of action during HBV entry.

**SAT206**

**Cholangiocarcinoma-on-chip: a platform for 3D liver tumour model**

Michela Anna Polidoro 1, Arianna Rosina 2, Erika Ferrari 2, Marco Rasponi 2, Ana Lleo 1–4, Simona Marzorati 1. 1Humanitas Clinical and Research Center IRCCS, Hepatobiliary Immunopathology Lab, Rozzano, Italy; 2Politecnico di Milano, Department of Electronics, Information and Bioengineering, Milan, Italy; 3Humanitas University, Department of Biomedical Sciences, pieve emanuele, Italy; 4Humanitas Clinical and Research Center IRCCS, Department of gastroenterology, division of internal medicine and hepatology, milano, Italy

**Background and aims:** Intrahepatic cholangiocarcinoma (iCCA) is a deadly cancer of biliary epithelium with very limited therapeutic options. This highlights the importance of decipher iCCA mechanisms for effective therapeutic strategies. Nevertheless, in-vivo cellular interactions complexity has hindered an effective recapitulation of in-vitro human milieu through 2D culture systems. We aim to develop an in-vitro 3D microfluidic device with patient-specific co-cultures of the main cells involved in iCCA.

**Method:** Primary iCCA cells were isolated from patients surgically resected at the Hepatobiliary Surgery Department, Humanitas Clinical Institute. A PDMS microfluidic device, composed by three adjacent microchannels separated by pillars and with independent accesses, was fabricated at Polytechnic of Milan.

**Results:** Firstly, proliferation assays, morphology assessments and RT-PCR were performed for three cell types to verify the phenotype retaining with an ad-hoc medium composition. After medium optimization, to recapitulate iCCA microenvironment, iCCA cells and primary fibroblasts were co-cultured in the central channel embedded in an optimized fibrin/collagen hydrogel, displaying an high cell viability and 3D organization after 96 h in culture. Endothelial cells were seeded in one lateral channel forming a tubular vessel, corroborated by fluorescence microscopy with specific antibodies. Dextran diffusion assays and COMSOL simulations were performed to assess the hydrogel diffusion ability to molecules and the endothelial barrier functional integrity within the chip.

**SAT207**

**Regulation of cholangiocyte ciliogenesis by soluble adenyly cyclase**

Hang Lam Li 1, Arthur Verhoeven 1, Simei Go 1, Jung-Chin Chang 1, Ronald Oude-Elferink 1. 1Tygat Institute for Liver and Intestinal Research, Amsterdam, Netherlands

**Background and aims:** Sec61 subunit beta (SEC16B) is involved in endoplasmic reticulum (ER) import of a selected group of N-linked glycosylated proteins Mutations in SEC61B and Polycystin 1 (PC1) are both causative for polycystic liver disease (PCLD), which is characterized by disturbed ciliogenesis and disturbed cyclic adenosine monophosphate (cAMP) homeostasis. Soluble adenyly cyclase (sAC) is highly expressed in H69 cholangiocytes. Therefore, we investigated the role of sAC in ciliogenesis of H69 cells.

**Method:** Phosphoproteomics, western blotting and immunofluorescence staining were performed in H69 cholangiocytes in the presence and absence of the sAC-specific inhibitor LRE1 or by knockdown of sAC with lentiviral shRNA. Deglycosylation of H69 lysates was performed with PNGase F and endo H. 

**Results:** Phosphoproteomic analysis of H69 cells incubated with the sAC-specific inhibitor LRE1 acutely and drastically reduced phosphorylation of SEC61B at serine 17. The function of this phosphorylation site is unknown. Since mutations in Sec61B are known to disturb the maturation of PC1, a primary ciliary protein, we studied the effect of sAC knockdown on PC1. Chronic sAC knockdown by lentiviral shRNA led to impaired glycosylation of PC1, while no difference was observed in protein levels (as determined by deglycosylation with PNGase F). Conversely, knockdown of sAC did not affect the protein level, nor the glycosylation of GLUT1, which is a strongly glycosylated plasma membrane protein that is not associated with the primary cilium. We also studied the effect of sAC knockdown on ciliogenesis. Immunofluorescence staining of cilia (with ADF/Arp2/3 capping factor-like protein 13B (ARL13B) as a marker) revealed disappearance of cilia upon sAC knockdown. This was accompanied by intracellular accumulation of ARL13B.

**Conclusion:** These data suggest that sAC-dependent phosphorylation is essential for proper co-translational glycosylation of a specific set of proteins that travel through the ER, including PC1. As a consequence, ablation of sAC expression leads to the absence of cilia in cholangiocytes. Our observations suggest that sAC may be a regulator of ciliogenesis.
SAT208
CRISPR perturbation in iPSC-derived hepatic stellate cells reveals role for TNF-driven interferon response in chronic liver disease
Kelly Haston1, Navpreet Ranu1, Lorn Kategaya1, Eric Lubeck1, Michael D. Bereket1, Francesco Paolo Casale1, Panagiotis Stanitsas1, Alicia Lee1, Owen Chen1, Bobby Leitmann1, Srivisavan Sivanandan1, Ahmed Sandalki1, Pooja Prasad1, Rohit Loomba2, Arun Sanyal3, Stephen Harrisson4, Zobair Younossi5, Catherine Jia6, Grant Budas6, James Trevaskis6, Robert Myers6, David Breckinridge6, Ajamete Kaykas1, Daphne Koller1, Matthew Albert1, Insitro, South San Francisco, United States; 2University of California San Diego, La Jolla, United States; 3Virginia Commonwealth University, Richmond, United States; 4Oxford University, Radcliffe Department of Medicine, Oxford, United Kingdom; 5Inova Fairfax Medical Campus, Fairfax, United States; 6Gilead Sciences, Inc., Foster City, United States; 7insitro, South San Francisco, United States
Email: research_operations@insitro.com

Background and aims: Activation of hepatic stellate cells (HSC) by inflammatory cytokines plays a central role in the progression of fibrosis. We aimed to: (i) define the interplay between NF-kappa-B and TGF-beta pathways using induced pluripotent stem cell (iPSC)-derived hepatic stellate cells (iHSCs); and (ii) discover insights that align with non-alcoholic steatohepatitis (NASH) progression.

Method: We developed an iHSC model that showed evidence of cellular maturation and extracellular matrix production. We employed Cas9-engineered cells and barcoded guide RNAs to execute pooled optical screening in human cells (POSH); and single-cell RNA-seq to analyze cytokine-treated iHSCs. For characterization of NASH phenotypes, we used 4,641 whole-slide images of liver biopsies from multiple trials. We trained end-to-end deep convolutional neural networks (CNN) to predict histological features [Casale et al, EASL 2020]. RNA-seq was performed on matched samples. For each clinical end point, we assessed the (multiple-hypothesis corrected) enrichment of TNF-alpha and IL1-beta response genes at multiple cutoffs using GSEA as implemented in the gseapy prerank module.

Results: Using a 400-guide RNA CRISPR library, we characterized the genes critical for TNF-alpha and IL1-beta-mediated activation of NF-kappa-B p65 response in iHSCs (Figure 1A and not shown). Molecular characterization of gene expression changes demonstrated that NF-kappa-B induces type I interferon response genes in iHSCs, constituting a distinct activation state as compared to TGF-beta (Figure 1B). Supporting the disease relevance of these signatures, we observed that TNF-alpha and IL1-beta signatures were enriched for genes associated with the CNN fibrosis stage and progression, as well as the serum fibrosis biomarker ELF score at FDR 5%.

Conclusion: This work constitutes an advancement above the state-of-the-art methodology, with optimized protocols and cell lines for genetic editing of iHSCs. Notably, this constituted the first time that POSH with image-based phenotyping has been achieved in iPSC derived cells. These studies also revealed a model of cytokine-driven fibrosis that aligned with clinical histological and biomarker features of NASH progression. Finally, we highlight the identification of NF-kappa-B p65 induced type I interferon in iHSCs. These results provide insights that will support the development of new therapeutic approaches for NASH.

SAT209
Regulation of cholangiocyte ciliogenesis by soluble adenylyl cyclase
Hang Lam Li1, Simei Go1, Jung-Chin Chang1, Arthur Verhoeven1, Ronald Ouwe Elferink1, Amsterdam UMC, Tytgat Institute, Amsterdam, Netherlands
Email: r.p.oude-elferink@amc.uva.nl

Background and aims: Sec61 subunit beta (SEC61B) is involved in endoplasmic reticulum (ER) import of nascent plasma membrane, secreted and vacuolar proteins. Mutations in the genes for SEC61B and PC1 are (amongst others) causative for polycystic liver disease.
conclusion: These data suggest that sAC-dependent phosphorylation of SEC61B is essential for proper cotranslational glycosylation of a specific set of proteins that travel through the endoplasmic reticulum, including PC1. As a consequence, ablation of sAC expression leads to absence of cilia in cholangiocytes. Our observations suggest that sAC may be a regulator of ciliogenesis.

SAT210
Signal transducer and activator of transcription 3 (STAT3)-driven hepatic transcriptional changes are indicative of a shift from immune tolerance to immune activation in chronic hepatitis B (HBV) infection
Jinglin Tang1, Jiaxuan Zhang1, Gao Li Zhang2, Ning Ling3, Min Chen1.
1Chongqing Medical University, Key Laboratory of Molecular Biology for Infectious Diseases (Ministry of Education), Institute for Viral Hepatitis, The Second Affiliated Hospital, Chongqing, China
Email: mchen@hospital.cqmu.edu.cn

Background and aims: Various immune cells and mediators were reported to be significantly changed in immune activation stage during chronic HBV (CHB) infection. However, it is still unknown what key upstream regulators drive these numerous changes in gene expression, especially during the transition from immune tolerance to immune activation.

Method: A HBV transgenic (HBV-Tg) mice model with spontaneous development of hepatic immune activation was applied to comprehensively investigate the dynamic changes in hepatic gene expression and immune cells by RNA sequencing, flow cytometry and immunohistochemistry. The transcriptomic and immunologic characters were analyzed by Gene Set Enrichment Analysis (GSEA) and ImmPort, and upstream transcriptional factors (TFs) were predicted by ENCODE CHIP-seq library in immune tolerance and immune activation phases both in HBV-Tg mice and CHB patients (GSEB3148 and GSE65359 from GEO datasets). Expression and activation of predicted transcriptional factors and the signal pathway components were identified and confirmed by western blot and quantitative real time PCR.

Results: Compared to 1-month-old HBV-Tg mice (in immune tolerance phase), a number of inflammatory and immune-related genes and pathways were significantly up-regulated in 3-month-old HBV-Tg mice (in early immune activation phase). Similar hepatic gene expression patterns were found between HBV-Tg mice in 1 month or 3 month and CHB patients in immune tolerance or immune activation phase respectively. STAT3 was predicted to be the top-ranking transcription factor in early immune activation phase of HBV-Tg mice (3 month). Furthermore, expression of total and phosphorylated STAT3, and several genes involving STAT3 pathway was significantly enhanced in 3-month-old HBV-Tg mice.

Conclusion: Activation of STAT3 with enhanced expression of immune- and inflammation-related genes indicated a shift from immune tolerance to immune activation in chronic HBV infection.
bioavailability. Here, we evaluate in a rat model the possible benefit against HF of encapsulated Gly in polymeric nanomicelles based on polygalacturonic acid and polyacrylic acid (Gly-NMs) previously characterized and known to increase drug bioavailability.

Method: Gly and Gly-NMs role against fibrosis were tested in a CCl4-induced HF rat model. Morphological, hematic and hepatic data were collected to monitor disease progression.

Results: In terms of body weight, liver weight, and serum parameters of hepatic function, Gly-NM appeared to provide better recovery from hepatic fibrosis than Gly. Molecular markers and histopathological analysis showed that Gly-MN demonstrated marked antifibrotic properties, reducing collagen deposition in liver tissue and decreasing the activation of hepatic stellate cells. Furthermore, we remarked an improved CCl4-induced fatty-degeneration following Gly-MNs treatment. The latter was associated with a gene downregulation of carnitine palmitoyl-transferase 1A (Cpt1a) which can impose a protective action against CCl4 insult as reported in the literature for mice lacking the enzyme.

Conclusion: Our results show that encapsulated Gly reduces fibrosis and related disease markers and improve the fatty degeneration better than free drug in a in vivo rat model.

SAT212
3D bioprinted hepatocyte and mesenchymal stem cell spheroids as a cell therapy for liver disease
Christopher Dickman1, Stephanie Campbell1, Haley Tong1, Reza Jalili1, Simon Beyer1, Tamer Mohamed1, Sam Wadsworth1, Spiro Getsios1
1 Aspect Biosystems, Vancouver, Canada
Email: chrisd@aspectbiosystems.com

Background and aims: Individuals with severe liver failure or metabolic liver disease, often have limited treatment options aside from transplantation. Liver transplantation is a complex and invasive surgery with limited availability of donor organs. Furthermore, recipients require life-long immune suppression, increasing the risk of infection and cancer. Recently, isolated hepatocytes have been transplanted into pediatric patients with acute liver failure with improvements in survival. Long term function of transplanted hepatocytes remains a challenge for treatment of chronic disease. The goal of this study is to demonstrate the ability of our unique bioprinting technology to generate hepatocyte implants capable of long term viability and function in vitro as well as in vivo in the intraperitoneal space of transplanted mice.

Method: Primary human hepatocytes (PHHs) were formed into spheroids with the addition of CD166 positive mesenchymal stem cells (MSCs). These spheroids were manufactured into a 3D bioprinted implant using Aspect Biosystems’ RX1 bioprinter. Spheroids were embedded in a hydrogel core and surrounded by an immune isolating shell in a core-shell micro-architecture. Live/Dead; albumin, and alpha-1 antitrypsin (α-1AT) production as well as ammonia detoxification assays were used to confirm in vitro function of printed implants. Hepatocytes were then implanted into the IP space of NOD-scid IL2γRnull mice. Function was examined over 28 days by monitoring the levels of plasma albumin and α-1AT. At day 28 fibers were retrieved to analyze function and viability.

Results: When cultured in vitro 1 million cell hepatocyte and MSC implants were able to synthesize >20 ug/million PHH/day. When implanted into mice plasma levels of albumin remained steady for 28 days and reached levels >2000ng/ml. The hepatocytes retained function and the ability to detoxify ammonia when retrieved from mice at the study end-point.

Conclusion: Our hepatocyte and MSC bioprinted implants demonstrate promise for the treatment of liver disease. We aim to build upon our research with studies demonstration efficacy of these implants in a small and large animal model of acute liver failure.
SAT214
Glycine ameliorates paracetamol-induced liver injury in non-alcoholic fatty liver disease by supporting glutathione biosynthesis
Alia Ghrayeb1, Shani Drucker1, Bella Agranovich1, Daniel Peled1, Oren Rom2–3, Ifat Abramovich1, Sara Fernandes1, Natan Weissman1, Jonatan Fernandez Garcia1, James Traylor2, Chen Eugene2, Eyal Gottlieb1, Inbal Mor1. 1The Ruth and Bruce Rappaport Faculty of Medicine, Cell Biology and Cancer Science Department, Haifa, Israel; 2University of Michigan, Internal Medicine Department, Ann Arbor, United States; 3Louisiana State University Health Shreveport, Pathology and Translational Pathobiology Department, Shreveport, United States

Background and aims: Non-alcoholic fatty liver disease (NAFLD) is the most common chronic liver disease worldwide. NAFLD patients are more susceptible to drug-induced hepatotoxicity compared to healthy individuals, yet a clear understanding of the predisposing factors and dedicated therapeutic interventions are still lacking. Overdose of paracetamol, a common analgesic drug, is one of the leading causes of acute liver injury in general. Paracetamol is oxidized in the liver to N-acetyl-p-benzoquinone imine (NAPQI), a highly reactive metabolite, which is detoxified by the cellular antioxidant, glutathione (GSH). In toxic doses, GSH levels cannot eliminate NAPQI, leading to reactive oxygen species (ROS)-induced damage. Glycine, a substrate of GSH synthesis, is lower in plasma of NAFLD patients and mouse models. It has recently been shown that in mice, administration of glycine can elevate GSH in the liver. We examined the mechanistic link between steatosis and paracetamol toxicity and the role of glycine in glutathione replenishment as therapeutic intervention.

Method: AML12 mouse hepatocyte cell line was incubated with palmitate (PA), which induced an increase in lipid droplets and ROS levels as detected by BOIDPY and DHE staining, respectively. Metabolomics analysis of PA treated cells by liquid chromatography and mass spectrometry demonstrated a decrease in glycine and GSH levels, which was further exacerbated by exposure to paracetamol. Cell viability analysis showed paracetamol toxicity and PA lipotoxicity were synergistic, indicating lipid accumulation increases oxidative stress and paracetamol toxicity. Glycine supplementation elevated cellular levels of glycine and GSH, even in the presence of paracetamol.

Results: C57BL/6] mice fed western diet (WD) for 8 weeks, demonstrated liver steatosis and decreased circulating glycine compared to mice on standard chow diet (CD). Unbiased metabolomic profiling of liver tissue followed by pathway analysis, exhibited significant changes in GSH and glycine metabolism in WD compared to CD. Following the 8 week diet, mice received a single dose of paracetamol. WD-paracetamol treated mice displayed higher ALT levels and more severe liver histopathology compared to CD-paracetamol treated mice, demonstrating steatosis increased sensitivity to paracetamol hepatotoxicity. Metabolomic analysis of the livers 6hrs following paracetamol administration showed significantly lower GSH and glycine levels in WD compared to CD. Glycine administration to WD-paracetamol treated mice increased hepatic levels of GSH. Indices of liver injury: ALT levels, liver pathology and tissue marker for oxidative stress, were all improved following glycine administration.

Conclusion: These results indicate that decreased glycine in the plasma and the liver in NAFLD lead to lower hepatic GSH synthesis and increase paracetamol sensitivity which can be alleviated by glycine administration.

SAT215
Hepatocyte-specific deletion of the anti-apoptotic Mcl-1 in mice induces polyploidization, mitotic errors and chromosomal instability.
Laure-Alix Clerbaux1,2, Pierre Cordier3, Nina Desboeufs1,2, Kristian Unger4, Gabriel Semere2, Lap Kwan Chan2, Chantal Desdouets3, Massimo Lopes1, Achim Weber1,2. 1Institute of Molecular Cancer Research, University of Zürich, Zurich, Switzerland; 2Department of Pathology and Molecular Pathology, Zürich Hospital, Zurich, Switzerland; 3Team Proliferation, Stress and Liver Physiopathology, INSERM, Paris, France; 4Research Unit of Radiation Cytogenetics, Helmholtz Zentrum München, Germany

Background and aims: Mcl-1 is a widely recognized pro-survival protein and a promising target for cancer therapy. We previously showed that hepatocyte-specific deletion of Mcl-1 (Mcl-1Dhep) triggers apoptosis and proliferation in livers of young mice, and found that higher apoptotic levels at early age correlate with spontaneous HCC development later on. Aiming to characterize further non-apoptotic roles of Mcl-1, we here investigated its role in ploidy and mitosis in vivo.

Method: Mcl-1Dhep mice of 2 months old mice were analyzed for ploidy profile, formation and polarization of mitotic spindles. Whole exome sequencing (WES) of tumors of 12 months old Mcl-1Dhep mice was performed to assess extent of chromosomal instability (CIN) via SNVs and indels frequency. To evaluate the impact of Mcl-1 loss in livers upon induced hyperproliferation, 2 months old Mcl-1Dhep and WT mice were subjected to two-third partial hepatectomy (PHx). Ploidy contingent, mitotic figures and chromosome segregation were analyzed at the peak of proliferation (48 h post-PHx). WES was performed in regenerated livers when hepatocytes stop proliferating (7d post-PHx) to monitor associated genetic alterations.

Results: Mcl-1Dhep livers of young mice displayed a high proportion of polyploid hepatocytes (Fig. A), which were associated neither with higher apoptosis, nor with higher proliferation, age or oxidative stress. Moreover, Mcl-1Dhep hepatocytes entered into mitosis, thus excluding endoreplication. Gene set enrichment analysis showed an association between genes upregulated upon Mcl-1 deletion and genes of the mitotic spindle assembly checkpoint (SAC), which ensures correct chromosomes segregation during mitosis. Around
50% of the mitotic events in Mcl-1Dhep livers were aberrant (Fig. B), with abnormal chromosome segregation. WES of Mcl-1Dhep tumors of 12 months old mice showed a mean CN of 33.8% (Fig. C). Following PHx, liver weight to body weight ratios were similar in Mcl-1Dhep and WT mice during liver regeneration, while Mcl-1Dhep livers were smaller prior to PHx (Fig. E). Mcl-1Dhep hepatocytes progressed faster through G2/M. At the proliferative peak, abnormal mitotic figures were observed with similar frequency in Mcl-1Dhep and WT livers (Fig. F). After regeneration, the ploidy profile was comparable in WT and Mcl-1Dhep livers (Fig. G). Both WT and Mcl-1Dhep livers harbored very low level of SNVs and indels.

Conclusion: In 2 months old mice, hepatocytes lacking Mcl-1 exhibit nuclear polyplody, mitotic errors and abnormal chromosome segregation leading to CIN. Surprisingly, similar rates of aberrant mitosis were observed in WT and Mcl-1Dhep livers upon hyperproliferation. And after hyperproliferation, WT and Mcl-1Dhep livers exhibited similar levels of abnormal nuclear morphology, of low mutational burden and of high proportion of polyploid nuclei.

SAT216

Hepatic inflammation elicits production of proinflammatory netrin-1 through exclusive activation of translation

Romain Barnault1,2,3,4, Claire Verzeroli1,2,3,4, Carole Fournier5, Michele Maud6,7,8, Anna-Rita Redavid9,3,4,7, levgenia Chicherova2,3,4,6, Marie-Laure Plissonnier2,3,4,6,8, Annie Adrait9, Olga Khomich2,3,4,6, Fleur Chapus10, Mathieu Richaud2,4,7,8, Maëva Hervieu2,4,7,8, Veronika Reiterer11, Romain Barnault1,2,3,4, Claire Verzeroli1,2,3,4, Carole Fournier5, Michele Maud6,7,8, Anna-Rita Redavid9,3,4,7, levgenia Chicherova2,3,4,6, Marie-Laure Plissonnier2,3,4,6,8, Annie Adrait9, Olga Khomich2,3,4,6, Fleur Chapus10, Mathieu Richaud2,4,7,8, Maëva Hervieu2,4,7,8, Veronika Reiterer11, Frederica-Grazia Centonze11, Julie Lucifora2,4,7,8, Birke Bartosch2,4,7,8, Michel Rivoire2,3,4,6,13, Fabien Zoulin2,3,4,6,13, Romain Parent2,3,4,6,1, Centre de Recherche en Cancérologie de Lyon, Inserm U1052-LabEx DEVweCan, France; 2Université de Lyon, France; 3CNRS UMR 5286, France; 4Centre Léon Berard, Lyon, France; 5Institute for Advanced Biosciences, La Tronche, France; 6Pathogenesis of Chronic Hepatitis B and C Laboratory-Centre de Recherche en Cancérologie de Lyon, Inserm U1052-LabEx DEVweCan, France; 7Apolo, Cancer an development Laboratory-Cancer research Center of Lyon, Inserm U1052-LabEx DEVweCan, France; 8Centre de Recherche en Cancérologie de Lyon, Lyon, France; 9University of Grenoble-Alpes, Inserm, CEA, UMR biosanté U1292, Grenoble, France; 10The National Institute of Environmental Health Sciences, Durham, United States; 11Medizinische Universität Innsbruck, Institute of Pathophysiology, Innrainstrasse 1, Innsbruck; 12Universitätsklinikum Tübingen Anaesthesiologie und Intensive Care Medicine, Tübingen, Germany; 13Service de Hepato-Gastroenterologie, Hospice civils de Lyon, Lyon, France

Email: romain.barnault@inserm.fr

Background and aims: Chronic liver diseases (CLDs) affect more than 1 billion people worldwide. Though CLDs exhibit a high degree of diversity in terms of causal effects, including infectious (HBV and HCV), metabolic, toxic, and genetic, they all converge toward hepatic inflammation and represent a pertinent model for its study. Inflammation in turn drives hepatocyte turnover, extracellular matrix (ECM) accumulation, histological worsening, and the long-term induction of tumorigenic mediators such as IL-6, eventually leading to the development of HCC. Hence, the identification of factors involved in the harmful consequences of inflammation may lead to its clinical improvement.

Netrin-1 is well known for preventing cellular apoptosis through its binding to "dependence receptors," and we demonstrated that it is HBV- HCV induced and endowed hepatocytes with resistance to apoptosis during the unfolded protein response (UPR), a hallmark of CLDs and cirrhosis. Owing to the causal link between inflammation, cancer in general, and HCC, we hypothesized that hepatic inflammation and netrin-1 may be reciprocal influencers in the liver. This prompted us to test its inducibility and inflammatory contribution in the liver in the context of previous descriptions in inflammatory bowel disease and colorectal cancer.

Method: A panel of cell biology and biochemistry approaches (RT-qPCR, reporter assays, run-on, polysome fractionation, CLIP, filter binding assay, subcellular fractionation, western blotting, IP, stable isotope labeling by amino acids in cell culture) on in vitro- grown primary hepatocytes and liver cell lines from mouse samples and clinical samples was used.

Results: We identify netrin-1 as a hepatic inflammation-inducible factor and decipher its mode of activation through an exhaustive eliminative approach. We show that netrin-1 up-regulation relies on a hitherto unknown mode of induction, namely its exclusive translational activation. This process includes the transfer of NTN1 mRNA to the endoplasmatic reticulum and the direct interaction between the Staufen-1 protein and this transcript as well as netrin-1 mobilization from its cell-bound form. Finally, we explore the impact of a phase 2 clinical trial-tested humanized anti-netrin-1 antibody (NP137) in two distinct, toll-like receptor (TLR) 2/TLR3/TLR6-dependent, hepatic inflammatory mouse settings. We observe a clear anti-inflammatory activity indicating the proinflammatory impact of netrin-1 on several chemokines and Ly6C+ macrophages.

Conclusion: These results identify netrin-1 as an inflammation-inducible factor in the liver through an atypical mechanism as well as its contribution to hepatic inflammation.

SAT217

A meta-analysis to identify novel candidate genes in the development of hepatocellular carcinoma

Andrew Walakira1, Cene Krubic1, Nejc Nadžar1, Miha Mraz2, Miha Moskon2, Tadeja Rezen1, Damjana Rozman1, University of Ljubljana, Centre for Functional Genomics and Bio-Chips, Ljubljana, Slovenia; 2University of Ljubljana, Faculty of Computer and Information Science, Ljubljana, Slovenia

Email: andrew.walakira@mf.uni-lj.si

Background and aims: Hepatocellular carcinoma (HCC) is a major health problem worldwide. In 2020, there was about 900,000 new
cases of liver cancer, which is the third-highest number of cancer-related deaths (8.3% of 9.9 million) in the same year. Hepatitis B and C infections are still the major risk factors but with vaccination and effective treatment, these are steadily being overtaken by other factors, such as metabolic associated fatty liver disease and diabetes. Prevention efforts have been useful but the HCC burden is on the rise. To alleviate this problem, there is an urgent need for new tools, such as non-invasive diagnostics and effective treatments. We aim to unravel novel candidate genes that are important in HCC.

**Method:** We did a meta-analysis using 8 transcriptomics datasets (GSE19665, GSE39791, GSE41804, GSE57957, GSE64041, GSE84402, GSE84598, and HCCDB15/TCGA-LIHC). These datasets were from tumour and surrounding non-tumour tissue biopsies of the liver. First, we did differential gene expression analysis on each of the datasets individually by fitting linear models using the Limma package. This was followed by a meta-analysis by fitting random effects models using log fold change (LogFC) as effect size. Genes were considered significant if their p value was less than 0.05. Significant genes from the meta analysis were further analysed for KEGG pathway enrichment, network analysis in STRING database and searched DisGeNET to discover gene-disease associations. All statistical analyses were done in R software.

**Results:** After the meta-analysis, 690 genes were significantly differentially expressed. Thirty pathways were enriched with the majority (28) associated with metabolism. The two other enriched pathways were the cell cycle and p53 signalling pathways. Genes in the cell cycle and p53 signalling pathways were generally upregulated, while the genes in metabolism related pathways were generally downregulated. When searched DisGeNET database, 128 genes (of the 690 genes) were found not to be associated with HCC or other forms of liver cancer. Some of these genes like KIAA1010, SERPINA10 and ROR5 have been associated with HCC in smaller studies. Searching in STRING database revealed several important protein-protein interactions and hubs that are worth further investigation.

**Conclusion:** Four genes namely; C8A, HA01, PIPOX and PROZ were identified as key hub genes and will be studied further in the laboratory.

---

**SAT229**

**Outcomes of living liver donors are worse than those of matched healthy controls: nationwide cohort study**

Jong Man Kim1, Jin Yong Choi2, Jae Heon Kim2, Hyun Jung Kim4, Jae-Won Jo1.1 Samsung Medical Center, Sungkyunkwan University School of Medicine, Department of Surgery, Seoul, Korea, Rep. of South; 2Myongji Hospital, Goyang-si, Korea, Rep. of South; 3Soonchunhyang University Seoul Hospital, Korea, Rep. of South; 4Korea University, Korea, Rep. of South.

**Background and aims:** Donor death is the most serious complication of living liver donation, but is reported rarely. We investigated the actual mortality of living liver donors (LLDs) compared with matched control groups based on analysis of the Korean National Health Insurance Services (NHIS) database.

**Method:** This cohort study included 12, 372 LLDs who donated a liver graft between 2002 and 2018, and were registered in the Korean Network for Organ Sharing. They were compared to three matched control groups selected from the Korean NHIS and comprising a total of 123, 710 subjects: healthy population (Group I); general population with comorbidities (Group II); and general population with comorbidities (Group III).

**Results:** In this population, 78.5% of living liver donors were 20–39 years old, and 64.7% of all donors were male. Eighty-nine donors (0.7%) in the LLD group died (68 males and 21 females), a mortality rate (1000 person/year) of 0.91 (0.74–1.12). Mortality rate ratio and the adjusted hazard ratio of the LLD group was 2.03 (1.61–2.55) and
Background and aims: Hepatocellular carcinoma (HCC) recurs after liver transplantation and provide a potential prognostic biomarker: a proof-of-concept study

Xavier Verhelst1,2, Heline Engels1, Anja Geerts1,2, Ade Vandevelde3, Luis Abreu de Carvalho3, Helena Degroot3,4, Leander Meuris3,5, Frederik Bertevoet1, Nico Callewaert1,4, Hans Van Vlierberghen1,2,3

1Ghent University Hospital, Gastroenterology and Hepatology, Gent, Belgium; 2Ghent University, Liver Research Center Ghent, Gent, Belgium; 3Ghent University Hospital, General, hepatobiliary and transplant surgery, Gent, Belgium; 4VIB-Ugent, Center for Medical Biotechnology, Gent, Belgium; 5Ghent University, Department of Biochemistry and Microbiology, Gent, Belgium

Email: xavier.verhelst@ugent.be

Background and aims: Hepatocellular carcinoma (HCC) recurs after liver transplantation (LT) in 10% of patients. Changes in protein glycosylation have been described during the development of HCC. Study goal was to assess the risk of HCC recurrence after LT, according to changes in serum protein glycosylation before LT.

Method: A prospective study was performed in patients receiving LT between July 2011 and September 2018. A whole serum protein N-glycan profile was assessed using DNA sequencer assisted fluorophore assisted capillary electrophoresis, using a validated high-glycan profile was assessed using DNA sequencer assisted fluorophore assisted capillary electrophoresis, using a validated high-glycan profile. Specific changes in serum protein glycosylation profiles were analysed in patients with HCC recurrence compared to patients without.

Results: Amongst 225 consecutive liver transplant patients, 76 patients suffered from HCC before LT. Main indications were related to changed behavior of cirrhosis (47.4%), HCV infection (21.1%) and NASH (15.8%). Eight patients (10.5%) developed HCC recurrence after a median follow-up time of 9.5 months after LT. Seventy-four patients (97%) fulfilled Milan criteria.

Significant differences in the relative abundance of 5 serum glycans were present in patients with HCC recurrence compared to patients without (Cox regression analysis). Based on these changes, a composite biomarker was developed (GlycoHCCRecurrenceScore). This score integrates an increased presence of triantennary glycans with and without branch and core fucosylation (NA3, NA3Fbc and NA3Fb) and a decreased presence of undergalactosylated glycans NGALF and NGALB in patients with HCC recurrence. This biomarker panel shows an AUC of 0.855 (p = 0.001; 95% CI 0.731–0.979) for association with HCC recurrence. Using an optimized cut-off (-4.24), sensitivity was 87.5% and specificity 67.6%. Only 2.1% of patients with a value below this cut-off showed HCC recurrence, compared to 24.1% of patients with values above this cut-off (p = 0.011). PPV was 72.98% and NPV 84.3%. Figure 1 illustrates the discriminative value of this biomarker. In a univariate cox regression analysis other factors related to HCC recurrence in this cohort were diameter of the largest lesion before LT and the presence of perineural or lymphovascular invasion in the explant liver. In a multivariate analysis, the biomarker showed an independent relation with HCC recurrence (HR 1.931; p = 0.008:1.184–3.149).

Conclusion: A glycomics based serum biomarker panel is strongly associated with tumor recurrence in a cohort of LT patients with HCC, even if adhering to Milan criteria. In a multivariate analysis, this biomarker was the only pretransplant discriminative parameter of HCC recurrence in this cohort. The biomarker could potentially increase the prediction of HCC recurrence and improve allocation strategies in LT candidates with HCC.
Method: We performed random probability sampling among 3 US LT ACLF in UNOS. Network for Organ Sharing (UNOS) database are being used to inform failure (ACLF) among liver transplant (LT) candidates from the United States regarding acute-on-chronic liver.

SAT232
Discordance in categorization of acute-on-chronic-liver-failure in the national transplant database
Brian Lee1, Giuseppe Cullaro2, Aidan Vosooghi3, Frederick Yao4, Sarjukumar Panchal5, David Goldberg6, Norah Terrault. 1 University of Southern California, Los Angeles, United States; 2 University of California San Francisco; 3 University of Southern California; 4 University of Pennsylvania; 5 University of Miami

Background and aims: Studies regarding acute-on-chronic liver failure (ACLF) among liver transplant (LT) candidates from the United Network for Organ Sharing (UNOS) database are being used to inform LT policy changes worldwide. We assessed the validity of identifying ACLF in UNOS.

Method: We performed random probability sampling among 3 US LT centers between 2013 and 2019 to obtain a representative patient sample across ACLF grades. We compared the concordance of ACLF classification by UNOS vs. blinded manual chart review, according to EASL-CLIF. We compared the association of ACLF by UNOS and chart review was independently associated with waitlist dropout within 90 days of listing.

Results: Among 481 sampled LT registrants, 250 (52%) had no ACLF, 75 (16%) had ACLF grade 1, 79 (16%) had ACLF Grade 2, and 77 (16%) had ACLF Grade 3 per UNOS categorization. Concordance of ACLF grade by UNOS vs. chart review was: 72%, 64%, 56%, and 64% for no ACLF, Grade 1, Grade 2, and Grade 3, respectively, with overall Cohen’s kappa coefficient 0.48 (95%CI 0.42 – 0.54). Absence of acute compensation was the most common reason for overestimation, and discordant brain and respiratory failure categorization were the most common reasons for underestimation of ACLF by UNOS. In multivariable analysis, ACLF by chart review was independently associated with waitlist dropout (Grade 1: p = 0.44; Grade 2: p = 0.003; Grade 3: p = 0.004), but this association was not present by UNOS classification with waitlist dropout (Grade 1: p = 0.44; Grade 2: p = 0.003; Grade 3: p = 0.004). The remaining 5 patients are alive at a mean of 4 years (range: 2–9 years) post-transplant. One patient was documented to have an underlying risk factor that likely contributed to its development. LT may be required to treat refractory complications, with acceptable long-term outcomes.

Conclusion: Patients presenting with complications of HPSc usually have an underlying risk factor that likely contributed to its development. LT may be required to treat refractory complications, with acceptable long-term outcomes.

SAT233
Hemoluric response to 2-dose BNT162b2 mRNA vaccine for COVID-19 in liver transplant recipients
Maria Guarino1, Ilaria Esposito2, Giuseppe Portella3, Valentina Cossiga1, Ilaria Loperto4, Luca Pignata1, Raffaella Tortora2, Maria Rosaria Attanasio1, Michele Cennamo3, Mario Capasso1, Daniela Terracciano5, Francesco Maria Cutolo1, Alfonso Galeota Lanza2, Raffaele Lieto1, Sarah di Somma5, Francesco Paolo Picciotto2, Filomena Morisco1, 1 University of Naples “Federico II”, Department of clinical medicine and surgery, Gastroenterology and hepatology Unit, naples, Italy; 2 Hepatology Unit, AORN A. Cardarelli, Naples, Italy; 3 Department of translational medical science, University of Naples “Federico II”, Naples, Italy; 4 UOC Epidemiologia e prevenzione e registro tumori, ASL Napoli 1 Centro, Naples, Italy

Background and aims: In the context of the Italian SARS-CoV-2 vaccination program, liver transplant (LT) recipients were prioritized for vaccine administration, although the lower response to vaccines is a well known problem in this population. We aimed to evaluate immunogenicity of BNT162b2 mRNA vaccine in LT recipients and healthy controls and to identify factors associated with negative response to vaccine.

Method: We prospectively evaluated a cohort of adult LT patients the humoral response (with anti-Spike protein IgG-LIAISON SARS-CoV-2 S1/S2-IgG chemiluminescent assay) at 1 and 3 months after 2-dose vaccination. A group of 307 vaccinated healthcare workers, matched by age and sex, served as controls.

Results: Overall, 492 LT patients were enrolled (75.41% male, median age 64.85 years). Detectable antibodies were observed in the 75% of patients with a median value of 73.9 AU/ml after 3 months from 2-dose vaccination. At multivariable analysis, older age (>40yrs, p = 0.016), shorter time from liver transplantation (<5 years, p = 0.004), and immunosuppression with antimetabolites (p = 0.029) were significantly associated with non-response to vaccination. Moreover, the LT recipients showed antibody titers statistically lower than the control group (103 vs 261 AU/ml, p <0.0001) (figure). Finally, both in controls and LT patients we found a trend of inverse correlation between age and antibody titers (correlation coefficient: −0.2023 and −0.2345, respectively).

Conclusion: In this retrospective multi-center study, ACLF categorization by UNOS showed weak agreement with manual chart review. We confirmed the independent association of ACLF with waitlist outcomes. These findings are informative for ongoing allocation policy discussions and highlight the importance of prospective studies regarding ACLF in LT and UNOS reform.

Figure: Humoral response to 2-dose BNT162b2 vaccine after 1 and 3 months in LT patients and healthcare workers (controls).

Conclusion: Three months after vaccination, LT recipients showed humoral response in 75% of cases. Older age, shorter time from transplantation and use of antimetabolites were factors associated with non-response to vaccination and needed to be kept under close monitoring.
SAT234
A predictive model for mortality within one year of liver transplantation at the time of wait-listing for transplant: a novel approach using machine learning algorithms in a large US multi-ethnic cohort
Sripriya Balasubramanian1, Megha Bhatnagar2, Jian Wang2, Lisa Edelman3, Malou Valencia4, Aaron Rosenberger2, Robert Freed4, Amandeep Sahota2, Varun Saxena5,6, Nizar Mukhtar2, Suk Seo5, Brock McDonald5, Joanna Ready5,1 Kaiser Permanente, Gastroenterology and Hepatology, Roseville, United States; 2Kaiser Permanente, Information Support for Care Transformation, United States; 3Kaiser Permanente, National Transplant Services; 4Kaiser Permanente, Vascular and Interventional Radiology; 5Kaiser Permanente, Gastroenterology and Hepatology, United States; 6University of California, San Francisco, Hepatology, United States
Email: priya.b.manian@gmail.com

Background and aims: Pre-liver transplant (LT) sarcopenia, malnutrition and frailty are implicated in increased mortality following LT. Tests for these entities are expensive (CT for sarcopenia assessment) or require one-on-one testing not readily available at all centres (frailty testing), limiting widespread use. A predictive tool using readily available clinical data at waitlisting would be valuable to identify patients at risk, allowing for targeted evaluation and intervention.

Method: All Kaiser Permanente adult members nationally who underwent a first LT between 2010 and 2019 for indication other than hepatocellular carcinoma were included. Data extracted from the electronic medical record included demographics, laboratory values and diagnoses by ICD 9/10 codes. Frailty was assessed by previously published associated ICD codes; malnutrition by ICD codes and calculated Nutritional Risk Index. One year mortality was calculated from the day of transplant. Vote-based approach was used to identify variables of interest derived from six machine learning algorithms. Variables with two or more votes were included. Cohort was split 80:20 for model training and validation. Models were developed with repeated iterations and hyperparameter tuning using cross-validation for maximal improvement. Model assessments done with ROC curves, confusion matrix and decile plots with KS statistic.

Results: A total of 1,056 patient were included, of whom 98 (9.3%) died within one year of surgery. Variables deemed important by the "vote-based approach" included pre-LT bilirubin, creatinine, WBC count, albumin, MELD at Waitlist ≥31 and more (figure). Random forest, decision tree with bagging classifier and linear support vector classifier (SVC) performed best. Linear SVC model was selected as the final model based on sensitivity/recall, specificity, AUC statistic and F1 score. With a threshold of 50%, model had high sensitivity (80%), specificity (79%) and accuracy (79%) in identifying patients with poor outcome. Linear SVC Model performance assessed with KS statistic and decile plots achieved a value of 55 in the 3rd decile with the validation cohort, indicating excellent performance.

Conclusion: We have identified a model that predicts one year mortality after liver transplantation at the time of waitlisting with excellent performance. This enables early detection of patients at risk; studies on targeted interventions to improve post-transplant outcomes are planned.

SAT235
Monitoring patients with anti HBs trough levels can minimise hepatitis B immune globulin therapy after liver transplant
Erica Nicola Lynch1, Stefania Petruccelli1, Claudia Campiani1,3, Gabriele Dragoni1,4, Tommaso Innocenti1, Paolo Forte4, Stefano Milan1, Andrea Galì1, Gastroenterology Research Unit, Department of Experimental and Clinical Biomedical Sciences “Mario Serio,” Florence, Italy; 2Hepatobiliary Surgery and Liver Transplantation, University of Pisa Medical School Hospital, Pisa, Italy; 3Department of Experimental and Clinical Medicine, University of Florence, Florence, Italy; 4Department of Medical Biotechnologies, University of Siena, Siena, Italy; 5Division of Gastroenterology, University Hospital “Careggi,” Florence, Italy
Email: ericanicola.lynch@unifi.it

Background and aims: Hepatitis B virus (HBV) is still among the most frequent causes of liver transplantation (LT) in Europe. Combined prophylaxis with anti-HBs immunoglobulins (HBIG) and nucleos(t)ide analogues (NUCs) has virtually eliminated the risk of a disease relapse, although there is growing evidence that HBIG therapy could be safely withheld in most patients. The aim of our study was to evaluate the effectiveness of a combined HBV prophylaxis with a minimised and personalised fixed-dose HBIG therapy and a target anti-HBs trough level of 50–100 IU/L.

Method: All patients transplanted for HBV-related diseases (at least 12 months post LT) who attended our tertiary referral centre between January 2019 and June 2021 were prospectively included in our study. All patients received a combined HBV prophylaxis with NUCs (tenofovir, entecavir, or lamivudine) and intramuscular HBIG therapy administered at individualised multiple-week intervals, aiming at obtaining anti-HBs trough levels of 50–100 IU/L.

Results: Out of a total of 40 patients, there were no cases of HBV-DNA or HBsAg recurrence. The median (IQR) interval between 1000 UI HBIG doses was 5 weeks (4–6 weeks), with a maximum of 9 weeks and a minimum of 4 weeks. No patient characteristic-including LT indication (cirrhosis, hepatocellular carcinoma, or acute hepatitis), HDV coinfection, and type of NUC-was significantly associated with HBIG dosage, nor did the latter correlate with body mass index, estimated glomerular filtration rate, or follow-up duration after LT. The mean anti-HBs trough level reduction per one week increase in inter-HBIG dose interval was 40 IU/L (95% CI 32.96–47.04 UI/L).

Conclusion: Our data support the use of a minimised HBIG for the prevention of HBV recurrence in LT recipients who should prudently continue combined prophylaxis (e.g. HDV coinfection). Anti-HBs trough levels rather than random assessments are rationally a more effective tool to lower the anti HBs level cut-off and therefore minimise HBIG dosage and costs. Individual HBIG consumption...
profiles are highly variable and can be as low as <500 UI/month to maintain anti-HBs trough levels of 50–100 UI/L, thus treatment should be personalised.

SAT236
Formal referral networks optimise patient selection for liver transplantation
Oliver Tavabie1, Victoria Kronsten1, Talal Valliani2, Deepak Joshi1, Johnny Cash3, Abid Siddique1, Matthew Cramp4, Andreas Prachalias1, Krishna Menon1, Kosh Agarwal1, Michael Heneghan2, Varuna Aluvihare1, 1King’s College Hospital, United Kingdom; 2North Bristol NHS Trust, United Kingdom; 3Royal Victoria Hospital, United Kingdom; 4Derriford Hospital, United Kingdom
Email: oliver.tavabie@nhs.net

Background and aims: In the United Kingdom, liver transplant (LT) referral pathways for patients (PTs) with chronic liver disease (CLD) are not standardized. This is unlike other conditions with high mortality such as hepatocellular carcinoma (HCC). King’s College Hospital (KCH) developed a network of satellite LT centres (SLTCs) with standardized referral pathways to improve access to LT. We aimed to evaluate the impact of SLTCs in LT candidacy evaluation in CLD PTs and those within the established HCC pathway.

Method: All PTs discussed at the KCH LT meeting between 10/2014–10/2019 were included. Second opinions from other LT centres and non-CLD/non-HCC PTs were excluded. Geographic, referral (KCH, SLTC or conventional referrer (CR)), clinical, demographic and laboratory data were retrospectively recorded. HCC PTs had tumor related variables recorded. CLD and HCC PTs were analyzed separately. Univariate (UVA) and multivariate analyses (MVA) were utilized to evaluate the effectiveness of SLTCs in PT selection for LT.

Results: 1102 assessments from CLD PTs (CR = 512 SLTC = 299 KCH = 291) and 240 assessments from HCC PTs (CR = 110 SLTC = 72 KCH = 58) were included. HCC PTs were not more likely to be; referred from any centre, listed or have a contraindication to LT than CLD PTs. 725 CLD PTs were listed and 216 had contraindications to LT. Variables associated with listing were; younger age, autoimmune liver diseases (AILD), biliary atresia (BA), previous LT, higher CLD prognostic scores, shorter referral to decision time and SLTC referral. Variables negatively associated with listing were; non-alcoholic fatty liver disease (NAFLD), alcohol related liver disease (ARLD), hepatitis C and CR referral. MVA including significant and variables of interest was utilized to demonstrate that SLTC referrals were independently associated with listing (adjusted odds ratio (aOR) 2.92 (95% confidence interval (CI) 2.07–4.17)). This was confirmed on sensitivity analyses excluding KCH and ARLD PTs. Variables associated with contraindication to LT were; older age, ARLD, NAFLD, higher CLD prognostic scores and CR referral. Variables negatively associated with contraindication to LT were; AILD, BA, previous LT or SLTC referral. MVA including significant and variables of interest was utilized to demonstrate that SLTC referrals were independently negatively associated with contraindications (aOR 0.33 (95%CI 0.21–0.50)). This was confirmed on sensitivity analyses excluding KCH and ARLD PTs. 168 HCC PTs were listed and 55 had contraindications to LT. No variables were significantly associated with listing including SLTC referral on UVA or MVA. Older HCC PTs were more likely to have a contraindication to LT but SLTC referral did not influence likelihood on UVA or MVA.

Conclusion: Formal referral pathways through SLTCs improve PT selection and access to LT for PTs with CLD but do not impact on the established HCC pathway.

SAT237
Efficacy and safety of SARS-CoV-2 vaccination in liver transplant recipients
Lucy Meunier1, Mathilde Sanavio1, Magdalena Meszaros1, Stéphanie Faure1, José Urcis Redoya1, Maxime Echenne1, Antoine Debordureau1, Georges-Philippe Pageaux1, 1CHU Montpellier, St Eloi, Montpellier, France
Email: lucy.meunier@chu-montpellier.fr

Background and aims: Liver transplant recipients have a poorer vaccine response than the general population (1), so a booster dose is now recommended for these patients. Real-life data on SARS-CoV-2 vaccination in liver transplant recipients are limited. The objective of this study was to evaluate the efficacy and safety of the vaccine and identify factors associated with vaccine response.

Method: This was a retrospective observational study of consecutive liver transplant recipients attending CHU de Montpellier. Inclusion criteria were patients who had received at least one vaccine dose and serological assessment of SARS-CoV-2 spike protein antibody titers. Data on the vaccination indication, immunosuppression, vaccine type, and serology 28 days after the last vaccine dose were collected. Serology below 30 BAU/ml (WHO units) defined non-responders, 30–260 BAU/ml low responders, and >260 BAU/ml responders.

Results: 494 patients were included between 1 January and 15 March 2021. 366 (74%) patients were vaccinated: 280 with 3 doses, 63 with 2 doses, and 3 with 1 dose. 260 patients were excluded from the analysis: 128 (25.5%) unvaccinated, 130 without serology, and 2 with serology prior to the first dose. Complete data were available for 234 patients. 164 (70.1%) patients were male, with a mean age of 59 ± 12 years. Indications for vaccination were alcoholic (n = 92; 39.3%), viral (n = 37; 15.8%), NASH (n = 17; 7.3%), autoimmune (n = 14; 6%), and other cirrhosis (n = 74; 31.6%), with a mean time to transplantation of 4.9 ± 5.9 years. No serious adverse events were reported. Of 201 (85.9%) patients with complete vaccination and post-vaccination serology, 104 (51.7%) were responders, 45 (22.4%) poor responders, and 52 (25.9%) non-responders. In multivariate analysis, factors associated with no or low response were vaccination with Vaxzevria alone (HR 6.8 [1.46–31.67], p = 0.046), mycophenolate mofetil (MMF) therapy (HR 2.1 [1.1–3.9], p = 0.025), previous SARS-CoV-2 infection prior to vaccination (HR 3.6 [1.025–12.89], p = 0.046), and female gender (HR 2.4 [1.15–4.99], p = 0.02).

Conclusion: Only half of our patients were vaccine responders after three injections. MMF, female gender, and Vaxzevria vaccination were associated with a poorer response, while previous SARS-CoV-2 exposure was associated with a better response. Even after three injections, serological responses were much lower than in the general population. It is now essential to determine the value of a fourth dose, the incidence of COVID-19 in transplant patients with poor serological responses after three doses, and the value of suspending MMF in liver transplant recipients to improve responsiveness.

Reference
Background and aims: Data on immunogenicity of SARS-CoV-2 vaccination in liver transplant (LT) recipients is limited. Homologous vaccination protocol in a number of studies demonstrated variable responses. We aimed to explore SARS-CoV-2 specific humoral response in heterologous prime-boost immunization with ChAdOx1 nCoV-19 AstraZeneca (AZ) and BNT162b2 Pfizer-BioNTech (BNT) among LT patients.

Method: LT recipients receiving SARS-CoV-2 vaccine at King Chulalongkorn Memorial Hospital between April and October 2021 were enrolled. Patients received either heterologous prime-boost protocol (AZ/BNT) or homologous regimen (AZ/AZ) depending on national policies. Blood samples were collected before vaccine administration and 4 weeks after the second dose. SARS-CoV-2 spike receptor-binding-domain (RBD) IgG was measured using electrochemiluminescence immunoassay (Roche Diagnostics) with positive cut-off of ≥0.8 U/ml. The neutralizing antibody was detected by enzyme-linked immunosorbent assay-based surrogate virus neutralization test (sVNT) (GenScript) with positive cut-off of ≥30% inhibition. Adverse events following vaccination were recorded by questionnaires.

Results: Eighty LT recipients were enrolled: 68.8% male with mean age of 58.0 ± 14.6 years. Median time since transplant was 5.7 years (IQR 2.8–11.8). 58 (72.5%) and 22 (27.5%) patients received AZ/BNT and AZ/AZ, respectively. Comparable seroconversion rate of anti-RBD antibody and sVNT after vaccination were observed in both AZ/BNT and AZ/AZ group (89.7% vs 81.8%, p = 0.45 and 77.6% vs 59.1%, p = 0.10, respectively). However, median IgG titer was significantly higher in AZ/BNT group compared to AZ/AZ group (843.9 U/ml vs 147.1 U/ml, respectively). However, median IgG titer was significantly higher in AZ/BNT group compared to AZ/AZ group (843.9 U/ml vs 147.1 U/ml, respectively). However, median IgG titer was significantly higher in AZ/BNT group compared to AZ/AZ group (843.9 U/ml vs 147.1 U/ml, respectively). However, median IgG titer was significantly higher in AZ/BNT group compared to AZ/AZ group (843.9 U/ml vs 147.1 U/ml, respectively). However, median IgG titer was significantly higher in AZ/BNT group compared to AZ/AZ group (843.9 U/ml vs 147.1 U/ml, respectively). However, median IgG titer was significantly higher in AZ/BNT group compared to AZ/AZ group (843.9 U/ml vs 147.1 U/ml, respectively). However, median IgG titer was significantly higher in AZ/BNT group compared to AZ/AZ group (843.9 U/ml vs 147.1 U/ml, respectively).

Conclusion: Nearly 90% and 80% of patients had positive anti-RBD antibody and sVNT, respectively, following heterologous prime-boost immunization. AZ/BNT vaccination was well-tolerated and yields greater SARS-CoV-2 specific humoral response than AZ/AZ. Cell-mediated response and immune durability of this mix-and-match strategy among LT recipients are eagerly awaited.
In univariate analysis, risk factors associated with rPSC were age <30 years at LT (p = 0.03), inflammatory bowel disease (IBD) at placement on LT waiting list (p = 0.001), maintenance steroid therapy (p < 0.0001), acute rejection after LT (p = 0.05), right liver transplant (p = 0.02). Maintenance treatment with AUDC after LT did not reduce the risk of rPSC.

Our large study with long follow-up strongly confirms that rPSC after LT for CSP is common, leading in a significant number of cases to one or more reLT. Independent risk factors were age <30 years at LT, 8995 were in Covid era. LT activity decreased since September 2020 by 3.4% every month for any transplant and 22% for HCC. LT activity increased by 4.5% for ALD since 11/2020 and 17% for ACLF 2 since 03/2021. LT activity decreased for NASH and HCV by 2.5% and 1% respectively every month and increased for alcoholic hepatitis by 4.5% without any jointpoint in Covid era. Monthly MELD score increased by 0.7 (Std. Error 0.17) and 0.36 (Std. Error 0.13) since 06/2020 for HCV and HCC respectively. Regional analysis showed Covid impact with 12.4–24.1% decrease in LT activity across the four regions. However, this was heterogeneous for overall number of LT, etiology, and for ACLF 2–3 (Table).

**Conclusion:** Covid–19 pandemic impacted LT activity in the US, with a decrease in LT for HCC, and increase for ALD and severe ACLF. Impact across regions is homogeneous for HCC, but not on other changes. Strategies are needed to reorganize cirrhosis patients in community to overcome after effects of Covid-19.

**Table: (abstract: SAT240): Joinpoints in trends of monthly LT.**

<table>
<thead>
<tr>
<th>Indication</th>
<th>Northeast</th>
<th>Time</th>
<th>Slope (95% CI)</th>
<th>Midwest</th>
<th>Time</th>
<th>Slope (95% CI)</th>
<th>South</th>
<th>Time</th>
<th>Slope (95% CI)</th>
<th>West</th>
<th>Time</th>
<th>Slope (95% CI)</th>
</tr>
</thead>
<tbody>
<tr>
<td>HCV</td>
<td>04/18–05/21</td>
<td>–2.8</td>
<td>(–3.7––1.9)*</td>
<td>04/18–05/21</td>
<td>–2.1</td>
<td>(–3.2––1.0)*</td>
<td>04/18–05/21</td>
<td>–2.4</td>
<td>(–3.1––1.7)*</td>
<td>04/18–05/21</td>
<td>–2.3</td>
<td>(–3.1––1.4)*</td>
</tr>
<tr>
<td>ALD</td>
<td>04/18–05/21</td>
<td>1.9</td>
<td>(1.6–2.3)*</td>
<td>04/18–05/21</td>
<td>1.3</td>
<td>(1.0–1.6)*</td>
<td>04/18–05/21</td>
<td>2.0</td>
<td>(1.7–2.3)*</td>
<td>04/18–05/21</td>
<td>11/20–05/21</td>
<td>6.6</td>
</tr>
<tr>
<td>NASH</td>
<td>04/18–05/21</td>
<td>–1.0</td>
<td>(–1.8––0.1)*</td>
<td>04/18–05/21</td>
<td>–0.2</td>
<td>(–0.7–0.3)</td>
<td>04/18–05/21</td>
<td>0.3</td>
<td>(0.1–0.8)</td>
<td>04/18–05/21</td>
<td>0.4</td>
<td>(–1.1–0.2)</td>
</tr>
<tr>
<td>HCC</td>
<td>04/18–05/21</td>
<td>–1.8</td>
<td>(–2.9––0.7)*</td>
<td>04/18–05/21</td>
<td>–12.4</td>
<td>(–21.1––9.5)*</td>
<td>04/18–05/21</td>
<td>–2.0</td>
<td>(–2.6––1.5)*</td>
<td>04/18–05/21</td>
<td>–2.4</td>
<td>(–3.3––3.3)</td>
</tr>
<tr>
<td>ACLF 2–3</td>
<td>04/18–05/21</td>
<td>–1.4</td>
<td>(–2.1––0.2)*</td>
<td>04/18–05/21</td>
<td>1.7</td>
<td>(1.3–2.1)*</td>
<td>04/18–05/21</td>
<td>1.7</td>
<td>(1.3–2.1)*</td>
<td>04/18–05/21</td>
<td>1.1</td>
<td>(0.7–1.5)</td>
</tr>
<tr>
<td>Alcoholic hepatitis</td>
<td>04/18–05/21</td>
<td>3.8</td>
<td>(2.5–5.2)*</td>
<td>04/18–05/21</td>
<td>3.0</td>
<td>(1.7–4.3)*</td>
<td>04/18–05/21</td>
<td>3.3</td>
<td>(1.9–4.8)*</td>
<td>04/18–05/21</td>
<td>4.3</td>
<td>(3.1–5.4)</td>
</tr>
<tr>
<td>All LT**</td>
<td>04/18–05/21</td>
<td>–0.8</td>
<td>(–1.1––0.4)*</td>
<td>04/18–05/21</td>
<td>–0.6</td>
<td>(–0.9––0.3)*</td>
<td>04/18–05/21</td>
<td>–0.7</td>
<td>(–1.1––0.4)*</td>
<td>04/18–05/21</td>
<td>–0.2</td>
<td>(–0.7–0.2)</td>
</tr>
</tbody>
</table>

*p < 0.05.
SAT241
Perinatal outcomes in liver transplant patients—possible positive effect of aspirin prophylaxis
Marius Braun1, Gil Ze'evit2, Eran Haradi3, Arnon Wiznitzer2, Alyssa Hochberg2, Michal Cohen-Naffaly4, Assaf Issachar1, Orly Sneh Arbi5, Yael Haridi6, Eviatar Nesher2, Eelin Oxtud6, Amir Shlomai1, Ran Tur-Kaspa1, 1Liver Institute, Petah Tikva, Israel, 2Ob Gyn, Petah Tikva, Israel, 3Transplant, Petah Tikva, Israel
Email: m.braun_md@yahoo.com

Background and aims: To describe perinatal outcomes in liver transplanted (LT) women and evaluate the effect of low-dose aspirin treatment in these women.

Method: An observational retrospective study examining perinatal outcomes among liver transplant recipients, between 2016 and 2020 at a single university-affiliated tertiary medical center in Israel. Demographic, obstetric and clinical data were obtained from electronic health records. The role of aspirin was explored.

Results: Ten LT patients delivered 13 babies. All the patients received tacrolimus, 9 (69%) low dose prednisone and the liver kidney transplant (LKT) also received azathioprine. The 2 patients that were pregnant during the first year after LT had premature deliveries (week 31, 32) Regarding maternal outcomes, 2 women (16%) developed preeclampsia, 2 (16%) gestational diabetes, three (24%) postpartum infection, and one -postpartum hemorrhage. Median gestational age at delivery was 37 weeks (31–39 weeks), with 6 preterm births (31–36 weeks) and a median birthweight of 3072 g (1450–4100 g). All the babies had high Apgar scores and normal development, but the baby born at week 31 had to be ventilated for a week and is healthy with normal development at 2 year follow-up. Low-dose aspirin (100 mg daily) was administered to LT patients beginning 2018 and was given in 5 (38%) of the pregnancies. Of the women receiving low-dose aspirin, none developed hypertensive disease or suffered excessive bleeding during pregnancy.

SAT242
Antibody response after a third dose of the mRNA-1273 SARS-CoV-2 vaccine in liver transplant recipients
Aitor Odriozola Herrán1, María Del Barrio1, Antonio Cuadra1, José Ignacio Forcén2, Lidia Amigo1, David San Segundo Arribas3, María Rodríguez-Cundín4, María Rebollo5, Roberto Fernandez4, Federico Castillo4, María Achalandabaso4, Juan Andrés Echeverría4, Juan Carlos Rodríguez-San Juan5, Marcos López-Hoyos5, Juan Carlos Rodríguez Duque1, Álex García Tellado5, Javier Crespo1, Emilio Fabrega1, 1University Hospital Marqués de Valdecilla, Gastroenterology and Hepatology Service, Santander, Spain; 2University Hospital Marqués de Valdecilla, Immunology, Santander; 3University Hospital Marqués de Valdecilla, Preventive Medicine, Santander, Spain; 4University Hospital Marqués de Valdecilla, General Surgery, Santander, Spain; 5University Hospital Marqués de Valdecilla, Internal Medicine, Santander, Spain
Email: aodrihe54@gmail.com

Background and aims: Recent studies showed that antibody titers after vaccination against severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in liver transplant recipients (LTR) are diminished as compared to the general population, suggesting the possible value of a third booster dose. We aimed to characterize the humoral response after three doses of the Moderna mRNA-1273 vaccine in LTR.

Method: The cohort comprised 129 adult LTR who received a third homologous dose of the mRNA-1273 SARS-CoV-2 vaccine. Humoral response was evaluated using plasma levels of anti-SARS-CoV-2 spike protein S1 immunoglobulin (Abbott® SARS-CoV-2 anti-spike IgG II assay, positive >50 AU/ml) measured a median of 30 days (IQR, 30–37.7 days) after the third vaccine injection.

Results: LTR (median age 63 [IQR, 56–68] years, 76.7% men) had a mean anti-S1 antibody level of 8,388 [SD, ± 10,836.9] AU/ml after the third vaccine injection; and their antibody titers increased significantly from 9426 [SD, 11,057.5] AU/ml to 29,449 [SD, 15,460.5] AU/ml (p = 0.01).

<table>
<thead>
<tr>
<th>Laboratory parameters (SD)</th>
<th>3rd dose of moderna (129)</th>
<th>Seropositive (125)</th>
<th>Seronegative (4)</th>
<th>p</th>
</tr>
</thead>
<tbody>
<tr>
<td>Haemoglobin (g/dL)</td>
<td>14.9 (<em>± 9.3</em>)</td>
<td>12.7 (± 1.5)</td>
<td>0.635</td>
<td></td>
</tr>
<tr>
<td>Platelets (G/L)</td>
<td>169.9 (<em>± 61.3</em>)</td>
<td>150.0 (± 25.2)</td>
<td>0.518</td>
<td></td>
</tr>
<tr>
<td>Leukocytes (G/L)</td>
<td>5.9 (<em>± 1.6</em>)</td>
<td>6.5 (± 1.4)</td>
<td>0.474</td>
<td></td>
</tr>
<tr>
<td>Lymphocytes (G/L)</td>
<td>3.4 (<em>± 1.8</em>)</td>
<td>1.5 (± 0.8)</td>
<td>0.832</td>
<td></td>
</tr>
<tr>
<td>eGFR (ml/min/1.73 m²)</td>
<td>69.4 (± 18.9)</td>
<td>32.3 (± 17.3)</td>
<td>&lt;0.001</td>
<td></td>
</tr>
</tbody>
</table>

Conclusion: Successful pregnancy is feasible in stable liver transplant patients. Patients with unstable liver grafts within the first year post transplant have poorer maternal fetal outcomes. Aspirin use is safe in pregnant LT patients and might improve the pregnancy outcome.
Sixteen patients (12.4%) were non-responders after the second vaccine dose. After the third dose, twelve of the sixteen (75%) initial non-responders produced anti-spike antibody (3, 633 [SD, 8, 361] AU/ml). Non-response after third dose was associated with mofetil mycophenolate treatment (75% vs 23.2%) (p < 0.001), a higher dose of this drug (1, 666.7 [SD, ± 577, 6] vs 1068, 9 [SD, ± 394, 7]) (p = 0.02), and lower estimated glomerular filtration rate (32.3 [SD, ± 173] vs 69.4 [SD, ± 18.9]) (p = 0.001).

Conclusion: our study showed that administration of a third dose of the mRNA-1273 SARS-CoV-2 to LT improved the immunogenicity of the vaccine. Lower estimated glomerular filtration rate and immunosuppressive regimens with mycophenolate were associated with a poorer response to vaccination.

SAT243
Early post liver transplant rescue treatment with sofosbuvir/velpatasvir/voxilaprevir in patients experienced to NS5A-inhibitors
Margherita Saracco1, Francesco Tandoi2, Alberto Calleri1, Donatella Cocchis2, Giorgia Rizza2, Renato Romagnoli2, Silvia Martini1, 1AOU Città della Salute e della Scienza di Torino, General Surgery 2U, 2AOU Città della Salute e della Scienza di Torino, Gastrohepatology Unit; 1AOU Città della Salute e della Scienza di Torino, General Surgery 2U, Liver Transplantation Center
Email: margherita.saracco@gmail.com

Background and aims: Direct acting antivirals (DAA) revolutionized the HCV treatment landscape. In patients (pts) who are HCV viremic at liver transplant (LT), early post-LT DAA therapy (tx) prevents graft damage and extrahepatic HCV involvement. Few data are available regarding pts who are HCV NS5B+NS5A inhibitors experienced at LT. We aimed to describe our first 6 pts treated early after LT with sofosbuvir/velpatasvir/voxilaprevir (SOF/VEL/VOX) for 12 weeks.

Method: From January 1th 2019 to November 1th 2021, 436 pts underwent LT in our Center. Among 46 pts who were viremic at LT, 6 were experienced to NS5A inhibitors. SOF/VEL/VOX was started as soon as graft function was optimal with stable immunosuppression tx (standard combination: steroid, tacrolimus, mycophenolate mofetil).

Results: At LT, the median age of our 6 pts was 54 years and median MELD 13. Median donor age was 70 years. Median cold ischemia time (CIT) 448 minutes. Pt #4 received a graft from a HBCAb-positive donor with 50% macrovesicular steatosis and pt #6 received a graft from a 82-year-old donor; both grafts underwent hypothermic oxygenated machine perfusion. Five pts were HCV genotype (GT) 3 and one 1a; the median post-LT HCV RNA was 618,180 UI/ml, before tx. Pt #6 (GT3) received HCV viremic donor (naive GT2; Ishak: grading 3/18, fibrosis 1/6) and donor HCV strains replaced the recipient’s (shift from GT3 to GT2). The median time from LT to DAA tx was 15 days. Four pts reached sustained virological response after 12 weeks by the end of tx (SVR12) and remained negative after a median follow-up of 587 days, range 42–831 days. Pt #6 is still on tx (week 3 with HCV RNA <15). Pt #3 interrupted the DAA tx at week 8 for cholestatic hepatitis (AST/ALT 62/56 UI/L, GGT/ALP 576/1294 UI/L, bilirubin 12 mg/dl); liver biopsy was consistent with drug-induced hepatitis. Bilirubin dropped to 4 mg/dl at day 7 after tx withdrawal and normalized within 28 days; HCV RNA remained negative from day 14 of tx (follow-up of 400 days). Immunosupression levels were stable on DAA tx.

Conclusion: Early use of post-LT DAA tx was successful in pts who were HCV viremic at LT and experienced to NS5B+NS5A inhibitors. One pt developed cholestatic hepatitis which reverted after prompt interruption of tx. Early post-LT DAA tx prevented liver damage by HCV and allowed the use of suboptimal grafts (old donor, HCV viremic donor or with moderate macrovesicular steatosis).

SAT244
Inclusion of body composition parameters in MELD score leads to optimization of predictive performance in patients with cirrhosis
Maryam Ebadi1, Rhonda J. Rosychuk2, Elora Rider1, Abha Dunichand-Hoedl3, Maryam Motamedrad3, Rahima A. Bhanji1, Aldo J Montano-Loza1, 1University of Alberta, Division of Gastroenterology and Liver Unit, Edmonton, Canada; 2University of Alberta, Division of Infectious Diseases, Department of Pediatrics, Edmonton, Canada; 3University of Alberta, Human Nutrition and Metabolism, Edmonton, Canada
Email: montanol@ualberta.ca

Background and aims: Model for end-stage liver disease (MELD) score has been shown to estimate the risk of short-term mortality in patients awaiting liver transplant (LT). Given the decreasing predictive performance of MELD and the improved prognostication using body composition parameters in cirrhosis, inclusion of these parameters may lead to optimization of the organ allocation criteria in LT candidates. The aim of this study was to determine the performance of individual and combined body composition parameters by sex and to compare their performance with MELD in predicting pre-LT mortality.

Method: CT images, from LT evaluation of 860 patients with cirrhosis were used to determine height-normalized indices and radiodensity of muscle, visceral and subcutaneous adipose tissue (SAT) expressed by cm2/m2 and Hounsfield Unit (HU), respectively. Performance of body composition features and MELD score for mortality prediction was assessed at 3-, 6-, and 12-months by area under the receiver operating characteristic curve (AUROC) in the presence of competing risks.

Results: Sixty-six percent of the patients were male with the MELD score of 14 ± 8. Evaluated patients were followed for a mean time of 24 months. Performance of MELD and body composition features for mortality prediction is presented in Table. Among individual body composition features in male patients, SAT radiodensity outperformed other features when considering each time-point. Among various combinations in males, performance of combined skeletal muscle index and SAT radiodensity were superior to that of MELD. Addition of skeletal muscle index and SAT radiodensity to the MELD outperformed MELD at each time point in males. In females, inclusion

<table>
<thead>
<tr>
<th>Pt #</th>
<th>Age, years</th>
<th>Sex</th>
<th>HCC</th>
<th>MELD at LT</th>
<th>HCV GT</th>
<th>Previous DAA</th>
<th>HCV RNA at LT (U/ml)</th>
<th>Macroversicular Steatosis</th>
<th>Age, years</th>
<th>CIT (min)</th>
<th>Days from LT to DAA</th>
<th>HCV RNA &lt;15 U/ml</th>
<th>SVR12</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>46</td>
<td>M</td>
<td>No</td>
<td>14</td>
<td>3</td>
<td>SOF/VEL</td>
<td>1370000</td>
<td>&lt;5%</td>
<td>55</td>
<td>312</td>
<td>6</td>
<td>26500</td>
<td>Week 1</td>
</tr>
<tr>
<td>2</td>
<td>56</td>
<td>M</td>
<td>Yes</td>
<td>8</td>
<td>3</td>
<td>SOF/VEL</td>
<td>7066296</td>
<td>&lt;5%</td>
<td>76</td>
<td>439</td>
<td>9</td>
<td>211200</td>
<td>Week 2</td>
</tr>
<tr>
<td>3</td>
<td>48</td>
<td>M</td>
<td>Yes</td>
<td>15</td>
<td>3</td>
<td>SOF/VEL</td>
<td>62400</td>
<td>25%</td>
<td>43</td>
<td>391</td>
<td>21</td>
<td>779000</td>
<td>Week 1</td>
</tr>
<tr>
<td>4</td>
<td>57</td>
<td>M</td>
<td>No</td>
<td>20</td>
<td>1a</td>
<td>SOF/VEL/EDV</td>
<td>3716</td>
<td>50%</td>
<td>63</td>
<td>456</td>
<td>47</td>
<td>457360</td>
<td>Week 2</td>
</tr>
<tr>
<td>5</td>
<td>58</td>
<td>M</td>
<td>Yes</td>
<td>9</td>
<td>3</td>
<td>SOF/VEL</td>
<td>1250000</td>
<td>10%</td>
<td>83</td>
<td>511</td>
<td>20</td>
<td>18500000</td>
<td>Week 3</td>
</tr>
<tr>
<td>6</td>
<td>51</td>
<td>M</td>
<td>No</td>
<td>11</td>
<td>3</td>
<td>SOF/VEL</td>
<td>1490000</td>
<td>0%</td>
<td>82</td>
<td>578</td>
<td>8</td>
<td>5370000</td>
<td>Week 3</td>
</tr>
</tbody>
</table>

Table: (abstract: SAT243)
of SAT and muscle radiodensity within MELD score improved the discriminative performance of MELD, but this was not significant.

<table>
<thead>
<tr>
<th>Gender</th>
<th>3-month</th>
<th>6-month</th>
<th>12-month</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Male</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Skeletal muscle index (SMI)</td>
<td>66.5 (58.2–74.7)</td>
<td>66.5 (59.9–73.1)</td>
<td>62.3 (56.5–68.2)</td>
</tr>
<tr>
<td>Subcutaneous adipose (SAT) radiodensity</td>
<td>74.7 (68.0–81.5)</td>
<td>69.1 (62.9–75.3)</td>
<td>62.7 (56.9–68.6)</td>
</tr>
<tr>
<td>SAT radiodensity + SMI</td>
<td>76.4 (69.7–83.0)</td>
<td>72.7 (66.9–78.4)</td>
<td>66.1 (60.6–71.7)</td>
</tr>
<tr>
<td><strong>Female</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Muscle radiodensity</td>
<td>65.9 (56.6–75.3)</td>
<td>64.8 (56.5–73.1)</td>
<td>63.2 (55.4–70.9)</td>
</tr>
<tr>
<td>SAT radiodensity</td>
<td>66.1 (58.3–73.8)</td>
<td>61.5 (53.6–69.5)</td>
<td>62.9 (55.6–70.3)</td>
</tr>
<tr>
<td>SAT radiodensity + SMI</td>
<td>72.0 (64.4–79.6)</td>
<td>69.4 (62.3–76.4)</td>
<td>68.7 (62.0–75.5)</td>
</tr>
<tr>
<td><strong>MELD</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MELD + SAT radiodensity + SMI</td>
<td>76.9 (69.0–84.7)</td>
<td>71.2 (64.0–78.4)</td>
<td>68.5 (61.7–75.3)</td>
</tr>
<tr>
<td><strong>P value</strong></td>
<td>0.004</td>
<td>0.001</td>
<td>0.009</td>
</tr>
</tbody>
</table>

**Conclusion:** Inclusion of skeletal muscle index and SAT radiodensity within MELD was associated with an improvement in the prediction of mortality in male patients with cirrhosis.

**SAT245**

Long-lasting seropositivity after anti SARS-CoV-2 vaccination in pre liver transplant patients

Alberto Calleri1, Margherita Saracco 1, Renato Romagnoli2, Silvia Martini1, 1AOU Città della Salute e della Scienza di Torino. Gastrohepatology Unit, Turin, Italy; 2AOU Città della Salute e della Scienza di Torino, General Surgery 2U, Liver Transplantation Center, Turin, Italy

Email: alberto.calleri.md@gmail.com

**Background and aims:** Since the beginning of COVID-19 pandemic, global vaccination represents the goal to fight the virus spreading. Anti SARS-CoV-2 vaccines demonstrated a high rate of success in preventing severe COVID-19 and decreasing the infection rate, but few data are available about special population such as pre liver transplant (LT) patients (pts). Serological tests for IgG anti Spike reflect the humoral response to vaccination. We aimed to evaluate the longevity of the humoral response to mRNA vaccine in pts listed for LT in our Center.

**Method:** From January 2021 to October 2021 we consecutively enrolled all pts on our LT waiting list who completed anti SARS-CoV-2 mRNA vaccination. Pts with previous COVID-19 received a single vaccine dose within 6 months after infection. All the other pts received 2 doses, administered 21 (Pfizer-BioNTech) or 28 days (Moderna) apart. Pts were tested for SARS-CoV-2 IgG antibodies (LIASON® SARS-CoV-2 Triumeric® IgG assay, positive value ≥33.8 BAU/ml) 1 month after mRNA vaccination and then every 2 months until LT. Mask wearing indoors and physical distancing measures were recommended for all pts.

**Results:** During the study period, 91 pre-LT pts completed the anti-SARS-CoV-2 vaccination: 80 pts received 2 vaccine doses, while 11 pts received only 1 dose, as per protocol. 94% of the pts received Pfizer-BioNTech and 6% Moderna COVID-19 vaccine. 65% were male, median age 56 years, BMI 25 kg/m², eGFR 95 ml/min, MELD 12 (IQR 8–15). 32% was affected by viral cirrhosis and 43% by hepatocellular carcinoma; 6 pts were treated with steroid and 1 with mycophenolate mofetil due to autoimmune cirrhosis and 1 pt was affected by common variable immunodeficiency.

After a median time of 23 days from the last vaccine dose (T1), 86/91 (95%) seroconverted (median titer 1970 BAU/ml, IQR 645–2080). During follow-up none of retested pts became IgG negative, however their titer progressively decreased: -after a median time of 72 days from the last vaccine dose (T2), 61/64 (95%) tested again IgG positive (median titer 1480 BAU/ml, IQR 307–2040); -at T3 (113 days from vaccination) 42/43 (98%) pts remained positive and their titer significantly dropped (779 BAU/ml, IQR 307–2040). –23 pts were retested at T4 (140 days after vaccination) and all of them remained IgG positive (median titer 320 BAU/ml, IQR 148–2080). (T1 vs T2, paired p = 0.22; T2 vs T3 p < 0.001; T3 vs T4, p = 0.02; T1 vs T4, p = 0.008). (Figure 1).

At the end of a median follow-up period of 190 days (IQR 175–202) from vaccination, none of the patients developed COVID-19. No serious adverse events were registered following vaccination.

**Conclusion:** In our 91 pre-LT patients, mRNA anti-SARS-CoV-2 vaccination elicited a high rate of seroconversion (95%) within 1 month. We observed a progressive significant decrease in IgG titer during a median follow-up of 190 days after vaccination. Nevertheless, none of our pre-LT pts developed COVID-19.

**SAT246**

The outcome of living donor versus deceased donor liver transplantation for hepatocellular carcinoma: a systematic review and meta-analysis

Beshoy Effat Elkomos1, Amr Abdelaal1, Mostafa Abd1, Remon Mamdouh1, 1Faculty of Medicine, Ain Shams University, General surgery, Cairo, Egypt

Email: beshoy3ff@gmail.com

**Background and aims:** A potential solution to the deceased donor organ shortage is to expand the organ donor pool to include living donors. Many studies have analyzed outcomes of living donor transplantation (LDLT) versus deceased donor liver transplantation (DDLT) for hepatocellular carcinoma (HCC) and the predictors of recurrence after transplantation.

**Method:** PubMed, Scopus, Web of science, Cochrane library were searched for eligible studies from inception to 1 July 2021 and a systematic review and meta-analysis were done to detect patient overall survival (OS), Intention to treat overall survival (ITT-OS), disease-free survival (DFS), and recurrence for LDLT vs DDLT recipients.
Patients were grouped by gender and age (>65 and ≤65). The etiology was established based on histology, combined radiological and laboratory features. Treatments were divided into curative (orthotopic liver transplantation, radiofrequency ablation, microwave ablation, surgical resection), non-curative (stereotactic body radiation therapy, transarterial chemoembolization, transarterial embolization, target drugs) and best supportive care (BSC). Cox multivariate regression analysis was performed to identify the risk factors for survival.

**Results:** The cohort consisted of 419 (84.1%) men, who had a higher median body mass index (26.8 vs 25.4, p = 0.037), more frequently both alcohol and non-alcoholic fatty liver disease (12.9% vs 3.8%, p <0.05), cirrhosis (80.7% vs 70.9%, p = 0.050), and diabetes (35.8% vs 22.8%, p = 0.025) in comparison to women. For the patients younger than 65 years of age, the median OS of men was 856 vs 828 days (p = 0.025) in comparison to women.

**Conclusion:** This study is in consonance with the view that the cancer biology (not the graft type) is the most important determinant of recurrence and survival after LT. However, LDLT provided a much better survival benefit to HCC patients especially in regions that suffer from low deceased organ availability.

**SAT247**

**Impact of gender on survival of hepatocellular carcinoma**

Chaoran Jin1, Birgit Schwacha-Eipper1, Jean-François Dufour2, Pompilia Radu2.

**Background and aims:** Risk of hepatocellular carcinoma (HCC) is considerably higher in men compared to women; however, there is inconclusive evidence on the effect of gender on HCC prognosis. We aimed to evaluate whether gender influences overall survival (OS).

**Method:** A prospective cohort, consisting of 498 HCC patients included between 2010 and 2020 at University Clinic for Visceral Surgery and Medicine, Inselspital, Bern, was retrospectively analysed.

**Results:** 35 studies with total of 7822 patients were included. The 1-, 3-, and 5-year OS showed trivial improvement for LDLT recipients. However, LDLT and DDLT recipients had similar 5-, 6- and 10-year OS. Moreover, our subgroup analysis showed equal long term OS between LDLT and DDLT for those who were within Milan criteria (MC). Nevertheless, beyond MC, there was a better prognosis for the patients who underwent LDLT. In addition to that, a significant improvement in the ITT-OS was observed for LDLT recipients. In the group >65 the median OS was 856 vs 828 days (p = 0.920).

**Conclusion:** This study is in consonance with the view that the cancer biology (not the graft type) is the most important determinant of recurrence and survival after LT. However, LDLT provided a much better survival benefit to HCC patients especially in regions that suffer from low deceased organ availability.
Conclusion: Our single-center experience suggests that HCC females <65 years have inferior survival and a lower assignment rate to curative therapies, particularly liver transplantation than HCC males <65 years.

SAT248
Effectiveness of MRI methods in the assessment of hepatic steatosis in living liver donors
Digdem Kuru Öz1, Zeynep Melekoğlu Elliott2, Ayşegül Gürsoy Çoruh1, Mehmet Adıgüzel1,1, Mesut Gumussoy2, Serkan Duman2, Ramazan Erdem Er2, Onur Kırkmker3, Deniz Balci3, Hale Gökcen2, Ramazan İdilman1, Ayse Erdem1, 1Ankara University School of Medicine, Radiology, Ankara, Turkey; 2Ankara University School of Medicine, Gastroenterology; 3Ankara University School of Medicine, General Surgery
Email: digdem_k@hotmail.com

Background and aims: Liver biopsy is still gold standard diagnostic method for accurate quantification of steatosis. However, there is still no consensus in terms of which diagnostic methods to use for donor selection and which threshold value to acceptable. The aims of the present study, to determine utility of proton density fat fraction (PDFF) measurements for quantifying the liver fat content in potential donor candidates, and compare these results with liver biopsy findings.

Method: Between January 2017 and March 2021, a total of 134 living liver donor candidates imaged on a 1.5 tesla Magnetic Resonance Imaging (MRI) device were included. Magnetic resonance spectroscopy (MRS) was performed with a multiecho T2-corrected stimulated echo acquisition mode sequence. MRS fat fraction (FF) was calculated by placing an independent voxel in the right lobe of the liver. PDFF was calculated by 2 radiologists from the parametric FF map obtained with a multi-echo Dixon sequence using at least 4 regions of interest placed in the right lobe of the liver. The MRI measurement results were compared with pre- and/or intraoperative biopsy results. All liver biopsy specimens were evaluated by the Kleiner’s method. Spearman correlation analysis was performed to determine the relationship between MRS and PDFF and histopathology. Receiver Operating Characteristic analysis was used for the diagnostic efficiency of the methods.

Results: Median age was 31 years. The gender was predominantly male (59.7%). On the liver biopsy evaluation, 25 (18.7%) had grade I steatosis, whereas 109 (81.3%) did not have steatosis. Median PDFF calculated with MRI was 3% (0.5–15%). Signal fat fractions obtained by MRS and PDFF methods were statistically different in the groups with and without steatosis (p < 0.001, p = 0.019). There was a high degree of positive linear correlation between MRS and PDFF methods (r = 0.819, p < 0.001). The area under the curve was 0.848 and 0.824 (p < 0.001) at the cut-off of 5.05% and 3.25% for MRS and PDFF, respectively.

Conclusion: The present study indicates the MRS and PDFF measurements provided a non-invasive, accurate estimation of the presence and grading of hepatic steatosis in liver donor candidates. Such modalities can be used effectively in donor selection for living donor liver transplantation.

SAT249
Long-term outcomes of donation after cardiac death and living donor liver transplant for primary sclerosing cholangitis
Dilip Moonka1, Yoshihiro Kitajima4, Tommy Ivanics2, Kelly Collins2, Michael Rizzari2, Atsushi Yoshida2, Marwan Abouljoud3, Shunj Nagai2, 1Henry Ford Health System, Gastroenterology and Hepatology, Detroit, United States; 2Henry Ford Health System, Transplant Institute, Detroit
Email: dmoonka1@hfhs.org

Background and aims: The use of donation after circulatory death (DCD) grafts is reported to be a risk factor for worse outcomes after liver transplant (LT) for primary sclerosing cholangitis (PSC) due to a higher risk of biliary complications. However, long-term outcomes comparing DCD, donation after brain death (DBD) donors, and living donor LT (LDLT) have not been fully investigated in a recent cohort. This study aims to assess outcomes of LT for PSC with each graft type.

Method: Using OPTN/UNOS data, we analyzed adult LT patients with PSC or primary biliary cholangitis (PBC) between 2002 and 2020. Patients with exception scores, multi-organ or re-transplant were excluded. One, 5, and 10-year graft survival (GS) were compared between PSC and PBC groups (as control). Next, outcomes were compared between DBD-LT, DCD-LT, and LDLT in each group. In PSC, the three types of donor grafts were compared for cause of graft loss. Finally, transplant outcomes were analyzed in an early era (2002–2010) and late era (2011–2020). Risks were adjusted by recipient variables.

Results: 3, 946 PSC and 2, 675 PBC patients were eligible. Among PSC patients, 3, 099 (78.5%), 151 (3.8%), and 696 (17.7%) received DDB-LT, DCD-LT, and LDLT, respectively. One, 5, and 10-year GS were comparable between PSC and PBC groups. In PSC, DCD-LT had significantly higher risks of 1, 5, and 10-year graft loss than DBD-LT (1-year: HR 1.87, p = 0.007, 5-year: HR 1.74, p = 0.001, 10-year: HR 1.60, p = 0.003) whereas LDLT had similar risks of 5 and 10-year graft loss. In contrast, outcomes were comparable between donor types in PBC. As a cause of graft loss, DCD-LT had a significantly higher incidence of both biliary complications and PSC recurrence than other graft types. 16.5% of DCD-LT lost grafts because of PSC recurrence or biliary issues vs 4.5% for DBD-LT and 5.1% for LDLT. Incidence of re-transplant was highest in DCD-LT (DCD-LT 18.5% vs DBD-LT 10.2% vs LDLT 10.6%, p = 0.005). This finding was more prominent in the early era, whereas risks of 3- and 5-year graft loss were similar among all graft types in the late era (Figure). When comparing profiles of DCD donors for PSC between eras, CIT was shorter in late era (6.5 vs 5.2 hours, p = 0.001)

S778 Journal of Hepatology 2022 vol. 77(S1) | S665–S939
whereas age and proportion of organ sharing were similar between 2 groups.

**Conclusion:** In PSC patients, the use of DCD grafts was associated with significantly worse post-transplant outcomes because of PSC recurrence and biliary complications. LDLT had similar outcomes to DBD-LT. However, the negative effect of DCD grafts was blunted in the more current era. The use of DCD grafts is an appropriate option for PSC with appropriate donor selection.

**SAT250**

**Patients with acute-on-chronic liver failure have significantly greater healthcare resource utilization after liver transplantation**

Vinay Sundaram, Christina Lindenmeyer, Kirti Shetty, Robert Rahimi, Atef Alattar, Gianina Flocco, Brett Fortune, Cynthia Gong, Suryanarayan Challa, Haripriya Maddur, Janice Jou, Michael Kriss, Lance Stein, Ross Vyhmeister, Ellen Green, Braide Campbell, Josh Levitsky, Constantine Karvellas.

1Cedars-Sinai Medical Center, Los Angeles, United States; 2Cleveland Clinic Main Campus, Cleveland, United States; 3University of Maryland, College Park, United States; 4Baylor Scott and White Medical Center-Grapevine, Grapevine, United States; 5Weill Cornell Medicine, New York, United States; 6University of Southern California, Los Angeles, United States; 7Tampa General Hospital, Tampa, United States; 8Oregon Health and Science University, Portland, United States; 9University of Colorado Denver, Denver, United States; 10Piedmont Atlanta Hospital, Atlanta, United States; 11Northwestern Medical Center, Chicago, United States; 12University of Alberta, Edmonton, Canada

Email: vinaysundaram@yahoo.com

**Background and aims:** Data is lacking regarding healthcare resource utilization after liver transplantation (LT) for patients with acute-on-chronic liver failure (ACLF).

**Method:** We retrospectively reviewed data from 10 centers in North America of patients transplanted from years 2018–2019, who required management in the intensive care unit prior to LT. ACLF was identified using the EASL-CLIF criteria.

**Results:** We studied 318 patients of whom 106 patients (33.3%) had no ACLF, 61 (19.1%) had ACLF-1, 77 (24.2%) had ACLF-2, and 77 (24.2%) had ACLF-3 at LT. Multivariable negative binomial regression analysis demonstrated a significantly longer length of stay for patients with ACLF-1 (1.9 days, 95% CI 0.8–7.51), ACLF-2 (6.7 days, 95% CI 2.5–24.3), and ACLF-3 (19.3 days, 95% CI 1.2–38.7), compared to recipients without ACLF. Presence of ACLF-3 at LT was also associated with longer length of dialysis post-LT (9.7 days, 95% CI 4.6–48.8) relative to lower grades. Logistic regression analysis revealed greater likelihood of discharge to a rehabilitation center among recipients with ACLF-1 (OR = 1.79, 95% CI 1.09–5.73). Development of bacterial infection post-LT also predicted LOS (20.9 days, 95% CI 6.1–38.5) and 30-day readmissions (OR = 1.39, 95% CI 1.17–2.25). Cost estimates based on post-LT LOS demonstrated that expenditures were significantly greater for patients transplanted with ACLF, and especially for ACLF-3 (No ACLF: $65,359, ACLF-1: $102,698, ACLF-2: $129,893, and ACLF-3: $244,406, p < 0.001).

**Table:** Multivariable negative binomial regression and logistic regression regarding predictors of post-LT healthcare resource utilization

<table>
<thead>
<tr>
<th>ACLF grade</th>
<th>Post-LT length of stay (days) (Coefficient, 95% CI)</th>
<th>Post-LT length of dialysis (days) (Coefficient, 95% CI)</th>
<th>30-day readmission (OR, 95% CI)</th>
<th>Discharge to rehabilitation center (OR, 95% CI)</th>
</tr>
</thead>
<tbody>
<tr>
<td>No ACLF (reference)</td>
<td>1.9 (0.8, 7.5)</td>
<td>5.1 (2.2–14.0)</td>
<td>1.27 (0.62, 2.57)</td>
<td>1.79 (1.09, 4.54)</td>
</tr>
<tr>
<td>ACLF-1</td>
<td>6.7 (2.5, 24.3)</td>
<td>5.8 (-1.4, 18.5)</td>
<td>1.37 (0.62, 3.04)</td>
<td>2.23 (1.40, 5.73)</td>
</tr>
<tr>
<td>ACLF-2</td>
<td>19.3 (12.3, 38.7)</td>
<td>9.7 (4.6, 48.8)</td>
<td>1.75 (0.87, 3.46)</td>
<td>2.12 (1.11, 5.01)</td>
</tr>
<tr>
<td>ACLF-3</td>
<td>Age</td>
<td></td>
<td></td>
<td>1.05 (1.01, 1.09)</td>
</tr>
<tr>
<td>Braden score &lt;16</td>
<td>13.2 (5.1, 44.0)</td>
<td></td>
<td>5.14 (1.89, 14.0)</td>
<td></td>
</tr>
<tr>
<td>In ICU at LT</td>
<td>7.7 (2.1, 18.1)</td>
<td></td>
<td>1.36 (1.12, 1.57)</td>
<td></td>
</tr>
<tr>
<td>Dialysis at LT</td>
<td>9.2 (2.0, 29.1)</td>
<td>4.9 (1.9, 18.6)</td>
<td>2.00 (1.17, 3.41)</td>
<td></td>
</tr>
<tr>
<td>Mechanical ventilation at LT</td>
<td>5.5 (2.96, 16.0)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Pre-transplant bacterial infection</td>
<td>20.9 (6.1, 38.5)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Post-transplant bacterial infection</td>
<td>2.23 (95% CI 1.17, 4.54)</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**Conclusion:** Patients with ACLF at LT, particularly ACLF-3, have greater post-transplant healthcare resource utilization and costs.
SAT251
Use of statins after liver transplantation is associated with improved survival: results of a nationwide study
Chiara Becchetti1, Melissa Dirichwolf1,2, Jonas Schropp1,4, Giulia Magini1, Beat Mullhaupt5, Franz Immer6, Jean-François Dufour1, Banz Vanessa1, Annalisa Berzigotti1, Jaime Bosch1,8, Inselspital, University Hospital, University of Bern, Department for Visceral Surgery and Medicine, Berne, Switzerland; 2Hospital Privado de Rosario, Santa Fe, Argentina, Liver Unit, Argentina; 3Open University of Cyprus, Cyprus, Department of Computer Science, Cyprus; 4University of Cyprus, Cyprus, Department of Psychology, Cyprus; 5Hôpitaux Universitaires de Genève, Geneva, Switzerland, Service de Transplantation, Geneve, Switzerland; 6University Hospital Zurich, Switzerland, Swiss HPB (Hepato-Pancreato-Biliary) Center and Department of Gastroenterology and Hepatology, Zurich, Switzerland; 7Swisstransplant, the Swiss National Foundation for Organ Donation and Transplantation, Bern, Switzerland, Berne, Switzerland; 8University of Bern, Bern, Switzerland, Department of Biomedical Research, Switzerland
Email: becchettichiara@tiscali.it

Background and aims: Statins are known to have pleiotropic effects that can act favorably on the liver, including protection from endothelial dysfunction and from ischemia reperfusion injury, as well as to increase cold preservation time in experimental grafts. However, there is limited data on the benefit that statins might confer in the liver transplant (LT) setting, either with regard to statin administration in LT recipients or its use in donors. This study aimed at analyzing the effect of statin exposure on recipient and on graft survival.

Method: We included all consecutive adult LT candidates nationwide who received a liver from a deceased donor. The statistical analysis adopted was a multistate modelling approach examining the effect of statin exposure (recipient under statin treatment or liver from donor exposed to statins) on the transition hazards between LT, biliary and/or vascular (B-V) complications, and death, while allowing for recurring events. The observation time was 3 years.

Results: Overall, 998 (696 male, 70%, mean age 54.5 ± 11.1 years) LT recipients were included. 19% of recipients were exposed to statins during the study period. Over the 3-year follow-up period, 141 patients died; there were 40 re-LT and 363 B-V complications. Recipient statin use protected from mortality after-LT (HR = 0.35; 95% CI 0.12–0.97; p = 0.039). However, it was not significantly associated with the occurrence of B-V complications (HR = 1.22; 95%CI = 0.83–1.78; p = 0.307) or re-LT (HR, 1.8e-7; 95%CI, 0-Inf; p = 1). In patients developing B-V complications, statin use significantly protected from mortality (HR = 0.10; 95%CI = 0.01–0.75; p = 0.023) and reduced recurrence of B-V complications (HR = 0.42; 95%CI = 0.18–0.100; p = 0.049). Donor’ statins use prior LT had no significant influence on post-LT outcomes.

Conclusion: Our results show that statin use in recipients appears to confer a survival advantage. Statin administration should therefore be encouraged when indicated.

SAT252
Liver transplantation for hepatocellular carcinoma with extended criteria: performance and applicability of the AFP score after official adoption by the French Organ Sharing Organization ABM: 5-year outcomes
Christophe Duvoux1, Mathilde Petit Dumont2, Georges-Philippe Pageaux3, Ephrem Salamé4, Jérôme Dumortier5, Sylvie Radenne6, Sébastien Dharancy7, Pauline Houssel-Debruy8, Philippe Bacheller9, Laurence Chiche10, François Durand11, Fabrice Muscar12, Jean Gugenheim13, Filomena Conzi14, Jean Hardwigsen15, Christian Jacqulinet16, Corinne Antoine17, Norbert Ngongang18, Vincent Leroy19, Thomas Decaens19, Daniel Cherqui20, Nadia Oubaya21, Henri Mondor Hospital APHP, Paris Est University, ME, Créteil, France; 2Grand Hôpital de l’Est Francilien Site de Meaux, Hepatology and Gastroenterology Department, Meaux, France; 3Saint Eloi Hospital, Liver Department, Montpellier, France; 4Trousseau University Hospital, Liver and Digestive Surgery, Liver Transplantation Unit, Tours; 5Edouard Herriot University Hospital, Liver Department and Liver Transplantation Unit, Lyon, France; 6Hospices Civils de Lyon-, Croix Rousse University Hospital, Liver Department and Liver Transplantation Unit, Lyon; 7Lille University Hospital, Liver Department and Liver Transplantation Unit, Lille, France; 8Rennes University Hospital, Liver Transplantation and Digestive Surgery, Rennes, France; 9Strasbourg University Hospital, Liver and Digestive Surgery, Liver Transplantation Unit, Strasbourg, France; 10Bordeaux University Hospital, Department of Digestive Surgery and Liver Transplantation, Bordeaux, France; 11Beaujon University Hospital-APHP, Liver Department and Liver Transplantation Unit, Clichy, France; 12Toulouse
Background and aims: Composite scores for selection of patients who are candidates for liver transplantation (LT) for HCC with extended criteria are being considered by scientific societies (EASL), subject to a demonstration of the superiority of these models over the Milan criteria and to their audit. The first composite score developed, the AFP score, has been shown superior to Milan criteria and adopted by the French Organ Sharing Organization, ABM, in January 2013 as a selection tool. The aim of this study was to evaluate the applicability and performance of this new strategy.

Method: Adult patients listed and then transplanted for HCC in 15 French TH centers between March 1, 2013, and March 1, 2014, were studied. The primary end point was the incidence of recurrence at 5 years in patients with AFP score ≤2, or >2 or after down-staging. The secondary end points were 5-year survival rates in the same subgroups and the % of transplanted patients with an AFP score ≤2.

Agreement for extraction of the centralized ABM data was obtained among all centers before the start of the study. The statistical analysis was performed with cumulative analysis taking into account death as a competitive event of recurrence.

Results: Over the enrolment period, 507 patients were consecutively listed, among whom 334 (65.9%) were transplanted and are the basis of this study. Median age at listing was 60 [55–63] and 84.7% were male. The median MELD was 10 [8; 15]; 74 patients (22.2%) were outside the Milan criteria. The AFP score was assessed in 331 patients (99.4%) at listing and in 333 patients (99.7%) within 3 months prior to LT. Overall, 297 (89.7%), 12 (3.6%) and 22 (6.7%) patients were transplanted with a final AFP score ≤2, >2, or after down-staging ≤2.

The 5-year recurrence rates were 12.2% [8.9; 16.5], 50% [26.4; 79.2], and 84.7% [71.8; 81.4%] and 33.3% (10.3; 58.8%) respectively.

Conclusion: In this real-life prospective cohort study, including 22% of patients beyond Milan criteria, applicability of the AFP score was high with only 3.6% of patients transplanted with an AFP score >2. The 12%-observed recurrence rate in patients listed and transplanted with an AFP score ≤2 was in strict agreement with the prediction of the model, with a corresponding 77% 5-year survival rate. The AFP score complies with 2018 EASL requirements for an expansion of Milan criteria and can be proposed as a new selection tool for HCC patients.
SAT254
SARS-CoV-2 vaccination in liver transplant recipients: factors affecting immune response and refusal to vaccine
Joanna Raszeja-Wyszomirska1, Maciej K. Janik1, Maciej Wójcicki1, Piotr Milkiewicz1,2, 1Medical University of Warsaw, Liver and Internal Medicine Unit, Warsaw, Poland; 2Pomeranian Medical University, Translational Medicine Group, Szczecin, Poland
Email: joanna.wyszomirska@wum.edu.pl

Background and aims: The effectiveness of SARS-CoV-2 vaccination in liver transplant (LT) recipients varies between 47.5% to 81% with majority of reports focusing on the immune response assessed in the first month after the vaccination. Data on LT recipients willingness to receive vaccine is limited to only a few reports. Here, we analysed the immune response to the SARS-CoV-2 vaccination, factors affecting response and reasons for refusal to receive this vaccine.

Method: Among 300 consecutive LT recipients, 225 (75%) were vaccinated. Seventy-four (25%) subjects were not vaccinated, including 45 (15%) who refused to be vaccinated and 29 (10%) who did not get the vaccine due to medical reasons. The humoral response was assessed by quantitative determination of anti-trimeric spike-protein-specific-IgG antibodies to SARS-CoV-2 by LIAISON® SARS-CoV-2 TrimericS IgG assay (DiaSorin, Italy), which is a chemiluminescence immunoassay (CLIA). Thirty-four vaccinated patients with prior COVID-19 infection were analysed separately.

Results: Among 192 LT recipients vaccinated without prior COVID-19, 65% of them had an immune response (median time of 125 days after the second dose). Older age, worse kidney function and dual immunosuppression negatively affected the humoral response. Mycophenolate mofetil increased the risk of non-response (OR 3.0, 95% CI 1.43–6.25). LT recipients with prior COVID-19 presented with a robust immune response (100%) and with significantly higher IgG antibodies (median 2080 vs 134 BAU/ml; p < 0.001). The antibodies concentration was higher in the first 90 days from the second dose (p = 0.034) and stable when compared between patients who received the vaccination within 90–150 or more than 150 days (Figure 1). Female gender, living in rural area, lower BMI (all p < 0.05) and younger age (p = 0.001) were associated with refusal of the vaccine due to non-medical reasons. In contrast, liver recipients with diabetes and impaired kidney function (both p < 0.01) were more prone to get a vaccine.

Conclusion: Lower immune response after the vaccine among LT recipients may support administration of a third dose. Previous COVID-19 infection dramatically improves response to vaccination in these patients. Sociodemographic factors may play a role in refusal of being vaccinated but this finding require further investigations in other cohorts of transplanted patients.

SAT255
The effect of clinicopathologic findings of hepatocellular carcinoma on posttransplant survival: a multicenter cohort from TASL liver transplantation special interest group
Murat Akylidiz1, Genc Gencdal1, Volkan Ince2, Mülsin Murat Harputluoglu3, Birkan Bozkurt4, Murat Zeytunlu5, Murat Kilic6, Rasim Farejo6, Ilker Turan7, Fulya Günsar7, Zeki Karasu8, Utku Tonguç Yılmaz9, Mesut Akarsu10, Gökhlan Kabaçam10, Elvan Onur Kırımkır11, Ali Atay12, Meral Akdogan Kayhan12, Hale Gökcan13, Gupse Adalı14, Yaman Tokat15, Remzi Emiroğlu15, Kamil Yalçın Polat16, Sezai Yılmaz17, Sedat Karademir17, Ramazan İldıman1, 2Koç University, School of medicine, Center of Liver Transplantation, Department of Gastroenterology, Turkey; 3İnönü University, School of medicine, Center of Liver Transplantation, Department of General Surgery, Turkey; 4İnönü University, School of medicine, Center of Liver Transplantation, Department of Gastroenterology, Turkey; 5İstanbul Bilim University, School of medicine, Center of Liver Transplantation, Department of General Surgery, Turkey; 6Ege University, School of medicine, Center of Liver Transplantation, Department of General Surgery, Turkey; 7İzmir kent Hospital, School of medicine, Center of Liver Transplantation, Department of General Surgery, Turkey; 8Ege University, School of medicine, Center of Liver Transplantation, Department of General Surgery, Turkey; 9Çukurova University, School of medicine, Center of Liver Transplantation, Department of General Surgery, Turkey; 10Çukurova University, School of medicine, Center of Liver Transplantation, Department of General Surgery, Turkey; 11Ankara City Research and Training Hospital, Center of Liver Transplantation, Department of General Surgery, Turkey; 12Ankara City Research and Training Hospital, Center of Liver Transplantation, Department of Gastroenterology, Turkey; 13Ankara University, School of medicine, Center of Liver Transplantation, Department of General Surgery, Turkey; 14Umraniye Research and Training Hospital, Center of Liver Transplantation, Department of Gastroenterology, Turkey; 15Acibadem University, School of medicine, Center of Liver Transplantation, Department of General Surgery, Turkey; 16Memorial Atasehir Hospital, Center of Liver Transplantation, Department of General Surgery, Turkey; 17Çukurova University, School of medicine, Center of Liver Transplantation, Department of General Surgery
Email: akylidizmr@yahoo.com

Background and aims: The aim of the present study was to determine the effect of clinicopathological findings of hepatocellular carcinoma (HCC) on posttransplant survival.

Method: This was a multicenter retrospective study of patients with HCC undergoing LT from 10 tertiary center in Turkey between 2002 and 2020. Datas were retrieved from standardized electronic case report forms in each center.

Results: A total of 1428 patients with HCC underwent LT were included into the study. Viral hepatitis was the most common etiology accounting for 75.6% of patients. Hepatitis B infection was the most cause (58.6%) followed by hepatitis C (12.6%), and cryptohepatitis (13.8%). The mean overall survival (OS) was 178.2 months, whereas the mean progression free survival (PFS) was 44 months. The one and five-year estimated overall survival rate was found 88% and 80. Overall and disease-free survival did not significantly differ between patients with Living Donor LT and patients with Deceased Donor LT (Log Rank for OS p = 0.148 and for PFS p = 0.137, respectively). In univariate analysis, serum AFP level, histologic differentiation, tumor size, Milan and UCSF criteria, the number of tumors, the presence of microvascular and macrovascular invasion were significantly associated with patient survival (p < 0.005). In multivariate analysis, serum AFP level, poor differentiation
microvascular invasion remained significantly associated with disease-free survival (p < 0.05).

Table: The correspondence of Recurrence and Non-Recurrence groups

<table>
<thead>
<tr>
<th></th>
<th>Recurrence Group</th>
<th>Non-Recurrence Group</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age</td>
<td>54.7 ± 9.8</td>
<td>56.1 ± 8.2</td>
<td>&gt;0.05</td>
</tr>
<tr>
<td>Gender (Male)</td>
<td>87.9</td>
<td>84.2</td>
<td>&gt;0.05</td>
</tr>
<tr>
<td>Cirrhosis (%)</td>
<td>95.4</td>
<td>91.7</td>
<td>P = 0.495</td>
</tr>
<tr>
<td>AFP</td>
<td>1825 ± 16311</td>
<td>1352 ± 739.2</td>
<td>P &lt; 0.001</td>
</tr>
<tr>
<td>0–9 (%)</td>
<td>35.9</td>
<td>52.3</td>
<td>P &lt; 0.001</td>
</tr>
<tr>
<td>10–99 (%)</td>
<td>33.1</td>
<td>33.5</td>
<td>P &lt; 0.001</td>
</tr>
<tr>
<td>100–499 (%)</td>
<td>18.2</td>
<td>10.2</td>
<td>P &lt; 0.001</td>
</tr>
<tr>
<td>500–999 (%)</td>
<td>5.4</td>
<td>1.9</td>
<td>P &lt; 0.001</td>
</tr>
<tr>
<td>&gt;10000 (%)</td>
<td>7.4</td>
<td>2.1</td>
<td>P &lt; 0.001</td>
</tr>
<tr>
<td>Transplantation Type</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Cadaveric (%)</td>
<td>69.1</td>
<td>67.2</td>
<td>p &gt; 0.05</td>
</tr>
<tr>
<td>MELD (0–14%)</td>
<td>30.9</td>
<td>32.8</td>
<td></td>
</tr>
<tr>
<td>Total Tumor Diameter</td>
<td>79.7 ± 53.8</td>
<td>46.3 ± 37.4</td>
<td>P &lt; 0.001</td>
</tr>
<tr>
<td>The Largest Tumor Diameter</td>
<td>53.8 ± 38.6</td>
<td>33.1 ± 24.4</td>
<td>P &lt; 0.001</td>
</tr>
<tr>
<td>Total Tumor Number</td>
<td>4 ± 3.6</td>
<td>2.2 ± 2.2</td>
<td>P &lt; 0.001</td>
</tr>
<tr>
<td>Milan (in/out) (%)</td>
<td>38.7/61.3</td>
<td>70.6/29.4</td>
<td>p &gt; 0.05</td>
</tr>
<tr>
<td>UCSF (in/out) (%)</td>
<td>49/51</td>
<td>78.3/21.7</td>
<td></td>
</tr>
</tbody>
</table>

Conclusion: Based on the results of the study, viral hepatitis remains the most frequent etiology of HCC in Turkey. High serum AFP levels, poor histologic differentiation and microvascular invasion significantly affect the posttransplant outcome. Donor type does not significantly affect posttransplant survival in patients with HCC.

SAT256
Utility and prognostic value of diagnosing metabolic dysfunction-associated fatty liver disease in patients undergoing liver transplantation for alcohol-related liver disease

Benedict Vanlerberghe1,2,3,4, Hannah Van Malenstein1,2, Mauricio Sainz-Barriga5,6, Christoffel Schalk van der Merwe1,2, Jacques Pirenen3,6, Frederik Nevens1,2, Jef Verbeek1,2, University Hospitals Leuven, Department of Gastroenterology and Hepatology, Leuven, Belgium; 3KU Leuven, Department of Chronic Diseases and Metabolism, Leuven, Belgium; 4Maastricht University Medical Center, Department of Internal Medicine, Maastricht, Netherlands; 5Maastricht University, NUTRIM School of Nutrition and Translational Research in Metabolism, Maastricht, Netherlands; 6University Hospitals Leuven, Abdominal Transplantation Surgery, Leuven, Belgium; 7KU Leuven, Department of Microbiology, Immunology and Transplantation, Leuven, Belgium

Email: b.vanlerberghe@maastrichtuniversity.nl

Background and aims: Metabolic dysfunction-associated fatty liver disease (MAFLD) is a recently proposed term, which allows diagnosing liver disease associated with metabolic dysfunction in patients with alcohol-related liver disease (ALD). We assessed the prevalence of MAFLD in ALD patients undergoing liver transplantation (LTx) and its prognostic value on post-LTx outcome.

Method: We retrospectively analyzed all patients transplanted for ALD between 1990 and August 2020 at our center. MAFLD was diagnosed at LTx based on the presence or history of hepatic steatosis and a BMI ≥25 kg/m² or type 2 diabetes (DMII) or ≥2 metabolic risk abnormalities (dyslipidemia, hypertension, pre-diabetes). Overall survival and potential risk factors for recurrent liver steatosis (based on imaging or biopsy) and cardiovascular (CV) events were analyzed by Cox regression (presented as hazard ratio (HR) with 95% confidence interval).

Results: Of the 371 included ALD patients, 255 (68.7%) had concomitant MAFLD at LTx. Median follow-up post-LTx was 72 months (Table 1). Patients with ALD-MAFLD were older, more often male, and more frequently had hepatocellular carcinoma (HCC) at LTx (Table 1). Perioperative mortality and overall survival (HR: 0.991 (0.702–1.401); p = 0.960) did not differ between MAFLD and non-MAFLD ALD patients (Table 1). Multivariate analysis identified MAFLD at LTx (HR: 2.092 (1.412–3.098)), weight gain in the 1st year post-LTx (HR: 1.092 (1.043–1.143)) and any alcohol relapse (HR: 4.606 (3.097–6.850)) as independent risk factors for recurrent hepatic steatosis (p < 0.001). MAFLD at LTx was not associated with CV events post-LTx (HR: 1.519 (0.790–2.922); p = 0.210), in contrast with the traditional risk factors age (HR: 1.064 (1.016–1.14); p = 0.008) and DMII (HR: 2.068 (1.134–3.770); p = 0.018).

Table: Patient characteristics (at LTx)

<table>
<thead>
<tr>
<th>All (n = 371)</th>
<th>ALD-MAFLD (n = 255)</th>
<th>ALD-non-MAFLD (n = 116)</th>
<th>p value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age (years)</td>
<td>60.0 (56.0–63.0)</td>
<td>61.0 (56.0–63.0)</td>
<td>58.0 (52.5–64.0)</td>
</tr>
<tr>
<td>(IQR)</td>
<td>66.0</td>
<td>76.0</td>
<td>64.0</td>
</tr>
<tr>
<td>Male sex (%)</td>
<td>80.1</td>
<td>86.3</td>
<td>66.4</td>
</tr>
<tr>
<td>HCC (%)</td>
<td>38.3</td>
<td>44.3</td>
<td>25.0</td>
</tr>
<tr>
<td>Follow-up</td>
<td>72.0 (34.5–122.0)</td>
<td>68.0 (33.5–116.5)</td>
<td>82.0 (35.5–127.5)</td>
</tr>
<tr>
<td>(months)</td>
<td>(IQR)</td>
<td>(IQR)</td>
<td></td>
</tr>
<tr>
<td>Perioperative mortality (%)</td>
<td>2.43</td>
<td>2.75</td>
<td>1.72</td>
</tr>
</tbody>
</table>

Legend: * statistically significant/IQR: interquartile range

Conclusion: The presence of MAFLD in ALD is associated with a distinct patient profile at LTx and is a risk factor for recurrent hepatic steatosis irrespective of alcohol relapse. These novel findings demonstrate the utility and prognostic value of diagnosing MAFLD at LTx.

SAT257
Severe acute respiratory syndrome coronavirus type 2 (SARS-CoV-2) specific cellular and humoral immunity in Coronavirus Disease-2019 (COVID-19) convalescence after liver transplantation-a prospective six month follow-up

Theresa Kirchner1, Hagen Sauer1, Sophia Heinrich1, Agnes Bonfacius2, Ruhl Louisa3, Isabell Pink3, Bastian Engel1, Emily Saunders1, Joerg Martens2, Marius M. Hoeper4, Rainer Blasczyk2, Heiner Wedemeyer1, Elmar Jaeckel1, Christine Falk1, Britta Eiz-Vesper1, Richard Taubert1, Hannover Medical School, Department of Gastroenterology, Hepatology and Endocrinology, Hannover, Germany; 2Institute of Transfusion Medicine and Transplant Engineering, Hannover, Germany; 3Institute of Transplant Immunology, Hannover, Germany; 4Department of Pneumology, Hannover Medical School, member of the German Centre for Lung Research (DZL), Hannover, Germany

Email: kirchner.theresa@mh-hannover.de

Background and aims: Data on protective immunity against SARS-CoV-2 in liver transplantation recipients (LTR) after mild/moderate
COVID-19 are limited. The aim of the study was to analyse the immune response in LTR convalees with ongoing immunosuppressive therapy in the first six months and to assess the impact of vaccination in LTR convalees in comparison to matched convalees without immunosuppression (non-IS).

**Method:** Immune response in LTR and non-IS was measured prospectively 1–2 (LTR: n = 15; non-IS: n = 14), 3–5 (LTR: n = 16; non-IS: n = 16) and ≥5 (LTR: n = 14; non-IS: n = 36) months after positive PCR test. Immunity after post-COVID-19 booster vaccination in convalese LTR was measured in n = 11.

Specific T cell reactivity was detected by IFN-γ ELISPOT against 4 antigens (membrane, nucleocapsid, spike protein1/2). Specific antibodies (IgG and A) were detected against 4 different antigens (S1/2, receptor binding domain (RBD), nucleocapsid). Pre-pandemic samples were retrieved from our prospective LTR biorepository.

**Results:** The majority of LTR (93%) had a mild or moderate COVID-19 (outpatients: 87%). No T cell reactivity or IgG was detectable in pre-pandemic samples.

IgG antibodies in LTR were detectable in 62–85% (1–2 month), 70–90% (3–5 month) and 56–100% (≥5 month and vaccination). Although IgG antibodies against nucleocapsid were reduced in LTR in comparison to non-IS, IgG and IgA antibodies against all other antigens including RBD of the spike protein of convalese LTR were not reduced, neither in frequency nor in concentration.

In initial analysis convalese LTR had no reduced IFN-γ production normalized to numbers of PBMCs compared to non-IS in the first 6 months. In addition, cellular and humoral immune response did not decline significantly over the first 6 months. However, booster vaccination non-significantly increases cellular (S1 p = .093, S2 p = .096) or humoral (S1 p = .055, S2 p = .096) reactivity against spike protein in convalese LTR.

The prospective follow-up will be continued for 1 year after COVID-19.

**Conclusion:** In conclusion, LTR convalees achieved cellular and humoral immune responses against SARS-CoV-2 comparable to non-IS, even after mild or moderate COVID-19. Cellular and humoral immunity showed no decline but could be booster with additional vaccination in the first months after COVID-19 in LTR convalees. The development of a robust immunity without triggered rejection justifies the continuation of immunosuppression during infection.

**SAT258**

A third dose of the BNT162b2 mRNA vaccine significantly improved immune response among liver transplant recipients

Yana Davidov1, Victoria Indenbaum2, Keren Tsara1, Oranit Cohen- Ezra1, Mariya Likhter2, Gil Ben Yaacov1, Rebecca Halperin3, Itzhak Levy3,y Orna Mor4,5, Nancy Agmon-Levin4,5, Arnon Afek6,7, Galia Rahav1,4, Yaniv Lustig6,7, Ziv Ben Ari1,4, 1Sheba Medical Center, Liver Diseases Center, Tel Aviv-Yafo, Israel; 2Central Virology Laboratory, Ministry of Health, Tel-HaShomer, Tel Aviv-Yafo, Israel; 3Sheba Medical Center, Infectious diseases unit, Tel Aviv-Yafo, Israel; 4Tel Aviv University, Sackler School of Medicine, Tel Aviv-Yafo, Israel; 5Sheba Medical Center, Clinical Immunology Angioedema and Allergy Unit, The Zabludowicz Center for Autoimmune Diseases, Tel Aviv-Yafo, Israel; 6Sheba Medical Center, Tel Aviv-Yafo, Israel.

**Email:** y.davidov@gmail.com

**Background and aims:** Immune responses of solid organ transplant recipients to two doses of the BNT162b2 mRNA anti-SARS-CoV-2 vaccine is impaired. The immunogenicity and safety of a third dose among liver transplant (LT) recipients is unknown. This work aimed to evaluate the immune response of LT recipients to a third dose of the BNT162b2 mRNA vaccine.

**Method:** Consecutive LT recipients (n = 64) in follow-up at Sheba Medical Center were included. Receptor-binding domain (RBD) IgG and neutralizing antibody (NA) titers and T cell levels before (test 2) and 21–28 days a third vaccine dose (test 3) were determined and compared to their levels measured a median 38 days after the second vaccine dose (test 1). IgG antibody titers ≥1/150 were defined as positive antibody. Adverse effects after the third dose were monitored.

**Results:** The LT recipients were of a median age of 64 years; 59.4% were male. The percentage of responders to the second vaccine (69.4%) decreased after a median time of 174 days (54%) and improved significantly after the third vaccine (97%). Geometric mean anti-RBD IgG levels, NA levels and T cell count also increased significantly after the third dose. Anti-RBD IgG and NA titers after the third vaccine negatively correlated with age (p = 0.0001), renal failure (p > 0.0001), mycophenolate mofetil treatment (p = 0.004), and combined immunosuppression vs. calcineurin inhibitors monotherapy (p = 0.001). After the third dose, adverse events were reported by 37% of recipients and were mostly mild (local pain and fatigue).

**Conclusion:** The immune response after a third BNT162b2 mRNA vaccine improved significantly among LT recipients, without serious adverse effect. Further studies are needed to evaluate immune response durability and to determine the optimal number and schedule of boost vaccines.

**SAT259**

Everolimus combined with low-dose tacrolimus controls histological graft injury and liver fibrosis as sufficiently as high-dose tacrolimus combined with mycophenolate after liver transplantation

Fabian Dranicki1, Emily Saunders1, Theresa Kirchner1, Bastian Engel1, Björn Hartleben2, Heiner Wedemeyer1, Elmar Jaeckel1, Richard Tauber1, 1Hannover Medical School, Dept. Gastroenterology, Hepatology and Endocrinology, Hannover, Germany; 2Hannover Medical School, Institute for Pathology, Hannover, Germany

**Email:** dranicki.fabian@mh-hannover.de

**Background and aims:** After liver transplantation (LTX), there are multiple regimens for immunosuppression (IS). The combination of everolimus (EVR) and low-dose tacrolimus prevents T cell-mediated rejection (TCMR) of liver grafts as sufficiently as the standard of care (SOC) with high-dose tacrolimus (highTAC) and mycophenolate, but is associated with a preserved kidney function within the first years after liver transplantation (LT). However, none of the available studies assessed the histological pattern of graft injury or liver graft fibrosis in surveillance biopsies (sVLbx), especially in the first year after LTX.

**Method:** All surveillance biopsies in our protocol biopsy program taken under at least 1 month of stable immunosuppression with either EVR (aim 3–8 ng/ml) and lowTAC (aim 3–5 ng/ml) or SOC with tacrolimus (aim 3–8 ng/ml) and mycophenolate (500–1500 mg/day) within the first 3–4 years after LTX at our center were included. Patients who were switched to EVR because of insufficient control of alloreactivity through SOC were excluded. Reasons for switches to EVR were malignancies before or after LT, chronic kidney injury, intolerance of SOC or CMV reactivations.

**Results:** So far, we could include 21 patients for the everolimus/low dose tacrolimus group, and 39 patients for the SOC/high dose tacrolimus group. The switch to EVR took place at a median of 116 days after LTX. EVR/lowTAC group exhibited lower TAC through levels at sVLbx than SOC (p < 0.001). Histological graft injury quantified by the rejection activity index and hepatitis activity index according to Ishak were not significantly different between the EVR/lowTAC group and SOC. Similarly, liver graft fibrosis in all compartments (portal/periportal, sinusoidal, perivenular) was not significantly different between both groups. Likewise, patterns of TCMR, NAFLD/NASH and bile duct abnormalities exhibited similar frequencies in both treatment groups.

**Conclusion:** The combination of everolimus with low dose tacrolimus seems to control alloreactivity and histological graft injury as sufficiently as SOC with tacrolimus/mycophenolate within the first 3–4 years after LTX. These histological safety data suggest a broader application of this CNI-sparing regimen.
SAT260
The portrait of adult liver transplant recipients in the United States from 2002 to 2020
Zobair Younossi1,2,3, Reem Al Shabeeb1, Michael Harring1, Janus Ong4, Saleh Alqahtani1,6, Linda Henry1,7, Maria Stepanova1,7
1Inova Health System; 2Betty and Guy Beatty Center for Integrated Research, IHS; 3Inova Health System, Medicine Service Line; 4University of the Philippines, College of Medicine; 5King Faisal Specialist Hospital and Research Center; 6Johns Hopkins University, Division of Gastroenterology and Hepatology; 7Center for Outcomes Research in Liver Disease
Email: zobair.younossi@inova.org

Background and aims: Aging population, the epidemics of obesity and metabolic syndrome, and decreasing burden of viral hepatitis are changing the portrait of liver transplant (LT) candidates in the U.S. We aimed to assess changes in demographics and clinical presentation of LT candidates in the U.S. over the last two decades.

Method: The Scientific Registry of Transplant Recipients (SRTR) data 2002–2020 was used to select adult candidates for LT. Patients with acute liver disease, hepatocellular carcinoma, or without known LT etiology were excluded. Trends in the proportions of common LT etiologies of chronic liver disease at the time of LT listing, such as chronic hepatitis B (CHB), chronic hepatitis C (CHC), non-alcoholic steatohepatitis (NASH, including cryptogenic cirrhosis if accompanied by obesity or type 2 diabetes), alcoholic liver disease (ALD) without and with CHC, autoimmune hepatitis (AIH), primary biliary cirrhosis (PBC), and primary sclerosing cholangitis (PSC), were assessed over time along with other clinico-demographic parameters.

Results: There were 149,910 LT candidates included in this study: n = 28,581 in 2002–2005, n = 30,158 in 2006–2009, n = 31,824 in 2010–2013, n = 32,925 in 2014–2017, and n = 26,422 in 2018–2020. Over time, the mean ± SD age of LT candidates increased from 52 ± 10 years in 2002–2005 to 55 ± 11 years in 2018–2020, and the proportion of patients ≥65 years increased from 8% to 20% (trend p < 0.0001). The proportion of male candidates decreased from 65% to 60%, respectively, and so did the proportion of white patients: from 75% to 72%, respectively (p < 0.0001). During the same period, the proportion of liver re-transplants decreased from 6.0% to 3.5%, respectively (p < 0.0001). The rates of obesity (BMI >30 kg/m²) and diabetes increased from 33% and 8%, respectively, in 2002–2005 to 40% and 27%, respectively, in 2018–2020 (p < 0.0001). The rates of obesity (BMI >30 kg/m²) and diabetes increased from 33% and 8%, respectively, in 2002–2005 to 40% and 27%, respectively, in 2018–2020 (p < 0.0001) (Figure). In 2002–2005, the most common etiology of chronic liver disease in LT candidates without HCC was CHC without or with ALD (total 45%), while NASH accounted for 7% of listings. In contrast, in 2018–2020, NASH was the second most common LT etiology at 27%, following ALD (38%), while CHC with or without ALD decreased to a total of 10%. Other common etiologies (CHB, AIH, PBC, and PSC) accounted for 2–7% listings each throughout the study period.
Heterologous regimen viral-vector/mRNA produces significantly higher SARS-CoV-2 humoral response than homologous viral-vector and inactivated vaccines in liver transplant recipients

Manuel Mendizabal1, Nicolas Ducasa2, Paula Benencio3, Maria Margarita Anders4, Fernando Cairo5, Adriana Alter6, Patricia Etcheves7, Giampaolo Scarton8, Mirna Biglione9, Ezequiel Mauro10, Hospital Universitario Austral, Hepatology and Liver Transplant Unit, Pilar, Argentina; Instituto de Investigaciones Biomédicas en Retrovirus y SIDA (INIBIROS), CONICET-Universidad de Buenos Aires, Argentina; Hospital Italiano, Buenos Aires, Argentina; Buenos Aires, Argentina

Background and aims: Knowledge of the immunogenicity of vaccines against SARS-CoV-2 in liver transplant recipients (LTR) is mainly limited to mRNA vaccines. We aimed to assess independent predictors of humoral response, in regimens based on homologous non-replicating viral vectors, inactivated vaccines, and heterologous combination.

Method: Multicenter and prospective study, in which consecutive and volunteering LTR and immunocompetent controls were recruited. COVID-19 Spike 1–2 IgG (S-IgG), neutralizing antibodies (NA) and nucleocapsid protein (N) were evaluated 21–90 days after receiving the second doses of vaccine ChAdOx1 (AstraZeneca), rAd26-rAd5 (Sputnik V), inactivated BBIBP-CorV (Sinopharm), and the heterologous combination rAd26/mRNA-1273 (Sputnik V/Moderna), according to the Argentinean immunization program. Vaccine side effects and clinical data was collected.

Results: After excluding 3 LTR for having a positive N protein test, 120 LTR and 27 immunocompetent controls were analyzed. No significant baseline differences were found between LTR and controls. Twenty-four (89%) controls and 74 (61%) LTR were positive for S-IgG (p = 0.007). NA titers were significantly higher in controls compared to LTR [64 (8–128) vs 16 (8–64); p = 0.02]. The correlation between S-IgG and NA titers was high [Pearson’s correlation 0.89 (0.8–0.9); p < 0.001]. In a multivariate analysis, Increased BMI [OR 0.8 (0.8–0.9); p = 0.004] and the use of MMF [OR 5.1 (2.0–12.8); p < 0.001] were independently associated with a negative humoral response, while the use of the rAd26/mRNA-1273 combination [OR 0.11 (0.02–0.6); p = 0.001] was independently associated with a higher humoral response rate. No significant differences were detected regarding adverse effects between controls and LTR.

Conclusion: The portrait of LT candidates in the U.S. is changing to include more elderly patients, patients with metabolic syndrome, and diagnosis of NASH.

SAT262

Evolution of pretransplant cardiac risk factor burden and major adverse cardiovascular events in liver transplant recipients over time

Claire Harrington1, Paul Levy1, Elizabeth Cabrera1, Jing Gao1, Dyanna Gregory1, Cynthia Padilla1, Gonzalo Crespo1, Lisa VanWagner1, Northwestern Memorial Hospital, Chicago, United States

Background and aims: Non-alcoholic steatohepatitis (NASH) is associated with high cardiac risk factor burden in liver transplant recipients (LTRs). Major adverse cardiovascular events (MACE) are a major cause of complications in LTRs. The contemporary prevalence and temporal trends in pretransplant cardiac risk factor burden among LTRs are unknown. Therefore, the aim of this study is to evaluate the evolution of MACE and pre-LT cardiac risk factors in LTRs over time.

Method: This is a retrospective cohort of 1739 adult LTRs at a single, large U.S. academic transplant center (2003–2020) using the electronic health record. NASH was defined using primary or secondary listing diagnosis for NASH or cryptogenic cirrhosis plus one metabolic risk factor. MACE was defined as death or hospitalization for myocardial infarction (MI), revascularization, stroke, or heart failure (HF). Logistic regression analysis was used to assess factors a priori that are associated with 1-year MACE among LTRs.

Results: Figure 1 shows trends in pre-LT cardiac comorbid conditions. Comparing 2003 and 2020, there was a significant increase in pre-LT obesity, chronic kidney disease (CKD), atherosclerotic (ASCVD) and NASH (p < 0.05 for all). There was no significant change in proportion of LTRs with older age (≥65 years old), diabetes, or HF. The mean 1-year MACE rate was 18.7%. Higher 1-year MACE was observed in LTRs transplanted for NASH compared to other etiologies (26.4% vs 16.5%, p < 0.0001). There was a trend toward a decrease in MACE in 2020 vs 2003 (13.3% vs 25.0%, p = 0.052). In multivariable modeling, age, ASCVD, diabetes, HF, and CKD were significantly associated with MACE within 1 year of LT.
There was an increase in all cardiac risk factors over time. Factors marked with an asterisk had a significant increase between 2003 and 2020 (p < 0.05).

**Conclusion:** There has been an overall increase in cardiac risk factor burden among LTRs between 2003 and 2020 that are also significantly associated with MACE within 1 year of LT. Unexpectedly, overall MACE decreased in our cohort. This may reflect advancement in the identification and management of cardiovascular risk factors in LTRs. With projected continued increase in cardiac risk burden and the proportion of patients transplanted for NASH, it is critical for LT programs to develop and implement quality improvement efforts to improve cardiovascular care in LTRs.

**Posters**

SAT263

Retransplantation (reLT) outcomes of patients who were initially transplanted for ACLF

Gandhi Lanke¹, Feng Li¹, Paul J. Thuluvath¹,². ¹Mercy Medical Center, Baltimore, United States; ²University of Maryland School of Medicine, Baltimore, United States

Email: thuluvath@gmail.com

**Background and aims:** The outcomes of early retransplantation (within 90-days of initial transplantation) of the liver (reLT) in those who initially underwent LT for acute on chronic liver failure (ACLF) are unknown.

**Method:** Using the national data from the United Network for Organ Sharing (UNOS) for all adult patients aged ≥ 18 years who were listed for LT in the United States from Jan 11, 2016, to Aug 31, 2020, we identified those who had reLT. We defined organ failure (OF) and graded ACLF as described by EASL-CLIF. The primary outcomes of interest were 3-month mortality and all-time mortality after reLT in those initially transplanted with or without ACLF. Kaplan Meier survival analysis was used to compare survival probabilities.

**Results:** During the study period, 100 ACLF and 299 non-ACLF patients underwent reLT, and of those 47 ACLF and 159 non-ACLF underwent reLT within 90 days of initial LT. The mean age of ACLF and non-ACLF patients who underwent reLT was 48.6 ± 12.5 and 52.8 ± 11.8 years, respectively (p <0.001). Alcoholic liver disease was the predominant etiology in ACLF patients (58% vs. 24% in non-ACLF, p <0.001). Respiratory (7% vs. 0%, p <0.001) and circulatory (18% vs. 0%, p <0.001) were more common at the time of reLT in the ACLF group compared to non-ACLF group. The overall survival rates in ACLF and non-ACLF groups who underwent reLT within 90 days were similar (72.3% vs. 75.5%, p = 0.66). However, patients with 3 or more organ failures (n = 71) at the time of reLT (reLT within 90 days of initial LT) had worse outcomes (63.4% vs. 80.7%, p = 0.006) compared to those (n = 135) with less than 3 organ failures (Figure 1A). Irrespective of the interval between initial LT and reLT (anytime reLT), the survival was lower (68.6% vs. 81.8%, p = 0.008) in those with 3 or more organ failures (n = 86) at the time of reLT than those (n = 313) with less than 3 organ failures (Figure 1B). On multivariable logistic regression analysis, respiratory failure, circulatory failure, and ACLF grade were independent predictors of survival after reLT.
SAT264
The ratio of Activin A and Follistatin-related gene allows prediction of posthepatectomy liver failure and postoperative morbidity in patients prior to liver surgery
Jonas Santol1,2, David Pereyra2, Stefanie Haegelge2, Daphni Ammon2, Anita Pirabe1, Philipp Jonas3, Stefan Schuster2, Sarang Kim2, Toni Nguyen2, Thomas Grünberger1, Alice Assinger1, Patrick Starlinger2.

Background and aims: Even though outcome after hepatic resection has improved, patient outcome is significantly worse if posthepatectomy liver failure (PHLF) develops. With no causal treatment available, research focusing on the prediction of PHLF and elucidating its potential causes, is of great importance. Here, we evaluate the predictive potential for PHLF of Activin A and its inhibitory protein Follistatin-related gene (FLRG) and examine their involvement in the development of PHLF.

Method: Activin A and FLRG were measured in plasma of 59 patients undergoing liver resection using commercially available ELISA kits. Plasma was prepared from blood taken prior to the operation (preOP), as well as on the first and fifth postoperative day (POD). Postoperative outcome was prospectively documented.

Results: We saw a significant decrease in plasma for Activin A and FLRG from preOP to POD1 (p = 0.045 and p = 0.005, respectively). Subsequently FLRG increased from POD1 to POD5 (p = 0.004). Interestingly, neither activin A nor FLRG differed between patients with and without PHLF at any timepoint. However, the ratio of Activin A/FLRG was significantly higher in patients without PHLF preOP (p = 0.037). There was no peroperative dynamic for Activin A/FLRG. PreOP Activin A, FLRG and Activin A/FLRG did not differ between patient in the context of underlying malign or benign liver primary or in the context of low-grade (grade 0–1) or high-grade (grade 2–4) fibrosis. Using Receiver operating curve analysis, we aimed to further investigate the predictive potential of preOP Activin A/FLRG for PHLF. The Activin A/FLRG ratio was able to significantly predict postOP PHLF (Area under the curve = 0.789, p = 0.038, 95%-CI: 0.609–0.969). Using the median of Activin A/FLRG ratio values, we further divided the cohort in a high and low Activin A/FLRG ratio group. When comparing the 2 groups, we could identify all patients with postOP PHLF in the low Activin A/FLRG ratio group, with none of the patients in the high Activin A/FLRG ratio group developing PHLF (5 of 21 [23.8%] vs 0 of 21 [0.0%], p = 0.017). Further, patients in the low Activin A/FLRG ratio group were found to suffer from a significantly higher risk for postoperative morbidity (14 of 21 [66.7%] vs 5 of 21 [23.8%], p = 0.005).

Conclusion: While the circulating dynamics of activin A and FLRG showed no association with PHLF, the preOP ratio of Activin A/FLRG was significantly decreased in patients suffering from PHLF. While further research into the pathophysiology behind these results is needed, Activin A and the ratio of Activin A/FLRG show potential as possible predictors of PHLF and Morbidity.

SAT265
Derivation of a cardiac risk index for use in liver transplantation for non-alcoholic steatohepatitis
Paul Levy1, Claire Harrington1, Elizabeth Cabrera1, Jing Gao1, Dyanna Gregory1, Cynthia Padilla1, Gonzalez Crespo1, Lisa VanWagner1, Patrick Starlinger2.1, McGraw Medical Center of Northwestern University, Internal Medicine, Chicago, United States

Background and aims: Cardiovascular events (CVEs) are the most common cause of early mortality after liver transplant (LT). LT candidates with non-alcoholic steatohepatitis (NASH) are at highest risk for CVEs. The Cardiovascular Risk in Orthotopic LT (CAR-OLT) score quantifies risk for post-LT CVEs, but its accuracy in LT candidates with NASH is unknown. We propose a new prediction model for risk of CVEs among NASH LT candidates and compare its performance to the CAR-OLT score.

Method: All adults who underwent first LT at a large United States urban transplant center (2/1/2002–12/31/2020) were included. Data were drawn from the Organ Procurement and Transplant Network (OPTN) and linked to data from the electronic health record. Primary outcome was 1-year CVE, defined as death from a CV cause or hospitalization for myocardial infarction (MI), cardiac revascularization, heart failure, atrial fibrillation (AF), cardiac arrest, and/or stroke. NASH was identified based on OPTN primary or secondary listing diagnosis for LT or cryptogenic cirrhosis plus metabolic syndrome comorbidity. All pre-LT variables with p ≤ 0.15 on bivariate analysis were considered for model inclusion. Akaika Information Criterion was used for model selection using backward selection. Receiver operating curve analysis was used to compare model discrimination.

Results: Among 1788 LT recipients, 330 (18.5%) were listed for NASH. Of these, 115 (34.9%) had 1 year CVE. Variables included in the final model were pre-LT recipient age, sex, functional status, hepatic encephalopathy, peritonitis, hepatorenal syndrome, MI, AF, hypertension, and venous thromboembolism. Only age, sex, history of AF and hypertension were shared risk factors within the CAR-OLT score. The discriminative performance of the new point based score (C statistic = 0.72) was superior to the CAR-OLT score (C statistic = 0.69) for 1-year post-LT CVEs in candidates with NASH (Figure 1).

Conclusion: Patients being considered for LT for NASH cirrhosis have a unique cardiovascular risk profile not captured by existing risk prediction models. This study proposes a novel point based risk prediction tool to guide future cardiac risk stratification in patients with NASH cirrhosis being considered for LT.
The prognostic effect of adequate lymphadenectomy in clinically node-negative patients undergoing liver resection for intrahepatic cholangiocarcinoma

Carlo Sposito1,2, Marianna Maspero1, Francesca Ratti3, Elena Panettieri4, Stefano Di Sandro5, Fabrizio Di Benedetto5, Felice Giuliante4, Luca Aldrighetti3, Vincenzo Mazzaferro1,2.

1Fondazione IRCCS Istituto Nazionale Tumori di Milano, HPB surgery and Liver Transplantation, Milano, Italy; 2University of Milan, Oncology and Hemato-Oncology, Milano, Italy; 3Ospedale San Raffaele, Hepatobiliary Surgery Division, Milano, Italy; 4Fondazione IRCCS Policlinico Gemelli, General and HPB Surgery, Roma, Italy; 5Policlinico di Modena, HPB Surgery and Liver Transplant Unit, Modena, Italy

Email: carlo.sposito@istitutotumori.mi.it

Background and aims: The prognostic effect of lymphadenectomy (LND) in the surgical treatment of intrahepatic cholangiocarcinoma (iCC) with no clinical evidence of lymph-node metastases (clinically node-negative, cN0) is still a matter of debate. The aim of this study is to assess the role of lymphadenectomy in cN0 iCC, and which patients might benefit most.

Method: Consecutive patients who underwent surgery for cN0 iCC at four Italian Centers between 2000 and 2020 were included. A multivariate analysis for factors associated with overall survival (OS) was performed. The cohort was divided into two groups according to LND adequacy, defined as at least 6 excised nodes, and survival analysis was carried out. An analysis of the subgroups of patients that benefited the most from LND was also performed.

Results: Out of 818 surgically resected iCC patients, 632 were cN0. In this cohort, 359 (57%) patients received adequate LND (AD-LND).

Figure 1: Discriminative performance of NASH scoring model compared to CAR-OLT

Variables selected for inclusion were age, sex, functional status, history of hepatic encephalopathy, peritonitis, hepatorenal syndrome, atrial fibrillation, hypertension, myocardial infarction, and venous thromboembolism.

The original CAR-OLT model (dotted red line) included age, sex, race, working status, education level, history of atrial fibrillation, respiratory failure requiring ventilator support, hepatocellular carcinoma, hypertension, diabetes, and heart failure.

Figure: (abstract: SAT266)
Impact of MELD 3.0 Versus MELD-Na in patients with renal dysfunction
Allison Kwong, Ajitha Mannalithara, W. Ray Kim.

Background and aims: MELD 3.0 is a proposed model that improves upon MELD-Na, incorporating sex and albumin as additional variables, updating existing coefficients and adding relevant interactions, and resetting the upper bound of serum creatinine to 3.0 from 4.0 mg/dL. This analysis evaluates the impact of replacing MELD-Na with MELD 3.0 on waitlist priority among patients with advanced renal dysfunction.

Method: New adult waitlist registrations for liver transplantation from June 15, 2016 to June 30, 2021 were identified using OPTN data. MELD, MELD-Na, and MELD 3.0 scores from registration were calculated by the following equations:

\[
\text{MELD} = 9.57 \times \log_{10} \text{creatinine} + 3.78 \times \log_{10} \text{bilirubin} + 11.20 \times \log_{10} \text{INR} + 6.43; \\
\text{MELD-Na} = \text{MELD} + 1.32 \times (137-\text{Na}) - 0.033 \times \text{MELD} \times (137-\text{Na}); \\
\text{MELD 3.0} = 1.33 \times (\text{female}) + 4.56 \times \log_{10} \text{bilirubin} + 0.82 \times (137-\text{Na}) - 0.24 \times (137-\text{Na}) \times \log_{10} \text{creatinine} + 1.85 \times (3.5-albumin) - 1.83 \times (3.5-albumin) \times \log_{10} \text{creatinine} + 6. \\
\]

Differences between MELD-Na and MELD 3.0 were evaluated by sex and serum creatinine at listing.

Results: There were 68, 111 new waitlist registrations for liver transplantation during the study period. The median serum creatinine at listing was 1.0 (IQR 0.7–1.5), with 1439 (2.1%) of listings with creatinine between 3 and 4 mg/dL and 6369 (9.4%) receiving maximum points for being on dialysis. On average, MELD 3.0 added 1.47 points for women and 0.14 for men compared to MELD-Na. For patients where the initial creatinine was between 3 and 4 mg/dL, MELD 3.0 added an average of 1.66 points for women and 0.50 for men compared to MELD-Na, whereas for patients on dialysis, MELD 3.0 added 0.16 points for women and subtracted 1.14 for men. Compared to MELD-Na, MELD 3.0 reduced the maximum number of potential creatinine-derived points from 13 to 12.

Conclusion: The MELD 3.0 scoring system increases the weight of the serum creatinine and thus the calculated MELD for patients with renal dysfunction — but not those with Cr ≥4 mg/dL or dialysis. If implemented in liver allocation, MELD 3.0 may increase waitlist priority for patients with acute kidney injury (e.g. hepatorenal syndrome); earlier access to liver transplant for this population could improve post-transplant renal outcomes including the need for kidney transplant.

Sustainability of humoral immunity induced by the SARS-CoV-2 vaccine and response to booster dose among Liver Transplant recipients

Background and aims: Liver Transplant (LT) recipients were among the first to receive the BioNTech-BNT162b2 SARS-CoV-2 vaccine, with preliminary data indicating reduced humoral response compared to the general population. Our aim was to assess immunogenicity to the SARS-CoV-2 vaccine and response to a third booster dose among Liver Transplant recipients.

Method: LT recipients followed at the Tel-Aviv Sourasky Medical Center and healthy volunteers were tested for SARS-CoV-2 IgG antibodies against the Spike-protein (S) and Nucleocapsid-protein (N) at four time points: 10–20 days after the second Pfizer-BioNTech BNT162b2 SARS-CoV-2 vaccine dose, after 3 months follow-up, prior to (6 months follow-up) and 10–20 days after a third booster dose.
Information regarding vaccine side effects and clinical data was collected from patients and medical records.

**Results:** Following the second vaccine dose, immunogenicity among 80 LT recipients was significantly lower compared to the control group, with positive serology in 52% compared to 100% among controls \((p < 0.001)\). Antibody titer was also significantly lower among LT recipients (median 368.3 AU/ml vs. 12, 538 AU/ml in controls, \(p < 0.001\)). After 3 months follow-up, the antibody titer declined by 58% among LT compared to 86% decline in the controls (median titer 192 AU/ml vs 1, 995 AU/ml, \(p = 0.7\)). By 6 months the titers decreased by 21% and 62% in the LT and controls, respectively (median titer 225 AU/ml vs 385 AU/ml). Following a third dose given to 61 LT recipients received a third booster dose positive response rate increased to 85%. The median antibody titer significantly increased in both groups, but remained lower in LT recipients (3, 542 AU/ml vs. 28, 358 AU/ml among controls). Predictors for negative response among LT recipients were older age, lower eGFR, and treatment with high dose steroids and MMF.

**Conclusion:** LT recipients are at risk for lower humoral response to Pfizer-BioNTech SARS-CoV-2 mRNA based vaccine. The decline over-time is lesser in comparison to the general population. A booster dose was able to increase the response rate significantly, although antibody titers remained lower in comparison to control.

**SAT269**

**Acute-on-chronic liver failure due to severe intrahepatic vaso-occlusion and recurrence of the initial disease: 2 major features in liver transplantation for severe sickle-cell-related hepatopathy**

Christophe Duvoux¹, Francky Mubenga², Jean Jacques Matimbo³, Lorraine Blaise⁴, Eric Levesque⁵, Jean Claude Merle⁵, Norbert Ngongang⁶, Justine Gellen-Dautremer⁷, Maryvonnick Carmagnat⁸, Frederic Galacteros⁹, Daniel Cherqui¹⁰, Vincent Leroy⁶, Alexis Laurent¹¹, Anoosha Habibi¹², Pablo Bartolucci¹³.

¹Henri Mondor Hospital APHP, Paris Est University, Medical Liver Transplant Unit, liver Unit, Créteil, France; ²Agence Régionale de Santé, Guyanne, Cayenne, France; ³Avicenne University Hospital, Liver Department, Bobigny, France; ⁴Henri Mondor Hospital APHP, Paris Est University, Anesthesiology and Intensive Care, Créteil, France; ⁵Henri Mondor Hospital APHP, Paris Est University, Department of Anesthesiology and Intensive Care, Créteil, France; ⁶Henri Mondor Hospital APHP, Paris Est University, Medical Liver Transplant Unit, liver Unit, Créteil, France; ⁷Poitiers University Hospital, Internal Medicine, Poitiers, France; ⁸Saint Louis University Hospital, Immunohistocompatibility Laboratory, Paris, France; ⁹Henri Mondor Hospital APHP, Paris Est University, Red Cells Genetic Disorders Unit, Créteil, France; ¹⁰Paul Brousse Hospital, Centre Hépato-Biliaire, Villejuif, France; ¹¹Henri Mondor Hospital APHP, Paris Est University, Department of Digestive Surgery, Créteil, France

Email: christophe.duvoux@aphp.fr

**Background and aims:** The prognosis of severe sickle cell disease hepatopathy (SCDH) is dismal. Liver transplantation (LT) can be a salvage option but the worldwide experience, less than 70 reported LTs, is very limited and results controversial. The aim of this study was to describe presentation patterns and outcomes of LT for severe SCDH in a reference center for sickle cell disease.

**Method:** 24 patients, 16 men and 8 women, median age 37.4 years, transplanted between 1992 and 2020 were studied. Data on complications and management of SCD before LT, patterns of SCDH, liver explants, and post-LT outcomes were reviewed.

**Results:** SCD was SS, SC and S/Jβ thal in 62, 8 and 30% of cases. The indications for LT were ACLF in 14 (58%) cases, triggered by severe intrahepatic vaso-occlusive (VOC).
in 11/14 (78.5%) cases, severe acute liver failure (ALF) in 5 cases, due to massive VOC in 4 cases and autoimmune hepatitis in 1 case. Five patients were transplanted electively: cirrhosis without ACLF in 3 cases (12.5%) (HCV 2, alcoholic hepatitis on cirrhosis 1), sclerosing cholangitis (SC) (8.5%) in 2 cases, with mild intrahepatic vaso-occlusive injury in 3 cases. Among patients with ACLF 3 cases were ACFL grade 2, and 9 (64%) grade 3, with a median number of organ failures of 3; the underlying liver disease consisted of chronic SCD-related liver hepatopathy in 11/14 cases (71.5%). The median MELD score at LT was 37.4, reaching 40 in ACLF patients. Median bilirubin was 700, 553, and 293 μmol/L in ACLF, ALF and elective patients, respectively. 16 patients (67%) received induction immunosuppression. The incidence of acute cellular rejection was 13%. Six patients (25%) developed serious neurological complications (seizures 4 and/or PRES syndrome 3). Postoperative mortality was 0, 20% and 30% in elective patients, ALF and ACLF. The 5-year overall survival was 65%, ranging from 100% in elective patients to 60 and 50% in patients transplanted in ALF and ACLF. With a median post LT Fu of 6.4 years, a liver biopsy was performed in 10/19 patients beyond the 3rd month post LT because of liver lab tests suggestive of rejection. The recurrence of VOC injury was observed in 8/10 cases, significant graft fibrosis, F2/F3, in 4 cases (HCV 1 case). Recurrent SCD vaso-occlusive injury in the graft justified a preventive strategy combining transfusion exchanges and/or hydroxyurea, with HbS target <30%.

Conclusion: This largest worldwide series of LT for SCDH shows that severe intrahepatic VOC causes ALF or ACLF in 75% of cases. Associated organ failures account for results inferior to those observed in other indications. In this rare indication, LT was associated with a reasonable 60% 5-year survival yet, transforming the prognosis of severe SCDH. LT should therefore be considered in expert multidisciplinary centers as a treatment option for SCDH. Identification of ACFL patients at high risk of post-operative death should be improved.

SAT270
Post-operative complications and short-term survival in obese cirrhotic patients undergoing liver transplantation
Javier Tejedor-Tejada1, Carmen Alonso Martin1, Samuel Juan Fernández Prada2, Laura Juan3, Violeta Mauriz2, Abdelaleem Helal2, Rifaat Safadi3, Esteban Fuentes Valenzuela4, Carolina Almohalla1, Félix García Pajares1, 1Hospital Universitario Rio Hortega, Department of Gastroenterology, Hepatology and Liver Transplantation Unit, Spain; 2Complejo Hospitalario Universitario de Santiago de Compostela, Department of Gastroenterology, Spain; 3Hospital Universitari Vall d’Hebron, Department of Gastroenterology, Egypt; 4Hadassah Medical Organization, Hadassah Hebrew University Medical Centre, The Liver Unit, Israel
Email: jtejedor1991@gmail.com

Background and aims: Obesity is considered a risk factor for perioperative complications, but its effect on patients undergoing liver transplantation (LT) remains unclear. This study was conducted to analyze the impact of the body mass index (BMI) on morbidity and mortality risk following LT.

Method: A multicenter study of outcomes in patients submitted to LT between 2001 and 2019. Recipients were stratified in obese (BMI ≥30 kg/m²) and non-obese patients (BMI <30 kg/m²). The following exclusion criteria were considered: Patients with no BMI available, refractory ascites, polycystic liver disease or multiorgan transplant. Post-LT outcomes and 1-year patient and graft survival were compared.

Results: A total of 1410 patients were included in the study, non-obese (989, 70.1%) and obese patients (421, 29.9%). There were not significant differences in Charlson comorbidity score, race, MELD, waiting time, total ischemia time, length of stay, ICU stay (Table 1). The rate of postoperative vascular and biliary complications were significantly higher in the obese recipients (23.3%, p = 0.015 and 36.6%, p <0.01) versus the non-obese recipients (17% and 27.1%). There was a significantly increased risk for long-term graft failure. However, there was no difference in patient survival after LT.

Conclusion: Obese patients have significantly increased morbidity in terms of vascular and biliary complications after LT. They have a higher risk for worse 1-year graft survival in comparison to controls.

SAT271
Impact of comorbidities on liver transplantation: a prospective and multicentric study
Trinidad Serrano1, Sergio Sabroso2, Luis M. Esteban3, Miguel Ángel Gómez Bravo3, Pablo Ruiz2, Rosa Martin-Mateos2, Alejandra Otero Ferreiro7, Francisco Javier Bustamante Schneider8, Sonia Pascual3, Carolina Almohalla5, Marta Guerrero1, Itxaron Bilibio12, Valle Cadahia-Rodrigo13, Ángel Rubin4, Luis Cortes Garcia1, Elena Oton15, Ana Arias16, Esther Molina17, Ursula Ewa Gajownik18, Jose Ignacio Herrero15, Magdalena Salcedo19, 1Hospital Clínico Universitario Lozano Blesa, Zaragoza, Spain; 2National Cancer Research Center, Madrid, Spain; 3Escuela Universitaria Politécnica de la Alumunia, Madrid, Spain; 4Hospital Virgen Del Rocio, Sevilla, Spain; 5Clinic, Barcelona, Spain; 6Hospital Ramón y Cajal, Madrid, Spain; 7Coruña University Hospital, A Coruña, Spain; 8Hospital Universitário Cruces, Barakaldo, Spain; 9General University Hospital of Alicante, Alicante, Spain; 10Río Hortega University Hospital, Valladolid, Spain; 11Hospital Universitario Reina Sofia, Córdoba, Spain; 12Hospital Universitari Vall d’Hebron, Barcelona, Spain; 13Central University Hospital of Asturias, Oviedo, Spain; 14La Fe University and Polytechnic Hospital, Valencia, Spain; 15Hospital Universitario de Canarias, San Cristóbal de La Laguna, Spain; 16Puerta de Hierro Majadahonda University Hospital, Majadahonda, Spain; 17Santiago Clinic Hospital CHUS, Santiago de Compostela, Spain; 18Parking Hospital Virgen De La Arrixaca, Murcia, Spain; 19Clínica Universidad de Navarra, Pamplona, Spain; 20Gregorio Marañón Hospital, Madrid, Spain
Email: tserrano.aullo@gmail.com

Background and aims: Comorbidity plays an important role in the mortality of patients both on the waiting list and after liver transplantation (LT). To analyze the impact of comorbidities on LT, a prospective and multicentre study (HEPA_TIC) has been launched and the preliminary results are presented here.

Method: Analysis of 996 consecutive patients included in LT waiting list, in 18 Spanish hospitals, from October 2019 to October 2021. Retransplantation, multivisceral transplantation and patients younger than 16 years were excluded. Comorbidities at the time of
listing, and follow-up variables were collected. The analysis of comorbidities was disaggregated by sex.

**Results:** Patients were predominantly male (77.2%) with a median age of 61 years IQR (56–66); 60 years in females IQR (54–66) and 61 in males (56–66) (p = n.s). Median follow-up was 7.9 months IQR (4.9–12.1). Decompensated cirrhosis was the most frequent indication with no differences in both sexes. Hepatocellular carcinoma was significantly more frequent in males (45.9% vs. 24.6%; p < 0.001). The most frequent comorbidities were diabetes and arterial hypertension. Diabetes, chronic obstructive pulmonary disease and cardiovascular disease were significantly higher in men (p < 0.05), while chronic kidney disease was higher in women (p < 0.05). Only 11.7% of the listed patients had no comorbidities. The number of comorbidities was higher in males than in females (p < 0.001). 20.3% of the listed men and 15.1% of the women had more than three comorbidities. During follow-up, 4.8% of females and 2.5% of males died on the waiting list. Comorbidity was the cause of 13.3% of these deaths. In our cohort, 735 patients were transplanted during follow-up. Among all analyzed variables, only hyperuricemia was associated with a decrease in intention-to-treat survival (p = 0.02). Also, the presence of more than four comorbidities was related to a lower survival, although it did not reach statistical significance (p = 0.07).

**Conclusion:** Comorbidities are highly prevalent in patients with liver disease on the LT waiting list and are the second leading cause of waiting list mortality. Hyperuricemia is the only comorbidity associated with lower survival, although further follow-up is needed to determine the impact of other comorbidities on survival.

**SAT272**

Liver transplant patients infection rate with SARS-CoV-2 is lower but depend upon the infection rate in the general population and have a better outcome  
Michal Cohen-Naftaly, Evelin Oxtrud, Orly Sneh Arbib, Assaf Issachar, Yael Harif, Amir Shlomai, Marius Braun, Rabin Medical Center, Liver Institute, Israel  
Email: michal_c_n@yahoo.com

**Background and aims:** Conflicting results regarding the susceptibility to SARS-CoV-2 infection and outcome in liver transplant (LT) patients (pts) were reported. Israel adopted early active policies to control the epidemic. Initially of severe travel restrictions and social distancing were enforced, followed by a lockdown. The relaxation of the restrictions led to 2 more severe waves, which triggered 2 new lockdowns. Israel was the first in the world to begin immunization with BNT162b2 on 20.12.2020, prioritizing first the elderly and immune compromised and rapidly extending to vaccination of the whole adult population. A fourth wave triggered the administration of booster doses in the same order. Guidelines encouraging social distancing, hygiene, and vaccination were disseminated to our pts and active follow-up was maintained using tele medicine. The immune suppression was not changed.

To assess the pattern of COVID19 pandemic among LT pts followed at Rabin Medical Center, compared to the general population in Israel.  
**Method:** Retrospective study from 2019 to 2021. Demographic data on 420 LT pts were collected from the electronic medical records, immunosuppressive therapy, dates of vaccination with BNT162b2, antibody levels after vaccination, data on SARS-COV-19 infection, severity of the disease, treatments and outcome. The data were compared to data reported on the Ministry of Health website: number of those infected in Israel, the vaccination rate. Comparison according to the waves of eruptions in Israel: 1st wave 2–5.2020, 2nd wave 6–11.2020, 3rd 11.2020–4.2021 and 4th wave 6–10.2021.

**Results:** 41 LT pts were diagnosed with Covid-19 out of 420 LT pts followed up: prevalence of 9.7%, significantly less than the 14.53% reported for the whole population (p < 0.05). There were 4, 6, 19 and 12 COVID-19 cases respectively in waves 1 to 4. In waves 3 and four the number a COVID-19 patients that received 1, 2 and 3 vaccine doses was 2, 10 and 3 respectively, vs 16 unvaccinated. The vaccinated pts were infected at a median of 167 and 27 days after the second and third vaccine, respectively. The risk of infection was proportional to the risk in the population. (Fig 1).

Seven patient were hospitalized and treated with steroids, 3 of them died. All the other patients had mild disease, two pts received monoclonal antibodies. Three pts died from COVID-19 while 4 pts died of unrelated causes. There was no increase in the mortality of LT pts due to the COVID epidemic.

**Conclusion:** In our LT cohort the outcome of COVID-19 was better than reported in the literature regarding both morbidity and mortality. Our data indicate that despite the population vaccination and the increase in the antibody titer after the third vaccine, there is still a considerable risk for LT recipients to develop COVID19, which is affected by the infection rate in the general population and not the immunization rate.
SAT273
Sarcopenia predict complications after hepatic resection for primary hepatocellular carcinoma (HCC) in patients with advanced chronic liver disease (ACLD) and clinically significant portal hypertension (CSPH)
Federico Ravaioli, Giovanni Marasco, Elton Daji, Vanessa Alemanni, Matteo Zenulli, Matteo Serenari, Matteo Ravaioli, Amanda Vestito, Giulio Vara, Davide Festi, Rita Golffieri, Matteo Cescon, Antonio Colechia. IRCCS Ospedaliero-Universitaria di Bologna, Department of Medical and Surgical Sciences, Bologna, Italy
Email: f.ravaioli@unibo.it

Background and aims: Patients with advanced chronic liver disease (ACLD) complicated by early-stage hepatocellular carcinoma (BCLC-0/A) are the best candidates for surgical liver resection. Despite the latest improvements in clinical management and surgical techniques, hepatic resection is burdened with an incidence of major complications (MC) and post-hepatectomy hepatic failure (PHLF) with significant perioperative mortality and morbidity. Sarcopenia assessed by measuring skeletal muscle index (SMI) was associated with a higher risk of waiting list mortality and worse outcome after transplantation in patients with ACLD. In the absence of data on the role of sarcopenia in the post-hepatectomy setting, we aimed to investigate the prognostic role of SMI on the incidence of PHLF and surgical complications in patients with ACLD in a tertiary European referral centre.

Method: All patients with available preoperative abdominal CT performed 3 months before surgery who underwent hepatic resection for primary HCC enrolled consecutively from 2014 to 2019 were included. Sarcopenia was defined according to the EASL as SMI, as measured by CT-images, <50 cm²/m² in males and SMI <39 cm²/m² in females. Surgical complications were assessed according to the Clavien-Dindo classification. The diagnosis of PHLF was performed according to the International Study Group of Liver Surgery (ISGLS) definition.

Results: 159 patients underwent hepatic resection for primary HCC, within inclusion criteria were included in the final analyses. Sarcopenia was present in 82 patients (51.6%). The median SMI was 39.2 (35.7–42.4) cm²/m² and 48.9 (43–55.3) cm²/m² in female and male patients, respectively. SMI values were significantly correlated with age (r = −0.229, p value = 0.004) and BMI (r = 0.369, p value <0.0001), but not with the of liver disease severity, as assessed by liver stiffness, platelet count, or MELD score. During the 30-days postoperative observation, 13 (8.2%) patients developed MC and 48 PHLF (30.2%; 14 PHLF-B/C). Overall, the presence of sarcopenia was not independently associated with post-hepatectomy and PHLF complications; however, in the group of patients with clinically significant portal hypertension (CSPH), SMI was independently associated with MC and PHLF B/C (OR 0.889 [0.798–0.990]; p value 0.032). Indeed, the MC rate was significantly higher in patients with (16.3%) than in patients without (0%) sarcopenia (p = 0.012).

Conclusion: the assessment of sarcopenia by SMI may aid physicians and surgeons in preoperative evaluation for hepatectomy for primary hepatocellular carcinoma in patients with advanced chronic liver disease complicated by clinically significant portal hypertension. However, further studies are still needed to evaluate the impact of perioperative nutritional and rehabilitation intervention.

SAT274
A comparison of hispanic living liver donor candidates approved and denied at a high-volume urban transplant center
Dana Toy, Brian Horwich, Ashwini Mulgaonkar, Ana Padilla, Jennifer Dodge, Navpreet Kaur, Hyosun Han, University of Southern California, Medicine, Los Angeles, United States; University of Southern California, Transplant Institute, Los Angeles, United States;
University of Southern California, Population and Public Health Sciences, Los Angeles, United States; University of Southern California, Gastrointestinal and Liver Diseases, Los Angeles, United States;
University of Southern California, Surgery, Los Angeles, United States
Email: dana.toy@med.usc.edu

Background and aims: Hispanics account for 20% of candidates waiting for liver transplantation (LT). Although living donor LT is comparable to deceased donor LT, minorities receive a disproportionately low percentage of living donor LT. From 2018–2019, living donor LT increased by one-third, while percentage of Hispanic living donors decreased. This study aims to compare Hispanic living liver donor candidates who were approved versus declined by a multidisciplinary selection committee at a large urban transplant center.

Method: The Living Liver Donor Referrals Database was reviewed between December 1, 2017 and August 31, 2021 for donor applicants (n = 195) who (1) completed a questionnaire and clinic evaluation, (2) were presented at a multidisciplinary selection committee, and (3) were formally approved/declined to serve as living liver donors. Statistical analysis was performed using Student’s t-test and chi-squared test.

Results: Of 1, 689 living liver donor applicants, 11.5% (n = 195) were presented at a multidisciplinary selection committee. Half of those presented were approved (52.3%, n = 102), while the other half were declined (47.7%, n = 93). Hispanics who were approved (n = 55) and declined (n = 47) as living liver donor candidates had similar baseline demographics: mean age (34 v. 35 years, p = 0.71), mean body mass index (27.9 v. 28.8 kg/m², p = 0.40), female (61.8% v. 63.8%, p = 0.83). There was no significant difference in social history among Hispanics who were approved and declined: full time employment (62.3% v. 55.6%, p = 0.15), female (61.8% v. 63.8%, p = 0.83). There was no significant difference in social history among Hispanics who were approved and declined: full time employment (62.3% v. 55.6%, p = 0.50), some college education (67.9% v. 68.9%, p = 0.92), married (47.2% v. 42.2%, p = 0.62), without alcohol use (20.6% v. 26.7%, p = 0.49). Both approved and declined Hispanic living liver donor candidates had nearly one-fourth who reported no medical insurance (28.3% v. 22.2%, p = 0.49) and no primary care doctor (25.5% v. 31.9%, p = 0.47). Hispanic living liver donor candidates were referred by intended transplant recipient or their friend/family (74.5% v. 83%, p = 0.30). Mean length of time from questionnaire to formal decision by a selection committee did not differ significantly when comparing approved and declined Hispanic candidates (165.4 v. 144.2 days, p = 0.55).

Conclusion: the assessment of sarcopenia by SMI may aid physicians and surgeons in preoperative evaluation for hepatectomy for primary hepatocellular carcinoma in patients with advanced chronic liver disease complicated by clinically significant portal hypertension. However, further studies are still needed to evaluate the impact of perioperative nutritional and rehabilitation intervention.
The results of our study suggest that there is interest in living donor liver transplantation among Hispanics, given that nearly half (44.9%) of all living liver donor applicants were Hispanic. Our study shows that there is interest in living donor liver transplantation among Hispanics, given that nearly half (44.9%) of all living liver donor applicants were Hispanic. Our study suggests that the standard demographic and clinical data do not adequately capture factors that influence approval for living donor candidacy among Hispanics. There are ongoing efforts to establish comprehensive donor candidate registries that will better elucidate how the donor evaluation process may adapt to reduce racial and ethnic disparities in living donor LT.

SAT276
SARS-CoV-2 infection in liver transplant recipients: a single center case series from Romania
Ioana-Alexandra H usur-Shurlan1, Raluca Roxana Grigorescu1, Elena Cristina Radu1, Daniela Tabacel1, Madalina Florescu1, Florina Nitc2, Radu Dumitru1, Ana Stanila3, Alexandru Martinu4, Nicolae Bolesa5, Dragos Chirita4, Laura Popa-Dan5, Cesal Stroescu4, Narcis Copca1, 1Saint Mary Hospital, Gastroenterology, Bucuresti, Romania; 2Saint Mary Hospital, Radiology, Bucuresti, Romania; 3Fundeni Clinical Institute, Radiology, Bucuresti, Romania; 4Saint Mary Hospital, Surgery, Bucuresti, Romania; 5Saint Mary Hospital, Anaesthesiology and Intensive Care Unit, Bucuresti, Romania.

Background and aims: The COVID-19 pandemic has affected people and medical care and led to changes in solid organ transplant programs. Recipients of liver transplantation (LT) represent a special group of patients with chronic immunosuppression and frequently associated comorbidities that may present with different progression of the disease than the general population.

Method: We report a case series of patients undergoing post-liver transplantation evaluation, from a single centre in Romania, who were diagnosed with SARS-CoV-2 infection by RT-PCR from respiratory swaps. We analysed their clinical traits, prognostic factors, management and outcome.

Results: In this case series, we report 11 cases of SARS-CoV-2 infection in liver transplant recipients at different times after transplant, varying from 7 days to 77 months. 45% of patients included were asymptomatic, while in the symptomatic group dyspnea was the most common manifestation (83.33%), followed by fever (50%), dry cough and gastrointestinal symptoms. COVID-19 therapies included antibiotics, antivirals, immunomodulators, steroids, low molecular weight heparin, antifungal, high dose vitamin therapy and Quercetine. Dyspnea as a symptom, and neutrophil-to-lymphocyte-ratio (NLR) as biological marker were significantly associated with a severe clinical course. Other inflammatory markers like leucocytosis, platelet-to-lymphocyte-ratio (PLR), C-reactive protein (CRP), fibrinogen at diagnosis failed to show significant prognostic value. Patients who progressed to severe forms of the disease were often already hypoxic and tachypneic at presentation, highlighting once again that these patients may be presenting at a late stage of their infection, which limited their therapeutic options. In our study in 68% of patients immunosuppression was Tacrolimus, 9% had Tacrolimus with low dose corticoid, 9% had Sirolimus, and two patients were in the induction immunosuppression phase. Tacrolimus immunosuppression remained unchanged during COVID-19 infection in almost all cases. COVID-19-related mortality was 27.27%. No difference was observed in mortality between those infected within one-year vs after one year of liver transplantation.

SARS-CoV-2 infection in liver transplant recipients—a single center case series from Romania
Ioana-Alexandra H usur-Shurlan1, Raluca Roxana Grigorescu1, Elena Cristina Radu1, Daniela Tabacel1, Madalina Florescu1, Florina Nitc2, Radu Dumitru1, Ana Stanila3, Alexandru Martinu4, Nicolae Bolesa5, Dragos Chirita4, Laura Popa-Dan5, Cesal Stroescu4, Narcis Copca1, 1Saint Mary Hospital, Gastroenterology, Bucuresti, Romania; 2Saint Mary Hospital, Radiology, Bucuresti, Romania; 3Fundeni Clinical Institute, Radiology, Bucuresti, Romania; 4Saint Mary Hospital, Surgery, Bucuresti, Romania; 5Saint Mary Hospital, Anaesthesiology and Intensive Care Unit, Bucuresti, Romania.

Background and aims: The COVID-19 pandemic has affected people and medical care and led to changes in solid organ transplant programs. Recipients of liver transplantation (LT) represent a special group of patients with chronic immunosuppression and frequently associated comorbidities that may present with different progression of the disease than the general population.

Method: We report a case series of patients undergoing post-liver transplantation evaluation, from a single centre in Romania, who were diagnosed with SARS-CoV-2 infection by RT-PCR from respiratory swaps. We analysed their clinical traits, prognostic factors, management and outcome.

Results: In this case series, we report 11 cases of SARS-CoV-2 infection in liver transplant recipients at different times after transplant, varying from 7 days to 77 months. 45% of patients included were asymptomatic, while in the symptomatic group dyspnea was the most common manifestation (83.33%), followed by fever (50%), dry cough and gastrointestinal symptoms. COVID-19 therapies included antibiotics, antivirals, immunomodulators, steroids, low molecular weight heparin, antifungal, high dose vitamin therapy and Quercetine. Dyspnea as a symptom, and neutrophil-to-lymphocyte-ratio (NLR) as biological marker were significantly associated with a severe clinical course. Other inflammatory markers like leucocytosis, platelet-to-lymphocyte-ratio (PLR), C-reactive protein (CRP), fibrinogen at diagnosis failed to show significant prognostic value. Patients who progressed to severe forms of the disease were often already hypoxic and tachypneic at presentation, highlighting once again that these patients may be presenting at a late stage of their infection, which limited their therapeutic options. In our study in 68% of patients immunosuppression was Tacrolimus, 9% had Tacrolimus with low dose corticoid, 9% had Sirolimus, and two patients were in the induction immunosuppression phase. Tacrolimus immunosuppression remained unchanged during COVID-19 infection in almost all cases. COVID-19-related mortality was 27.27%. No difference was observed in mortality between those infected within one-year vs after one year of liver transplantation.
Conclusion: In this case series, liver transplant recipients with COVID-19 disease, aged 60 years or older, who presented with dyspnoea and had diabetes mellitus had more severe outcomes. Neutrophil-lymphocyte ratio at diagnosis seems to be a prognostic factor for a more severe course of COVID-19 pneumonia. Other inflammatory markers had failed to show a significant prognostic role. Older liver transplant recipient patients with diabetes, that present dyspnoea related to COVID-19 pneumonia should be admitted and monitored because of the risk of severe course and high risk of mortality.

SAT277
Liver transplantation for hepatocellular carcinoma: outcome and prognostic factors for recurrence
Veronica Paon1, Ilaria Normelli2, Amedeo Carraro3, Paola Violi3, Andrea Dalbeni2, Donatella Ieluzzi1, Andrea Ruzzenente4, Alfredo Guglielmi4, David Sacerdoti1.
1Liver unit AOUI, medicine, Verona, Italy; 2General medicine AOUI, medicine, Verona, Italy; 3Liver transplant unit, surgery, Verona, Italy; 4Hepatobiliary surgery, surgery, Verona, Italy
Email: veronica.paon@aovr.veneto.it

Background and aims: Hepatocellular carcinoma (HCC) accounts for approximately 75% of primary liver cancers and is the fourth leading cause of death from malignancy worldwide. The 5-year survival rate is around 10–15%, often due to late diagnosis with detection of advanced neoplastic disease. Liver transplant (LT) is a curative treatment in some patients. The post-transplant recurrence rate of HCC is very wide, between 5 and 30%, due also to different listing policies. The aim of our study was to evaluate the recurrence rate of HCC after LT and to identify the main risk factors for recurrence.

Method: 230 patients (84% male, mean age 59 yr) with HCC transplanted between February 2007 and December 2020 were followed until recurrence or death. The majority of patients had Mayo End Stage Liver Disease (MELD) scores ≤ 19, while only 4.8% presented for transplant with MELD scores ≥ 30. Milan criteria were applied for listing. Etiology, biochemical data, comorbidities, pre-transplant treatments, and histological evaluation of the native liver were collected.

Results: 57% of patients had viral, 29.6% alcoholic, and 12.6% non-alcoholic fatty liver disease cirrhosis. 37% of patients had type 2 diabetes mellitus (T2DM) and 43.6% hypertension. 69% of patients had undergone pre-transplant treatments (percutaneous ethanol injection, radiofrequency ablation, transarterial chemioembolization, transarterial radioembolization, resection). The mean follow-up was 47 ± 39 months, with 77.4% survival. Average survival of patients without HCC recurrence was 48.6 ± 39.4 months, average survival of patients with recurrence was 23 ± 25.1 months. After LT, 9.1% of patients had HCC recurrence, and 22.6% died. Among those who had HCC recurrence, 57% of patients had recurrence within the first 12 months after transplantation; 19% at 24 months, 19% at 36 months and 5% at 60 months. In 66.6% of patients with relapsed HCC, the tumor started with extrahepatic localizations (lung, lymph nodes, mediastinum).

In the multivariate analysis the only factors that predicted the outcome (death or HCC relapse) were: extranodal microvascular invasion (p < 0.001), size of the largest nodule (p < 0.005) and number of pre-transplant local-regional treatments (p < 0.04). High pre LT MELD and T2DM identified patients with a worse overall outcome and poorer survival.

Conclusion: In our 13 years experience, recurrence of HCC after transplantation was low (9%). Number of pre-transplant treatments, size of nodules and microvascular invasion were the only predictors of recurrence of HCC after transplantation.
SAT278

The liver outcomes and equity (LOEq) index: neighborhood social determinants independently predict outcomes in liver transplantation

Kali Zhou1, Leane Kuo1, Jennifer Dodge1, Laura Thompson1, Norah Terrault1, Myles Cockburn1. 1University of Southern California, Los Angeles, United States
Email: kalizhou@usc.edu

Background and aims: The impact of social determinants of health (SDOH) at the neighborhood-level on patient outcomes in adult liver transplantation (LT) is unknown. We constructed the novel Liver Outcomes and Equity (LOEq) index to characterize area-based SDOH specific to the population with liver disease in the United States (US) and examined association with LT outcomes.

Method: The LOEq index was derived from 16,713 unique ZIP codes (42% of all US ZIP codes) of adult waitlisted patients in the Scientific Registry of Transplant Recipients database between 6/18/2013–5/18/2018. We selected 38 ZIP code-level variables across five SDOH domains from the 2014–2018 American Community Survey as a comprehensive measure of neighborhood SDOH. Principal component analysis conducted with a structured and iterative process identified the most influential 13 variables to be included in the final index. Primary predictor was the LOEq index categorized into quintiles (Q1 = lowest to Q5 = highest SDOH). Outcomes were 1) waitlist (WL) mortality (= delisting for too sick/death) and 2) post-LT patient survival, examined with competing risk and Cox regression, respectively. Models were adjusted for transplant region and relevant demographic/clinical factors, with insurance tested as an effect modifier.

Results: Adult LT patients disproportionately resided in neighborhoods with higher SDOH, with 14.0% vs 30.3% of waitlisted patients (n = 59,298) and 13.9% vs 30.2% of transplanted patients (n = 37,598) in Q1 vs Q5, respectively. Lower LOEq quintiles had higher proportion minorities, public insurance, hepatitis C etiology, diabetes, and obesity. 47% in Q1 vs 17% in Q5 lived in transplant regions with a short wait time to LT; 5.6% in Q5 vs 2.4% in Q1 underwent living donor LT. The 3-year cumulative incidence of WL mortality was higher in Q1 (22.9%) vs Q5 (20.6%), while 3-year post-LT survival was lower in Q1 (85.8%) vs Q5 (87.4%). In the multivariable model of waitlisted patients, LOEq Q1–4 were associated with increased WL mortality compared to Q5 (all p < 0.01), with Q1 patients incurring 23% excess deaths compared to Q5 (HR 1.23, 95% CI 1.16–1.31). Among transplanted, risk of post-LT death was also elevated for LOEq Q1 (HR 1.14, 1.04–1.24) and Q3 (HR 1.12, 1.03–1.21) compared to Q5. There was a non-significant interaction between LOEq and insurance type: higher WL mortality for Q1 vs Q5 (HR 1.28 for private vs 1.15 for public; p = 0.08) and lower post-LT deaths for Q1 vs Q5 (HR 1.01 for private vs 1.17 for public; p = 0.09).

Conclusion: More LT patients living in higher LOEq quintiles highlights a neighborhood-level disparity in access to LT. Lower neighborhood SDOH predicted worse outcomes in LT independent of patient demographics and clinical characteristics. The liver disease-specific LOEq index might be leveraged to identify the most vulnerable patients for interventions in clinical settings to increase LT equity.

SAT279

Prevalence, prognosis, clinical, biological and histological features of incidentally found hepatocellular carcinoma after liver transplantation

Emilie Kerstens1, Samuele Iesari2,3, Eliano Bonaccorsi1, Laurent Coubeau1, Géraldine Dahlqvist1, Olga Ciccarelli1, Bénédicte Delire1,2UCLouvain; 2Fondazione IRCCS Ca’ Granda Ospedale Maggiore Policlinico, General surgery and kidney transplantation, Milan, Italy; 3Institut de Recherche Expérimentale et Clinique, UCLouvain, Pôle de Chirurgie Expérimentale et Transplantation, Brussels, Belgium
Email: benedicte.delire@saintluc.uclouvain.be

Background and aims: An incidentally found hepatocellular carcinoma (iHCC) is an HCC diagnosed postoperatively after the analysis of the liver explant from patients who underwent liver transplantation (LT) for non-oncological indication. Data about the prevalence and prognosis of iHCC are scarce. The aim of this study is to evaluate the prevalence of iHCC in our LT patients and to compare the mortality, the risk of recurrence and the clinical, biological, and histological features between patients who underwent LT for postoperatively known HCC (pHCC) and patients with a postoperative diagnosis of iHCC.
Method: We retrospectively reviewed 268 adult patients who underwent LT at the Cliniques Universitaires Saint-Luc, Brussels, Belgium, from January 2010 to January 2020. Results were compared using Fisher’s exact test or Mann-Whitney U test as appropriate. The Kaplan-Meier method was used to analyze the rate of death and graft loss. Log-rank tests were run to compare the survival curves. The significance of statistical tests was taken at a P value of <0.05. Analyses were run with SPSS Statistics.

Results: Among the 268 adult patients who underwent LT, 98 cirrhotic patients were transplanted for a pkHCC. Prevalence rate of iHCC was 12%. Alcoholic cirrhosis was predominant in the iHCC cohort (88.9% vs 48%, p = 0.032). As expected, the patients of the iHCC cohort had a higher MELD score (19.0 (17.0–20.0) vs 10.0 (8.0–13.0); p <0.001) both, at the registration on the waiting list and at LT. Value of Child-Pugh score was also higher for the iHCC cohort compared to pkHCC patients (10.0 (9.0–11.0) vs 5.0 (5.0–6.0); p <0.001). None of the iHCC patients got Child–Pugh A score vs 76, 3% of the patients with pkHCC (p <0.001). Child-Pugh class C cirrhosis at LT was mainly found in the iHCC cohort (55.6% vs 62%; p <0.001). No statistical difference was observed between the 2 cohorts for the level of alfaprotein, neither at time of registration nor at LT. However, des-carboxy-prothrombin level was significantly higher at time in the LT cohort in the iHCC cohort (273.8 (228.9–551.1) vs 42.0 (22.5–96.0); p = 0.022). The interval between the last imaging and LT was longer in iHCC cohort than pkHCC (2.7 months (1.9–3.7) vs 1.0 (0.5–1.7); p <0.004). Based on histological analysis, Edmondson grade II lesions were more frequently found in the iHCC cohort. However, there was no difference regarding the microvascular invasion rate. None of the 9 iHCC patients got recurrence of HCC post-LT. Cumulated recurrence at 1, 3 and 5 years post-LT for pkHCC patients were respectively 3%, 7% and 11%. No significant difference was observed for 1, 3 and 5-year survivals rates for pkHCC patients compared to iHCC patients (respectively 100%, 88% and 53% vs 90%, 87% and 65%; p = 0.565).

Conclusion: While the prevalence of iHCC is not negligible (12% in our patients), it impacts neither the neoplasic recurrence rate nor the survival rate compared to pkHCC patients.

SAT280
Survival benefit from liver transplantation for patients with and without hepatocellular carcinoma
Ben Goudsmith1, Ilaria Prosepe2, Maarten Tushuizen1, Serge Vogelaar2, Tan Alwayn2, Bart Van Hoek1, Andries Braat1, Hein Putter1, 1Leiden University Medical Center (LUMC), Gastroenterology and Hepatology, Leiden, Netherlands; 2Leiden University Medical Center (LUMC), Biostatistics, Leiden, Netherlands; 3Foundation Eurotransplant International Foundation, Leiden, Netherlands; 4Leiden University Medical Center (LUMC), Surgery, Leiden, Netherlands
Email: b.f.goudsmith@lumc.nl

Background and aims: In the US, inequal liver transplantation (LT) access exists between patients with and without hepatocellular carcinoma (HCC). Survival benefit considers survival without and with LT and could equalize LT access. We calculated and compared LT survival benefit scores for patients with (out) HCC, based on longitudinal data in a recent US cohort.

Method: Adult LT candidates with (out) HCC between 2010 and 2019 were included. Waitlist survival over time was contrasted to posttransplant survival, to estimate 5-year survival benefit from the moment of LT. Waitlist survival was modeled with bias-corrected time-dependent Cox regression and posttransplant survival was estimated through Cox proportional hazards regression.

Results: Mean HCC survival without LT was always lower than non-HCC waitlist survival. Below MELD (−Na), 30, HCC patients gained more life-years from LT than non-HCC patients at the same MELD (−Na) score. Only non-HCC patients below MELD (−Na) 9 had negative benefit. Most HCC patients were transplanted below MELD (−Na) 14 and most non-HCC patients above MELD (−Na) 26. Liver function (MELD (−Na), albumin) was the main predictor of 5-year benefit. Therefore, during five years, most HCC patients gained 0.12 to 1.96 years from LT, whereas most non-HCC patients gained 2.48 to 3.45 years.

Conclusion: On an individual level, transplanting patients with HCC resulted in survival benefit. However, on a population level, benefit was indirectly wasted, as non-HCC patients were likely to gain more survival due to decreased liver function. Based on these data, we now provide an online calculator to estimate 5-year survival benefit given specific patient characteristics. Survival benefit scores could serve to equalize LT access.
Background and aims: In the era of nucleos (t)ide analogues (ANs), we investigate the outcomes of liver transplantation (LT) using HBsAg (+) grafts using Korean national registry database.

Method: Among 4265 LTs which were registered in KOTRY database between April 2014 and January 2020, 20 (0.5%) LTs using HBsAg (+) grafts were identified. We investigated the overall outcomes of LT using HBsAg (+) liver grafts (n = 4100, S (+) group) compared to those of HBsAg (-) liver grafts. S (+) group were compared to those for LT using HBsAg (-) and HBcAb (+) (n = 882, C (+) group) and HBsAg (-) and HBcAb (-) (n = 3132, SC (-) group) after propensity-score matching (1:1).

Results: Twenty HBsAg (+) grafts from deceased donors were transplanted to HBsAg (+) recipients. HBIG was maintained in 16 patients (80%). Most common NA was tenofovir. S (+) group showed comparable patient survival (26.5 ± 21.8 vs 22.8 ± 18.2 months, p = 0.332) and graft survival (26.5 ± 21.8 vs 21.3 ± 18.2 months, p = 0.152) compared to those of HBsAg (-) group.

Age (HR = 1.03, p = 0.016), HCC (HR = 4.61, p < 0.001), MELD score (HR = 2.82, p = 0.001), ascites (HR = 2.14, p = 0.002), and encephalopathy (HR = 2.53, p < 0.001) were the risk factors affecting patient survival. For graft survival, HCC (HR = 4.01, p = 0.001), pre-operative treatment to HCC (HR = 0.54, p = 0.006), MELD score (HR = 2.14, p = 0.012), ascites (HR = 2.52, p < 0.001), and encephalopathy (HR = 1.99, p < 0.001) were significant factors.

After PSM matching between S (+) and C (+), and S (+) and SC (-), there was no significant difference in patient survival (24.3 ± 20.7 vs 38.2 ± 23.0 months, p = 0.865, 24.3 ± 27 vs 38.2 ± 23.0 months p = 0.547), and graft survival (26.5 ± 21.8 vs 36.3 ± 17.4 months, p = 0.576, 26.5 ± 21.8 vs 36.3 ± 18.4 months, p = 0.327, respectively).

Conclusion: HBsAg (+) liver grafts can expand the donor pool without compromising the outcomes in the era of NA in the HBV endemic area.

SAT283
A panel of three micro RNAs allows robust prediction of overall survival after liver resection

David Pereyra1,2, Hubert Hackl3, Susanna Skalicky4, Jonas Santol1,2, Thomas Grünberger2, Matthias Hackl1, Alice Assinger2, Patrick Starlinger1.1Medical University of Vienna, Department of General Surgery, Division of Visceral Surgery; 2Medical University of Vienna, Center of Physiology and Pharmacology, Institute of Vascular Biology and Thrombosis Research; 3Medical University of Innsbruck, Division of Bioinformatics, Biocenter; 4TamiRNA GmbH; 5Clinic Favoriten, Department of Surgery, Hepatico-Pancreato-Biliary Center Email: david.pereyra@meduniwien.ac.at

Background and aims: Overall survival (OS) after liver resection (LR) is influenced by posthepatectomy liver failure (PHLF), disease recurrence, and chronic deterioration of liver function. We previously reported on a panel consisting of the three micro RNAs (miR) miR-122, miR-151a, and miR-192, summed up as the hepatomiR score, which allows accurate preoperative prediction of PHLF. Here, we aimed for investigation of the hepatomiR score in prediction of long-term OS.

Method: Blood was taken prior to LR in 175 patients followed by optimized plasma preparation. Plasma was used for evaluation of miRs using quantitative polymerase chain reaction, and hepatomiR was calculated. Patients were followed up for disease recurrence and mortality. Statistical analysis was carried out on SPSS version 26 and was based on receiver operating characteristic analysis (ROC), non-parametric tests, log-rank tests, and Cox-regression.

Results: HepatomiR showed a high predictive potential for PHLF with an area under the curve of 0.794 upon ROC. Further, hepatomiR was significantly associated with OS upon univariable Cox-regression (hazard ratio [HR] = 3.104, 95% confidence interval [95%CI] 1.77–8.184, p = 0.022), and remained significant in a multivariable model (HR = 6.326, 95%CI 1.994–20.066, p = 0.022). The previously evaluated cut-offs for hepatomiR (>0.59 and >0.68) were applied in order to divide the cohort into three risk groups. In Kaplan-Meier analysis OS after LR was reduced in the intermediate-risk group (median OS = 44 months, 95%CI 0–96, p = 0.651), and patients in the high-risk group (hepatomiR >0.68) showed a significantly shorter OS (median OS = 11 months, 95%CI 5–18, p = 0.001) when compared to the low-risk group, respectively (median OS = 53 months, 95%CI 31–74). Accordingly, we focused on the high-risk group and observed a significantly higher incidence of 90-day mortality (3.7% vs 27.3%, p = 0.001), and mortality within 1 year (16.3% vs 63.6%, p <0.001), 3 years (42.9% vs 81.8%, p = 0.012), and 5 years (58.4% vs 90.0%, p = 0.048). An association with disease-free survival could not be observed. In order to evaluate the relevance of hepatomiR for PHLF independent prediction of OS, we further excluded patients with 90-day mortality. We observed that the high-risk cut-off was still able to identify patients with reduced OS (median OS = 68 ± 59 months, 95%CI 35–84; median OS >68 ± 12 months, 95%CI 7–17, p = 0.040), and patients with mortality within 1 year (13.0% vs 50.0%, p = 0.004), 3 years (40.5% vs 75.0%, p = 0.055), and 5 years (56.5% vs 85.7%, p = 0.127).

Conclusion: We here present the hepatomiR score as a marker for risk stratification prior to LR. HepatomiR allows identification of patients at risk for PHLF, and patient with reduced OS after LR independently from PHLF. Accordingly, the evaluation of hepatomiR might improve patient selection and ultimately increase personalized outcome of liver surgery.

SAT284
Liver transplantation for primary sclerosing cholangitis and predictors of disease recurrence

Julie Zhu1, Dennis Lim2, Larry James3, Eric Yoshida3, Kevork Peltekian2.1Dalhousie University, Atlantic Liver Transplant Program, Canada; 2Dalhousie University, Medicine; 3University of British Columbia, Medicine Email: julie.zhu@ualberta.ca

Background and aims: In liver transplantation (LT) for PSC, pre-transplant colectomy may lower the risk of PSC recurrence (rPSC), and well-controlled or lack of IBD may protect against rPSC, however, these findings are not consistent across all studies. It is unknown whether recipient/donor sex plays a role in rPSC. The aim is to study factors associated with PSC recurrence in the post-transplant population.

Method: This is a retrospective study on adults who received LT for PSC in Halifax NS from 1985 to 2020. Graft and patient outcomes are analyzed by logistic regression models.

Results: A total of 92 patients underwent deceased donor LT for PSC with a mean follow-up time of 9.2 yrs (SD 7.1). Fifty-three remain active in the program, 2 were lost to follow-up and 37 died. The mean age at transplant was 43 (SD13, range 18.9–67.8). Seven patients had a second transplant. The five- and 10-year patient survival rate of the entire cohort was 78.7% and 66% respectively. In the active cohort, the
prevalence of rPSC was 23.5% (12/51). Retransplantation for rPSC occurred in 8.3% (1/12). The prevalence of IBD was 82.4% (42/51), consisted of ulcerative proctitis (64.7%, 33/51), ulcerative colitis (19.6%, left-sided UC (2%) and Crohn’s disease (9.8%). Males are much more likely than females to undergo a colectomy at any time (OR 5.5, 95% CI 1.07–28.22, p = 0.041). Refractory IBD was the predominant indication for a colectomy (10/16), followed by dysplasia or colon cancer (6/16). In the post-transplant period, 69% had stable IBD without therapy escalation, 11.5% were escalated to a biologic, 19% underwent a colectomy for active IBD symptoms. Pretransplant colectomy negatively predicted rPSC, in this subgroup 0% (0/6) developed rPSC. Neither recipient sex (OR 1.14, 95% CI 0.26–5.0, p = 0.86) or recipient age predicted the likelihood of rPSC. There was no association between donor sex on rPSC (OR 1.25, 95% CI 0.30–5.27, p = 0.76). A trend towards increased rPSC was observed in male donors to female recipients versus female-to-female transplants (OR 6, 95% CI 0.76). A trend towards increased rPSC was observed in male donors to female recipients versus female-to-female transplants (OR 6, 95% CI 0.33–10.74, p = 0.224). Overall, having a post-transplant colectomy, subtotal or total, irrespective of timing, did not significantly impact rPSC (OR 0.389, 95% CI 0.09–1.66, p = 0.20). Diagnosis of IBD was not associated with an increased risk of rPSC (OR 1.21, p = 0.83).

Conclusion: Several factors were associated with rPSC after liver transplant in patients with PSC and IBD, pre-transplant colectomy was found to be protective, male donor to female recipient was a potential risk factor. It is important to study these factors in multi-centered cohorts to understand the pathogenesis of rPSC. Pretransplant total colectomy may be beneficial for several reasons, reducing rPSC, controlling IBD activities, and lowering dysplasia and colon cancer rates in the post-transplant population.

SAT285 Predictive factors of antibody response after anti-SARS-CoV-2 vaccine in liver transplant recipients

Ilias Kounis1, Bruno Roche1, Lea Duhault1, Rodolphe Sobesky1, Eleonora De Martin1, Edouardo Poli1, Alia Pascale1, Gabriella Pittau1, Oriana Ciocio1, Jean-Charles Duclos-Vallée1, Didier Samuel1, Cyrille Feray1, Audrey Coilly1, 1AP-HP Hôpital Paul-Brousse, Centre Hépato-Biliaire; Inserm, Université Paris-Saclay, UMR-S 1193; Université Paris-Saclay, Inserm, Villejuif, France

Email: ilias.kounis@aphp.fr

Background and aims: A weak immune response to 2 doses of anti-SARS-CoV2 vaccine was observed in solid-organ transplant recipients, encouraging the authorities to recommend a third dose in immunosuppressed patients. The aim of our study was to search for predictive factors of an antibody response to the vaccines and describe their efficacy and tolerance in a large population of liver transplant (LT) recipients.

Method: This is a retrospective monocenter study conducted at Paul Brousse Hospital in France. All adult LT recipients followed up in our transplant center and vaccinated with at least one dose of vaccine from January 2021 to September 2021 were included. A strong immune response to vaccination was defined as the presence of antibodies titration to SARS-CoV-2 spike protein up to 250 U/ml after 2nd or 3rd dose of vaccine.

Results: 745 patients were included. Of them, 642 (85.5%) had 2 doses and 343 (46%) patients had three. Mean age at vaccination was 59.1 (± 14.5) years and mean time from LT to vaccination was 12.1 (± 9.7) years. Immunosuppression was due to one immunosuppressive drug in 29.7% of patients, 2 drugs in 57.6% and 3 drugs in 12.5%. The prevalence of anti-SARS-CoV-2 antibodies was 11% (19 patients) before the first dose, 40.8% (53 patients) before the second dose, 66.2% (392 patients) before the third dose, and 72.5% (271 patients) after the third dose. 190 (36.7%) patients had a strong antibody titration after 2nd injection and 139 (47.6%) after 3rd injection. Patients who had strong antibody response had, in time of vaccination, lower Tacrolimus blood concentrations (p = 0.04), lower Mycophenolate (p < 0.001) and corticosteroid doses (p = 0.009), lower creatinine (p = 0.04), higher hemoglobin (p < 0.001) levels and longer time between LT and vaccination (p = 0.004). In multivariate analysis, predictive factors of strong response were time since LT >9.8 years (p = 0.001), while creatinine levels >95 μmol/l (p = 0.014), use of corticosteroids (p < 0.001) and high mycophenolate dose (p < 0.001) in time of vaccination were correlated with an absence of strong response to the vaccine. Fifteen (2%) patients had COVID after vaccination, 2 of them after 3 doses of vaccine. No serious adverse events were for 99.7% of patients.

Conclusion: A strong immune response was detected to less than a half of LT recipients after 3 doses of anti-SARS-CoV-2 vaccine. These patients remain at risk for Covid-19, especially if they had a recent LT or have high levels of immunosuppression.

SAT286 Immunotherapy before solid organ transplantation: an international transplant community-focused survey

Tommy Ivanic1,2,3, Marco Claasen1,4, David Al-Adra3, Gonzalo Sapisochin1, 1University Health Network, Multi-Organ Transplant Program, Toronto, Canada; 2Henry Ford Hospital, Department of Surgery, Detroit, United States; 3Uppsala University, Department of Surgical Sciences, Akademiska Sjukhuset, Uppsala, Sweden; 4Erasmus MC, Department of Surgery, Rotterdam, Netherlands; 5University of Wisconsin-Madison, Division of Transplantation, Madison, United States

Email: tommy.ivanics@uhn.ca

Background and aims: The use of immunotherapy for cancer has increased and is expected to continue to grow. The outcomes after solid organ transplantation (SOT) in patients having received immunotherapy before SOT remain unclear. We sought to evaluate the global transplant surgery community’s attitude and experience with patients who have received immunotherapy for malignancy before SOT.

Method: An online-based survey was sent to North American transplant directors in December-2020 and to members of the International Liver Transplant Society (ILTS) in November-2021 to evaluate experiences with, and attitudes towards, SOT in recipients with previous immunotherapy for cancer. Descriptive summary statistics were reported.

Results: 134 respondents provided consent to participate in the survey and 91 completed the survey for a completion rate of 68%. Respondents represented center experience from North America, South America, Europe, Asia, and Australia. Most represented centers from the United States (n = 22, 24%), followed by India (n = 9, 10%), and Spain (n = 4, 4%). Fifty-eight (64%) respondents would consider receiving immunotherapy for cancer before a SOT. Thirty (33%) respondents were aware of such recipients from the United States (n = 22, 24%), followed by India (n = 9, 10%), and Spain (n = 4, 4%). Fifty-eight (64%) respondents would consider offering a SOT to a patient with previous history of immunotherapy for cancer. Thirty (33%) respondents were aware of such recipients receiving immunotherapy for cancer before a SOT. The majority (n = 69, 77%) of respondents reported an absence of institutional clinical management policies in this setting.

Conclusion: Though this survey’s response rate was relatively low, it provides preliminary insight into the attitudes and experiences with SOT after immunotherapy for cancer in the international transplant community. This represents a clinical scenario for which outcomes should be clarified and consensus guidelines established to inform future clinical management, especially as immunotherapy for cancer is likely to increase in coming years.
## SAT287

Evaluating the predictive performance and transferability of machine learning-based prediction models using national liver transplant data registries

Tommy Ivanics1,2,3, Delvin So4, Marco Claasen5-6, David Wallace7-8, Madhukar Patel9, Annabel Gravely5, Kate Walker7, Thomas Cowling7, Lauren Erdman4, Gonzalo Sapisochin5.  
1University Health Network, Toronto, Canada; 2Henry Ford Hospital, Department of Surgery, Detroit, United States; 3Uppsala University, Department of Surgical Sciences, Uppsala, Sweden; 4The Hospital for Sick Children, The Centre of Computational Medicine, Toronto, Canada; 5University Health Network, Multi-Organ Transplant Program, Toronto, Canada; 6Erasmus MC Transplant Institute, University Medical Centre Rotterdam, Department of Surgery, division of HPB and Transplant Surgery, Rotterdam, Netherlands; 7London School of Hygiene and Tropical Medicine, Department of Health Services Research and Policy, United Kingdom; 8Guy’s and St Thomas’ Hospital, Department of Nephrology and Transplantation, United Kingdom; 9University of Texas Southwestern Medical School, Division of Surgical Transplantation, Dallas, United States  
Email: tommy.ivanics@uhn.ca

### Background and aims:
Large, national registries of liver transplant (LT) data are collected in many countries. We compared data from

### Table: Predictive Performance and Transferability of Machine Learning-Based Prediction Models

<table>
<thead>
<tr>
<th>Question</th>
<th>Overall (N=139)</th>
<th>48</th>
<th>58</th>
</tr>
</thead>
<tbody>
<tr>
<td>1a. Would you consider offering an organ transplant to a patient with a previous history of immunotherapy treatment for cancer?</td>
<td></td>
<td>48</td>
<td>58</td>
</tr>
<tr>
<td>1b. Do you consider offering an organ transplant to a patient with a previous history of immunotherapy treatment for cancer?</td>
<td></td>
<td>13(32%)</td>
<td>58(48%)</td>
</tr>
</tbody>
</table>

### Figure: (abstract: SAT286)
three national registries and developed machine learning algorithm (MLA)-based models that were used to evaluate performance predictions both within and across these different countries.

**Method:** We studied adults (≥ 18-years) who underwent primary LT between Jan-2008 and Dec-2018 from United Network for Organ Sharing (UNOS-US), National Health Service Blood and Transplantation (NHSBT-UK), and the Canadian Organ Replacement Registry (CORR-Canada). MLA models for 90-day post-LT mortality were built firstly on each individual registry’s capacity (based on variables inherent to the individual database) and then based on the overlapping variables available in all three registries (based on harmonized variables). The predictive abilities of the harmonized registry models were evaluated externally across countries using area-under-the-receiver-operator-curve (AUROC) and area-under-the-precision-recall-curve (AUPRC).

**Results:** The total number of patients were as follows: training (2008–2015) (Canada:n = 827; UK: n = 3,388; US: n = 40,454), validation (2016) (Canada:n = 126; UK:n = 621; US:n = 6,128), and testing (2017–2018) (Canada:n = 261; UK:n = 1,278; US:n = 12,976). The best performing MLA-based model was the ElasticNet across both multiply imputed independent and harmonized datasets (best performance in the US: AUROC: 0.70; Range: 0.70–0.71). Model performance diminished from the independent to the harmonized (only using variables that were in common between the three registries) registries, especially in the UK (independent ElasticNet: AUROC:0.54; Range: 0.52–0.56 to harmonized AUROC:0.48; Range: 0.48–0.50) and the US (independent ElasticNet: AUROC:0.70; Range:0.70–0.71 to harmonized AUROC:0.65; Range:0.64–0.65). Model performance after external validation across countries was overall poor (Table 1).

**Conclusion:** MLA-based models can be constructed using international LT registries, with independent ElasticNet models demonstrating optimal predictive performance. While MLA-based model performance yields fair discriminatory potential, a diminishing number of variables and granularity results in decreased performance. Moreover, the external validity of such MLA-based models is poor when applied to other transplant registries. This is likely due to inherent limitations and variability within each dataset. As such, it is conceivable that these limitations may be overcome in the future by increasing the granularity of datasets (for example, with linkages to other administrative datasets), and placing an increased emphasis on consensus for variable standardization (such as with increased collaboration and communications across transplant data collecting organizations).

**SAT288**
Liver transplant recipients have a higher incidence of lung cancer than general population
Paula Pujols1, Fanny Meylin Caballeros2, Mercedes Iñarraíraegui3, Javier Zulueta4, Gorka Bastarrika Alemán3, Jose Ignacio Herrero5.
1University of Navarra, Pamplona, Spain; 2Clínica Universidad de Navarra, Pamplona, Spain; 3Clinica Universidad de Navarra, Pamplona, Spain; 4Mount Sinai Morningside, New York, United States
Email: iherrero@unav.es

**Background and aims:** De novo malignancies are frequent complications after liver transplantation. Liver transplant recipients (LTRs) have a higher risk of lung cancer than the general population, but it may be due to a higher frequency of smoking. Our aim was to compare the incidence of lung cancer in LTRs with respect to a matched group of control candidates.

**Method:** In this retrospective study, 124 LTRs and 496 controls participating in a lung cancer screening program with low-dose computed tomography (LDCT) were compared. Four controls were matched for each LTR according to gender, age (± 10 years), current smoking status, cumulative smoking (± 10 pack-years) and presence of emphysema on initial LDCT examination. The results of our lung cancer screening program in LTRs were also evaluated.

**Results:** Twelve LTRs (9.7%) and 28 controls (5.6%) were diagnosed with lung cancer. The actuarial risks of lung cancer at 3, 5, 7 and 10 years were 3.3%, 4.5%, 8.3% and 18.2% for LTR and 3%, 3.4%, 4% and 7.1% for controls, respectively (p = 0.038). The most important predisposing factors for lung cancer were a higher age and the presence of emphysema.

Ten of the 12 LTRs with lung cancer were diagnosed with stage IA. At the end of the follow-up, six patients had died (two of them from lung cancer progression and one from chemotherapy-related sepsis). Nine patients were free of malignancy at their last follow-up.
SAT289
Survival benefit-based priority of liver transplantation in HBV-related acute-on-chronic liver failure
Peng Li1, Xi Liang2, Jinjin Luo1, Jiaqi Li3, Jiaojiao Xin1, Jiaqi Li4, Dongyan Shi5, Yingyan Lu5, Hozeifa Mohamed Hassan2, Qian Zhou1, Shaowei Hao1, Huaofeng Zhang5, Tianzhu Wu2, Tan Li5, Heng Yao1, Keke Ren1, Beibei Guo5, Xingping Zhou1, Jiaxian Chen1, Lulu He1, Hui Yang1, Wen Hu1, Shiwen Ma1, Bingli Li1, Shaoli You4, Shaojie Xin1, Yingyan Lu3, Jun Li1, 1The First Affiliated Hospital, Zhejiang University School of Medicine, State Key Laboratory for Diagnosis and Treatment of Infectious Diseases, Hangzhou, China; 2Taizhou Central Hospital (Taizhou University Hospital), Precision Medicine Center, Taizhou, China; 3Tongde Hospital of Zhejiang Province, Key laboratory of cancer prevention and therapy combining traditional Chinese and Western Medicine, Hangzhou, China; 4The Fifth Medical Center of PLA General Hospital, Senior Department of Hepatology, Beijing, China; 5Beijing Youan Hospital, Capital Medical University, Beijing Municipal Key Laboratory of Liver Failure and Artificial Liver Treatment Research, Fourth Department of Liver Disease, Beijing, China
Email: ljjun2009@zju.edu.cn

Background and aims: Acute-on-chronic liver failure (ACLF) is a lifethreatening syndrome characterized by multiorgan failure and high short-term mortality rates. Liver transplantation (LT) is an effective therapy but is limited by organ shortages. Survival benefit-based priority for LT is important to decrease the risk of futile transplantation and develop new clinical strategies for ACLF patients.

Method: Hospitalized patients with acute deterioration of hepatitis B virus-related chronic liver disease (n = 4577) from the Chinese Group on the Study of Severe Hepatitis B (COSSH) study cohort were enrolled between January 2015 and December 2020. The performance of five commonly used scores (COSSH-ACLF IIs, COSSH-ACLFs, CLIF-C ACLFs, MELDs and MELD-Nas) for predicting the outcome on the waitlist and post-LT at days 28/90/180/365 were evaluated. The survival benefit based on the extra lifespan derived from LT was calculated by the difference in the area under the survival curve between patients with and without LT.

Results: A total of 368 ACLF patients and 98 non-ACLF patients received LT. The 1-year survival probability of 368 ACLF-LT patients (77.2%) was significantly higher than that of non-LT patients in both the ACLF entire cohort (52.3%) and the propensity score matching (PSM) cohort (27.6%) (all p < 0.001). However, 98 non-ACLF patients who underwent LT showed a lower survival probability than 2625 without LT (88.8%/92.3%, p = 0.20), and PSM analysis demonstrated no significant improvement in survival probability (88.8%/81.4%, p = 0.16). The receiver operating characteristic curve showed that the COSSH-ACLF II score had the highest performance (0.849) for identifying the 1-year risk of death on the waitlist and was also superior (0.864) for predicting 1-year outcome post-LT to the four other scores (COSSH-ACLFs/CLIF-C ACLFs/MELDs/MELD-Nas, 0.835/0.825/0.796/0.781; all p <0.05). Survival benefit rate analyses showed that 79.1% of ACLF patients with COSSH-ACLF IIs of 7-10 had a much higher 1-year survival benefit rate (39.2%-64.3%) than those with scores <7 or >10 (all p <0.001).

Conclusion: The COSSH-ACLF IIs not only identified the risk of death on the waitlist but also accurately predicted post-LT mortality and survival benefit rates for ACLF patients. Our findings can help to decrease the risk of futile transplantation and develop new clinical strategies for ACLF patients.

SAT290
Social determinants of health and racial disparities in liver transplant: a nation wide analysis
Mahmoud Mansour1, Adham Obeidat2, Mohammad Darweesh2, Rati Malfouz3, Sanket Basida3, Ahmad Alfi2, 1University of Missouri Columbia, Internal Medicine, Columbia, Missouri, United States; 2University of Hawaii, Internal Medicine, Honolulu, Hawaii, United States; 3East Tennessee State University, Internal Medicine, Johnson City, Tennessee; 4Kent Hospital/Brown University, Internal Medicine, Warwick, Rhode Island, United States; 5Upadhyay Medical College, Medicine, Gujarat, India; 6University of Missouri Columbia, Hepatology, Columbia, Missouri, United States
Email: aliah@health.missouri.edu

Background and aims: Liver transplantation is a life-saving treatment and standard of care for many forms of end-stage liver disease. Unfortunately, 20 percent of patients on liver transplant list die while on the waiting list, with several studies showing racial, gender and socioeconomic disparities among patients receiving a liver transplant. We sought to evaluate disparities amongst patients receiving liver transplant in the United States using the most recently available data from the National Inpatient Sample (NIS).

Method: We performed analysis of discharge data from the NIS between Jan 1st, 2016, to Dec 31st, 2019. We identified adult patients who underwent liver transplant using International Disease Classification of Disease 10th Procedure Coding System (ICD-10-PCS). Multivariate logistic regression was used to evaluate for differences in race, gender and socioeconomic status among those who received a liver transplant.

Results: A total of 29,050 liver transplants were performed during the study period. Compared to White patients, Black and Native America patients had increased transplant rates (adjusted odds ratio [aOR] 3.43, p < 0.001). Female gender was independently associated with decreased transplant rates (aOR 0.80, p < 0.001).
Conclusion: Our analysis showed that race and social determinants of health, including gender, income, and insurance status, are associated with the likelihood of receiving a liver transplant in the United States. Our study confirms, on a national level, previously described disparities in receiving liver transplantation. Patient-level studies are needed to understand better why disparities in liver transplant exist to achieve a more equitable distribution of this scarce resource.

SAT291 Reduced neutralization efficacy against SARS-CoV-2 Omicron variant after third boost of mRNA BNT162 vaccine among liver transplant recipients
Yana Davidov¹, Victoria Indenbaum², Michal Mandelboim²,³, Keren Asraf², Tal Gonen²,³, Keren Tsaraf³, Orenit Cohen-Ezra¹, Mariya Likhter¹, Gil Ben Yaacov¹, Itai Nemet², Limor Kliker²,³, Orna Mor²,³, Ram Doolman⁴, Carmit Cohen⁵, Arnon Afek⁶, Yitshak Kreiss⁶, Gili Regev⁶, Yaniv Lustig⁶, Ziv Ben Ari⁶, ¹Sheba Medical Center, Liver Diseases Center, Tel Aviv-Yafo, Israel; ²Sheba Medical Center, Central Virology Laboratory, Ministry of Health, Tel-Hashomer, Tel Aviv-Yafo, Israel; ³Tel Aviv University, Sackler School of Medicine, Tel Aviv-Yafo, Israel; ⁴Sheba Medical Center, The Dworman Automated Mega Laboratory, Tel Aviv-Yafo, Israel; ⁵Sheba Medical Center, Infection Prevention and Control Unit, Tel Aviv-Yafo, Israel; ⁶Sheba Medical Center, General Management, Tel Aviv-Yafo, Israel
Email: y.davidov@gmail.com

Background and aims: The immune response of solid organ transplant recipients to the two doses of the BNT162b2mRNA vaccine is impaired (72%). However, improved immune response was noted after the third boost. The durability and effectiveness of the

Figure: (abstract: SAT291)
Method: Consecutive 59 liver transplant (LT) recipients, who received three doses of BNT162b2mRNA vaccine and followed-up at the Sheba Medical Center were included. Receptor-biding domain (RBD) IgG, pseudo-virus (psVARS-2) neutralization antibody (NA) titers, and T cells levels were determined 4 ± 1 weeks and 19 ± 3 weeks after the third vaccine. IgG antibody titer above 214 BAU/ml was defined as a positive response. A comparison between the neutralization efficacy of the vaccine among wild type, omicron, and delta variants 4 ± 1 weeks after the third vaccine was conducted.

Results: The 59 LT recipients were of a median age of 61 years (ranges, 25–82); 53.5% were male. Four weeks after the third vaccine, a positive humoral immune response was detected in 81.4%. It decreased significantly 19 ± 3 weeks after the third boost to 76.1%, (p < 0.0001). The geometric mean titers (GMT) of anti-RBD IgG decreased from 483 BAU/ml to 204 BAU/ml (p < 0.0001), psVARS-2 NA 653 to 450 (p = 0.2), and T cell 223 to 30 cells per 10⁶ PMC (p < 0.0001) four weeks and 19 weeks respectively. Following multivariate analysis, the independent predictors associated with maintaining a positive immune response 19 weeks after the third vaccine were CNI monotherapy (p = 0.02) and Hemoglobin >11.5 g/dl (p = 0.02). The GMT of omicron neutralization was significantly lower than wild-type, and delta virus and were 21.72, 140, 131, respectively (p < 0.0001). We evaluated the impact of CNI monotherapy vs. combined immunosuppression (combination of CNI with MMF or mTOR or prednisone) on neutralization efficacy of VOC. The GMT of the wild type, delta, and omicron variants were significantly higher among LT recipients who received CNI monotherapy than combined immunosuppression and were 666, 563, 89 and 40, 39, 8, respectively (p < 0.01).

Conclusion: The immune response after the third BNT162b2mRNA boost vaccine decreased significantly and rapidly among LT recipients. CNI monotherapy was a predictor of durability. The neutralization efficacy against the omicron variant was reduced significantly. Further studies are needed to evaluate the efficacy of a fourth vaccine dose on the durability of the immune response and protection against symptomatic COVID 19 disease.

SAT292
Long-term outcomes (beyond 5 years) of liver transplant recipients-a transatlantic multicentre study
Naaventhan Palaniyappan1, Emily Peach1, Fiona Pearce1, Amritpal Dhalwah1, Isabel Campos-Varela2, Matthew Canr3, Cristina Dopazo3, Sapna Divani-Pate3, James F. Trotter4, Ayeshia Hatta2, Laurence Hopkins2, Giuliano Testa3, Zain Kasmani2, Sarah Faloon2, Darius F. Mirza2, Goran Klintmalm4, Jeanne-Marie Giard1, Catherine Vincent1, Ziad Hassoun1, Geneviève Soucy2, Bich Ngoc Nguyen2, Basil Nasir3, Pasquel Ferraro4, Julie Morisset4, Charles Poiret1, Genevieve Huard1, 1Centre hospitalier de l’Université de Montréal (CHUM), Liver division, Montréal, Canada; 2Centre hospitalier de l’Université de Montréal (CHUM), Department of Pathology, Montréal, Canada; 3Centre hospitalier de l’Université de Montréal (CHUM), Division of Thoracic Surgery; 4Centre hospitalier de l’Université de Montréal (CHUM), Division of pulmonary medicine, Canada
Email: naaventhan.palaniyappan@nottingham.ac.uk

Background and aims: Long-term (>5 year) outcomes following liver transplantation (LT) have not been extensively reported upon, in contrast to established short-term and medium-term outcomes. The aim was to evaluate survival outcomes of recipients who have survived the first 5 years following LT.

Method: A retrospective analysis of prospectively collected data from 3 high volume centres (Dallas, USA; Birmingham, UK; and Barcelona, Spain) was undertaken. Data were extracted of all adult patients, who underwent LT since the inception of the programme in the respective centres to 31 December 2010, and who survived at least 5 years since their first LT. Patient survival was the primary outcome measure. Age-standardised mortality rates stratified by sex were calculated for each centre and compared with respective jurisdiction mortality rates of the general population.

Results: A total of 3, 682 patients who survived at least 5 years following LT were included. Overall, median age at LT was 52 years (IQR 44–58); 53.1% were males; and 84.6% were Caucasians. 49.4% (n = 1, 820) died during a follow-up period of 36, 828 person-years (mean 10 years). 80.2% (n = 1460) of all deaths were premature deaths, defined as death before the age of 75 years (USA and UK) and 65 years (Spain). Age-standardised all-cause mortality as compared to general population was 3 times higher for males and 5 times higher for females. On adjusted analysis, besides older recipients (HR 2.09, 95%CI 1.44–3.04) and older donors (1.38, 95%CI 1.11–1.72), predictors of long-term mortality were pre-LT malignancy (HR 1.28, 95%CI 1.02–1.61), pre-LT CVD (HR 1.35, 95%CI 1.11–1.65) and post-LT dialysis (HR 2.40, 95%CI 1.56–3.68).

Conclusion: This study demonstrates an increased mortality rate in LT recipients even after 5 years of transplantation. It is likely that implementation of simple strategies such as non-invasive cancer screening measures, minimisation of immunosuppression and intensive primary/secondary cardiovascular prevention could further improve survival of organ recipients.

SAT293
Hepatic evaluation of patients with telomeropathies
Olivia Portolese1, Isaac Ruiz1, Julien Bissonnette1, Julian Hercunc1, Helene Castel1, Bernard Willems1, Marc Bilodeau1, Jeanne-Marie Giard1, Catherine Vincent1, Ziad Hassoun1, Geneviève Soucy2, Bich Ngoc Nguyen2, Basil Nasir3, Pasquel Ferraro4, Julie Morisset4, Charles Poiret1, Genevieve Huard1, 1Centre hospitalier de l’Université de Montréal (CHUM), Liver division, Montréal, Canada; 2Centre hospitalier de l’Université de Montréal (CHUM), Department of Pathology, Montréal, Canada; 3Centre hospitalier de l’Université de Montréal (CHUM), Division of Thoracic Surgery; 4Centre hospitalier de l’Université de Montréal (CHUM), Division of pulmonary medicine, Canada
Email: isaac.ruiz@me.com

Background and aims: Telomeropathies arise from an inheritable genes mutations resulting in decreased telomere length and impaired telomere maintenance. The most frequent manifestation of telomeropathy in adults is interstitial lung disease (ILD) that can lead to consideration for lung transplantation. Liver and bone marrow involvement have also been described. Liver assessment in this population is not well described in the current literature.

The aim of this study was to describe the liver evaluation and findings of patients with telomeropathies and ILD that were evaluated for liver and lung transplantation.

Method: This is a retrospective analysis of a prospectively recruited real-world cohort including all patients between January 2020 and December 2021 who consulted the pulmonary and hepatology units at the Centre hospitalier de l’Université de Montréal (CHUM) for liver and lung transplantation. Diagnosis of telomeropathy was confirmed by sequence analysis and/or telomere length (flow-fish analysis). Demographic, clinical, biological, radiological and pathological data were collected. Liver fibrosis was assessed by elastometry (FibroScan,
Echosens, France) and/or histological analysis of a transjugular liver biopsy.

Results: For this analysis, 17 patients were included. Table 1 shows the main characteristics of the cohort. Mean age was 60 years (50–69) and 10 of 17 patients (58.8%) were male. The main reason for the hepatology consultation was pre-operative evaluation for lung or liver transplantation. Sixteen of the 17 (94.1%) patients had at least one comorbidity. The biological evaluation showed a macrocytosis with a mean corpuscular volume of 95.1 fl (83.0–104.0). Mean platelet count was 203.3 x10^9/L (62.0–485.0).

Transient elastography was available for 15 of 17 (88.2%) patients, mean elasticity was 8.9 kPa (3.7–28.0) and the mean CAP was 247 dB/ Pa (168.0–358.0). Five of 17 (29.4%) patients had a transjugular liver biopsy following abnormal elastography result. Mean gradient was 9.4 (4.0–17.0). Steatosis was present in 4/5 cases (80.0%) and cirrhosis in 4/5 cases (80.0%).

One patient out of 17 (5.9%) had an isolated liver transplantation for decompensated cirrhosis and 10/17 (58.8%) had a lung transplantation. No patient underwent combined lung/liver transplantation.

Conclusion: In patients with telomeropathy undergoing liver/lung transplantation evaluation at least 4/17 (23.5%) had a cirrhosis. Transplantation evaluation should include a hepatology consultation, screening and management of comorbidities, a complete etiological assessment of liver diseases, assessment of the portal hypertension and non-cirrhotic portal hypertension and liver fibrosis via transient elastography and transjugular liver biopsy with hepatic venous pressure gradient measurement.

Figure: Main characteristics of patients.

SA1294
Third dose of SARS-CoV-2 mRNA-vaccine in liver transplant recipients: can it bridge the response gap?
Marzia Montalbano1, Raffaella Lionetti2, Ulbaldo Visco Comandini1, Silvia Meschi3, Chiara Agrati4, Federica Conte5, Vincenzo Puro6, Paola Piccolo7, Giulia Matusali1, Germana Grassi7, Tiziana Mereu1, Federica Angelone1, Enrico Girardi3, Giuseppe Maria Ettorre6, Giampiero D'Offizi1, National Institute for infectious diseases Lazzaro Spallanzani, POIT; 2National Institute for infectious diseases Lazzaro Spallanzani, POIT; 3National Institute for infectious diseases Lazzaro Spallanzani; 4Institute for Systems Analysis and Computer Science Antonio Ruberti; 5San Giovanni Calibita, Fatebenefratelli Hospital; 6San Camillo Hospital, POIT
Email: raffaella.lionetti@inmi.it

Background and aims: Liver transplant recipients (LRTs) show reduced immunological response after 2-dose mRNA vaccine against SARS-CoV2: stronger immunosuppression, time from transplant (TFT) and mycophenolate mofetil (MMF) were related to non-response (NR; D'Offizi, Liver Int 2021). Some studies indicated an additional vaccine dose could improve response. Aim of our study is to assess the effect of a third dose on mRNA vaccine response in LRTs.

Method: 181 consecutive LTRs (median age 63 years, M/F 149/32) were tested for humoral response before first dose (T0), before second dose (T1), 2 weeks after second dose (T2), before third dose (T3), at 4 (T4) and 12 weeks (T5) after third dose; and for cellular response via Th1 production of interferon-γ (IFN-γ) at T3, T4, T5. Anti-spike IgG (RBD) and neutralizing antibodies (N-Ab) were measured and results expressed as median. NR was defined as titre <7.1 binding antibody units (BAU) for RBD; Micro-Neutralization Assay <5 for N-Ab. NR was defined as <10 pg/ml for IFN-γ. T7 groups were defined by a cut-off of more or less than 6 years.

Results: After 2-dose vaccine, 31 LTRs (17%) were non-responders for RBD and 74 (40.6%) for N-Ab. After third dose, a positive response for RBD and N-Ab was observed in 27 (87%) and 61 (82.4%) LTRs with previous NR, respectively.

Overall, MMF was a significant negative predictive factor for RBD (p <0.001) and N-Ab (p = 0.003) response at T2, but not at T4 and T5. Among responders, RBD titre was lower in LRTs receiving MMF at T2 (180 BAU vs. 278 BAU, p <0.05) and at T4 (2331 BAU vs. 4009 BAU, p <0.05), while N-Ab titre was lower only at T4 (160 vs. 320, p <0.05). Overall, we observed significantly higher response among LTRs with TFT >6 years vs. <6 years at all time points (p = 0.0001 and p = 0.0004; p = 0.026 and p <0.0001; p = 0.025 and p <0.0001; p = 0.025 and p <0.0001 at T2, T4, T5 for RBD and N-Ab, respectively).

Among responders, RBD titre was higher among LTRs with TFT >6 years vs. <6 years at T2 (337 BAU vs. 113 BAU, p <0.05), at T4 (3407 BAU vs. 1802 BAU, p <0.05) and at T5 (1927 BAU vs. 693 BAU, p <0.0001). N-Ab titre was significantly higher only at T5 (160 vs. 320, p <0.05).

Overall, we observed significantly higher response among LTRs with TFT >6 years vs. <6 years at all time points (p = 0.0001 and p = 0.0004; p = 0.29, p = 0.0007 and p = 0.32, p = 0.0004 at T4; r = 0.4, p <0.0001 and r = 0.29, p = 0.0007 at T5; r = 0.3, p = 0.0006 and r = 0.35, p <0.0001 at T5 for RBD and N-Ab, respectively). None of the analysed variables influenced IFN-γ response.

Liver disease aetiology and comorbidities (diabetes, cancer, obesity, HIV positivity) did not influence response after third vaccine dose.

Conclusion: A third dose enhances antibody response in LTRs who had a poor response after an initial 2-dose mRNA vaccination to SARS-CoV2. However, MMF and TFT <6 years were associated with lower response after third vaccine dose.
SAT295
Protein-energy malnutrition is associated with worse outcomes in patients admitted for liver transplant: analysis of national inpatient sample

Mahmoud Mansour1, Ratib Mahfouz2, Mohammad Darweesh3, Adham Obeidat4, Nikolaos T. Pyrsopoulos5.
1University of Missouri Columbia, Internal Medicine, Columbia, Missouri, United States; 2Kent Hospital/Brown University, Internal Medicine, Warwick, Rhode Island, United States; 3East Tennessee State University, Internal Medicine, Johnson City, Tennessee, United States; 4University of Hawaii, Internal Medicine, Honolulu, Hawaii, United States; 5Rutgers-New Jersey Medical School, Gastroenterology and Hepatology, Rutgers, New Jersey, United States
Email: pyrsopni@njms.rutgers.edu

Background and aims: Protein-energy malnutrition (PEM) is a common complication in liver cirrhosis patients, with an estimated prevalence of 25.1 to 65.5%. PEM among cirrhotic patients has been associated with increased morbidity and mortality. The data on the in-hospital outcomes of patients who underwent liver transplantation with co-existing PEM is limited. In this study we sought to evaluate the impact of PEM on patients who underwent liver transplantation.

Method: The United States Nationwide Inpatient Sample was used to search for patients who underwent liver transplantation between Jan 1st, 2016, to Dec 31st, 2019. Using International Classification of Diseases 10th revision codes, we divided patients into two groups based on the presence or absence of PEM. The NIS-provided discharge-level weights were used to reflect prevalence estimates. The primary outcome was in-hospital mortality. Secondary outcomes were intensive care unit (ICU) admission, length of stay (LOS), and hospital charges. Multivariate logistic regression was used to adjust for comorbidities and demographic variables.

Results: Among the 29,050 patients who underwent liver transplantation, 7,650 (26.33%) had the diagnosis of PEM. Patients with PEM had higher mortality, ICU admission, mean LOS, and hospital charges compared to those without PEM. After adjusting for potential confounders, PEM was an independent predictor of worse outcomes in patients undergoing liver transplantation. Adjusted odds ratio was 1.64, (p = 0.008) for mortality, and 1.88 (p <0.001) for ICU admission. Adjusted mean for LOS and total hospital charges increased by 14.49* (12.15–16.82) days and $323, 270*, respectively, for liver transplant patients with PEM compared to those without PEM.

Table: In-hospital outcomes of patients undergoing liver transplant with and without a diagnosis of protein-energy malnutrition (PEM).

<table>
<thead>
<tr>
<th>Outcome</th>
<th>Without PEM</th>
<th>With PEM (p value)</th>
<th>aOR (95% CI)</th>
</tr>
</thead>
<tbody>
<tr>
<td>In-hospital mortality (%)</td>
<td>2.50%</td>
<td>4.05% (&lt;0.001)</td>
<td>1.64 (1.14–2.36)</td>
</tr>
<tr>
<td>ICU admission (%)</td>
<td>5.42%</td>
<td>9.76% (&lt;0.001)</td>
<td>1.88 (1.58–2.24)</td>
</tr>
<tr>
<td>Mean length of stay (days)</td>
<td>16.40</td>
<td>30.75 (&lt;0.001)</td>
<td>14.49* (12.15–16.82)</td>
</tr>
<tr>
<td>Mean hospital charges (US$)</td>
<td>513,902</td>
<td>832,365 (&lt;0.001)</td>
<td>322,270* (253,832–392,708)</td>
</tr>
</tbody>
</table>

*Adjusted mean difference
Abbreviations: PEM: protein energy malnutrition, CI: confidence interval, aOR: adjusted odds ratio

Conclusion: PEM is associated with increased morbidity, mortality, and hospital burden in patients admitted for liver transplantation. Timely nutrition assessment and intervention in liver transplant recipients may improve outcomes.

SAT296
COVID vaccination among liver transplant recipients: A EASL-ESOT/ELITA-ILTS multi society survey

Carmen Vinaixa1,2, Francesco Paolo Russo3, Luca Saverio Belli4, Wojciech Polak5, MANHAL IZZY6, Varvara Kirchner7,8, Tommaso Di Maira1,2, Ashwin Rammohan9, Thomas Berg10, Marina Berenguer11,12,13,1. Hospital Universitario y Politécnico La Fe, Hepatology and Liver Transplantation Section, Digestive Diseases Department, Valencia, Spain; 2Instituto de Salud Carlos III, Madrid, Spain; 3Azienda Ospedaliero-Universitaria Padova, Gastroenterology and Multivisceral Transplant Unit Department of Surgery, Oncology and Gastroenterology, Padua, Italy; 4Dipartimento Medico Poli specializzato, Milan, Italy; 5Erasmus MC, Department of Surgery Division of HPB and Transplant Surgery, Rotterdam, Netherlands; 6Vanderbilt University, Nashville, United States; 7Minessota, United States; 8Stanford University, Division of Abdominal Transplantation, Department of Surgery, Stanford, United States; 9Dr Rela Institut and Medical Center, Chennai, India; 10University Medical Center, Leipzig, Germany; 11University of Valencia, Department of Medicine, Valencia, Spain
Email: vinaixa.carmen@gmail.com

Background and aims: Liver transplant (LT) recipients have been prioritized for vaccination in most parts of the world. The aim of this multi-society survey was to explore and to describe the different policies and outcomes of vaccination in this population in a real-world setting.

Method: A web-based survey was available online from October 2021 to February 2022 to members of the EASL, ESOT/ELITA and ILTS. The survey was divided into 4 domains: (1)Vaccination policies, (2)Safety assessment, (3)Efficacy assessment, and (4)center data. No patient-related data were collected.

Results: 188 eight out of 470 centers responded to the survey. There was a wide geographic distribution: 41% Europe, 24% Asia and 23% North America (Fig 1).

The global response rate to the survey’s section on vaccination policies was 90%. Most transplant patients (86%) were vaccinated after 12 months post-LT. Prioritization of transplant patients was very common (85% of centers), this was the case for co-habitants in only 29% of centers. mRNA vaccines were used in most centers (76%); with restrictions to use only these vaccines in transplant recipients in 43% of these centers, followed by viral vector vaccines in 27%. Barriers to vaccination were reported in 23% of cases, related to patient’s fear (80%), public health policies (33%) and logistics (20%). Vaccination was ordered by health-care authorities or government in 56% of cases, and by the transplant provider in 30%. Other vaccines as flu were reported to be routinely recommended (92%).

The global response rate to the survey’s section on safety assessment was 75.4%. Only 1/3 of centers implemented specific monitoring policies for liver function tests (LFT) and/or immunosuppression (IS) levels post-vaccination, with variable frequencies. Most patients (59%) were monitored in the outpatient clinic, via telemedicine (26%) or patient self-reporting (9%). Only 28% of centers responded to the IS section, and only a minority of them (9%) reported that changes in IS were implemented before vaccination, with variable strategies. Regarding adverse events (AE) post-vaccination, 27% of centers observed LFT elevation, 11% thromboembolic events, 9% acute graft rejection and 17% other AE. 83% of centers answered the vaccine efficacy assessment section: 1/3 of centers tested for SARS-CoV-2 antibodies post-vaccination. COVID-19 positive cases post-vaccination were observed in 65% of the centers, and 33% amongst those were severe.

Journal of Hepatology 2022 vol. 77(S1) S665–S939 S807
**SAT297**

**Does m-RNA vaccination protect from Sars-Cov2 (asymptomatic) infection in liver transplant recipients?**

Ubaldo Visco Comandini, Marzia Montalbano, Raffaella Lionetti, Paola Piccolo, Daniela Nesticò, Silvia Meschi, Chiara Agrati, Chiara Taibi, Laura Vincenzi, Enrico Girardi, Giuseppe Maria Ettorre. 1National Institute for infectious diseases Lazzaro Spallanzani, POIT, rome, Italy; 2National Institute for infectious diseases Lazzaro Spallanzani, POIT; 3San Giovanni Calibita, Fatebenefratelli Hospital; 4National Institute for infectious diseases Lazzaro Spallanzani; 5San Camillo Hospital

**Background and aims:** Vaccination significantly reduces COVID-19 morbidity and mortality, as well as hospitalization, but it is less clear whether vaccination also prevents from asymptomatic infection. Liver Transplant recipients (LTRs) are less prone to develop severe COVID-19 compared to other solid organ transplant recipients (Trapani S, AJT 2021). A high frequency of asymptomatic Sars-CoV2 infections has been described in LTRs (Visco-Comandini, JLT 2021). The study aim is to compare the vaccine-induced humoral response in LTRs who developed Sars-CoV2 infection during or after three dose of mRNA vaccination, with those who did not

**Method:** The LTRs cohort is composed by 246 subjects, 182 of whom completed a 3-dose vaccination program in 2021. Subjects with Sars-CoV2 infection prior to 1st dose were excluded.

All LTRs were regularly screened through telephone-based questionnaire or clinical visits to detect systemic, respiratory or gastrointestinal symptoms. LTRs reporting symptoms compatible with COVID-19 or close contact to a positive subject underwent nasopharyngeal swab (NPS) to detect active infection.

Sars-CoV2 Receptor Binding Domain antibodies (RBD-Ab, detection limit >71 BAU/ml) were prospectively measured at T0 [before 1st dose], T2 [4 weeks (W) after 2nd dose], T3 [before 3rd dose], T4 (4 W after) and T5 (12 W after) in all. Anti-RBD and neutralizing antibodies (n-Ab, detection limit <1:5 for alpha and delta, <1:2.5 for omicron) were measured at T2, T3 and T5. Neutralizing activity was measured toward alpha variant (T2), alpha and delta variants (T3 and T4), delta and omicron variants (T5)

**Results:** Twenty-seven of 164 LTRs were infected by Sars-CoV2 (14.8%) after the 1st dose: 9 between the 2nd and 3rd dose (group A), and 18 after the 3rd dose (group B). Their RBD-Ab and n-Ab titres measured at the last time point before infection, were compared to the remaining vaccinated LTRs who never developed a positive NPS or a positive non RBD-serology (controls, n = 137) (Figure 1).

Moderate to severe COVID19 cases were observed in 2/9 (22.4%) subjects infected after the first/second dose of vaccine (alpha or delta variant), and in 1/18 (5.5%) infected after the third dose (delta or omicron variant).

The rate of non-response to vaccination was 22.2% in group A and 22.1% in controls at T2; 0% and 2.9%, in group B and controls respectively at T4.

Absence of neutralizing activity was 77.8% in group A and 46.0% in controls at T2 (p = 0.09); 22.2% and 7.8%, at T4 in group B and controls (p = 0.07).

At T5 infected LTRs showed higher RBD-Ab compared to controls (median 2019, IQR 691–3845 BAU/ml vs 1281, IQR 452–2994 BAU/ml p < 0.05) but similar n-Ab titers

**Conclusion:** Sars-CoV2 infection between 1st and 3rd vaccination doses was associated with lack of anti-RBD response or lower neutralizing activity, while infection after the 3rd dose seemed to be independent of humoral response to vaccination

Figure: (abstract: SAT297)
SAT298

Low dose interleukin-2 selectively expands circulating regulatory T cells but fails to promote transplantation tolerance in humans

Tiong Yeng Lim 1, Elena Perpinan 1, Maria Carlota Londoño 2, Rosa Miñiel 1, Paula Ruiz 1, Ada Kurt 1, Elisavet Codela 1, Amy Cross 3, Claudia Berlin 1, Joanna Hester 1, Fadi Issa 3, Abdel Douiri 4, Felix Volmer 5, Richard Taubert 5, Evangelia Williams 6, Jake Demetris 7, Andrew Lesniak 7, Gilbert Bensimon 8, Juanjo Lozano 9, Marc Martinez-Llordella 1, Timothy Tree 6, Alberto Sanchez-Fueyo 1.

1King’s College Hospital, Institute of Liver Studies, United Kingdom; 2Hospital Clinic Barcelona, Liver Unit, Barcelona, Spain; 3University of Oxford, Transplantation Research Immunology Group, Oxford, United Kingdom; 4King’s College London, School of Population Health and Environmental Sciences, London, United Kingdom; 5Hannover Medical School, Department of Gastroenterology, Hepatology and Endocrinology, Hannover, Germany; 6King’s College London, Department of Immunobiology, School of Immunology and Microbial Sciences (SIMS), London, United Kingdom; 7University of Pittsburgh, Department of Pathology, Pittsburgh, United States; 8Hôpital de la Pitie-Salpêtrière et UMR1171 Pharmacologie, Département de Pharmacologie Clinique, Paris, France; 9Carlos III Health Institute, ioinformatic platform, Biomedical Research Center in Hepatic and Digestive Diseases (CIBEREHD), Barcelona, Spain

Email: llty24@gmail.com

Background and aims: Low dose interleukin-2 (LDIL-2) can expand endogenous circulating CD4+CD25+Foxp3+ regulatory T-cells (Tregs) in vivo, but its role in promoting allograft tolerance in humans has not been investigated. We conducted a clinical trial in stable liver transplant (LT) recipients 2–6 years post-transplant to determine the capacity of LDIL-2 to suppress allospecific immune responses and allow for the complete discontinuation of maintenance immunosuppression.

Method: The LITE trial is a phase IV, open-label, activity, safety and efficacy, prospective single arm clinical trial in which stable LT recipients <50 years old and 2–6 years post-LT receive 6 months of daily 1 million IU injections of LDIL-2. After 4 weeks of LDIL-2 treatment, those recipients in whom circulating Tregs expand >2-fold gradually discontinue their immunosuppressive medication over 3 months. Patients who maintain stable serum liver tests and normal histology 1 year after immunosuppression withdrawal are considered tolerant.

Results: Six patients were recruited with a median age of 34 years (range 22–49) and 38.5 months (range 31–45) post-LT. All patients achieved a marked and sustained increase in circulating Tregs, in keeping with previous studies. Significant increases in circulating eosinophils, basophils, CD56bright NK cells and a reduction in the absolute numbers of circulating B cells were also observed. However, these findings were not associated with the preferential expansion of donor-reactive Tregs and did not promote the accumulation of intra-hepatic Tregs. Furthermore, LDIL-2 induced a marked interferon-γ orchestrated transcriptional response in the liver even before immunosuppression weaning was initiated. The trial was terminated after the first six trial participants failed to reach the primary end point due to rejection requiring immunosuppression reinstitution.

Conclusion: Our trial provides unique insight into the mechanisms of action of immunomodulatory therapies such as LDIL-2 and their limitations in promoting alloantigen-specific effects and immunological tolerance.

SAT299

Clinical significance of three-dimensional printing of the portal venous system in patients with extrahepatic portal hypertension

Binita Chaudhary 1, Utpal Anand 2, Rajeev Priyadarshi 3.

1All India Institute of Medical Sciences, Patna, Anatomy, Patna, India; 2All India Institute of Medical Sciences, Patna, Surgical Gastroenterology, Patna, India; 3All India Institute of Medical Sciences, Patna, Radiodiagnosis, Patna, India

Email: binitachaudhary18@gmail.com

Background and aims: Three-dimensional printing (3DP) is a novel technique that can generate 3D virtual image from multidetector computed tomography (MDCT) scan. The aim of the study was to investigate the feasibility of 3DP in visualization of portal venous system of patients with extrahepatic portal vein obstruction (EHPVO) to improve the surgical outcome (surgical time, blood loss).

Method: This retrospective study was performed in the Department of Anatomy in 24 patients of EHPVO who underwent shunt surgery from November 2018 to March 2022. The patients were divided into conventional planning group based on MDCT imaging (n = 12) and
planning with 3D printing group based on the 3D reconstruction of portal venous system (n = 12).

The image of MDCT was transferred to D2P software (dicom to print) and saved in a standard format DICOM (digital imaging and communication in medicine). Bone, soft tissue and blood vessels were semi-automatically segmented into separate areas. Segmented regions were combined to create a 3D object. These 3D objects were exported from D2P as STL files. STL files were repaired in 3D design software (Geomagic freeform plus) and a virtual 3D prototype was created. 3D virtual image prepared were used to see the exact location and depth of splenic and renal vein as well as surrounding collaterals.

Results: In conventional planning group, there were 12 patients (8 males and 4 females) with mean age of 24.00 ± 10.91. The time from day of surgery to the day of discharge from hospital was 7.08 ± 2.53 days. In planning with 3D printing group, there were 12 patients (10 males and 2 females) with mean age of 32.08 ± 16.57 years. The time from day of surgery to the day of discharge in 3D printing group was 7.16 ± 2.20 days.

The mean surgical time in planning with 3D printing group was 252.50 ± 115.79 min, which was significantly lower than that of conventional planning group (298.16 ± 12.87 min); P value < 0.05. The intraoperative mean blood loss in planning with 3D printing group and conventional planning group were 441.25 ± 44.52 ml and 624.16 ± 123.13 ml respectively; (P value < 0.05).

The rate of complication in the planning with 3D printing group and conventional planning group was 16.66% (2/12) and 8% (1/12) respectively.

Conclusion: Presurgical planning in 3D printing reduces guesswork and thus it remarkably reduces surgical time, blood loss, minimizes complication and improves surgical outcome.

SAT300
Liver transplantation (LT) and ethnicity in the United States: the impact of non-alcoholic steatohepatitis

Zobair Younossi1, Reem Al Shabeeb2, Michael Harring2, Dipam Shah2, Janus Ong2, Saleh Alqahthani1,5, Linda Henry1,6, Maria Stepanova1,2,6.

1Inova Health System, Medicine Service Line, Falls Church, United States; 2Inova Fairfax Medical Campus, Department of Medicine, Center for Liver Diseases, FALLS CHURCH, United States; 3College of Medicine, University of the Philippines, Manila, Philippines; 4Johns Hopkins Medical Center, Division of Gastroenterology and Hepatology, Baltimore, United States; 5King Faisal Specialist Hospital and Research Center, Liver Transplant Center and Biostatistics, Epidemiology and Scientific Computing Department, Riyadh, Saudi Arabia; 6Center for Outcomes Research in Liver Disease, Washington DC, United States

Email: zobair.younossi@inova.org

Background and aims: The burden of chronic liver disease (CLD) may vary by race and/or ethnicity. We aimed to assess distributions and trends of different CLD etiologies among liver transplant (LT) candidates from major racial/ethnic groups in the U.S. over the last two decades.

Method: The Scientific Registry of Transplant Recipients (SRTR) data 2002–2020 was used to select adult (≥18) candidates for LT. Patients without race/ethnicity data (white, black, Hispanic, or Asian) were excluded. Trends in the proportions of common LT etiologies, such as chronic hepatitis B (CHB), chronic hepatitis C (CHC), non-alcoholic steatohepatitis (NASH, including cryptogenic cirrhosis if accompanied by obesity or type 2 diabetes), alcoholic liver disease (ALD) were assessed over time.

Results: 204, 382 LT candidates with known race/ethnicity were included: n = 146, 535 non-Hispanic white (4.1 per 100, 000 per year with reference to the general U.S. population), n = 17, 653 non-Hispanic black or African-American (2.3 per 100, 000), n = 31, 086 Hispanic (2.7 per 100, 000), and n = 9, 108 Asian (2.4 per 100, 000). In whites, the most common etiologies were CHC (27% across all study years) followed by ALD (23%) and NASH (17%). In addition, in whites, there was a decreasing trend in CHC (34% in 2002–2005 to 12% in 2018–2020) but increasing trends in NASH (7% to 27%) (Figure) and ALD (17% to 35%) (all trend p < 0.0001). In blacks, CHC (41% in 2002–2005 to 25% in 2018–2020) decreased while ALD increased from 7% to 18% (all p < 0.0001). In Hispanics, the trends were similar to whites with CHC decreasing (40% in 2002–2005 to 13% in 2018–2020) while ALD (17% to 34%), and NASH (6% to 29%) increasing (all p < 0.0001). Finally, in Asians, the most common etiologies of LT remained CHB and CHC (decreasing from 39% to 28% and from 28% to 11% in 2002–2005 to 2018–2020, respectively) while ALD (3% to 14%) and NASH (1% to 16%) increased (all p < 0.0001). The proportions of HCC remained substantially elevated in Asians (28% in 2002–2005, 39% in 2014–2017, and 36% in 2018–2020), and over time was increasing from 2002 to 2005 (7–8%) to 2014–2017 (21–27%) in all other ethnic groups but then decreased in 2018–2020 (17–24%). In multivariate analysis, older age, female gender, obesity and type 2 diabetes were associated with the etiology of NASH in LT candidates of all ethnic groups (all p < 0.0001). Higher post-transplant mortality was associated with older age, diabetes, higher MELD score and HCC in all ethnic groups (p < 0.01).

Conclusion: CLD etiologies of liver transplant candidates in the U.S. vary across racial/ethnic groups and over time in the U.S. The proportion of NASH among LT candidates increased at least 4-fold between years 2002–2005 and 2018–2020 in all major ethnic groups.
SAT301
Can endothelial biomarkers before liver transplantation together with classical cardiovascular risk factors be useful to predict cardiovascular risk after liver transplantation
Julia Herreras López1, Angela Carvalho-Gomes2, Tommaso Di Maira1, Marina Berenguer1, Victoria Aguilera Sancho1,2, 1, La Fe University and Polytechnic Hospital, Valencia, Spain; 2 Instituto de Investigación Sanitaria La Fe de Valencia, Valencia, Spain.
Email: toyagui@hotmail.com

Background and aims: Cardiovascular (CV) disease is an important cause of morbidity and mortality after liver transplantation (LT). In the general population endothelial biomarkers have been associated to cardiovascular (CV) risk. Little is known about the relationship between endothelial biomarkers in LT candidates. To analyse pre-LT serum biomarkers (day 0) and to evaluate if they have an association with CV risk after LT alone or in combination with classical CV risk factors.

Method: Frozen plasma of 125 LT with a low FRS between 2014–2017 were analyze. At one year, patients with a high Framingham Risk Score (FRS) or with metabolic syndrome (MS) were considered of high risk, as a surrogate marker for CV events. Endothelial biomarkers measured were: LpPLA2 measured by ELISA and adiponectine, V CAM1, IL6, TNF αα and ProBNP by Lumexa. A multivariate analysis with clinical and endothelial biomarkers was done.

Results: Mean age was 56 years, 78% were men, HCV cirrhosis was the most frequent ethiology (36%) followed by alcohol (25%). Before LT, 20% had arterial hypertension and 19% diabetes. At one yr post-LT, 33% were considered to have a high CV risk by FRS or MS. Logistic regression showed that age before LT (OR = 1.06; p = 0.025), DM before LT (OR = 5.77; p < 0.001) were associated with high CV risk. Plasma levels of LpPLA2, adiponectine, TNF αα and ProBNP were associated with Liver function (MELD and Child) (p < 0.05). LpPLA2 showed a tendency through a high CV risk (OR = 2.82, p = 0.089). A model with clinical and endothelial biomarkers was created. DM (OR 9, 63–31 p < 0.001), obesity (OR, 5, 1 IC 1.62–16 p = 0.005), tobacco use (OR 4.44 IC 1.26–15 p = 0, 02) and LpPLA2 (OR 8, 18 IC 1.5–44 p = 0, 015) were statistically significant associated with CV risk post-LT.

Conclusion: Clinical variables such as age, obesity, DM before LT and tobacco use in combination with endothelial biomarkers (LpPLA2) could be useful to predict CV risk after LT.

SAT302
Factors contributing to late evaluation in liver transplant candidates undergoing inpatient liver transplant evaluation
Katherine Cooper1, Diana Liu1, Alessandro Colletta1,2, Deepika Devuni1,2. 1Mass Chan Medical School, Worcester, United States; 2UMass Memorial Medical Center-University Campus, Worcester, United States.
Email: katherine.cooper@umassmed.edu

Background and aims: Timely referral for liver transplant evaluation (LTE) is critical in patients with chronic liver disease (CLD) due to the high mortality associated with decompensation. Unfortunately, CLD can be under recognized resulting in the need for urgent transplant evaluation. We aimed to identify the proportion of late referrals in patients undergoing inpatient LTE and potential causes of late LTE.

Method: Patients undergoing inpatient LTE for CLD at our centre between October 2017 and August 2021 were included in the study. Charts were extensively reviewed for liver history focusing on earliest signs of liver dysfunction, imaging evidence of cirrhosis, time of diagnosis, decompensation history and barriers to referral. Patients were considered to have late referrals if they had a Model of End Stage Liver Disease score (MELD) >15 or decompensation without a substance-related contraindication to transplant.

Results: One hundred fifty-nine patients, mean age 57.7 (SD 9.6) undergoing inpatient transplant evaluation were identified. About half could have been referred earlier for outpatient transplant evaluation. Two-thirds of these patients were diagnosed at least two years prior to their evaluation and had an average of 4.0 (SD 1.3) decompensations (Table 1). Almost all had a primary care physician or saw a health care provider regularly. The most common barriers to referral included failure to obtain MELD labs/calculate MELD and misconceptions about the sobriety period needed for transplant (Table 1).

Conclusion: Many patients are referred for liver transplant late in their clinical course causing unnecessary health care utilization. Efforts to increase timely referral for liver transplant include improving awareness about routine labs and indications for liver transplantation for non-transplant providers. Further, efforts to improve patient insight into their condition may facilitate the referral process.

SAT303
CMV reactivation is associated with lower hepatocellular carcinoma (HCC) recurrence after liver transplantation (LT)
Victoria Aguilera Sancho1,2,3, Sarai Romero Moreno1,3, Isabel Conde1,2, Tommaso Di Maira1,2, Ángela Carvalho-Gomes1,4, Ángel Rubin1, Ángela Martínez-Arenas1, F Xavier Lopez-Labrador5, Marina Berenguer1,2,3,4, Instituto de Investigación Sanitaria La Fe de Valencia, Valencia, Spain; 2CIBERehd Instituto de Salud Carlos III, Valencia, Spain; 3La Fe University and Polytechnic Hospital, Valencia, Spain; 4Instituto de Salud Carlos III, CIBERehd; 5Fisabio, Valencia, Spain.
Email: toyagui@hotmail.com

Background and aims: There are data that link CMV reactivation (rCMV) with post-LT morbidity and mortality. Recent studies though suggest beneficial effects including a potential oncolytic effect
resulting in lower HCC recurrence after LT. To assess the effect of rCMV (before tumoral recurrence) in LT-patients with HCC.

**Method:** We included LT patients with HCC (2018-2020). Exclusion criteria were: late re-LT, early death <1month and combined Liver Kidney transplant. Variables: (i) Donor (D) and recipient (R) demographics, (ii) related with rCMV (defined if CMV viral load >400c/ml): DR CMV mismatch, preemptive therapy, CMV disease, (iii) related to HCC: bridging, downstage, vascular invasion, baseline AFP.

**Postoperative outcomes:** DR CMV mismatch, preemptive therapy, CMV disease, (iii) related to HCC: bridging, downstage, vascular invasion, baseline AFP. Prophylaxis with valganciclovir was used in high-risk patients while a preemptive approach was used in the remainder. The retreat score was used to establish posttransplant follow-up (AFP and Tomography).

**Results:** Out of 266 LT (83% men, median age 59 yrs) fulfilled inclusion criteria; the main etiology was HCV (31%) followed by alcohol (25%) and the functional Meld was 10 (6-27). Most (80%) were intraMilan at LT; 16 (13%) were included after downstaging and 73% received locoregional therapy either for bridging or downstaging. On explant 11.5% had vascular invasion. Median AFP was 43 (1.1-748 ng/ml). A minority were considered high-risk due to CMV Mismatch (11% D/R ± ). rCMV occurred in 50 patients (41%); 22 (18%) started early treatment and 5 (4%) developed CMV disease. Overall, 10 patients (8.2%) had HCC recurrence after a median of 288 days (Q1, Q3: 135–445). In multivariate analysis, vascular invasion [HR 11 (IC 3–44), p:0.08] and absence of rCMV were associated with HCC recurrence [HR 0.12 [IC:0.0006–0.25, p:0.004]. Survival at 1, 3 and 5 yrs post-LT was 89%, 82% and 77%, respectively.

**Conclusion:** In our series, vascular invasion, and absence of rCMV were associated with higher risk of HCC recurrence after LT.

**SAT304**

Managing HBV/HDV co-infection post liver transplant—Exploring a decade of experience

Almuthana Mohamed1, Lindsay Greenland1, Maria Guerra Veloz1, James Lok1, Khin Aye Wint Han1, Raquel Beckford1, Deepak Joshi1, Michael Heneghan1, Varuna Aluvihare1, Abid Suddle1, Ivana Carey1, Koshagarwal1, Institute of Liver Studies, King’s College Hospital, Hepatology, London, United Kingdom

Email: almuthana700@gmail.com

**Background and aims:** Liver transplantation is an important treatment modality for hepatitis B patients with delta co-infection (HBV/HDV), including those with hepatocellular carcinoma (HCC) or decompensated cirrhosis. Despite the judicious use of nucleos (t)ide analogues (NA) and hepatitis B immunoglobulins (HBIG), post-transplant management remains challenging, and there is an inherent risk of viral reactivation and graft failure. We describe ten years of experience in managing this patient cohort and explore their long-term clinical outcomes.

**Method:** In this retrospective study, all patients with HBV/HDV co-infection who underwent liver transplantation at King’s College Hospital between 2012 and 2022 were identified. Baseline demographics, date and type of liver transplant, post-surgical management, clinical outcomes, and virological markers (HBV DNA and HDV RNA) pre-, 6- and 12-months post-transplantation were assessed, and Kaplan-Meier survival curves were generated.

**Results:** Overall, 16 patients underwent liver transplant, including one individual with concomitant HBV, HDV and HIV infection. The median age was 51 years (Range 29–55, IQR 8), and dominant ethnic groups were Caucasian (n = 8, 50%), South Asian and Black African (18.8% each). The most common indication for transplantation was synthetic dysfunction from liver cirrhosis (87.5%). Prior to surgical intervention, 6 patients (37.5%) had detectable HBV DNA levels (Median = 229, Range 71-5.07E3 IU/ml) and 11 individuals (68.8%) had detectable HDV RNA (Median = 2.20E5, Range 1.00E4–3.11E7 IU/ml). In contrast, the vast majority (93.8%) had undetectable HBV DNA and HDV RNA titres at 6- and 12-months post-transplantation. There was also a significant difference in HBsAg levels pre-transplant, 6- and 12 months post-transplant (p = 0.006). All patients were administered HBIG intra and post-operatively and continued on long-term HBIG and NA. 56% received Tenofovir disoproxil fumurate, 6 individuals (37.5%) were prescribed Entecavir due to underlying renal impairment, and one received tenofovir alafenamide as part of their concurrent HIV treatment. Survival post liver transplant was compared to a control group of HBV mono-infected individuals, the mean survival of HBV/HDV co-infection post liver transplant was 78.6 months, with two fatalities secondary to viral reactivation or transplant-related complications and a mean follow-up of 40.94 months (SD 24.07 months).

**Conclusion:** This study demonstrates that liver transplantation successfully controls HBV/HDV co-infection expression. Whilst NA and HBIG effectively prevent viral reactivation and are associated with favourable long term outcomes; further work is needed to establish a consensus approach across different transplant centres in this patient group.

**SAT305**

Durability of SARS-CoV-2 specific immune response following different primary prime-boost vaccine platforms and subsequent humoral response to booster dose among liver transplant recipients

Supachaya Sri phoo sanapan1,2, Sirinporn Suksawat amnuay1,2,3, Nuntiya Srisoonthorn4,5, Nipapon Sirison5, Panarat Thaimai1, Wanwisar Makhassen1,2, Nawakodchamon Mungnamtrakul1,2, Kessarin Thanapirom1,2,3, Bunchoon Nonthatsoot1, Pokrath Hansasuta1, Pyawai Komolmit1,2,3, Division of Gastroenterology, Department of Medicine, Faculty of Medicine, Chulalongkorn University, Bangkok, Thailand; 2Center of Excellence in Liver Diseases, King Chulalongkorn Memorial Hospital, Bangkok, Thailand; 3Division of Surgery, Faculty of Medicine, Chulalongkorn University, Bangkok, Thailand; 4Division of Virology, Department of Microbiology, Faculty of Medicine, Chulalongkorn University and King Chulalongkorn Memorial Hospital, Thai Red Cross Society, Bangkok, Thailand

Email: supachaya.si@gmail.com

**Background and aims:** Suboptimal immunogenicity among liver transplant (LT) recipients after primary SARS-CoV-2 vaccination has aroused concerns about the longevity of protection and urgent need of a booster dose. There is a paucity of information on antibody kinetics and response following a third dose vaccine in this population. We aimed to investigate the durability of humoral response after primary immunization induced by different prime-boost vaccine platforms and subsequent response to booster dose in LT recipients.

**Method:** LT recipients who were vaccinated with ChAdOx1 nCoV-19 (AZ)/AZ or AZ/BNT162b2 (BNT) as primary vaccine series at King Chulalongkorn Memorial Hospital, Bangkok, Thailand, between April and December 2021 were enrolled. The mRNA-1273 (Moderna) was
administered as the booster vaccine at 3 months following the second dose. SARS-CoV-2 spike receptor-binding-protein (RBD) IgG was assessed at 1 month, 3 months after the second dose, and 1 month following the booster vaccine. Anti-RBD antibody was tested using electrochemiluminescence immunoassay (Roche Elecsys). According to the basis of plasma-neutralizing capacity in patients with convalescent SARS-CoV-2 infection, anti-RBD titer of ≤0.8 U/ml, 0.8–50 U/ml, and >50 U/ml were defined as negative, low-positive, and high-positive, respectively.

Results: Of 74 LT recipients, 51 (68.9%) were male and median age was 61 (IQR 52–68) years. Median time from transplantation was 5.8 (IQR 2.2–10.8) years. Sixty-one (82.4%) patients were taking tacrolimus, 60 (81.1%) anti-metabolite, and 8 (10.8%) steroids. Fifty-eight (78.4%) patients received AZ/BNT as primary vaccine series. Overall, median anti-RBD titer at 1 month after primary immunization were 609.1 (IQR 38.2–1,632) U/ml and the levels declined to 397.6 (IQR 77.7–1,098.5) U/ml at 3 months (p = 0.54). Antibody reduction rate was comparable between two vaccine platforms (32.1% in AZ/AZ versus 43.8% in AZ/BNT, p = 0.25). After the booster dose, median anti-RBD titers significantly rose to 9, 597.0 (IQR 3, 953–13, 497.5) U/ml (p < 0.001). The proportion of LT patients with high-positive titers significantly increased from 78.4% at 3 months after primary immunization to 98.6% following the third vaccination (p < 0.001). Patients who received heterologous prime-boost regimen as primary vaccine series had significantly greater anti-RBD levels after the booster (10, 346.0 U/ml in AZ/BNT/Moderna group versus 5, 134.0 U/ml in AZ/AZ/Moderna group, p = 0.04). (Figure 1)

Conclusion: SARS-CoV-2 specific antibody among LT recipients waned over time after primary immunization regardless of vaccine platforms. The booster strategy substantially provided high protective antibody titers in almost all LT patients. Further studies evaluating duration of protection after the booster as well as clinical effectiveness against the variants of concerns are warranted.

SAT306
Outcome of choledochal cysts with intrahepatic involvement (type IV-A) after extrahepatic cyst excision and roux-en-Y hepaticojejunostomy in adults
Utpal Anand1,2, Rajeev Priyadarshh2, Ramesh Kumar3. 1All India Institute of Medical Sciences, Patna, Surgical Gastroenterology, Patna, India; 2All India Institute of Medical Sciences, Patna, Radiodiagnosis, Patna, India; 3All India Institute of Medical Sciences, Pathna, Gastroenterology, Patna, India
Email: utpalanand2@gmail.com

Background and aims: Type I and type IV-A choledochal cysts (CC) according to Todani’s classification are the most frequent types. Unlike type I CC, in which the dilatation is confined to the extrahepatic bile duct, type IV-A affects both extra and intrahepatic ducts. The aim of this study was to evaluate outcomes in adult patients with type IV-A CC at least 2 years after resection of the extrahepatic bile duct cyst.

Method: Data was collected retrospectively from a cohort of 60 adult patients who underwent extrahepatic cyst resection for type IV-A CC from 2010 to 2020 in our institution. A total of 45 patients were included in the final analysis, with a minimum follow-up of two years.

Results: Follow-up time ranged from 2 years to 10 years (median, 25 months). Thirty-five patients remained asymptomatic; however, 5 patients had abnormal liver function tests (LFTs), requiring regular monitoring. Late complications in varying combinations were seen in 10 patients (16.6%), which included cholangitis and/or intrahepatic-hepatic stones in 9 (15%), intrahepatic bile duct stenosis with stones in 2, anastomotic stricture with or without stone formation in 6, and left lobar atrophy with intrahepatic stones in 3 patients. Magnetic resonance cholangiopancreatography and/or Computed tomography scans was done to evaluate the causes of stricture which revealed anastomotic stricture in 6 patients and web like stenosis of the left intrahepatic bile duct in 2 patients. Percutaneous transhepatic biliary dilatation was done in 2 patients with anastomotic stricture without cystolithiasis. Re-do hepaticojejunostomy (HJ) was required in the remaining 4 patients. The stenotic bile duct was incised and hepaticojejunostomy was performed in both patients with left intrahepatic web. The median time interval from primary surgery to reintervention was 24 months. The median follow-up period after reoperation was 5 years.

Conclusion: Residual intrahepatic dilatation of type IV-A cyst in adults did adversely affect the postoperative outcome after a conventional surgical repair. A long term follow-up is necessary to recognize and address late complications.

SAT307
The impact of COVID-19 on the duration of the liver transplant process in patients presenting for inpatient liver transplant evaluation
Katherine Cooper1, Arslan Talar1,2, Diana Liu1, Alessandro Colletta1,2, Deepika Devuti1,2. 1UMass Chan Medical School, Worcester, United States; 2UMass Memorial Medical Center-University Campus, Worcester, United States
Email: katherine.cooper@umassmed.edu

Background and aims: The SARS-CoV-2 pandemic (COVID-19) adversely affected liver transplantation internationally. At its peak, COVID-19 was associated with decreased transplant rates and increased waitlist mortality. Though many centres have resumed normal transplant activities, there is concern that reduction in health care services may mean patients present later in their disease course resulting in need for more urgent transplant evaluations. We aimed to evaluate differences in the inpatient liver transplant process before and after the COVID-19 pandemic to understand the impacts on the overall transplant care pathway.

Method: Medical records for all patients undergoing liver transplant evaluation (LTE) from 10/2017–8/2021 were reviewed. Patients undergoing LTE for chronic liver disease (CLD) were included; patients with a history of liver transplant or in fulminant liver failure were excluded. Records were categorized as Pre-COVID if evaluation was before 3/15/2020 and post-COVID if after 3/15/2020. Demographic and clinical history were collected for patients undergoing inpatient LTE. Variables were compared using Fisher’s exact test and students t-tests; significance was evaluated at p = .05.
**Results**: One hundred and fifty-nine evaluations occurred (54% Pre-COVID, 46% Post-COVID). Time from referral to the first day of LTE tended to be longer in the Post-COVID period than the Pre-COVID period. Conversely, there was a significant reduction in days from transplant referral to liver transplant in patients who underwent inpatient LTE in the Post-COVID period \( p = 0.0227 \). Time having elapsed There were no differences in age \( p = 0.85 \), MELD-Na \( (0.81) \), months since diagnosis \( p = 1.0 \). About 40%of patients who underwent inpatient LTE in the Post-COVID group had received a transplant at the time of data collection compared to 36.0% in the Pre-COVID group. Further, the rate of transplants performed per month has been around 70% higher for patients evaluated in the Post-COVID period compared to the Pre-COVID period (1.8 vs. 1.1 transplants per month, respectively).

**Conclusion**: The COVID-19 pandemic appears to have had a negative impact on the ability to undergo evaluation for liver transplant in the outpatient setting. Despite this, patients seem to be receiving transplants at a faster rate despite no differences in time since diagnosis or MELD-Na at the time of work up. The reason for this may be multifactorial and may include hospital capacity, varying disease progression, and clinical presentation.
**Results:** About one third (37.7%) of patients undergoing inpatient LTE have received a transplant since evaluation. Less than a quarter (15%) received a transplant during their index admission; with patients referred late tending to be transplanted less often (11.5% vs. 18.5%, p = 0.21). Overall, patients with missed referrals were more likely to die after approval (30.8% vs. 17.3%, p = 0.05) and less likely to receive a transplant than those without missed referrals (28.2% vs. 48.1%, p = 0.016). Even when adjusting for MELD-Na, disease etiology, and age, patients not receiving timely LTE referral are 2.2 times less likely to receive a liver transplant.

**Conclusion:** Failure to refer for LTE in a timely manner has an adverse effect on patient outcomes. It is crucial to improve education about liver transplant and for providers to remain up to date on liver transplant candidacy and the transplant referral process.

**SAT310 Nutritional intake after liver transplant: systematic review with meta-analysis and meta-regression**

Lynsey Spillman 1,2, Angela Madden 1,2, Holly Richardson 1, Fumiaki Imamura 1, Kirsten Rennie 1, Linda Oude Griep 1, Michael Allison 2, Simon Griffin 1.

**Objective:** To conduct a systematic review to synthesise evidence on nutritional intake of LT recipients (LTRs) and investigate causes of heterogeneity in reported intake between studies.

**Methods:** We searched Cochrane Library, MEDLINE, Embase, AMED, CINAHL, PsycINFO, BNI, Web of Science and OpenGrey electronic databases from the earliest date until 04/07/21 for peer-reviewed original studies of any design that recruited LTRs. Databases were searched from the earliest date until 04/07/21 for peer-reviewed papers. Extracted data and assessed risk of bias (ROB). Two independent reviewers assessed their nutritional intake. Two independent reviewers assessed their nutritional intake. The p-value was 0.05.

**Results:** We included 21 studies, and 19 provided dietary findings for meta-regression. Five studies were at low ROB. The pooled daily mean energy intake was 1,998 kcal (Figure); 17% from protein, 48% from carbohydrate, 34% from total fat, 10% from saturated fat and 20 g fibre. Average fruit and vegetable intake ranged from 105 to 418 g/day. Daily energy intake was lower at <1-month post-LT compared to all later time periods: 1-<6 months (-609 kcal mean difference (MD), p = 0.002), 6-<12 months (-251 kcal MD, p = 0.003), and ≥12 months (<135 kcal MD, p = 0.021). As age of LTRs increased, daily energy intake was estimated to be 49.7 kcal higher (p = 0.018) and energy from carbohydrates was 1.0% lower (p = 0.022). Energy from saturated fat increased as proportion of male participants increased (0.2%, p = 0.001). Total energy intake was higher (201 kcal, p = 0.042), energy from protein lower (<2.5%, p = 0.004) and energy from total fat higher (3.7%, p = 0.005) in European studies compared to other continents.

**Conclusion:** Diet quality is a potentially important area for post-operative intervention for LTRs. Compared to recommendations from the European Association for the Study of the Liver (35 kcal/kg body weight (BW) and 1.5 g protein/kg BW per day), on average LTRs are unlikely to meet energy or protein requirements for recovery in the first post-month LT. For protein and saturated fat LTRs follow recommendations for a healthy diet, however they consume a diet high in total fat and low in fibre, fruits and vegetables. The high energy diet for recovery may continue for longer than required, leading to energy imbalance and excess weight and body fat.

**SAT311 Impact of muscle mass on survival of patients with hepatocellular carcinoma after liver transplantation beyond the Milan criteria**

Berend Beumer 1, Jeroen van Vugt 1, Gonzalo Saposchnik 2, Peter Zucchelli 3, Marco Bongini 4, Di Lu 5, Xiao Xu 5, Paolo De Simone 6, Lorenzo Pintore 6, Nicolas Golse 7, Małgorzata Nowosad 8, William Bennet 9, Emmanuel Toschatzis 10, Evaggelia Koutli 11, Fariba Abbassi 11, Marco Claassen 12, Manuela Merli 12, Joanne Oorurke 13, Martina Gambato 14, Alberto Benito 15, Avik Majumdar 16, Ek Khoon Tan 17, Maryam Ebadi 18, Aldo J Montano-Loza 18, Marina Berenguer 19, Herold Metselaar 20, Wojciech Polak 1, Vincenzo Mazzaferrro 2, Jan Ijzermans 1.

**Objective:** To evaluate the impact of muscle mass on survival of patients with hepatocellular carcinoma after liver transplantation beyond the Milan criteria.

**Methods:** A retrospective cohort study was performed where all patients with HCC transplanted at our centre between 2000 and 2019 were included. Muscle mass was calculated using the dual energy X-ray absorptiometry (DXA) method and normalized for body surface area (BSA). Patients were stratified in two groups based on the Milan criteria (Group 1) and those who exceeded the Milan criteria (Group 2). The primary endpoint was overall survival (OS).

**Results:** A total of 161 patients with HCC transplanted during the study period were included. Patients in Group 2 had higher BMI, lower MELD and ALB than patients in Group 1. A total of 128 patients died during follow-up (no patients underwent LT for recurrence of HCC). Median OS time was significantly longer in Group 1 compared with Group 2 (17 months vs. 12 months, p = 0.002). Cox regression analysis showed that in Group 2, BMI, MELD and Creatinine were independent predictors of shorter OS. Patients with higher muscle mass normalized for BSA had significantly better OS in both groups (p = 0.03).

**Conclusion:** Muscle mass normalized for BSA is an independent predictor of survival beyond the Milan criteria. Further studies are needed to evaluate the impact of muscle mass on outcomes in HCC patients transplanted at early time points.
Liver Transplantation Unit and Ciberehd and ISS La Fe, Valencia, Spain; 2Erasmus MC Transplant Institute, Department of Gastroenterology and Hepatology, Rotterdam, Netherlands
Email: b.beumer@erasmusmc.nl

Background and aims: When listing for liver transplantation we can transplant as soon as possible or introduce a test of time to better select patients as the tumor’s biological behavior is observed. Knowing the degree of harm caused by time itself is essential to advise patients and decide on the maximum duration of the test-of-time. Therefore, we investigated the causal effect of waiting time on post-transplant survival for patients with HCC.

Method: We analyzed the UNOS-OPTN dataset and exploited the natural experiment created by blood groups. Relations between variables were described in a causal graph. Inverse probability weighting was used to address selection bias. Confounding biases were avoided using instrumental variable analysis, with an additive hazards model in the second stage. The causal effect was evaluated as a contrast between a scenario in which all patients waited 2 months and one in which all patients waited 12 months. Upper bounds of the test-of-time were evaluated for probable scenarios by means of simulation.

Results: The F-statistic of the first stage was 86.3. The effect of waiting 12 months versus 2 months corresponded with a significant drop in overall survival of 5.07% 95%CI [0.27; 9.69] and 8.33% 95% CI [0.47; 15.60] at 5- and 10-years post-transplant, respectively. The median survival significantly dropped by 3.41 years from 16.21 years 95%CI [15.98; 16.60] for those waiting 2 months to 12.80 years 95%CI [10.72; 15.90] for those waiting 12 months. No significant effect modification by tumor size or number was found.

Figure: (abstract: SAT310): Mean daily energy intake categorised by time post-transplant

Liver Transplantation Unit and Ciberehd and ISS La Fe, Valencia, Spain; 2Erasmus MC Transplant Institute, Department of Gastroenterology and Hepatology, Rotterdam, Netherlands
Email: b.beumer@erasmusmc.nl

Background and aims: When listing for liver transplantation we can transplant as soon as possible or introduce a test of time to better select patients as the tumor’s biological behavior is observed. Knowing the degree of harm caused by time itself is essential to advise patients and decide on the maximum duration of the test-of-time. Therefore, we investigated the causal effect of waiting time on post-transplant survival for patients with HCC.

Method: We analyzed the UNOS-OPTN dataset and exploited the natural experiment created by blood groups. Relations between variables were described in a causal graph. Inverse probability weighting was used to address selection bias. Confounding biases were avoided using instrumental variable analysis, with an additive hazards model in the second stage. The causal effect was evaluated as a contrast between a scenario in which all patients waited 2 months and one in which all patients waited 12 months. Upper bounds of the test-of-time were evaluated for probable scenarios by means of simulation.

Results: The F-statistic of the first stage was 86.3. The effect of waiting 12 months versus 2 months corresponded with a significant drop in overall survival of 5.07% 95%CI [0.27; 9.69] and 8.33% 95% CI [0.47; 15.60] at 5- and 10-years post-transplant, respectively. The median survival significantly dropped by 3.41 years from 16.21 years 95%CI [15.98; 16.60] for those waiting 2 months to 12.80 years 95%CI [10.72; 15.90] for those waiting 12 months. No significant effect modification by tumor size or number was found.

Figure: (abstract: SAT310): Mean daily energy intake categorised by time post-transplant

Liver Transplantation Unit and Ciberehd and ISS La Fe, Valencia, Spain; 2Erasmus MC Transplant Institute, Department of Gastroenterology and Hepatology, Rotterdam, Netherlands
Email: b.beumer@erasmusmc.nl

Background and aims: When listing for liver transplantation we can transplant as soon as possible or introduce a test of time to better select patients as the tumor’s biological behavior is observed. Knowing the degree of harm caused by time itself is essential to advise patients and decide on the maximum duration of the test-of-time. Therefore, we investigated the causal effect of waiting time on post-transplant survival for patients with HCC.

Method: We analyzed the UNOS-OPTN dataset and exploited the natural experiment created by blood groups. Relations between variables were described in a causal graph. Inverse probability weighting was used to address selection bias. Confounding biases were avoided using instrumental variable analysis, with an additive hazards model in the second stage. The causal effect was evaluated as a contrast between a scenario in which all patients waited 2 months and one in which all patients waited 12 months. Upper bounds of the test-of-time were evaluated for probable scenarios by means of simulation.

Results: The F-statistic of the first stage was 86.3. The effect of waiting 12 months versus 2 months corresponded with a significant drop in overall survival of 5.07% 95%CI [0.27; 9.69] and 8.33% 95% CI [0.47; 15.60] at 5- and 10-years post-transplant, respectively. The median survival significantly dropped by 3.41 years from 16.21 years 95%CI [15.98; 16.60] for those waiting 2 months to 12.80 years 95%CI [10.72; 15.90] for those waiting 12 months. No significant effect modification by tumor size or number was found.

Figure: (abstract: SAT310): Mean daily energy intake categorised by time post-transplant

Liver Transplantation Unit and Ciberehd and ISS La Fe, Valencia, Spain; 2Erasmus MC Transplant Institute, Department of Gastroenterology and Hepatology, Rotterdam, Netherlands
Email: b.beumer@erasmusmc.nl

Background and aims: When listing for liver transplantation we can transplant as soon as possible or introduce a test of time to better select patients as the tumor’s biological behavior is observed. Knowing the degree of harm caused by time itself is essential to advise patients and decide on the maximum duration of the test-of-time. Therefore, we investigated the causal effect of waiting time on post-transplant survival for patients with HCC.

Method: We analyzed the UNOS-OPTN dataset and exploited the natural experiment created by blood groups. Relations between variables were described in a causal graph. Inverse probability weighting was used to address selection bias. Confounding biases were avoided using instrumental variable analysis, with an additive hazards model in the second stage. The causal effect was evaluated as a contrast between a scenario in which all patients waited 2 months and one in which all patients waited 12 months. Upper bounds of the test-of-time were evaluated for probable scenarios by means of simulation.

Results: The F-statistic of the first stage was 86.3. The effect of waiting 12 months versus 2 months corresponded with a significant drop in overall survival of 5.07% 95%CI [0.27; 9.69] and 8.33% 95% CI [0.47; 15.60] at 5- and 10-years post-transplant, respectively. The median survival significantly dropped by 3.41 years from 16.21 years 95%CI [15.98; 16.60] for those waiting 2 months to 12.80 years 95%CI [10.72; 15.90] for those waiting 12 months. No significant effect modification by tumor size or number was found.

Figure: (abstract: SAT310): Mean daily energy intake categorised by time post-transplant
Conclusion: From a patient’s perspective the choice between ablate-and-wait versus immediate transplantation is in favor of immediate transplantation. From a policy perspective, the extra waiting time can be used to increase the utility of scarce donor livers, although the duration of the test-of-time is bound to be likely less than 8 months.

SAT312
Predictive factors of tumor recurrence after liver transplantation for hepatocellular carcinoma: analysis of a multicenter prospective study including 371 patients
Thomas Decaens1, René Adam2, Sébastien Dharancy3, Laurent Sulipce4, Didier Samuel2, Emmanuel Boleslawski5, Marianne Latourniere6, Georges-Philippe Pageaux7, Olivier Scatton8, Sylvie Radenne2, Eric Savier9, Claire Francoz7, Claire Vanleemmens10, Pierre-Henri Bernard9, Jean Hardwigen10, Jean Gugenheim11, Christophe Duvoix12, Nadia Oubaya12, Éric Grenoble Alpes, La Tronche, France; 1Assistance Publique-Hôpitaux de Paris, Paris, France; 2CHU De Lille, Lille, France; 3CHU Rennes-Pontchaillou Hospital, Rennes, France; 4CHU Dijon, Dijon, France; 5Hospital Center University De Montpellier, Montpellier, France; 6Hospices Civils de Lyon-HCL, Lyon, France; 7Hospital Jean-Minjoz, Besançon, France; 8CHU Bordeaux-Site Pellegrin, Bordeaux, France; 9Hôpital de Nice, France; 10Hospital Academic De Marseille, Marseille, France; 11Yespark-La Madeleine/Hôpital l’Archet 2-Nice, Nice, France

Background and aims: Hepatocellular carcinoma (HCC) has become the first cause of liver transplantation (LT) in France but also in most countries of the world. Patient selection criteria are based on retrospective studies of cohorts of transplant patients. They are mainly linked to predictive factors of tumor recurrence. The aim of our work was to analyze the predictive factors of tumor recurrence at 24 months after liver transplantation, from a prospective study of patients registered on the LT list for HCC in France.

Method: Prospective multicenter study with 15 French LT centers (NCT01198704). Quantitative variables are presented as mean ± standard deviation or median with IQR25–75. The qualitative variables are presented in percentage. The overall survival analysis was carried out by the Kaplan Meier method and recurrence-free survival by competitive risk analysis (Fine and Gray) considering death as a competitive event.

Results: 371 patients were included in this study, 18 patients were wrongly included. Among the 353 patients, 72 patients left the list, including 48 (66%) for tumor progression. 281 patients were transplanted, 90% of them men. The median waiting time was 7.56 months (3.78–12.16). During the baseline freeze in October 2021, 21 patients who had not died had a median follow-up of 60.1 months [95 CI: 58.8–61.2]. 45 patients showed tumor recurrence post-transplantation. The 5-year overall survival was 72% [95% CI 66.2–77.0], the cumulative incidence rate was 16% [95% CI 12.2–21.0] and the median survival of relapsed patients was 16.1 months [95% CI 13.0–24.0]. The multivariate analysis was divided into two for the construction of tumor recurrence scores based on the data accessible in pre-LT (registration and during the waiting time) and a model based on the data accessible after the transplant (pathology report, surgery data and clinical data within 6 months after LT). The remaining significant pre-LT parameters are the number of HCCs at enrollment >3 (HR = 2.67; p = 0.002) and progression of more than 7.5 ng/ml/month of AFP (HR = 2.25; p = 0.03). The progression of serum AFP level and the response to the waiting treatment disappear.

SAT313
Evaluation of predictive factors for postoperative nausea and vomiting in hepatobiliary cancer patients
Juliana Fernanda Holanda Bezerra Pereira1,2, Luciano Beltrão Pereira1,2, Zoka Milan1, Angela Sousa2, Claudia Marquez Simões1, Kings College Hospital, Anaesthesia and Critical Care, London, United Kingdom; 2State of São Paulo Cancer Institute, Anaesthesia and Pain Care Department, São Paulo, Brazil; 3King’s College Hospital, Institute of Liver Studies, Liver Transplant and Surgery Department, London, United Kingdom; 4Liver and Transplant Institute of Pernambuco-InP, Recife, Brazil

Background and aims: Postoperative nausea and vomiting (PONV) is associated with prolonged stay in post anesthesia care unit, patient's dissatisfaction, dehydration, wound dehiscence, bronchoaspiration, acute hypertension, increased intracranial pressure, acid base and electrolyte disorders and delayed hospital discharge. Thus, PONV prophylaxis is mandatory for anesthesia good practice as it poses a significant medical risk. This work aims to validate a simple predictor model for nausea and vomiting in the first 24 postoperative hours in hepatobiliary cancer patients.

Method: This single center retrospective study included adults patients undergoing medium to large hepatobiliary cancer surgeries. It was approved by the Ethics and Research Committee at King’s College Hospital. We assessed the PONV incidence after 24 hours. To evaluate possible factors influencing the occurrence of PONV, logistic regression analysis was applied, regression coefficient B, odds ratio (OR), 95% confidence interval of the odds ratio (95% CI OR), and p value were reported. We constructed a receiver operation characteristic (ROC) curve with the area under with possible risk factors for PONV, including the Apfel Score (female sex, non smoking status, postoperative opioid use, history of PONV/sickness).

Results: Over a six months period, a total of 137 patients, predominantly non-smokers (91%), and British race (77%), with the mean age of 61.80 ± 14.41 years and almost equal ratio of males and females (53% vs. 47%), were included in the study. PONV was presented in 29.9% cases; 100% used opioids in the postoperative period; Apfel score ranged from one to four, and most patients had Apfel score two or three (94%). It was obtained that younger age, female gender, and higher Apfel score increased the probability for PONV.

The remaining significant transplant and post-LT parameters are the number of viable HCC >3 (HR = 1.91; p = 0.039), the presence of satellite nodules (HR = 2.28; p = 0.01), and the presence of microscopic vascular invasion (HR = 2.41; p = 0.0006). The iron overload, the AFP rate at 6 months disappear.

Conclusion: This prospective multicenter study confirms the importance of the progression of the serum AFP level of more than 7.5 ng/ml/month as a predictive factor of tumor recurrence and underlines the importance of a low number of HCCs upon registration on listing. This study also shows the improvement in the prognosis of patients with tumor recurrence.
Figure 1. ROC curve for Apfel score as diagnostic marker for postoperative nausea and vomiting in hepatobiliary cancer patients.

Conclusion: We validated the Apfel Score in hepatobiliary cancer patients to guide the prophylaxis for PONV.

Liver transplantation and hepatobiliary surgery: Experimental and pathophysiology

SAT314

Immune responses before and after liver transplantation: a cohort study of the induced immune response

Dina Leth Møller1, Annemette Hald2, Andreas Dehlbæk Knudsen1,2, Ranya Houmami1, Nicoline Stender Arentoft1, Jens D. Lundgren1,4,5, Allan Rasmussen3, Sisse Rye Ostrowski1,4, Susanne Dam Nielsen1,4,5,1

1Rigshospitalet, University of Copenhagen, Viro-immunology Research Unit, Department of Infectious Diseases B632, Copenhagen, Denmark; 2Rigshospitalet, University of Copenhagen, Department of Cardiology, Copenhagen, Denmark; 3Rigshospitalet, University of Copenhagen, Centre for Excellence for Health, Immunity, and Infections, Department of Infectious Diseases, Copenhagen, Denmark; 4University of Copenhagen, Department of Clinical Medicine, Copenhagen, Denmark; 5Rigshospitalet, University of Copenhagen, Department of Surgical Gastroenterology and Transplantation, Copenhagen, Denmark; 6Rigshospitalet, University of Copenhagen, Department of Clinical Immunology, Copenhagen, Denmark

Email: dina.leth.moeller@regionh.dk

Background and aims: Reliable methods to assess the immune function after liver transplantation (LTx) are needed to guide dosing of immunosuppression and thereby prevent infections and rejections. The TruCulture assay is a standardized immunoassay that assesses the induced immune response in whole blood following ligand-stimulation of toll-like receptors (TLR).

We aimed to investigate the induced immune responses using TruCulture in LTx recipients before and three months after LTx and explore associations between methylprednisolone-treated acute rejection and cytokine levels post-LTx.

Method: A prospective observational study including LTx recipients transplanted at Rigshospitalet, Copenhagen University Hospital, Denmark from February 2018 to December 2020. The TruCulture analysis comprised 4 stimuli and a blank: A) Heat-killed Candida Albicans (HKCA, TLR1/2/4/6), B) Lipopolysaccharide (LPS, TLR4), C) Resiquimod R848 (R848, TLR7/8), D) Polyinosinic: polycytidylic acid (poly I:C, TLR3), and E) a blank containing only TruCulture media. After 22 hours of incubation, cytokine concentrations in the supernatants were measured by Luminex (TNF-α, IL-1β, IL-6, IL-8, IL-10, IL-12p40, IL-17A, IFN-α, and IFN-γ in pg/ml). Differences in cytokine concentrations before and after LTx were assessed using Wilcoxon signed-rank tests with subsequent Benjamini-Hochberg corrections for multiple comparisons. Associations were assessed using logistic regression.

Results: We included 67 LTx recipients. Median age was 50 years (IQR: 23–70) and 41 were males (61%). Methylprednisolone-treated acute rejection occurred in 10 (15%) recipients a median of 8.5 days (IQR: 7–9) post-LTx.

Most of the stimulated cytokine levels decreased post-LTx (Figure 1). Methylprednisolone-treated acute rejection was significantly associated with an increased relative risk for a large decrease in HKCA-stimulated IL-10 (RR: 2.3 (1.1–5.0), p = 0.03), IL-1beta (RR: 2.5 (1.0–5.8), p = 0.04) and IL-8 (RR: 2.5 (1.1–5.5), p = 0.03), LPS-stimulated IL-10 (RR: 2.1 (1.1–4.1), p = 0.03), and Poly I:C-stimulated IL-1beta (RR: 2.1 (1.1–4.0), p = 0.03).

Conclusion: Most of the investigated induced immune responses decreased after liver transplantation. Treatment for acute rejection was associated with a larger decrease in a subset of the stimulated cytokines. Thus, TruCulture is feasible and seems promising. Further studies to determine utility for prediction of infections and rejections post-LTx are warranted.

SAT315

Andrographolide can potentially rescue unusable liver grafts by reducing fat content, enhancing mitochondrial function, and inhibiting Th1/Th17 immunity

Zhenlin Huang1,2, Tengfei Si2, Xiaohong Huang2, Hanish Anand2, Celine Filippi2, Ragai Mitry2, Anil Dhawan2, Weyel Jassem2, Zhengtao Wang1, Nigel Heaton2, Lili Ji1, Yun Ma2, 1Shanghai University of Traditional Chinese Medicine, Institute of Chinese Materia Medica, Shanghai, China; 2King’s College London, Institute of Liver Studies, London, United Kingdom

Email: yun.ma@kcl.ac.uk

Background and aims: There is a great shortage of good quality donor liver grafts to meet the increasing demand of patients with end-stage liver disease. A large proportion of donated livers are discarded due to suspected sub-optimal quality. One of the major reasons for low quality liver grafts is that the fat content in it being too high (>50%). Normothermic machine perfusion (NMP) is a novel...
technique to preserve liver grafts which has been shown to improve marginal liver condition. Andrographolide (Andro), a newly defined active compound from traditional Chinese medicine (Chinese name: 穿心莲), has showed promising early results in vitro, so we are exploring using it in the NMP solution to reduce the fat content, improve the mitochondrial function, and inhibit the T cell induced immunity. This work is a deeper investigation of Andro’s effects in vitro experiments to justify its use during NMP.

**Method:** Human hepatocytes were isolated from 9 donor fatty liver grafts which were unsuitable for transplantation due to their fat content >50%. Hepatic T cells were isolated from an additional 12 donors’ liver perfusates. Hepatocytes and T cells were treated with sequentially increased dosage of Andro (5, 10, 25 μM) for 48 hours separately. After treatment, free and total cholesterol level in hepatocytes were detected using commercially available kits (Cholesterol Quantification Assay kit, CS0005, Merck); total DNA and RNA was extracted, mitochondrial DNA copy numbers and the expression of anti-oxidative genes was measured by qRT-PCR (SYBR™ Select Master Mix, 4472908, Thermo fisher); lipid droplets were stained using Oil Red (Lipid Staining Kit, MAK194, Merck). Cytokine levels in T cells including TNF-α, IFN-γ and IL-17 were measured.

Figure: (abstract: SAT315)
measure using flow cytometry; qRT-PCR and ELISA (Human DuoSet ELISA, DY210/DY285B, RandD systems).

**Results:** In hepatocytes, different dosage of Andro (5, 10, 25 μM) caused no toxicity. High dosage of Andro (25 μM) reduced the level of free/total cholesterol (p < 0.01) (Figure 1A), decreased amount of lipid droplets (Figure 1B), and increased the mitochondrial DNA copy numbers, mRNA expression of PGC-1α, GCLC, GCLM, HO-1 and NQO1 (p < 0.05) (Figure 1C). Furthermore, Andro (5, 10, 25 μM) decrease the percentage of TNF-α, IFN-γ or IL-17-producing T cells and reduced mRNA expression of TNF-α and IFN-γ in T cells (p < 0.05, p < 0.01, p < 0.0001). Andro (25 μM) also decreased the protein level of TNF-α and IFN-γ in T cell culture supernatant (p < 0.01) (Figure 1D).

**Conclusion:** Andro is effective in reducing lipid content, promoting mitochondrial biogenesis and activating anti-oxidative system in hepatocytes. In addition, Andro inhibited Th1 and Th17 immunity. These results show that Andro has a great potential to rescue those marginal liver grafts to ease graft shortage in the setting of human liver transplantation.

**SAT316**

**Trends and causes of etiology in adult liver transplant patients: multicenter study**


1Department of Gastroenterology, Dokuz Eylul University School of Medicine; 2Liver Transplantation Institute, Inonu University School of Medicine; 3Department of Gastroenterology, Koc University School of Medicine; 4Liver Transplant Center, Memorial Atasehir/Bahcelievler Hospitals; 5Department of Gastroenterology, Akdeniz University School of Medicine; 6Department of Gastroenterology, Ege University School of Medicine; 7Department of Gastroenterology, Ankara University School of Medicine; 8Department of Gastroenterology, Gazi University School of Medicine, Internal Medicine, Ankara, Turkey; 9Department of Gastroenterology, University of Health Sciences, Ankara City Hospital; 10Department of Gastroenterology, Uludag University School of Medicine; 11Department of Gastroenterology, Gaziantep University School of Medicine; 12Department of Gastroenterology, Hacettepe University School of Medicine; 13Department of General Surgery, Hacettepe University, Faculty of Medicine

**Email:** mesutakarsu71@gmail.com

**Background and aims:** The indications to liver transplantation (LT) are changing in western population over the years. The aims of the present study were to determine etiological trends in LT in Turkey.

**Method:** This is multicenter, retrospective study that evaluated the etiological factors of the patients with end-stage chronic liver disease who underwent LT between 2010 and 2020. A total of 5,880 adult patients who underwent LT was included into the study. The time frame was divided as January 1, 2010 to December 31, 2014 (first period) and January 1, 2015 to December 31, 2020 (second period) (Table 1).

**Results:** Mean age was 50.3 years; their gender was predominantly male (69.5%). Chronic viral hepatitis (46.4%) was the most common etiological factors leading to transplantation in the overall cohort. Hepatitis B virus (HBV) infection (35.2%) was the main etiology, followed by cryptogenic cirrhosis (CC) (23.5%), hepatitis C virus infection (8.2%), and ALD (6.2%). Hepatocellular carcinoma (HCC) was the LT indication for 939 patients (18.5%). In the second period, the proportion of viral hepatitis was decreased, whereas the proportion of NAFLD-related and ALD-related cirrhosis was increased (Table 1).

**Table:** Demographic data and etiologic changes in adult liver transplant patients

<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Age (year), mean ± SD</td>
<td>49.95 ± 1.92</td>
<td>50.68 ± 5.75</td>
<td>0.707</td>
</tr>
<tr>
<td>Male/Female, n (%)</td>
<td>74.2/25.8</td>
<td>74.6/25.4</td>
<td>0.124</td>
</tr>
<tr>
<td>Etiology, n (%)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Viral Hepatitis</td>
<td>668 (%39.8)</td>
<td>1125 (%33.1)</td>
<td>0.001</td>
</tr>
<tr>
<td>HBV</td>
<td>196 (%11.7)</td>
<td>223 (%6.6)</td>
<td>0.010</td>
</tr>
<tr>
<td>HCV</td>
<td>148 (%8.8)</td>
<td>110 (%3.2)</td>
<td>0.001</td>
</tr>
<tr>
<td>NAFLD</td>
<td>69 (%4.1)</td>
<td>250 (%7.3)</td>
<td>0.001</td>
</tr>
<tr>
<td>Miscellaneous</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CC</td>
<td>347 (%20.7)</td>
<td>849 (%24.9)</td>
<td>0.001</td>
</tr>
<tr>
<td>WD</td>
<td>57 (%3.4)</td>
<td>65 (%1.9)</td>
<td>0.004</td>
</tr>
<tr>
<td>BCS</td>
<td>28 (%1.7)</td>
<td>103 (%3)</td>
<td>0.004</td>
</tr>
<tr>
<td>HC</td>
<td>3 (%0.2)</td>
<td>9 (%0.3)</td>
<td>0.761</td>
</tr>
<tr>
<td>AAD</td>
<td>3 (%0.2)</td>
<td>10 (%0.3)</td>
<td>0.564</td>
</tr>
<tr>
<td>Others</td>
<td>55 (%3.3)</td>
<td>245 (%7.2)</td>
<td>0.001</td>
</tr>
</tbody>
</table>

**Email:** jychoi@catholic.ac.kr

**Background and aims:** Although liver transplantation (LT) patients have the possibility of rejection or tolerance, there have been no reliable models to predict the liver immune homeostasis of LT patients, which may give clinicians the chance to assess liver immunity and guide future treatment plans. Here, we developed a new patient-derived mouse model to predict the liver immune homeostasis of LT patients.

**Method:** The patient-derived avatar model was developed by injection of peripheral blood mononuclear cells from healthy controls (HCS) or LT patients with stable, rejection, or tolerance into NSG mice, followed by human hepatic stellate cells and CCL4 injections. After seven weeks of transferring the cells, the patient’s T-cell engraftment
and liver inflammation of the avatar model were evaluated and compared to the liver histology of LT patients.

Results: The CXCR3-dependently engrafted patient’s T cells caused different liver inflammation in our model according to the status of the LT patients. The livers of avatar models from rejection patients had severe inflammation with more T helper 17 and fewer regulatory T cells compared to that of the models from tolerance and HCs showing only mild inflammation. Moreover, our model could classify stable post-LT patients into severe and mild inflammation groups, which correlated well with the liver immunity of these patients.

Conclusion: Using our new patient-derived avatar model, we could predict real liver immune homeostasis and histologic inflammation in stable LT patients without liver biopsy.

Conflict of Interest: All authors disclose no conflicts.

Financial Support: This study was supported by a grant of the Korea Health Technology RandD Project through the Korea Health Industry Development Institute (KHIDI), funded by the Ministry of Health and Welfare, Republic of Korea (grant number: HI15C3062). This work was also supported by the National Research Foundation of Korea (NRF) grant funded by the Korea government (MSIT) (No. 2020R1F1A1075S18), and was supported by Basic Science Research Program through the National Research Foundation of Korea (NRF) funded by the Ministry of Education (No. 2021R111A1A01050954).

SAT318
Hepatocellular carcinoma and the risk of cancer onset after liver transplantation-role of immune activation and aging profiles
Sarah Shalaby1, Maria Raffaella Petrara2, Elena Ruffoni3, Martina Taborelli4, Francesco Carmona3, Paola Del Bianco3, Pierluca Piselli3, Francesca D’Arcangelo1, Debora Bizzaro1, Marco Senzolo1, Francesco Paolo Russo3, Patrizia Boccagni6, Umberto Cillo6, Paolo Feltracco7, Diego Serraino4, Anita De Rossi2, Patrizia Burra1.
1Multivisceral Transplant Unit, Department of Surgery, Oncology and Gastroenterology, Padua University Hospital, Padua, Italy; 2Oncology and Immunology Section, Department of Surgery, Oncology and Gastroenterology, Padua University Hospital, Padua, Italy; 3Immunology and Diagnostic Molecular Oncology Unit, Veneto Institute of Oncology IOV-IRCCS, Padua, Italy; 4Cancer Unit, CRO National Cancer Institute, IRCCS, Aviano, Italy; 5Department of Epidemiology, National Institute for Infectious Diseases L. Spallanzani, Rome, Italy; 6Hepatobiliary Surgery and Liver Transplantation Unit, Department of Surgery, Oncology and Gastroenterology, Padua University Hospital, Padua, Italy; 7Section of Anesthesiology and Intensive Care, Department of Medicine-DIMED, Padua, Italy
Email: sarahshalaby18@gmail.com

Background and aims: Patients with hepatocellular carcinoma (HCC) are at higher risk for post-transplant malignancies (PTM). Immune activation and senescence have been frequently implicated in cancer development, however, no data are available concerning their prognostic role in patients undergoing liver transplant (LT). The aim of the study was to analyze these profiles in patients transplanted for HCC (LT-HCC) and for other causes (LT-non-HCC).

Method: Patients who underwent LT between October 2016 and February 2021 at Multivisceral Transplant Unit, Padua University Hospital were enrolled. Patients characteristics, HCC presence and features and immunosuppression were recorded. Exclusion criteria: ≤18 years old, follow-up shorter than 30 days or previous neoplastic history other than HCC. All PTM were registered. Markers of T (CD3 +CD4+CD38+) and B (CD19+CD10-CD21-CD27+) cell activation, T (CD3+CD4+CD28-CD57+) and B (CD19+IgD-CD27+) cell senescence were evaluated by flow cytometry at transplantation (baseline).
Results: A total of 116 patients were included: 45 LT-HCC and 71 LT-non-HCC. LT-HCC patients were older than LT-non-HCC (median 60 vs 53 years, p = 0.011), but comparable for sex, liver disease etiology, immunosuppressive schedule. At baseline, levels of activated CD8, memory B-cells and senescent CD4, CD8 and B-cells were significantly higher in LT-HCC patients than LT-non-HCC ones. During 27.4 (7.7–41.7) months of follow-up, 6 PTM occurred: 4 in LT-HCC (8.9%) and 2 in LT-non-HCC (2.8%). Patients developing PTM showed significantly higher baseline levels of immune activation than patients without malignancies. Within LT-HCC group, levels of senescent cells were significantly higher in patients with PTM compared to the others [%CD8+CD28-CD57+: 22.45 (17.72–25.86) vs 10.82 (5.21–25.16), p = 0.098; %CD4+CD28-CD57+: 14.33 (10.23–21.12) vs 2.65 (1.05–13.11), p < 0.001].

Table: Differences of immunological parameters between LT-HCC and LT-non-HCC at baseline

<table>
<thead>
<tr>
<th>Parameter</th>
<th>LT-HCC (N = 62)</th>
<th>LT-non-HCC (N = 71)</th>
<th>p value*</th>
</tr>
</thead>
<tbody>
<tr>
<td>%CD8+CD28-CD57+</td>
<td>23.98 (17.72–25.86)</td>
<td>10.82 (5.21–25.16)</td>
<td>0.003</td>
</tr>
<tr>
<td>%CD4+CD28-CD57+</td>
<td>14.33 (10.23–21.12)</td>
<td>2.65 (1.05–13.11)</td>
<td>0.087</td>
</tr>
</tbody>
</table>

*Adjusted by age.

Conclusion: Our findings suggest that patients undergoing LT for HCC have a higher immune activation and senescence profile compared to other recipients, possibly representing an additional risk factor for PTM. Moreover, immune activation and senescence may be prognostic factors for PTM occurrence regardless of the cause of transplantation.

SAT319 The crucial role of PARP [poly (ADP-ribose polymerase)] on the post-ischemic liver injury and inflammation

Michtaka Ozaki1, Sanae Haga1, Naoki Morita2. 1National Institute of Advanced Industrial Science and Technology (AIST), Michitaka Ozaki1, Sanae Haga1, Naoki Morita2.

Background and aims: Ischemia/reperfusion (I/R) of liver is an unavoidable event in liver surgery and transplantation, which sometimes causes severe post-operative liver failure/complications. The mechanism of I/R-induced liver injury, however, is complicated so that we have not elucidated yet. I/R-induced ROS, various types of programmed cell death and the following sterile inflammatory reaction seem to be crucial. In the present study, we investigated the roles of PARP [Poly (ADP-ribose) polymerase] on hypoxia/reoxygenation (H/R)-induced, ROS-mediated programmed cell death and inflammation in mouse liver cells and macrophages.

Method: AML12 cells and Raw264.7 cells were used for the experiments as hepatocytes and macrophages, respectively. Cells were cultured in high-glucose DMEM supplemented with 10% FBS. H2O2 were administered directly to the culture medium for oxidative stress. Cellular hypoxic conditions were created and maintained in a chamber by flushing with a 95% N2/5% CO2 gas mixture for 10 min and then sealing the chamber. Following 6 h of hypoxia, cells were reoxygenated by opening the chamber and replacing the hypoxic medium with oxygenated medium. Protein and gene expressions were measured by western blot analysis/capillary-based immunoassay and RT-PCR, respectively. Cell survival and death were determined by plating the cells in the xCELLigence System (Roche) and the LDH release.

Results: H/R-induced cell death was inhibited significantly by PJ34, a specific inhibitor of PARP. Because an oxidative stress is one of the major causes of H/R-induced cell death, we challenged 1 mM H2O2 to AML12 liver cells. H2O2 induced cell death, PAR [Poly (ADP-ribose)] production and nuclear translocation of AIF (apoptosis inducing factor), which were suppressed significantly by the pre-treatment of PJ34. H2O2 also induced Receptor-Interacting Protein (RIP)1/RIP3 binding, which indicates the involvement of necroptosis in H2O2-induced cell death. H2O2-induced RIP1/RIP3 binding was inhibited by PJ34. These facts indicate that H/R and ROS potentially induce parthanatos and necroptosis in hepatocytes. Furthermore, H/R-induced inflammatory reaction (proinflammatory gene expression) was inhibited by PJ34 both in AML12 cells and Raw264.7 cells.

Conclusion: PARP is potentially involved in H/R- and oxidative stress-induced cell death in mouse liver cells, by inducing programmed cell death (parthanatos and necroptosis) and inflammatory reaction.

SAT320 Mitochondrial transplantation attenuates murine in vivo hepatic ischemia/reperfusion injury

Avinash Mukkala1, Raluca Petrut2, Zahra Khan1, Mirjana Jerkic2, Menachem Alenberg3, Shawn Rhind4, Marc Jessche5, Ana Andreazza4, Andras Kapus2, Ori Rotstein1,2, St. Michael’s Hospital, Keenan Research Centre for Biomedical Science, Toronto, Canada; 1University of Toronto, Institute of Medical Science, Toronto, Canada; 2St. Michael’s Hospital, Keenan Research Centre for Biomedical Science, Toronto, Canada; 4University of Toronto, Temerty Faculty of Medicine, Toronto, Canada; 5Defence Research and Development Canada/Recherche et développement pour la défense Canada, Ottawa, Canada; 6University of Toronto, Department of Immunology, Toronto, Canada; 7University of Toronto, Department of Pharmacology and Toxicology, Toronto, Canada; 8University of Toronto, Department of Biochemistry, Toronto, Canada; 9St. Michael’s Hospital, Department of Surgery, Toronto, Canada

Background and aims: Liver ischemia/reperfusion injury (LIRI) is a disease process implicated in organ dysfunction following hepatic surgery, traumatic injuries, and liver transplantation. LIRI causes mitochondrial perturbations which lead to organ death. Stringent mitochondrial quality control is vital in reinstating organ integrity in LIRI. Mitochondrial transplantation (MT) has recently surfaced as a biotherapeutic option in IRI. The effect and mechanism of MT in IRI are poorly characterized. We hypothesized that MT, using mitochondria derived from mouse skeletal muscle tissue, is hepatoprotective following murine LIRI.

Method: We utilized an in vivo murine model of LIRI by occlusion of the hepatic artery leading to the left lobe for 1 h to achieve lobe-specific ischemia. Mitochondria were isolated from hindlimb mouse skeletal muscle tissue by differential filtration followed by characterization for particle size and number, ATP, membrane potential, ultrastructural morphology, and protein purity. Inactivation of mitochondria was conducted using liquid nitrogen (LN2) immersion or incubation at 95°C. Active or inactive mitochondria were intrasplenically injected, to access the portal system, at the start of reperfusion. Mouse livers were reperfused for 2 h followed by sacrifice for blood and liver tissue collection for various molecular/histological analyses.

Results: Isolated active mitochondria (1–3um) retained membrane potential, cristae architecture and morphology, protein purity, and ATP content. LIRI animals had significantly greater circulating AST and ALT compared to sham animals. In addition, LIRI animals had extensive, left lobe-specific liver necrosis, congestion, and vacuolization, when compared to sham animals. Intrasplenic injection of 80 million active mitochondria into LIRI animals, significantly reduced plasma AST and ALT concentrations and normalized histology. Blinded Suzuki scoring of liver histology showed a significant attenuation of congestion, necrosis, and vacuolization as a result of MT in LIRI animals. Interestingly, inactivated mitochondrial particles (LN2 or 95°C) also significantly reduced plasma AST and ALT, albeit to a lesser extent.
a lesser degree. To rule out a confounding “particle effect” of MT, polyethylene beads (1–4μm) were injected and showed no protective effect against LIRI. Treatment with active mitochondria in LIRI animals significantly increased plasma IL-10 and decreased plasma IL-6 compared to control animals.

Conclusion: MT attenuated LIRI regardless of whether injected mitochondria were active or inactive. Future studies will focus on understanding how MT confers protection from LIRI and how their use in clinical scenarios might be optimized. Future avenues of this research include exploring metabolic reprogramming and liver regeneration as potential explanations for the hepatoprotection afforded by MT.

**Viral hepatitis B/D: therapy**

**SAT341**

Bulevirtide treatment of hepatitis D in Germany: multicentre real-world experience

Christopher Dietz¹, Frank Tacke², Caroline Zöllner², Münnever Demir³, Hartmut Schmid³, Christoph Schramm³, Katharina Willwot³, Christian M. Lange⁴, Gerald Denk⁴, Sabine Weber⁴, Christoph Berg⁴, Julia Grotenthaller⁵, Uta Merle⁶, Alexander Olkus⁶, Stefan Zeeuven⁶, Kathrin Sprinzl⁷, Thomas Berg⁸, Johannes Wiegand⁹, Florian van Bömmel⁸, Toni Herta⁸, Katharina Willuweit³, Christian M. Lange⁴, Gerald Denk⁴, Johannes Wiegand⁹, Florian van Bömmel⁸, Toni Herta⁸, Thomas Seufferlein¹⁰, Eugen Zieren¹⁰, Nektarios Dikopoulos¹⁰, Robert Thimme¹⁰, Christoph Neumann-Haefelin¹⁰, Peter Galle¹¹, Martin Sprinz¹¹, Ansgar W. Lohse¹², Julian Schulze zur Wiesch¹², Jan Kempski¹², Andreas Geier¹², Florian P Reiter¹³, Wolf Peter Hofmann¹⁴, Julia Kahlhöfer¹⁵, Benjamin Maasoumy¹⁵, Kersten Port¹, Markus Cornberg¹, Heiner Wedemeyer¹, Katja Deterding¹, ¹Medical High School Hannover, Dept. of Gastroenterology, Hepatology and Endocrinology, Hannover, Germany; ²Charité, Dept. of Hepatology and Gastroenterology, Berlin, Germany; ³University Hospital Essen, Dept. of Gastroenterology, Hepatology and Transplantational Medicine, Essen, Germany; ⁴Ludwig Maximilian University Munich, Dept. of Medicine II, Munich, Germany; ⁵University Tübingen, Medical clinic, Department of Gastroenterology, Hepatology, and Infectology, Tübingen, Germany; ⁶University Heidelberg, Department of Internal Medicine IV, Heidelberg, Germany; ⁷Goethe University Hospital, Internal Medicine Department, Frankfurt am Main; ⁸University Clinic Leipzig, Division of Hepatology, Clinic and Polyclinic for Gastroenterology, Hepatology, Infectiology, and Pneumology, Leipzig, Germany; ⁹University of Ulm, Department of Internal Medicine I, Ulm, Germany; ¹⁰University Medical Center Freiburg, Faculty of Medicine University Freiburg, Department of Medicine II, Freiburg, Germany; ¹¹University Medical Center of the Johannes-Gutenberg University Mainz, Department of Medicine I, Mainz, Germany; ¹²University Medical Center Hamburg-Eppendorf, Department of Medicine, Hamburg, Germany; ¹³University Hospital Würzburg, Dept. of Medicine II, Würzburg, Germany; ¹⁴MVZ for Gastroenterology at Bayerischer Platz Berlin, Berlin; ¹⁵German Center for Infection Research (DZIF), HepNet Study-House der Deutschen Leberstiftung, Hannover

Email: dietz.christopher@mh-hannover.de

Background and aims: Infection with hepatitis D virus (HDV) occurs as coinfection with hepatitis B virus. Chronic hepatitis D is the most debilitating form of viral hepatitis with a high risk of liver cirrhosis and hepatocellular carcinoma (HCC). Bulevirtide (BLV) is the first drug with a conditional approval for the treatment of chronic HDV infection in compensated liver disease. The aim of this project is the characterization of treatment response in terms of viral suppression and improvement of hepatic inflammation in a real-world setting.

Method: We collected anonymised longitudinal observational data from fourteen German centres treating patients with 2 mg of BLV. Individual case data from the participating centres were collected in a standardized data sheet. A paired t-test or Wilcoxon signed rank test was used for comparative data analysis. Analyses were carried out with R Studio. Statistical significance was assumed if p values were below 0.05.

Results: Baseline data was collected from 109 patients. In 103 cases BLV was given in combination with a nucleos (t)idanalogon. Currently, 47 and 26 patients reached treatment week 12 and 24 (Table 1). Elevated transaminases improved by 64 IU/ml at average with 24 cases reaching normal ALT levels (<45 U/l) at week 12. A 2log reduction in viral load was achieved by 4 (week 12) and 11 cases (week 24). Liver cirrhosis was present in 43 cases (FIB-4 > 3.6) with 4 patients being initially decompensated. Observed improvements regarding the amount of ascerles and levels of bilirubin. Hepatic decompensation occurred in two cirrhotic patients. No HCC or other drug-related SAE occurred. Fatigue was the most frequent AE reported (n = 7). A continuous improvement of FIB-4 was noted.

Table: Shown are key characteristics. p values were obtained from paired t-tests or Wilcoxon signed-rank test if medians were compared.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Baseline (n = 109)</th>
<th>Week 12 (n = 47)</th>
<th>Week 24 (n = 26)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Log10 HDV-RNA Median</td>
<td>5.7</td>
<td>4.5 (p &lt; 0.001)</td>
<td>3.5 (p &lt; 0.001)</td>
</tr>
<tr>
<td>2log reduction</td>
<td>/</td>
<td>4/47</td>
<td>11/26</td>
</tr>
<tr>
<td>ALT (U/l) Mean ± SD</td>
<td>53 ± 0.001</td>
<td>116 ± 105</td>
<td>47 (p &lt; 0.001)</td>
</tr>
<tr>
<td>AST (U/l) Mean ± SD</td>
<td>40 ± 0.001</td>
<td>49 ± 17</td>
<td>37 (p &lt; 0.001)</td>
</tr>
<tr>
<td>Albumin (g/l) Mean ± SD</td>
<td>40 ± 0.36</td>
<td>40 ± 6</td>
<td>42 (p &lt; 0.19)</td>
</tr>
<tr>
<td>Bilirubin (µmol/l) Mean ± SD</td>
<td>0.75</td>
<td>17 ± 12</td>
<td>14 (p = 0.83)</td>
</tr>
<tr>
<td>INR Mean ± SD</td>
<td>1.0 ± 0.015</td>
<td>1.0 ± 0.2</td>
<td>1.1 (p = 0.55)</td>
</tr>
<tr>
<td>Platelets (10³/µl) Median</td>
<td>115</td>
<td>115 ± 0.42</td>
<td>159 (p = 0.03)</td>
</tr>
<tr>
<td>Bile salts (µmol/l) (n = 15)</td>
<td>49 ± 49</td>
<td>60 ± 75</td>
<td>49 ± 49 (p &lt; 0.001)</td>
</tr>
</tbody>
</table>

Conclusion: Decreased platelets and a median FIB-4 of 2.8 indicate advanced liver disease and portal hypertension in patients selected for BLV treatment. After 12 weeks of treatment a decline in viral load is accompanied by a significant improvement in hepatic inflammation and FIB-4. Updated results will be presented at the meeting.
SAT342
Challenges with the cascade of HDV care in Mongolia
Enkhrjavt Altangerel1, Nandintsetseg Tsoggerel1, Suvid Batbaatar1, Uyanga Bat-Osor1, 1Academy of Medical Professionals, Department of Research, Mongolia
Email: ajargal8@gmail.com

Background and aims: Hepatitis D infection is highly endemic among individuals with chronic HBV infection in Mongolia. The anti-HDV prevalence among HBsAg-positive individuals, indicating likely HDV/HBV coinfection, ranged from 41% to 67% in the two major seroepidemiological studies. The study aimed to define the challenges within the care cascade among HDV patients.

Method: We conducted the cross-sectional survey designed with the inclusion and exclusion criteria for the selection among the patients diagnosed with a coinfection of HBV and HDV. The questionnaire covered topics of care cascade and linkage to the care. In total, 576 participants enrolled in the survey. Both online and paper modes were used to collect the questionnaire. The collected data was analyzed by SPSS 21.0 software.

Results: 65.0% of the participants were from urban areas. Most of the participants were women (59.8%), and the mean age was 43.57 ± 10.9. The duration of linkage to the specialized doctor varied: the most are within a month (33.3%), within 3–6 months (15.8%), 6–12 months (17.9%) and more than a year (18.8%). More than half of the participants enrolled to fibrosis assessment within a month (35.0%) and within 3–6 months (26.7%) after linked to the specialized care. However, many (34.5%) didn’t attend a specialist’s periodic exam and monitoring service after the fibrosis stage was defined. Except for 22.7% of the participants, all were on the antiviral treatment for HBV, including entecavir (11.1%), TAF (36.4%), and the remaining (29.8%) were on a combination of entecavir and TAF. Almost all participants (97.1%) did not get treatment with Peg-interferon, while only (2.9%) underwent the treatment. Peg-interferon treatment patients had the injection at the hospital (70.6%), Family Health Centers (17.6%) and at home (11.8%). The treatment duration was between one months to 1.6 years. The main reasons for the treatment interruption are combination of two or three of the reasons including an inability to bear the side effects, stock out of the injection, and lack of the money to pay for the injection. At the same time, the doctors recommended the Peg-interferon treatment to only 8.7% of the participants.

Conclusion: The most of patients spent a month and more time for the linkage to the care for HDV patients. The patients experience delays in the further steps of the cascade of care, including defining the fibrosis stage and attending periodic monitoring exams. Most doctors do not recommend Peg-interferon treatment, and very few patients are under the treatment. Side effect impact, poor supply, and high cost for injection are the main reasons for treatment interruption. Antivirals treatment for HBV is well practiced.

SAT343
Safety, tolerability and pharmacokinetics of single ascending doses of ALG-020572, a GalNAc-conjugated antiviral oligonucleotide, in healthy subjects
Edward J Gane1, Man-Fung Yuen2, Christian Schwabe3, Min Wu4, Kha Le2, Jen Rilo4, Kusum Gupta4, Christopher Westland4, Felix Lai4, Meenakshi Venkatraman4, Megan Fitzgerald4, Tse-I Lin4

Method: This is a two-part, double-blind, randomized, placebo-controlled, single- and multiple ascending dose study. In Part 1, cohorts containing 8 healthy subjects, including at least 4 Asians, were randomized to receive a single ascending subcutaneous (SC) dose of ALG-020572 or placebo in a 3:1 ratio. In Part 2, planned cohorts will consist of 8 CHB subjects that are randomized 3:1 to receive multiple ascending SC doses of ALG-020572 or placebo. Safety assessments, viral markers (Part 2) and plasma/urine PK samples are collected throughout the study. Preliminary blinded results from the first 2 cohorts of Part 1 are reported here. Additional available data will be presented at the conference.

Results: In Part 1, the first 2 cohorts of healthy subjects received a single 50 or 150 mg SC dose of ALG-020572 or placebo. Subjects were a mean age of 28 years, 94% male and 50% Asian. ALG-020572 was well tolerated; there were no serious adverse events (AEs) or dose limiting toxicities and all treatment-emergent AEs were mild in severity except one grade 2 injection site tenderness. All treatment-emergent laboratory abnormalities were Grade ≤2. No clinically significant physical examination, vital sign, or ECG abnormalities were reported. Plasma ALG-020572 exposures increased in a slightly greater than dose proportional manner between 50 and 150 mg, with low-to-moderate variability. ALG-020572 showed rapid absorption (tmax – 2hrs), high volume of distribution, high plasma clearance, and low urinary excretion. No differences in safety or PK were observed between Asian and non-Asian subjects. Based on observed exposures and nonclinical studies, ALG-020572 doses ≥150 mg are projected to have antiviral activity in CHB subjects.

Conclusion: ALG-020572 was safe and well tolerated with predictable PK properties when given to healthy subjects as single SC doses of up to 150 mg.
Background and aims: HBV/HDV coinfection is the most aggressive form of chronic viral hepatitis with a high risk for the development of liver cirrhosis and subsequent complications like hepatocellular carcinoma (HCC). In 09/2020 bulevirtide (BLV), a synthetic lipopeptide that blocks HBV/HDV uptake into hepatocytes by binding to the NTCP-receptor, has been approved for the treatment of HDV-related chronic hepatitis in Germany. So far, there is only limited data available on the efficacy of BLV treatment under real-life conditions.

We present our single-centre clinical and virological data on 12 HDV-infected patients with active chronic hepatitis in Germany. So far, there is only limited data available on the efficacy of BLV treatment under real-life conditions. From 11/2020 on, twelve HDV-infected patients with active chronic hepatitis were enrolled. Virological, biochemical and clinical parameters were measured at baseline and at monthly intervals thereafter. Furthermore, we measured liver stiffness by shear wave elastography.

Results: The median age of the 12 patients enrolled (4 female, all HDV-genotype 1) was 42.5. Five patients had compensated liver cirrhosis, ten received NUC-therapy and eight had a history of previous interferon treatment. Mean baseline parameters were: HDV-RNA 597, 000 IU/ml, ALT 117 IU/l, AST 64 IU/l, bile acids 11.5 mmol/l, platelets 160,000/ml, HBsAg 23.074 IU/ml, liver stiffness 10.0 kPa. Of note, shear wave elastography results revealed an improvement of liver stiffness to median values of 9.3 kPa after 3 and 8.1 kPa after 6 months. In total, 9 patients (75%) had improved by at least 1 kPa in liver-stiffness. At the time of final analysis (median treatment duration: 8.5 months), no patient had undetectable HDV RNA, 6 patients (50%) had a normalization of ALT and 4 (33%) had reached a combined response of ALT normalization and ≥2 log IU/ml HDV decrease. Mean values of viral loads changed to HDV-RNA 27, 600 IU/ml, bile acids 29 mmol/l, ALT 42 U/l and AST 29 U/l. Treatment was terminated for two patients, one because of non-response at week 48, and one for development of HCC.

Conclusion: Among Asian patients with EOT HBsAg levels ≤ 100 IU/ml, HBV genotype C, age and lower HBsAg and HBcrAg levels are associated with a higher probability of HBsAg clearance.

SAT345
Improvement of liver-stiffness after 6 months of therapy: real-life data for HBV/HDV co-infected patients treated with bulevirtide

Alexander Killer1, Mahyar Ghavemi1, Gliga Smaranda1, Johannes Bode2, Bjørn Jensen1, Jan Köhler1, Andreas Walker2, Nadine Lübbe2, Jörg Timm2, Tom Lüdde1, Hans Bock1, 1Uniklinik Düsseldorf, Klinik für Gastroenterologie, Hepatologie, Infektiologie, Düsseldorf, Germany; 2Uniklinik Düsseldorf, Institut für Virologie, Düsseldorf, Germany

Email: Alexander.Killer@med.uni-duesseldorf.de

Background and aims: HBV/HDV coinfection is the most aggressive form of chronic viral hepatitis with a high risk for the development of liver cirrhosis and subsequent complications like hepatocellular carcinoma (HCC). In 09/2020 bulevirtide (BLV), a synthetic lipopeptide that blocks HBV/HDV uptake into hepatocytes by binding to the NTCP-receptor, has been approved for the treatment of HDV-related chronic hepatitis in Germany. So far, there is only limited data available on the efficacy of BLV treatment under real-life conditions. From 11/2020 on, twelve HDV-infected patients with active chronic hepatitis were enrolled. Virological, biochemical and clinical parameters were measured at baseline and at monthly intervals thereafter. Furthermore, we measured liver stiffness by shear wave elastography.

Results: The median age of the 12 patients enrolled (4 female, all HDV-genotype 1) was 42.5. Five patients had compensated liver cirrhosis, ten received NUC-therapy and eight had a history of previous interferon treatment. Mean baseline parameters were: HDV-RNA 597, 000 IU/ml, ALT 117 IU/l, AST 64 IU/l, bile acids 11.5 mmol/l, platelets 160,000/ml, HBsAg 23.074 IU/ml, liver stiffness 10.0 kPa. Of note, shear wave elastography results revealed an improvement of liver stiffness to median values of 9.3 kPa after 3 and 8.1 kPa after 6 months. In total, 9 patients (75%) had improved by at least 1 kPa in liver-stiffness. At the time of final analysis (median treatment duration: 8.5 months), no patient had undetectable HDV RNA, 6 patients (50%) had a normalization of ALT and 4 (33%) had reached a combined response of ALT normalization and ≥2 log IU/ml HDV decrease. Mean values of viral loads changed to HDV-RNA 27, 600 IU/ml, bile acids 29 mmol/l, ALT 42 U/l and AST 29 U/l. Treatment was terminated for two patients, one because of non-response at week 48, and one for development of HCC.

Conclusion: Among Asian patients with EOT HBsAg levels ≤ 100 IU/ml, HBV genotype C, age and lower HBsAg and HBcrAg levels are associated with a higher probability of HBsAg clearance.

SAT346
Role of plasmatic and urinary TDF and TAF concentration in a cohort of HBV chronic hepatitis patients

Giacomo Stroffolini1, Valentina Dodaro1, Lucio Boglione2, Giuseppe Cariti1, Giovanni Di Perri1, 1Amedeo di Savoia Hospital, University of Torino, Medical sciences, Italy; 2University of Piemonte Orientale, Italy

Email: giacomo.stroffolini@unito.it

Background and aims: Tenofovir disoproxil fumarate (TDF) is the first-line therapy for chronic HBV infection. Currently, the proximal tubular kidney toxicity of the TDF is debated. Recently, tenofovir alafenamide fumarate (TAF) has been approved; virological and serological effectiveness are equal to TDF, but with lower kidney excretion and tubular toxicity. TAF is currently available for patients over sixty, pretreated with TDF or other NAs, with bone or kidney impairment; however, which categories of patients can benefit the most switching from TDF to TAF is still unclear.

Method: A cross-sectional study was conducted between November 2019 and January 2021. 42 patients were included (n = 42). At the baseline 17 patients who met the eligibility criteria were switched from TDF to TAF (n = 17), while the others continued treatment with TDF (n = 25). Patients were evaluated at baseline and after six months. The plasmatic and urinary dosage was performed for 16 patients treated with TAF (n = 16) and for 25 patients treated with TDF (n = 25).

Results: Patients treated with TDF were significantly younger than patients treated with TAF (38 vs 67 years). The plasmatic concentration of TAF was significantly lower for genotype E (27 vs 80 ng/ml) and higher for genotype C (114 vs 36.5 ng/ml) than other genotypes. Higher plasmatic concentration of TAF was found in patients whose liver stiffness was more than 9 kPa (8.20 vs 13.00 mg/ml, see figure). In the TAF group eGFR increased and urinary drug concentration reduced significantly compared to the TDF group (+9 vs 0 ml/min and − 0.5 vs +3 ng/ml). eGFR decreased and urinary TDF increased significantly for ADV-pretreated TDF patients compared to not-ADV-pretreated TDF patients (+9 vs +2 ml/min and +9 ng/ml vs +1 ng/ml). The increase of eGFR and the reduction of excreted urinary TAF was well-tolerated and led to a biochemical and virological response in the majority of patients. Treatment led to an early and marked decrease of liver-stiffness, suggesting improvement in liver fibrosis in a setting of chronic viral infection. Therefore, an improvement in liver-stiffness could be a way to predict a clinically relevant response and benefit for patients treated with BLV, warranting additional studies in larger patient cohorts.

Conclusion: BLV was well-tolerated and led to a biochemical and virological response in the majority of patients. Treatment led to an early and marked decrease of liver-stiffness, suggesting improvement in liver fibrosis in a setting of chronic viral infection. Therefore, an improvement in liver-stiffness could be a way to predict a clinically relevant response and benefit for patients treated with BLV, warranting additional studies in larger patient cohorts.
pretreatment with ADV for TDF patients (p < 0.005). In the multivariate analysis only eGFR and pretreatment with ADV for TDF patients resulted significant and directly proportional to the variation of urinary tenofovir concentration (<0.005).

Conclusion: According to these results, ADV-pretreated patients have a benefit from switching TDF to TAF. The correlation of genotype with plasmatic TAF concentration suggests a possible key role of TDF/TAF transporter polymorphisms. Finally, further studies are needed for a better understanding of TAF pharmacokinetics in relation to liver stiffness.

SAT347
Model to predict on-treatment restoration of functional HBV-specific CD8+ cell response foresees off-treatment HBV control in eAg-negative chronic hepatitis B
Julia Peña Asensio1,2, Henar Calvo1, Joaquin Miquel1, Eduardo Sanz de Villalobos1, Alejandro González Praterius1, Miguel Torralba1,2, Juan Ramón Larrubia1,2, 1Guadalajara University Hospital, Translational Hepatology Unit, Guadalajara, Spain; 2University of Alcala, Department of Biology of Systems, Alcala de Henares, Spain; 3University of Alcala, Department of Medicine and Clinical Specialties, Alcala de Henares, Spain
Email: hilda@juliaroma@gmail.com

Background and aims: Hepatitis B virus (HBV)-specific CD8+ cell response restoration during nucleos (t)ide analogue (NUC) treatment could lead to off-treatment HBV control in e-antigen-negative chronic hepatitis B (CHBe (-)). To predict this response with variables involved in T-cell exhaustion for use as treatment stopping tool.

Method: In NUC treated CHBe (-) patients, we considered a functional cure (HBsAg loss) or off-treatment sustained viral control. The immunological mechanisms that determine clinical outcome after treatment stop remain poorly understood, and predictors of clinical outcomes are lacking. We hypothesized that markers of systemic inflammation could identify key inflammatory pathways that are associated with and can predict clinical outcome after NA therapy cessation.

Method: Plasma cyto- and chemokines from 57 patients from the ongoing Nuc-Stop study were analyzed by Bio-Plex Pro Human Cytokine 27-plex Assay at baseline and three months after stopping NUC therapy. Statistical significance (p < 0.05) was determined using Kruskal-Wallis tests or one-way ANOVA followed by Bonferroni post-hoc tests.

Results: After three months, there was a significant increase in interferon gamma-induced protein 10 (IP-10) in patients with clinical relapse who restarted treatment (p = 0.001) (Figure). This group also had a stronger ALT flare compared with those who had a clinical relapse without restart (median peak ALT 216 vs. 103 U/L, p = 0.025). A significant, but less pronounced, increase in tumor necrosis factor (TNF) was observed in the same group (p = 0.010) (Figure). None of the other cyto- or chemokines were associated with clinical outcome at three months.

Conclusion: Short-term low-level antigen exposure and early long-term NUC treatment influence the restoration of a functional HBV-specific CD8+ cell response. Based on these predictors, high likelihood of detecting this response at treatment withdrawal associates with off-treatment HBV control and HBsAg decline and loss.

SAT348
Antiviral treatment cessation in HBeAg negative chronic hepatitis B: clinical outcome is associated with increase in specific pro-inflammatory cytokines
Marte Holmberg1, Dag Henrik Reikvam2, Olav Dalgard3, Hans Christian Dalsbotten Aas2, Ellen Samuelsen1, Niklas Björkström4, Asgeir Johannessen1.1Vestfold Hospital Trust, Tønsberg, Norway; 2Oslo University Hospital Ullevål, Oslo, Norway; 3Akershus University Hospital, Lørenskog, Norway; 4Karolinska University Hospital, Center for Infectious Medicine, Stockholm, Sweden
Email: mart.e.holmberg@online.no

Background and aims: Patients with HBeAg negative chronic hepatitis B may experience an immune response after stopping nucleos (t)ide analogue (NA) therapy, which may potentially trigger functional cure (HBsAg loss) or off-therapy sustained viral control. The immunological mechanisms that determine clinical outcome after treatment stop remain poorly understood, and predictors of clinical outcomes are lacking. We hypothesized that markers of systemic inflammation could identify key inflammatory pathways that are associated with and can predict clinical outcome after NA therapy cessation.

Method: Plasma cytokines and chemokines from 57 patients from the ongoing Nuc-Stop study were analyzed by Bio-Plex Pro Human Cytokine 27-plex Assay at baseline and three months after stopping NA therapy. All patients were HBeAg negative, non-cirrhotic, and virally suppressed for at least 24 months prior to stopping NA therapy. Outcome at three months was classified as immune control (HBV DNA <2000 IU/ml and ALT <2x baseline), viral relapse (HBV DNA >2000 IU/ml and ALT <2x baseline), clinical relapse (HBV DNA >2000 IU/ml and ALT >2x baseline), or clinical relapse with restart of treatment. Statistical significance (p <0.05) was determined using Kruskal-Wallis tests or one-way ANOVA followed by Bonferroni post-hoc tests.

Results: After three months, there was a significant increase in interferon gamma-induced protein 10 (IP-10) in patients with clinical relapse who restarted treatment (p = 0.001) (Figure). This group also had a stronger ALT flare compared with those who had a clinical relapse without restart (median peak ALT 216 vs. 103 U/L, p = 0.025). A significant, but less pronounced, increase in tumor necrosis factor (TNF) was observed in the same group (p = 0.010) (Figure). None of the other cyto- or chemokines were associated with clinical outcome at three months.
Background and aims: Data on long-term tenofovir alafenamide (TAF) therapy for pregnant women with active chronic hepatitis B (CHB) are lacking. The aim of this study was to investigate the safety and effectiveness of TAF (TAF) therapy for pregnant women with active chronic hepatitis B.

Method: Pregnant women with active CHB treated with TAF and tenofovir disoproxil fumarate (TDF) were enrolled in this multicenter (a total of 11 hospitals) prospective study, and infants received standard immunoprophylaxis. The primary outcomes were rates of adverse (safety) events in pregnant women and defects in infants and fetuses. The secondary outcomes were virological responses in pregnant women, infants’ safety, hepatitis B surface antigen (HBsAg) status, and growth conditions. Participants were assessed for eligibility from January 1, 2019, to March 31, 2020. The pregnant women and their infants were followed until at least 6 months after delivery and 7 months of age, respectively. The final follow-up date was the November 15, 2021.

Results: One hundred three and 104 pregnant women were enrolled, and 102 and 104 infants were born in the TAF and TDF groups, respectively. In the TAF group, 82 (79.6%) pregnant women were hepatitis B e antigen (HBeAg) positive, and the mean age, gestational age, alanine aminotransferase level, and viral loads at treatment initiation were 29.3 years, 1.3 weeks, 122.2 IU/L, and 5.1 log10 IU/ml, respectively. TAF was well tolerated, and the most common adverse event was nausea (30.1%) during a mean of two years (101.1 ± 24.3 weeks) of treatment. Notably, 1 (1.0%) TAF-treated pregnant woman exposed to agricultural chemicals during early pregnancy who initiated TAF from 12 weeks plus 2 days of gestation underwent induced abortion at 23 weeks plus 4 days of pregnancy due to the diagnosis of cleft lip and palate for the fetus at 22 weeks of gestation, this fetus was regarded as a congenital defect (most likely not related to TAF because the developmental processes of the lip and palate are completed by 6–10 weeks of embryogenesis). No infants in either group had birth defects. In the TAF group, the HBeAg seroconversion rate of mothers was 20.7% (17/82) at postpartum month 6, infants had normal growth parameters (weight, height, and head circumference) compared with Chinese and WHO standards, and no infants were positive for HBsAg at 7 months of age. As of November 15, 2021, 40 TAF-exposed mother–infant dyads completed the postpartum month 18 follow-up, the cumulative HBeAg seroconversion rate is 28.0% (23/82), and all infants have normal growth parameters compared with Chinese and WHO standards. The TDF group had comparable baseline characteristics, and safety and effectiveness profiles during therapy.

Conclusion: Clinical relapse requiring restart of antiviral treatment after NA cessation was associated with specific increase in IP-10 and TNF.

SAT349
Tenofovir alafenamide for pregnant Chinese women with active chronic hepatitis B: a multicenter, prospective, real-world study
Qing-Lei Zeng1, Hongxu Zhang2, Ji-Yuan Zhang3, Shuo Huang1, Wei-Zhe Li1, Guangming Li4, Ying-Hua Feng5, Guofan Zhang6, Jiang-Hai Xu7, Wan-Bao Lin8, Guang-Hua Xu9, Guoqiang Zhang10, Yan-Li Zeng11, Zu-Jiang Yu1, Pu-Sheng Wang1. 1The First Affiliated Hospital of Zhengzhou University, Department of Infectious Diseases and Hepatology, Zhengzhou, China; 2Luoyang Central Hospital, Department of Infectious Diseases, China; 3The Fifth Medical Center of Chinese PLA General Hospital, Treatment and Research Center for Infectious Diseases, Beijing, China; 4The Sixth People’s Hospital of Zhengzhou City, Department of Hepatology, China; 5The Sixth People’s Hospital of Kaifeng City, Department of Hepatology, China; 6The First Affiliated Hospital of Nanyang Medical College, Department of Infectious Diseases, China; 7The Fifth People’s Hospital of Anyang City, Department of Hepatology, China; 8Xinyang Central Hospital, Department of Infectious Diseases, China; 9The Affiliated Hospital of Yan’an University, Department of Infectious Diseases, China; 10Luoyang Central Hospital, Department of Infectious Diseases, China; 11Henan Provincial People’s Hospital, Department of Infectious Diseases, China
Email: zengqinglei2009@163.com

Background and aims: Data on long-term tenofovir alafenamide (TAF) therapy for pregnant women with active chronic hepatitis B (CHB, immune clearance and reactivation phases) are lacking. The primary aim of this study was to investigate the safety and effectiveness of TAF (TAF) therapy for pregnant women with active chronic hepatitis B (CHB, immune clearance and reactivation phases) are lacking. The secondary outcomes were virological responses in pregnant women, infants’ safety, hepatitis B surface antigen (HBsAg) status, and growth conditions. Participants were assessed for eligibility from January 1, 2019, to March 31, 2020. The pregnant women and their infants were followed until at least 6 months after initiation were 29.3 years, 1.3 weeks, 122.2 U/L, and 5.1 log10 IU/ml, respectively. TAF was well tolerated, and the most common adverse

Conclusion: TAF administered throughout or beginning in early pregnancy is generally safe and effective for pregnant women with active CHB and their infants.

SAT350
Suboptimal virological response to antiviral therapy in chronic hepatitis B as an independent predictor for occurrence of HCC and development of severe liver events
Chau-Ting Yeh1, Chao-Wei Hsu1. 1Chang Gung Memorial Hospital, Liver Research Center, Taoyuan, Taiwan
Email: chautingy@gmail.com

Background and aims: Although several potent antiviral drugs against chronic hepatitis B have been available worldwide with satisfactory virological suppression effect, incomplete virological suppression or suboptimal virological response can occur in a substantial proportion of patients. The definitions of suboptimal virological response varied among different international guidelines in terms of the remaining virological levels and the length of treatment periods. The suggested managements for patients experiencing suboptimal virological responses also varied, from continuation of the present antiviral drugs, switching to a more potent drug, to combination of two or more potent drugs. The long-term outcomes of these patients have never been interrogated.

Method: We retrospectively included 443 patients treated by entecavir in the Liver Clinic, Chang Gung Memorial Hospital, Taiwan, from 2008 to 2013. The HBV-DNA levels were assessed 6 months, 1 year, 2 years and 3 years after initiation of treatment. Suboptimal virological responses were defined as HBV-DNA levels above quantitative limit by Roche TaqMan Assay (>20 IU/ml) after the aforementioned treatment periods. The time-to-development of hepato cellular carcinoma (HCC) as well as the time-to-development of severe liver events (HCC or liver failure related death) were correlated with suboptimal responses and other clinical/virological factors. HBV X genes were sequenced from patients developing HCC.
Cell-based experiments were conducted to understand whether the HBV X mutants enhanced cccDNA accumulation.

Results: During the median follow-up period of 69 (range, 4 to 110) months, 6 patients developed HCC and 20 patients developed severe liver events. Kaplan-Meier analysis showed that suboptimal virological response detected at 6 months after treatment was an independent factor to predict HCC occurrence (p < 0.001). Univariate and Multivariate Cox proportion hazard ratio analysis showed that suboptimal virological response detected at 6 months after treatment was an independent factor to predict development of severe liver events (unadjusted p = 0.006; adjusted p = 0.001). Novel HBV X mutations were identified in 5 of the 6 patients developing HCC during the suboptimal response period. These HBV X mutants were capable of enhancing cccDNA accumulation in HCC cells.

Conclusion: Suboptimal response detected at 6 months after antiviral treatment by entecavir was an independent predictor for HCC occurrence and development of severe liver events. Novel HBV X mutations could be selected during the period of suboptimal virological response and these HBV X mutants enhanced cccDNA accumulation in HCC cells.

SAT351
Integrated efficacy analysis of 24-week data from two phase 2 and one phase 3 clinical trials of bulevirtide monotherapy given at 2 mg or 10 mg dose level for treatment of chronic hepatitis delta

Pietro Lampertico1,2, Soo Aleman3, Antje Blank4, Pavel Bogomolov5, Vladimir Chulanov6, Nina Mamonova6, Morozov Viacheslav7, Olga Sagalova8, Tatyana Stepanova9, Vithika Suri10, Markus Cornberg11, Maurizia Brunetto12,13, Heiner Wedemeyer11.

Background and aims: Bulevirtide (BLV) is a novel first-in-class entry analogue therapy; mean (SD) HDV RNA was 5.2 (1.33) log10 IU/ml and mean (SD) ALT was 107 (70.7) U/L. At Week 24, the combined response was achieved by 31.5% and 32.6% of patients in the BLV 2 mg and 10 mg groups, respectively. While the viral response rate was numerically lower in the BLV 2 mg group than in the BLV 10 mg group (53.3% and 71.6%), rates of ALT normalization were numerically higher for those treated with BLV 2 mg vs 10 mg (51.1% and 42.1%, respectively). For all efficacy end points, response rates were higher in the BLV groups compared to the Control or SOC groups.

Method: A total of 281 patients with CHD without cirrhosis or with compensated cirrhosis were included in this pooled analysis including 92 and 95 patients treated with BLV at 2 mg or 10 mg given s.c. once daily, respectively, compared with 79 receiving no active anti-HDV treatment (Control) during the analysis period, and 15 patients treated with Peginterferon alfa (Peg-IFNα), the current standard of care (SOC) which is not approved for CHD. The primary end point assessed at week 24 was the combined response of undetectable HDV RNA or decrease by ≥2 log10 IU/ml from baseline and ALT normalization; additional end points included viral response (undetectable HDV RNA or decline by ≥2 log10 IU/ml), ALT normalization and change in HDV RNA levels.

Results: At baseline, demographics of all groups were well balanced. Characteristics of the BLV 2 mg group included: mean (SD) age 42 (9.0) years, 60.9% males, 83.7% White, 44.6% with compensated cirrhosis, 96.7% with HDV genotype 1, 64.1% were on nucleos (t)ide analogues therapy; mean (SD) HDV RNA was 5.2 (1.33) log10 IU/ml and mean (SD) ALT was 107 (70.7) U/L. At Week 24, the combined response was achieved by 31.5% and 32.6% of patients in the BLV 2 mg and 10 mg groups, respectively. While the viral response rate was numerically lower in the BLV 2 mg group than in the BLV 10 mg group (53.3% and 71.6%), rates of ALT normalization were numerically higher for those treated with BLV 2 mg vs 10 mg (51.1% and 42.1%, respectively). For all efficacy end points, response rates were higher in the BLV groups compared to the Control or SOC groups.

Conclusion: In this integrated efficacy analysis of 24-week data from 281 patients, the combined response rates were comparable in the BLV 2 mg and BLV 10 mg groups; treatment with BLV was better than control or SOC groups. These results provide additional support for the use of BLV 2 mg once daily for treatment of compensated CHD.
SAT352
Integrated safety analysis of 24-week data from three phase 2 and one phase 3 clinical trials of bulevirtide monotherapy given at 2 mg and 10 mg dose level for treatment of chronic hepatitis delta
Pietro Lampertico1,2, Soo Aleman3, Tarik Asselah4, Marc Bourliere5, Adrian Strienu-Cercel6, Pavel Bogomolov7, Morozov Viacheslav8, Tatyana Stepanova9, Stefan Lazar10, Vithika Suri11, Dmitry Manuilov11, Lei Ye11, John F. Flaherty11, Anu Osinusi11, Maurizia Brunetto12,13, Heiner Wedemeyer14,15, Foundation IRCCS Ca’ Granda Ospedale Maggiore Policlinico, Division of Gastroenterology and Hepatology, Milan, Italy; 2CRC “A. M. and A. Migliavacca” Center for Liver Disease, University of Milan, Department of Pathophysiology and Transplantation, Milan, Italy; 3Karolinska University Hospital Karolinska Institutet, Department of Infectious Diseases, Stockholm, Sweden; 4Hôpital Beaujon APHP, Université de Paris, INSERM, Clichy, France; 5Hôpital Saint Joseph Marseille, Marseille, France; 6Matei Bals National Institute of Infectious Diseases, Bucharest, Romania; 7State budgetary institution of health care of Moscow region “Moscow regional research clinical institute after M.F. Vladimirsky”, Moscow, Russia; 8LLC Medical Company “Hepatologist”, Samara, Russian Federation; 9Limited liability company “Clinic of Modern Medicine,” Moscow, Russian Federation; 10Dr. Victor Babes Foundation-Infectious and Tropical Diseases Hospital, Bucharest, Romania; 11Gilead Sciences, Foster City, United States; 12University Hospital of Pisa, Hepatology Unit, Reference Center of the Tuscany Region for Chronic Liver Disease and Cancer, Pisa, Italy; 13University of Pisa, Department of Clinical and Experimental Medicine, Pisa, Italy; 14Medizinische Hochschule Hannover, Klinik für Gastroenterologie, Hepatologie und Endokrinologie, Hannover, Germany.

Method: A total of 355 patients with CHD were included in this pooled analysis: 92 and 145 patients treated with BLV alone at 2 mg or 10 mg given subcutaneously (s.c.) once daily, respectively, compared with 79 receiving no active anti-HDV treatment (Control) during the analysis period, and 39 patients treated with Peginterferon alpha (Peg-IFNα), the current standard of care (SOC) which is not approved for CHD. The assessed safety parameters included graded adverse events (AE) and laboratory abnormalities.

Results: At baseline, demographics of all groups were well balanced. Characteristics of the BLV 2 mg group included: mean (SD) age 42 (9.0) years, 60.9% males, 83.7% White, 44.6% with compensated cirrhosis, 96.7% with HDV genotype 1, 51.1% were Interferon experienced; mean (SD) HDV RNA was 5.2 (1.33) log10 IU/ml and mean (SD) ALT was 107 (70.7) U/L. By Week 24, the overall incidence of participants experiencing AEs was similar in BLV 2 mg and BLV 10 mg groups at 67.4% and 73.8%, respectively, compared to rates of 50% and 56%, respectively, in the Peg-IFNα group. Most AEs were mild or moderate in severity. Asymptomatic dose-dependent increase in serum bile acids is expected with BLV treatment based on its mode of action. Injection site reactions, considered as AEs of interest based on daily s.c. BLV administration mode, were more common in the BLV 10 mg group compared to 2 mg.

SAT353
Virologic response to bulevirtide is delayed in cirrhotic HDV patients with clinically significant portal hypertension
Mathias Jaehs1,2, Caroline Schwarz1, Marlene Panzer1, Lukas Hartl1,2, Simona Bota1,2, Petra Mund1, Albert F Stättermayer1,1, Ivo Grazier1,2, Stephan Aberle1, Michael Gschwantler1, Heinz Zoller1, Michael Trauner1, Mattias Mandorfer3, Peter Ferenci1, Thomas Reiberger1,2,3, Medical University of Vienna, Division of Gastroenterology and Hepatology, Department of Internal Medicine III, Vienna, Austria; 4Medical University of Vienna, Vienna Hepatic Hemodynamic Lab, Division of Gastroenterology and Hepatology, Department of Internal Medicine IV, Vienna, Austria; 5Klinik Ottakring, Division of Gastroenterology and Hepatology, Department of Internal Medicine, Vienna, Austria; 6Medical University of Innsbruck, Department of Internal Medicine I, Innsbruck, Austria; 7Klinikum Klagenfurt Wörthersee, Department of Internal Medicine and Gastroenterology, Hepatology, Endocrinology, Rheumatology and Nephrology, Klagenfurt; 8Landeskrankenhaus Hall, Department of Internal Medicine, Hall in Tirol; 9Medical University of Vienna, Center for Virology, Wien, Austria.

Method: The response to BLV therapy was assessed in HDV-related ACLD patients with evidence for CSPH, i.e., liver stiffness measurement (LSM) values ≥20 kPa by vibration-controlled transient elastography (VCTE), as compared to patients without evidence for CSPH.

Results: Twenty-one chronic HDV patients (median age: 47.6 years, sex: 10 male/11 female, baseline HDV-RNA: 100 to 2100000 copies/ml, HBV-DNA suppressed in all patients by NA therapy), were treated with BLV for ≥24 weeks and underwent pre-treatment VCTE-LSM. Median pre-treatment VCTE-LSM was 17.2 kPa (range: 5.4–48.0 kPa), and seven patients (33.3%) had CSPH by VCTE-LSM ≥20 kPa, further evidenced by thrombocytopenia (85.7%), splenomegaly (85.7%), or varices (66.7%). ALT levels ranged from 22 to 132 U/L in CSPH patients with 5 out of 7 showing ALT ≥50 U/L. At week 24, virological response (VR, defined by ≥2-log10 decrease or undetectable HDV-RNA) was achieved by only one CSPH patient (14.3%), while five patients (71.4%) showed partial response, i.e. any HDV-RNA decrease (range: –0.63 to –1.77 log10); one patient experienced even an HDV-RNA increase (+0.72 log10). In the 14 HDV patients without evidence for CSPH, seven (50.0%) patients achieved VR at W24, partial response was seen in 6 (42.9%) and one patient showed an increase in HDV-RNA.
Interestingly, five (71.4%) CSPH patients achieved normal ALT levels at W24, as compared to 12 out of 14 (85.7%) non-CSPH patients. Four HDV-ACLD patients with CSPH have already reached W48; two (50.0%) achieved HDV-RNA undetectability and all (100%) showed normal ALT levels.

Of note, four out of seven CSPH patients underwent a follow-up VCTE-LSM after one year of BLV therapy (range 40–52 weeks), and three (75.0%) showed VCTE-LSM decreases of ≥20%, two patients even achieved a reduction to a final VCTE-LSM ≤20kPa (i.e. a clinically relevant decrease as by Baveno VII consensus).

BLV treatment in HDV-CSPH was well tolerated, and no significant adverse events were observed despite substantial increases in serum bile acids levels (median +82% at 4 weeks; maximum levels: 38.0–208.6 µmol/L).

Conclusion: Virologic response to BLV in cirrhotic HDV patients with CSPH seems delayed, however, a high rate of decreases in VCTE-LSM suggests a treatment benefit. BLV is safe in patients with CSPH. Data on changes in HVPG—as a potential surrogate for treatment efficacy—are awaited.

SAT354 Response-guided long-term treatment of chronic hepatitis D patients with bulevirtide—Results of a “real world study”

Mathias Jachs1, Caroline Schwarz2, Marlene Panzer3, Teresa Binter1, Elmar Aigner4, Stephan Aberle5, Albert Stättermayer1, Ivo Graziaedi1, Petra Munda1, Heinz Zoller6, Michael Gschwantler2.

Background and aims: Bulevirtide (BLV) blocks hepatic uptake of the hepatitis D Virus (HDV) via the sodium/bile acid cotransporter NTCP. BLV was conditionally approved by EMA, but the optimal treatment duration is unknown. The aim of this real-world study was to define useful efficacy and futility endpoints.

Method: BLV was provided by MyrPharma (Leipzig/Germany) until 8/2020 and was subsequently prescribed and dosed at the discretion of the investigator. Based on the magnitude of HDV-RNA decline at week 24 patients were classified as responder (≥2log drop), partial responder (>1.0–<2log drop), or non-responder (<1log drop).

Results: 23 patients (m: 10/f:13; mean age: 47.9 years, cirrhosis: n = 15; median ALT:71 IU/ml (range 21–341); HDV-RNA: 9.5 × 10^5 [range:10–2.1 × 10^7] copies/ml) received BLV (2 mg/d in n = 21; 10 mg/day in n = 2). 21 patients (84.8%) were on concomitant NUCs (ETV n = 3; TDF n = 16; TAF n = 2); 19 were previous Peginterferon-alfa2a (PEGIFN) non-responders. 22 patients completed at least ≥24 weeks of BLV treatment (range: 24–130 weeks), one dropped out at week 8.

Twelve patients (54.5%) were classified as BLV responders: in 2 treatment was terminated as HDV-RNA was undetectable for >6 months after 63 and 130 weeks, respectively. Both became HDV-RNA positive again after 60 and 4 weeks, respectively; in the latter BLV treatment was resumed. One patient underwent liver transplantation at week 25 and one was lost to follow-up after week 26. In 2 patients PEGIFN was added after 39 and 48 weeks, respectively, because of no further decline or re-increase of HDV-RNA. Thus, 7 are still on BLV monotherapy.

Four partial responders (18.2%) are still on BLV monotherapy (24–29 weeks).

Six patients (31.8%) were non-responders. (PEGIFN) was added in 5 except for one who dropped out after 24 weeks. In 4 patients HDV-RNA courses under BLV+PEGIFN are available showing a rapid decline of HDV-RNA within 12 weeks (-0, 97; −1.19; −1.23; and −1.54 log-drop, respectively).

ALT levels normalized in 14/22 (63%) at week 24 and 8/10 (80%) at week 48, respectively. Treatment was well tolerated, bile acid levels increased without pruritus. HBsAg levels remained unchanged during BLV therapy.

Conclusion: Long-term BLV is safe and effectively decreases HDV-RNA and ALT. Responders likely require long-term treatment whereas in patients without virologic response response, the addition of PEGIFN seems to be of value. Our data indicate the need for an individualized approach for HDV treatment with BLV.

SAT355 HBV RNA levels are associated with virological response to treatment with pegylated interferon alpha in patients with chronic hepatitis D virus infection

Lisa Sandmann1, Birgit Bremer1, Cihan Yurdadaydın2,3, Katja Detertding1, Michael P. Manns1,4, Markus Cornberg3,4,5,6, Heiner Wedemeyer1,4,6, Benjamin Maasoumy1,4,5, Hannover Medical School, Department of Gastroenterology, Hepatology and Endocrinology, Hannover, Germany; 2University of Ankara Medical School, Department of Gastroenterology, Istanbul, Turkey; 3Koc University Medical School, Department of Gastroenterology and Hepatology, Istanbul, Turkey; 4German Center for Infection Research (DZIF), Partner Site Hannover-Braunschweig, Germany; 5Centre for Individualised Infection Medicine (CiIM), Helmholtz Centre for Infection Research, Germany; 6German Center for Infection Research (DZIF), Partner Site HepNet Study House, Hannover, Germany

Background and aims: Chronic hepatitis D virus (HDV) infection causes severe liver disease with rapid progression to liver cirrhosis. Treatment with pegylated interferon alpha (pegIFNα) leads to viral response in approximately 25%, including patients with long-term virological control. Since IFN treatment is accompanied by severe side effects, on-treatment markers to identify patients with high chances of virological response are needed. HBV RNA, which reflects HBV cccDNA activity, may serve as a novel marker during antiviral treatment.

Method: The HIDIT-II study included 120 HBV/HDV co-infected patients. Patients were treated for 96 weeks with pegIFNα and either tenofovir or placebo. 99 patients with HBV RNA results 24 weeks after end of treatment (FU24) were included in this analysis, of whom 32 patients (32.3%) had undetectable HDV RNA at FU24. HBV RNA was measured at baseline, week 12, 24, 48, 96 and FU24 using the Roche Cobas 6800 system (LLOQ 10 cp/ml). Additional virological parameters (HBV DNA, quantitative HBsAg, HBCrAg and HDV RNA) were measured by appropriate assays (Lumipulse® G (Fujirebio-Europe))
for HBcAg. Roche Cobas TaqMan system with an inhouse assay for HDV RNA).

**Results:** At baseline, mean HBV RNA levels were 1.71 ± 1.18 log cp/ml and HBV RNA levels were undetectable in 68.8% of patients. During treatment, mean HBV RNA levels did not differ between patients receiving either tenofovir or placebo. When separating between treatment responders (HDV RNA negative at FU24) and non-responders, mean levels of HBV RNA were significantly lower in responders at treatment week 24, 48 and end of treatment. Accordingly, the proportion of patients with undetectable HBV RNA was significantly higher in treatment responders at week 24 and 48 (79% vs. 50%, p = 0.0031; 75% vs. 50%, p = 0.0276) (Figure). However, HBV RNA levels of patients with viral relapse did not differ from those with maintained response at the end of treatment. No correlation between HBV RNA levels and HBV DNA, qHBsAg, HBcAg or HDV RNA levels was detected at any time-point during the study. Interestingly, only 36% of patients with undetectable HBV RNA showed undetectable HBcAg levels at baseline, whereas all but two patients with undetectable HBcAg were HBV RNA negative (n = 24/26, 92%).

**Conclusion:** On-treatment HBV RNA levels differ significantly between responders and non-responders. Along with other virological parameters, HBV RNA could be a supportive marker to identify patients benefiting from treatment with pegIFNα. However, overall HBV RNA levels were low throughout the study population.

**SAT356**

Management of chronic hepatitis B virus infection within a large integrated health care setting: treatment patterns among kaiser permanente members in southern california, 2008–2019

Deborah Malden1,2, Prabhu Gounder3, Katherine Oh1, Amandeep Sahota4, Robert Wong5, Amit Chitnis5, Theresa Im1, Vennis Hong1, Ana Florea6, Sara Tartof5,7 Kaiser Permanent Southern California Department of Research and Evaluation, Pasadena, United States; Centers for Disease Control and Prevention, Epidemic Intelligence Service, Division of Scientific Education and Professional Development, Atlanta, United States; The University of Hong Kong, Queen Mary Hospital, Hong Kong, China; University of Auckland, Faculty of Medicine, Auckland, New Zealand

**Email:** debbie.e.malden@kp.org

**Background and aims:** An estimated 1.89 million adults in the United States have chronic hepatitis B (CHB). Despite wide availability of treatment for CHB, many treatment-eligible patients remain untreated. To improve treatment rates, we investigated factors associated with receiving treatment among patients with CHB in a large, integrated health care setting in Southern California.

**Method:** Using data from Kaiser Permanente electronic medical records, we performed a retrospective cohort study among persons aged ≥18 years with CHB, defined as having two, positive hepatitis B surface antigen or hepatitis B virus (HBV) DNA tests >6 months apart during 2008–2019. Patients with HIV were excluded. CHB treatment eligibility was determined according to American Association for the Study of Liver Diseases guidelines based on hepatitis e antigen status, annual serum alanine aminotransferase levels, HBV DNA levels, and presence of fibrosis or cirrhosis. We used multivariate Cox proportional hazards regression to estimate adjusted hazard ratios (aHRs) and corresponding 95% CI for treatment receipt among those eligible for CHB treatment during the study period, defined as receiving antiviral treatment according to electronic medical records.

**Results:** Of 5, 314 patients with CHB, 16% (n = 857) were eligible for treatment. Treatment-eligible patients were older (mean age 53 vs 48 years) and included a greater proportion of men (56% vs 48%) and persons with diabetes (15% vs 8%), compared with all CHB patients. Among patients eligible for treatment, 49% (n = 417) received treatment. Patients who received treatment were on average 4 years younger (mean age 51 vs 55 years), but did not differ greatly by comorbidity status or Body Mass Index than those who did not receive treatment. Women were less likely to receive treatment than men (aHR 0.69; 95% CI: 0.55–0.85). Relative to non-Hispanic White race/ethnicity, persons of non-Hispanic White race/ethnicity were less likely to receive treatment (aHR: 0.66; 95% CI: 0.43–0.99). Patients who were referred to a health care specialist (infectious disease, hepatology or gastroenterology) were almost twice as likely to receive treatment, compared with those who were not (aHR 1.85; 95% CI: 1.26–2.70).

**Conclusion:** Among a large cohort of CHB patients, fewer than half of patients who were eligible for treatment received treatment. Increasing referral of CHB patients to a health care specialist may improve treatment rates.

**SAT357**

Dose-dependent durability of hepatitis B surface antigen reductions following administration of a single dose of VIR-3434, a novel neutralizing vaccine monoclonal antibody

Kosh Agarwal1, Man-Fung Yuen2, Heiner Wedemeyer3, Daniel Cloutier4, Ling Shen5, Andre Arizpe6, Sneha V. Gupta4, Marie C. Fanget4, Lillian Seul4, Andrea Cathcart4, Audrey H. Lai4, Carey Hwang4, Edward J Gane5, Kings College Hospital, Institute of Liver Studies, London, United Kingdom; The University of Hong Kong, Queen Mary Hospital, Hong Kong, China; Hannover Medical School, Department of Gastroenterology, Hepatology, and Endocrinology, Hannover, Germany; VIR Biotechnology, Inc., San Francisco, California, United States; University of Auckland, Faculty of Medicine, Auckland, New Zealand

**Email:** kosh.agarwal@kcl.ac.uk

**Background and aims:** Chronic hepatitis B virus (HBV) infection is associated with significant morbidity and mortality and contributes substantially to the overall global health burden. VIR-3434 is an Fc engineered human monoclonal antibody targeting the conserved antigenic loop of hepatitis B surface antigen (HBsAg) currently in development for the treatment of chronic HBV infection. Here, we report preliminary data from an ongoing phase 1 study evaluating the safety, tolerability, and antiviral activity of VIR-3434 in participants with chronic HBV infection.

**Method:** This randomized, double-blind, placebo-controlled, phase 1, single ascending dose study included adults with hepatitis B e antigen (HBeAg)-negative chronic HBV infection without cirrhosis. Participants had HBsAg <3,000 IU/ml at screening and had received nucleos (t)ide reverse transcriptase inhibitor (NRTI) therapy for ≥2 months. Eight participants in each cohort were randomized 6:2 to receive a single subcutaneous dose of VIR-3434 6 mg, 18 mg, 75 mg, or 300 mg, or placebo. Preliminary data through 8 weeks of follow-up are presented; dose escalation and follow-up are ongoing.

**Results:** Twenty-four participants were enrolled. Most participants achieved ≥1 log10 IU/ml reduction from baseline in HBsAg within 1–3 days of dosing. The largest and most durable HBsAg reductions were observed in the 75 mg cohort. Among the 6 participants per cohort with ≥0.2 log10 IU/ml reductions in HBsAg, mean reductions in the
Conclusion: A single dose of 6 mg, 18 mg, or 75 mg VIR-3434 demonstrated a rapid reduction in HBsAg; the 75 mg dose level was associated with larger and more durable HBsAg reductions through week 8. Preliminary safety data suggest that VIR-3434 was generally safe and well tolerated. These preliminary data support the further evaluation of VIR-3434 for functional cure of patients with chronic HBV infection.

SAT358
Quantification of HBV hepatocyte burden using novel multiplex immunofluorescence staining and image analysis reveals substantial reduction in HBV liver burden with anti-viral treatment
Abhishek Aggarwal1, Pamela Odorizzi1, Jens Brodbeck1, Nicholas Van Buuren1, Christina Moon1, Silvia Chang1, MaryVic Adona1, Torsten Trowe1, Scott Turner1, Patrick Marcellin2, Maria Buti3, Anuj Gaggar1, Lauri Diehl1, Becket Feierbach1, Scott Balsitis1.1Gilead Sciences, Inc., Foster City, United States; 2Hospital Beaujon AP-HP, Clichy, France; 3Hospital Universitari Vall d’Hebron, Barcelona, Spain
Email: pamela.odorizzi@gilead.com

Background and aims: Patterns of Hepatitis B virus (HBV) infection and integration before and after nucleotide (NUC) therapy have been previously described, but accurate quantification of HBV-infected hepatocytes in a large liver biopsy collection has not been reported. We developed novel immunofluorescence collection and image analysis techniques to quantify HBV-positive cells and applied them to over 200 liver biopsies.

Method: A 4-plex immunofluorescence assay was developed with HBsAg, core, membrane (Na+/K+-ATPase), and nuclear (Histone H3) markers to assign HBV staining to individual cells. An image analysis algorithm was also developed to quantify the percentage of hepatocytes positive for HBV proteins. Biopsies from HBeAg-positive (n = 76) and HBeAg-negative (n = 129) patients before or during NUC (tenofovir disoproxil fumarate or adefovir) treatment for 48 or 240 weeks were analyzed from GS-US-174-0102/0103. When available, matched serum samples were evaluated for HBV DNA, HBsAg, HBeAg, HBcAg, HBV RNA, and ALT. In fifteen cases, two biopsies were collected from different portions of the liver at the same timepoint and staining was compared to evaluate sampling effects.

Results: Two common and typically mutually exclusive staining patterns were observed: diffuse core staining and foci of HBsAg staining, thought to represent hepatocytes with cccDNA and integrated HBV DNA, respectively. Hepatocytes positive for both core and HBsAg were rare. Biopsies collected from the same patient and timepoint revealed enormous variability in HBV staining within individual patients, indicating that single biopsies are not representative of the entire liver. This intra-patient variability was confirmed in a liver resection sample. On a population level, NUC treatment was associated with >100-fold lower median frequency of core-positive cells (p <0.001), while reductions in HBsAg-positive cell frequency were modest and not statistically significant. HBeAg-negative Week 240 NUC-treated patients had the lowest HBV burden (median 3.8% hepatocytes positive for core and/ or HBSAg). Positive correlations between serum viral biomarkers and liver HBV burden were only observed in HBeAg-positive patients prior to NUC treatment.

SAT359
GST-HG141 inhibits de novo HBV cccDNA formation in cultured primary human hepatocytes
Dong Zhang1, Weniqiang Wu1, Shikui Chen1, Zhou Yu1, Vadim Bichko1, John Mao1, Jiang Zhigan2, Haiying He3, Li Jian4, Shuhui Chen5.1Fujian Cosunter Pharmaceutical Co., Ltd.; 2Domestic Discovery Service Unit, WuXi AppTec (Shanghai) Co., Ltd.
Email: vbichko@gmail.com

Background and aims: GST-HG141 is a novel, orally-bioavailable HBV capsid assembly modulator (CAM). It inhibits HBV pregenomic RNA packaging, leading to formation of "empty" capsids, devoid of genetic material. However, its mode of action and resistance profile appear to be distinct from other class I CAMs in development. GST-HG141 has an excellent antiviral potency in vitro, as well as efficacy in HBV mouse models. GST-HG141 was safe and well-tolerated in a first-in-man clinical study in healthy volunteers [Li et al, Antimicrob Agents Chemother. 2021; 65 (11) and is currently under phase Ib evaluation in chronic HBV patients. Here we report antiviral properties of GST-HG141 in cultured primary human hepatocytes (PHH).

Method: Cryopreserved PHHs from a single donor were infected with HepG2.2.15 cell-derived HBV. Treatment with GST-HG141, G5S4, or Entecavir (ETV) started concurrently with infection, or 5 days post-infection. After 7 days of treatment, the effects on the secreted HBV DNA were determined using qPCR. Secreted HBsAg and HBcAg were quantified by ELISA. Southern blot was performed to detect and quantify the HBV covalently closed circular DNA (cccDNA). The identity of the cccDNA band was confirmed by EcoRI digestion.
Results: All three tested compounds reduced secreted HBV DNA levels in a concentration-dependent manner, regardless of whether the treatment was started (GST-HG141 EC_{50} = 80 nM). The secreted HBsAg (EC_{50} ~ 1.5 microM) and HBcAg (EC_{50} ~ 1.6 microM) levels were also dose-dependently decreased by GST-HG141, but only if treatment started concurrently with infection. Similar observations were made with GLS4. ETV had no effect on HBsAg- and HBcAg levels in cell culture supernatants under neither condition. GST-HG141 potently and dose-dependently inhibited HBV cccDNA formation, but only when treatment started with the infection, and not at day 5 post-infection. No significant cytotoxicity was observed with neither compound in this study (CC_{50} >10 microM).

Conclusion: These data demonstrate that GST-HG141 prevents de novo synthesis of cccDNA, but has no effect on the established cccDNA pools in cultured PHH. It acts on different steps of the HBV life cycle, suggesting dual/multiple mechanisms of antiviral action. Further development of GST-HG141 for chronic HBV infections is warranted. Currently it is undergoing phase Ib-II clinical evaluations. The interim results from the ongoing phase Ib study show robust antiviral efficacy of GST-HG141 monotherapy and good safety/tolerability in chronic HBV patients.

SAT360 Predictive factors of virological response at one year in patients with chronic HBV/HDV co-infected treated with Bulevirtide

Victor de Lédinghen1, Paul Hermabessière2, Sophie Metivier3, Édouard Bardou-Jacquet4, Marie-Noëlle Hilleret4, Veronique Loustaud-Ratti5, Nathalie Ganne-Carrié6, Laurent Afric7,8, Isabelle Fouchard Hubert7, Louis d’Altercho8, Bruno Roche8, Fabien Zoulim9, Anne Gervais7, Hélène Fontaine7, Anne Minello Franza10, Christiane Stern11, Jérôme Dumortier11, Caroline Lascoux-Combe7, Juliette Foucher2, Christophe Garnier2, Jean-François Guillo3, Sébastien Desmare9, Rémi Dugast10, Dominique Roulot12, Xavier Causse3, Isabelle Ollivier-Hourmand14, Victor de Lédinghen1, Paul Hermabessière2, Sophie Metivier3, Édouard Bardou-Jacquet4, Marie-Noëlle Hilleret4, Veronique Loustaud-Ratti5, Nathalie Ganne-Carrié6, Laurent Afric7,8, Isabelle Fouchard Hubert7, Louis d’Altercho8, Bruno Roche8, Fabien Zoulim9, Anne Gervais7, Hélène Fontaine7, Anne Minello Franza10, Christiane Stern11, Jérôme Dumortier11, Caroline Lascoux-Combe7, Juliette Foucher2, Christophe Garnier2, Jean-François Guillo3, Sébastien Desmare9, Rémi Dugast10, Dominique Roulot12, Xavier Causse3, Isabelle Ollivier-Hourmand14, Karine Lacombe15, Patrick Mailhés16, Frederic Heluwaert17, Leon Muti18, Isabelle Rosa19, Valérie Canva18, Damien Lucidarme19, Dominique Larrey20, Bernard Prouvost-Keller21, Caroline Lascoux-Combe7, Juliette Foucher2, CHU Bordeaux, France; 2CHU Toulouse; 3CHU Rennes; 4CHU Grenoble; 5CHU Angers; 6CHU Tours; 7CHU Lyon; 8CHU Dijon; 9CHU Angers; 10CHU Tours; 11CHU Limoges; 12APHP; 13CHU Rangueil, Digestive Department Toulouse 3 University, Toulouse, France; 14CHU Angers; 15CHU Tours; 16CHU Lyon; 17CHU Clermont-Ferrand; 18CHU Créteil; 19CHU Lille; 20Hospital Saint Philibert; 21CHU Montpellier; 22CHU Nice

Email: victor.deledinghen@chu-bordeaux.fr

Background and aims: BLV monotherapy as well as combination with PEG-interferon α 2a (PEG-IFNα) for 48 weeks induced HDV RNA declines in the French ATU early access program. The aim of this study was to evaluate 12-month predictive factors of virological response in HBV/HDV patients receiving 2 mg BLV with or without PEG-IFNα 2a (real-life study).

Method: 145 patients with chronic HBV/HDV co-infection, with cirrhosis or moderate fibrosis and elevated ALT levels, without liver compensation, were included. Patients received 2 mg BLV qd sc alone in combination with PEG-IFNα once weekly for 12 months, according to physician’s choice. Univariate analysis was performed to evaluate predictive factors of undetectable HDV-RNA after one year of treatment.

Results: Characteristics of the 145 patients were: 99 (68.3%) males, 41 years, cirrhosis N = 91 (62.8%), median viral load of 6.2 log_{10} IU/ml. At month 12, in the BLV monotherapy and in the BLV + PEG-IFN group, the median decrease of HDV-RNA was – 3.64 et – 5.56 log_{10} IU/ml, respectively. Moreover, at month 12, HDV-RNA was undetectable in 39% and 85% of patients treated with BLV monotherapy and BLV + PEG-IFN group, respectively (per-protocol analysis). Factors associated with virological response are indicated in the table.

<table>
<thead>
<tr>
<th>HIV-1 Plasma (log10 IU/ml)</th>
<th>P</th>
<th>P</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>Median decrease</td>
<td>– 3.64 et – 5.56</td>
<td>0.03</td>
<td>0.03</td>
</tr>
</tbody>
</table>

Conclusion: In patients treated with BLV 2 mg alone, HDV-RNA is associated with virological response after one year of treatment. In patients treated with or without PEG-IFN, PEG-IFN treatment is associated with virological response. These preliminary results could help physicians for their clinical practice.

SAT361 Impact of baseline viral load on hepatocellular carcinoma risk during antiviral treatment in non-cirrhotic patients with HBAG2 positive chronic hepatitis B

Won-Mook Choi1, Gi-Ae Kim2, Jonggi Choi1, Seungbong Han3, Young-Suk Lim1. 1Asan Medical Center, Department of Gastroenterology, Liver Center, Seoul, Korea, Rep. of South; 2Kyung Hee University School of Medicine, Department of Internal Medicine, Korea, Rep. of South; 3Korea University College of Medicine, Department of Biostatistics, Seoul, Korea, Rep. of South

Email: limys@amc.seoul.kr

Background and aims: Early initiation of anti-viral treatment with high viral load is highly controversial in HBAG2-positive patients with chronic hepatitis B (CHB). Here, we investigated the impact of hepatitis B virus (HBV) DNA levels at the onset of antiviral treatment on the on-the-treatment risk of hepatocellular carcinoma (HCC) in non-cirrhotic patients with HBAG2-positive CHB.

Method: We conducted a multicenter cohort study including entecavir- or tenofovir-treated non-cirrhotic patients with HBAG2-positive CHB and baseline HBV DNA levels ≥ 5.00 log_{10} IU/ml at three centers in Korea between January 2007 and December 2016. We compared the on-treatment risk of HCC between high viral load (HBV DNA levels ≥ 8.00 log_{10} IU/ml) and moderate viral load (5.00–7.99 log_{10} IU/ml) groups.

Results: Of 2, 073 patients, 1, 108 patients were classified as high viral load group and 965 patients were moderate viral load group. After propensity score (PS)-matching, 930 pairs of patients were generated with well-balanced baseline characteristics. In the entire cohort, HCC was developed in 10 patients (0.15 per 100 person-years) in the high viral load group compared with 37 patients (0.67 per 100 person-years) in the moderate viral load group during a median 5.7 years of antiviral treatment. Patients with moderate viral load at baseline showed a significantly higher HCC incidence than those with high viral load in both the entire and PS-matched cohorts by Kaplan-Meier analysis (p < 0.001 for both; Figure). By multivariable analysis, the moderate viral load group had a significantly higher risk of HCC (hazard ratio, 3.48; 95% confidence interval, 1.72–7.06; P < 0.001) than the high viral load group, which was also consistently observed in the PS-weighted, PS-matched, and competing risk analyses.
Conclusion: In non-cirrhotic patients with HBeAg-positive CHB, decreased HBV DNA levels at baseline was associated with a significantly high risk of HCC during antiviral treatment. Early initiation of antiviral treatment with a high viral load (≥8.00 log_{10} IU/ml) would retain a low on-treatment risk of HCC in HBeAg-positive CHB patients.

SAT362
Therapeutic vaccination with CLB-3000 in a mouse model of chronic hepatitis B induces anti-HBs responses associated with functional cure
Renae Walsh1, Hans Netter1, Joan Ho1, Stephen Locarnini1, Ronald Farquhar2, Bharat Dixit2, Aileen Rubio2.
1Victorian Infectious Diseases Services, Parkville, Australia; 2Clearb Therapeutics, Inc., CONCORD, MA, United States
Email: arubio@clearbtherapeutics.com

Background and aims: Our therapeutic vaccine candidates previously achieved functional cure (FC) in a mouse model of chronic hepatitis B (CHB) [EASL 2021 poster 853, AASLD 2021 poster 829]. The vaccines consist of modified HBsAg displaying clearance profile (CP) associated epitopes identified from anti-HBs responses of FC clinical patients. CP-specific antibody responses are distinguished by the occupation of key loop 1 and 2 epitopes within HBsAg “a” determinant [Walsh, R et al 2019. Liver Int 39 (11) pp2066]. The vaccine candidate CLB-3000 consists of 2 modified HBsAg, expressed from Pichia pastoris and adjuvanted with Alhydrogel. Therapeutic vaccination with CLB-3000 achieved FC in CHB mice and were assessed for the presence of ‘clearing’ anti-HBs profiles consistent with those observed from clinical FC patients.

Method: CLB-3000 was subcutaneously delivered to CBA/CaJ mice with established CHB infection [Chou H-H et al 2015. PNAS 112 (7) pp2175]. Mice were monitored for FC by serological and liver immunohistochemistry (IHC). The quality of the anti-HBs immune response following FC was assessed for specificity to HBsAg CP epitopes defined clinically, HBsAg immune complexes to confirm serum clearance of HBsAg, and diagnostic anti-HBs titre.

Results: Therapeutic vaccination of CHB mice with CLB-3000 resulted in >2.5 log IU/ml reduction in serum HBsAg. Liver IHC confirmed clearance of HBV positive cells. Development of a vaccine-elicited CP-associated ‘clearing’ anti-HBs response was concomitantly detected in 80% of CLB-3000 treated CHB mice that achieved FC. Antibody specificity for CP-associated epitopes was detected, targeting both loops 1 and 2 of HBsAg, and mimicked that observed in FC patients. Immune complexes of residual HBsAg and anti-HBs were not typically detected following FC with an established ‘clearing’ anti-HBs response, indicative of complete HBsAg clearance. Placebo treatment resulted in no significant change in virological markers and no anti-HBs seroconversion.

Conclusion: CLB-3000 was highly efficacious in CHB mice as shown by rapid HBsAg decline, clearance from serum and liver, and seroconversion to CP-associated anti-HBs which mirrored clinical FC-associated anti-HBs responses. The data further support CLB-3000 development for the treatment of CHB.

SAT363
Evaluation of the disposition and mass balance recovery of vebicorvir, a first generation hepatitis B core inhibitor, in rats and humans
Katie Zomorodi1, Luisa M Stamm1, William Delaney1, Michael Shen1, 1Assembly Biosciences, Inc., South San Francisco, United States
Email: kzomorodi[assemblybio.com

Background and aims: Vebicorvir (VBR) is a first-generation hepatitis B virus (HBV) core inhibitor that targets multiple aspects of the viral replication cycle. VBR is in Phase 2 development for the treatment of chronic HBV infection (cHBV). Here we report the disposition and mass balance recovery of VBR in rats and healthy human subjects.

Method: 27 male rats were dosed with 30 mg/kg [14C]-VBR radio-labeled with 5.5 MBq/kg. Three animals were placed in metabolism cages for up to 120 h post-dose. Total radioactivity was measured in urine, feces, cage rinse and carcass. Pharmacokinetic (PK) profiles were obtained in blood, plasma and liver samples collected at selected timepoints over 48 h post-dose from three additional terminal animals per timepoint. The human study (NCT04637139) was a single-arm, non-randomized, open-label Phase 1 trial. Following an overnight fast of ≥8 hours, 6 healthy subjects received a single oral dose of 300 mg VBR solution containing a microdose of approximately 2 μCi of [14C]-VBR. Samples of blood, urine, and feces were collected for PK, metabolite, and radiolabel assessments for up to 240 h post-dose.

Results: In rats, 86% and 12% of the radio-labeled VBR dose were eliminated in feces and urine, respectively, with excretion of unchanged VBR in the feces accounting for the majority of the administered drug; unchanged VBR was the only radio-component detected in plasma. Total radioactivity showed very high distribution in the liver with partitioning ratios ranging from 18 to 30 over 48 h post-dose (calculated with respect to blood). Similarly, mean cumulative radioactivity recovery in humans was 88%, with 62% excreted in feces and 26% in urine (Figure 1); and unchanged VBR was the major component in both sexes (50% of dose) and urine (10% of dose). Unchanged VBR was the predominant component in plasma with low overall circulating metabolite-related radioactivity. Plasma VBR concentrations reached peak by ∼2.5 h and declined with terminal half-life of 27.7 h. Renal clearance of unchanged VBR (1.62 L/h) was a minor contributor to the total body clearance of VBR (17.9 L/h).

Conclusion: Fecal excretion of unchanged drug is the primary route of VBR elimination in both rats and humans. VBR is the predominant component in the systemic circulation with low overall circulating metabolite-related radioactivity. VBR showed high liver loading in the rat indicating favourable distribution to the target organ for treatment of chronic HBV infection.
Background and aims: Integrated analysis of the impact of nucleos (t)ide treatment on intrahepatic HBV antigen expression together with immune cell subset frequency is lacking. In this study, we performed concurrent analysis of the intrahepatic viral burden and the liver immune microenvironment in chronic hepatitis B (CHB) patients with minimally elevated serum alanine aminotransferase (ALT) before and after treatment with tenofovir disoproxil fumarate (TDF).

Method: CHB patients with serum viral load above 2000 IU/ml and mild ALT elevation between 1-2 folds the upper limit of normal were enrolled in a double-blind, placebo-controlled, randomized trial of either oral 300 mg TDF or placebo once daily for 3 years (NCT01522625). Paired core liver biopsies were collected at baseline and year 3 and analyzed by bulk RNA-Seq (n = 56 placebo and n = 64 TDF treated patients) as well as by a custom multiplex immunofluorescence (mIF) assay (Ultivue InSituPlex) in a subset of biopsies (n = 15 placebo and n = 15 TDF treated patients). Cell type proportions from RNA-Seq were calculated using the EPIC algorithm. Quantification of mIF images for immune cell subsets and viral burden was performed using Visiopharm software.

Results: Following 3 years of treatment, patients that received TDF showed significant reduction in serum ALT (p <0.05) and HBV DNA levels (p <0.001) compared to the placebo group. In line with RNA-Seq cell type estimates, mIF analysis revealed a decrease in CD3+ T-cell (p <0.001), CD4+ T-cell (p <0.001), CD8+ T-cell (p <0.001), CD20+ B-cell (p <0.001), CD4+ T-cell (p <0.001), CD8+ T-cell (p <0.001), CD20+ B-cell (p <0.01) and HBV core+ hepatocyte frequencies (p <0.001) after 3 years of TDF vs. placebo treatment. PD-1 expression was also significantly reduced on both CD4+ and CD8+ T-cells (p <0.001) with TDF treatment. Conversely, NK cell and monocyte gene signatures, as well as CD68+ macrophage density and HBsAg+ hepatocyte frequency did not significantly change with TDF treatment. mIF analysis also showed a reduction in periportal lymphoid aggregates (defined by dense CD20+ B-cell clusters, p <0.05) in TDF-treated vs. placebo patients.

Conclusion: Multiparametric analysis of the liver immune microenvironment revealed intrahepatic immune cell infiltration in patients with minimally elevated serum ALT. TDF treatment significantly reduced the number of HBV core+ (but not HBsAg+) hepatocytes, which was accompanied by a decrease in both intrahepatic T cells and B cells. These findings suggest that (i) CHB patients with minimally elevated ALT levels may benefit from nucleos (t)ide treatment and (ii) that intrahepatic T and B cell frequency is associated with the HBV core+ cell burden.

Background and aims: To evaluate the safety, pharmacokinetic, and antiviral activity of ALG-000184, an oral prodrug of ALG-001075, a novel, pan-genotypic class II capsid assembly modulator (CAM) with picomolar potency.

Method: This is an ongoing three-part, multicenter, double-blind, randomized, placebo-controlled study. In Parts 1 and 2, single and multiple doses of ALG-000184 were well tolerated in healthy volunteers (Gane et al, APASL, HBV TAG, 2021). Part 3 is evaluating untreated subjects with chronic hepatitis B (CHB) (N = 10/cohort; 8 active:2 placebo) receiving daily doses of ALG-000184 or placebo × 28 days. Reported here are preliminary blinded safety, PK, and antiviral data.

Results: To date, 36 subjects have completed dosing in Cohorts 1 (100 mg; N = 10 HBeAg neg), 2 (50 mg; N = 10 HBeAg neg), and 4 (100 mg; N = 10 HBeAg pos); enrollment in Cohort 3 (10 mg; N = 6 HBeAg neg) is ongoing. Most subjects were male (56%), Asian (58%), with a mean age of 40 years, a mean BMI of 24.6 Kg/m2 and genotype B or D. At baseline, mean HBV DNA by cohort ranged from 4.4 to 8.1 log10 IU/ml and most subjects’ (81%) baseline ALT concentrations were within the normal range. Study medication was well tolerated. There was 1 unrelated serious adverse event (hospitalization for back pain management). There were no treatment emergent adverse events (TEAEs) resulting in premature discontinuation. All TEAEs were Grade 1 or 2 in severity, except for three Grade 3 ALT elevations. These were asymptomatic, occurring post dosing and were associated with significant changes in HBV DNA and RNA. There were no changes in synthetic liver function. Plasma ALG-001075 exposures increased dose proportionally between 10, 50 and 100 mg dose levels, with low-to moderate variability and minimal accumulation. A similar magnitude of HBV DNA decline (~3–4 log10 IU/ml) was observed in all cohorts and a similar percentage (≥75%) of HBcAg negative subjects achieved HBV DNA below the lower limit of quantitation (LLOQ; <10 IU/ml). Mean HBV DNA level changes from baseline are shown in Fig 1. HBV RNA declined below LLOQ (10 copies/ml) in 100% of subjects in Cohorts 1 and 2 and by ~3.1 log10 copies/ml at day 28 in Cohort 4.
Deeper virologic suppression with the addition of vebicorvir, a first-generation hepatitis B core inhibitor, to entecavir correlates with reduced inflammation and fibrosis-4 index in treatment-naïve patients with HBeAg positive chronic hepatitis B

Mark S Sulkowski1, Scott K Fung2, Xiaoli Ma3, Tuan T Nguyen4, Eugene R. Schiff5, Hei-Won L Hann6, Douglas T Dieterich7, Ronald G Nahass8, James S Park9, Sing Chan10, Steven-Huy B Han11, Edward J Gane12, Michael Bennett13, Ran Yan14, Jieming Liu14, Ira M Jacobson9, Walid S Ayoub10, Frank Weilert17, Natarajan Ravendran18, Ainoor Ramji19, Paul Yen Kwo20, Magdy Elkhishab1, Tarek Hassanein22, Ho S Bae23, Jacob P Lalezari15, Kosh Agarwal24, Man-Fung Yuen25, Johns Hopkins University School of Medicine, Baltimore, United States; University of Toronto, Toronto, Canada; Office of Xiaoli Ma, Philadelphia, United States; Ng Nguyen, Research and Education, Inc., San Diego, United States; Schiff Center for Liver Diseases, University of Miami School of Medicine, Miami, United States; Thomas Jefferson University Hospital, Philadelphia, United States; Icahn School of Medicine, Mount Sinai Hospital, Department of Medicine, Division of Liver Diseases, New York, United States; Infectious Disease Care, Hillsborough, United States; NYU Langone Health, New York, United States; Sing Chan, MD, New York, United States; Pfleger Liver Institute, University of California, Los Angeles, United States; Aukland Clinical Studies Ltd, Auckland, New Zealand; Medical Associates Research Group, San Diego, United States; Assembly Biosciences, Inc., South San Francisco, United States; Quest Clinical Research, San Francisco, United States; Cedars-Sinai Medical Center, Los Angeles, United States; Waikato Hospital, Hamilton, New Zealand; Gastrohealth of Maryland, Catonsville, United States; Gastrointestinal Research Institute, Vancouver, Canada; Stanford University Medical Center, Stanford, United States; Toronto Liver Centre, Toronto, Canada; Southern California Research Center, Coronado, United States; Asian Pacific Liver Center, Los Angeles, United States; Institute of Liver Studies, King’s College Hospital, London, United Kingdom; Queen Mary Hospital, The University of Hong Kong, Department of Medicine and State Key Laboratory of Liver Research, Hong Kong

Background and aims: The goal of NrtI therapy for chronic hepatitis B virus infection (cHBV) is suppression of HBV DNA. While NrtIs reduce HBV DNA in most patients (pts), low-level viremia remains which is associated with disease progression. Therapies providing deeper levels of virologic suppression may improve long-term clinical outcomes. Previous reports from Study 202 (NCT03577717) in treatment-naïve, HBeAg positive pts demonstrated deeper reductions in HBV DNA and pre-genomic RNA (pgRNA) and more rapid normalization of ALT when vebicorvir (VBR) was added to entecavir (ETV). This report explores associations between the reductions in viral parameters with Fibrosis-4 (FIB-4) index, an indicator of liver health.

Method: In Study 202, 13 pts received 300 mg VBR+0.5 mg ETV and 12 pts received PBO+0.5 mg ETV for 24 weeks. Entry criteria included ALT ≤10xULN, platelets ≥100, 000/mm 3, Metavir F0-F2/8kPa. HBV DNA, pgRNA, and quantitative HBV antigens were measured at each visit. FIB-4 was calculated according to \( \frac{(age*AST)}{(platelet count*\sqrt{ALT})} \). Correlation analyses were performed, and Pearson correlation coefficients \( r \) calculated to describe associations between viral parameters and FIB-4.

Results: At Week 24 reductions in ALT and AST were observed with VBR+ETV but not PBO+ETV: ALT – 47.2 U/L vs +1.6 U/L and AST – 25.3 U/L vs +8.4 U/L respectively. For platelet counts, the mean change from baseline (CFB) at Week 24 was +3.5 × 10 9/L for VBR+ETV and +23.2 × 10 9/L for PBO+ETV. Changes in these parameters were reflected in the mean CFB in FIB-4 index, which was significantly greater for VBR+ETV than PBO+ETV: -0.21 vs -0.05, p = 0.034. For VBR+ETV but not PBO+ETV, significant associations were observed between FIB-4 and pgRNA \( r = 0.70; p = 0.008 \) and HBcrAg \( r = 0.78; p = 0.003 \). There were no significant associations between FIB-4 and HBV DNA for either group.

Conclusion: The addition of VBR to NrtI therapy provides deeper suppression of HBV DNA and pgRNA and more rapid normalization of ALT and AST than NrtI alone over 24 weeks of treatment. The deeper

Figure: Mean (SEM) HBV DNA levels change from baseline through the end of the treatment period by Cohort

**Conclusion:** All dose levels of ALG-000184 were well tolerated, exhibited predictable PK, and resulted in similar, substantial antiviral activity in untreated CHB subjects, regardless of HBeAg status.

SAT366

Deeper virologic suppression with the addition of vebicorvir, a first-generation hepatitis B core inhibitor, to entecavir correlates with reduced inflammation and fibrosis-4 index in treatment naïve patients with HBeAg positive chronic hepatitis B

Mark S Sulkowski1, Scott K Fung2, Xiaoli Ma3, Tuan T Nguyen4, Eugene R. Schiff5, Hei-Won L Hann6, Douglas T Dieterich7, Ronald G Nahass4, James S Park9, Sing Chan10, Steven-Huy B Han11, Edward J Gane12, Michael Bennett13, Ran Yan14, Jieming Liu14, Ira M Jacobson9, Walid S Ayoub10, Frank Weilert17, Natarajan Ravendran18, Ainoor Ramji19, Paul Yen Kwo20, Magdy Elkhishab1, Tarek Hassanein22, Ho S Bae23, Jacob P Lalezari15, Kosh Agarwal24, Man-Fung Yuen25, Johns Hopkins University School of Medicine, Baltimore, United States; University of Toronto, Toronto, Canada; Office of Xiaoli Ma, Philadelphia, United States; Ng Nguyen, Research and Education, Inc., San Diego, United States; Schiff Center for Liver Diseases, University of Miami School of Medicine, Miami, United States; Thomas Jefferson University Hospital, Philadelphia, United States; Icahn School of Medicine, Mount Sinai Hospital, Department of Medicine, Division of Liver Diseases, New York, United States; Infectious Disease Care, Hillsborough, United States; NYU Langone Health, New York, United States; Sing Chan, MD, New York, United States; Pfleger Liver Institute, University of California, Los Angeles, United States; Aukland Clinical Studies Ltd, Auckland, New Zealand; Medical Associates Research Group, San Diego, United States; Assembly Biosciences, Inc., South San Francisco, United States; Quest Clinical Research, San Francisco, United States; Cedars-Sinai Medical Center, Los Angeles, United States; Waikato Hospital, Hamilton, New Zealand; Gastrohealth of Maryland, Catonsville, United States; Gastrointestinal Research Institute, Vancouver, Canada; Stanford University Medical Center, Stanford, United States; Toronto Liver Centre, Toronto, Canada; Southern California Research Center, Coronado, United States; Asian Pacific Liver Center, Los Angeles, United States; Institute of Liver Studies, King's College Hospital, London, United Kingdom; Queen Mary Hospital, The University of Hong Kong, Department of Medicine and State Key Laboratory of Liver Research, Hong Kong

Background and aims: The goal of NrtI therapy for chronic hepatitis B virus infection (cHBV) is suppression of HBV DNA. While NrtIs reduce HBV DNA in most patients (pts), low-level viremia remains which is associated with disease progression. Therapies providing deeper levels of virologic suppression may improve long-term clinical outcomes. Previous reports from Study 202 (NCT03577717) in treatment-naïve, HBeAg positive pts demonstrated deeper reductions in HBV DNA and pre-genomic RNA (pgRNA) and more rapid normalization of ALT when vebicorvir (VBR) was added to entecavir (ETV). This report explores associations between the reductions in viral parameters with Fibrosis-4 (FIB-4) index, an indicator of liver health.

Method: In Study 202, 13 pts received 300 mg VBR+0.5 mg ETV and 12 pts received PBO+0.5 mg ETV for 24 weeks. Entry criteria included ALT ≤10xULN, platelets ≥100, 000/mm 3, Metavir F0-F2/8kPa. HBV DNA, pgRNA, and quantitative HBV antigens were measured at each visit. FIB-4 was calculated according to \( \frac{(age*AST)}{(platelet count*\sqrt{ALT})} \). Correlation analyses were performed, and Pearson correlation coefficients \( r \) calculated to describe associations between viral parameters and FIB-4.

Results: At Week 24 reductions in ALT and AST were observed with VBR+ETV but not PBO+ETV: ALT – 47.2 U/L vs +1.6 U/L and AST – 25.3 U/L vs +8.4 U/L respectively. For platelet counts, the mean change from baseline (CFB) at Week 24 was +3.5 × 10 9/L for VBR+ETV and +23.2 × 10 9/L for PBO+ETV. Changes in these parameters were reflected in the mean CFB in FIB-4 index, which was significantly greater for VBR+ETV than PBO+ETV: -0.21 vs -0.05, p = 0.034. For VBR+ETV but not PBO+ETV, significant associations were observed between FIB-4 and pgRNA \( r = 0.70; p = 0.008 \) and HBcrAg \( r = 0.78; p = 0.003 \). There were no significant associations between FIB-4 and HBV DNA for either group.

Conclusion: The addition of VBR to NrtI therapy provides deeper suppression of HBV DNA and pgRNA and more rapid normalization of ALT and AST than NrtI alone over 24 weeks of treatment. The deeper

Figure: Mean (SEM) HBV DNA levels change from baseline through the end of the treatment period by Cohort

**Conclusion:** All dose levels of ALG-000184 were well tolerated, exhibited predictable PK, and resulted in similar, substantial antiviral activity in untreated CHB subjects, regardless of HBeAg status.
level of viral suppression and reduced inflammation is reflected in greater reductions in FIB-4 for VBR+ETV compared to ETV alone. In post hoc analyses, reductions in pgRNA, a marker for cccDNA, replicative activity, and HBcAg are associated with improved response in FIB-4 over 24 weeks of treatment. Regimens providing deeper levels of viral suppression and reduced inflammation may further improve long-term clinical outcomes including fibrosis, cirrhosis and HCC.

SAT367
Safety, tolerability, pharmacokinetics, and preliminary antiviral activity of the capsid assembly modulator (CAM) ZM-H1505R after multiple escalating oral doses in patients with chronic hepatitis B (CHB) Infection
Jiali Ma1, Hong Zhang2, Min Wu3, Hong Chen2, Yue Hu2, Xiaoxue Zhu4, Xiuhong Jiang2, Bo Hua1, Tian Xia2, Gang Liu1, Aiyun Deng1, Bo Liang1, Ruoling Guo4, Hui Li4, Zhe Wang4, Ming Ben3, Huaming Chen2, Zhijun Zhang1, Junqi Niu1, Yanhua Ding1, 1The First Hospital of Jilin University, Jilin, China, Phase I Clinical Research Center, Changchun; 2The First Hospital of Jilin University, Jilin, China, Phase I Clinical Research Center, Changchun; 3Shanghai Zhimeng Biopharma, Inc., Shanghai Zhimeng Biopharma, Inc., Shanghai, China
Email: dingyuanhua2003@126.com

Background and aims: ZM-H1505R is a newly discovered hepatitis B virus (HBV) capsid inhibitor with a novel pyrazole structure. It interferes with the assembly of HBV particles by inducing the formation of viral capsids devoid of genomic material. The safety, tolerability pharmacokinetics (PK), and preliminary antiviral activity of ZM-H1505R were evaluated in a double-blind, randomized, placebo-controlled, dose escalating study in treatment-naive chronic hepatitis B (CHB) patients.

Method: Non-cirrhotic and treatment-naïve CHB patients were divided into three cohorts (10 patients each) and randomized within each cohort in a ratio of 4:1 to receive an ascending dose of 50, 100, or 200 mg of ZM-H1505R, or placebo once a day for 28 consecutive days.

Results: All results were analyzed in the blind state, because the blindness was still not uncovered. A total of 30 patients was randomized and completed the study. The cohorts were well matched and balanced with sex, age, baseline HBV DNA level and HBcAg status of the subjects. ZM-H1505R was safe and well tolerated from 50 to 200 mg qd oral administration, with most AEs being grade 1 or 2 and the symptoms being mild to moderate. No SAEs was observed and no withdrawal was caused due to AEs. The rates of AEs were 30%, 60% and 60% in the 50, 100, or 200 mg cohorts, respectively. The most common adverse reactions to ZM-H1505R were the elevation of alanine aminotransferase and aspartate aminotransferase in grade 1 or 2 severity (CTC-AE version 5.0), with the incidence of 10%-50% within a cohort. ZM-H1505R showed a linear pharmacokinetics proportional to the doses. ZM-H1505R reached mean plasma Tmax at 2.3–3.5 hours postdose with mean terminal half-life of 11.975–12.999 hours after last dosage. A steady-state was achieved –3.454, which indicates that the accumulation is mild. At day 28, the mean plasma Cmax was 2.7, 7.0, and 14.6 folds of its Clinical Research Center, Changchun; The First Hospital of Jilin University, Jilin, China, Phase I Clinical Research Center, Changchun; 2The First Hospital of Jilin University, Jilin, China, Phase I Clinical Research Center, Changchun; 3Shanghai Zhimeng Biopharma, Inc., Shanghai Zhimeng Biopharma, Inc., Shanghai, China

S837 Journal of Hepatology

POSTER PRESENTATIONS

SAT368
Evaluation of renal and bone safety at 4 years in post-liver transplant patients with chronic kidney disease receiving Tenofovir Alafenamide for HBV prophylaxis
Edward J Gane1, Rica Dagooe1, Dominic Ray-Chaudhuri1, Thomas Mules1, Frida Abramov2, Curtis Holt3, Hongyuan Wang4, Vithika Suri5, Anu Osnisius2, John F. Flaherty2, 1Auckland City Hospital and University of Auckland, New Zealand Liver Transplant Unit, Auckland, New Zealand; 2Gilead Sciences, Inc., Clinical Development, Foster City, United States; 3Gilead Sciences, Inc., Medical Affairs, Foster City, United States; 4Gilead Sciences, Inc., Biotostatistics, Foster City, United States
Email: frida.abramov@gilead.com

Background and aims: Chronic HBV remains a leading indication for orthotopic liver transplantation (OLT) worldwide. Renal dysfunction and osteopenia are commonly observed long-term complications of maintenance immunosuppression in OLT recipients. In this at-risk population, tenofovir alafenamide (TAF) may have an advantage over tenofovir disoproxil fumarate (TDF) due to its improved renal and bone safety profile. We previously reported similar efficacy and improved safety with TAF vs TDF up to 192 weeks in this population. Presented here is a comprehensive analysis of long-term bone and renal safety.

Method: In this Phase 2 open-label study (NCT02862548), 51 liver transplant recipients on HBV prophylaxis with TDF-containing treatments and ≥Stage 2 chronic kidney disease were randomized 1:1 to TAF 25 mg/day or TDF for 48 weeks, after which all received TAF through Week 192 (i.e. TAF vs. TDF→TAF). Week 192 safety end points included changes in estimated glomerular filtration rate (eGFR) by CG, CKD-EPI, and Chromium-EDTA Renal Scan (Cr-EDTA) methods, serum creatinine (sCr), exploratory markers of renal tubular dysfunction, bone mineral density (BMD) at spine and hip by DXA, and markers of bone turnover.

Results: Baseline characteristics included: mean age 60 years, 75% males, 53% Pacific Islander, median eGFR 50 ml/min/1.73m2 with 76% of patients at CKD stage 3 or greater, and median baseline surface area corrected GFRCr-EDTA was 58 ml/min/1.73m2. 46/51 (90%) patients completed 192 weeks of treatment. Overall safety results have been previously described. Renal parameters improved from baseline at Week 192 (Table). Increases from baseline in spine and hip BMD were observed with TAF (mean % change at Week 192: 3.4% and 1.1%, respectively) and TDF→TAF after switching to TAF (mean % change at Week 192: 3.8% and 2.1% for spine and hip, respectively); greater decreases in markers of bone turnover were observed in TAF vs TDF→TAF group (Table).

Table: Median (Q1, Q3) Change from Baseline at Week 192

<table>
<thead>
<tr>
<th></th>
<th>TAF 25mg (N = 26)</th>
<th>TDF → TAF (N = 24)</th>
</tr>
</thead>
<tbody>
<tr>
<td>eGFR (m/min/1.73 m²)</td>
<td>2.5 (−1.4, 8.2)</td>
<td>1.1 (−0.0, 9.3)</td>
</tr>
<tr>
<td>eGFRc (m/min)</td>
<td>2.8 (−1.3, 12.3)</td>
<td>0.2 (−0.0, 10.7)</td>
</tr>
<tr>
<td>sCr (mg/dL)</td>
<td>−0.08 (−0.39, 0.01)</td>
<td>−0.06 (−0.22, 0.09)</td>
</tr>
<tr>
<td>Cr EDTA (mL/min/1.73 m²)</td>
<td>0.1 (−3.1, 6.4)</td>
<td>−3.3 (−8.0, 5.6)</td>
</tr>
<tr>
<td>B2M (µg/mL)</td>
<td>−40 (−1.5, 115)</td>
<td>−38 (−58, 88)</td>
</tr>
<tr>
<td>sCr:2M:Cr ratio (g/g)</td>
<td>−54 (−87, 278)</td>
<td>−45 (−76, 223)</td>
</tr>
<tr>
<td>GCTX ng/ml (%Y)</td>
<td>−39.0 (−60.5, −14.3)</td>
<td>−26.9 (−60.3, 8.9)</td>
</tr>
<tr>
<td>PIFP ng/ml (%Y)</td>
<td>−36.98 (−55.13, −5.65)</td>
<td>−19.42 (−37.96, 12.75)</td>
</tr>
</tbody>
</table>

*Week 96 results presented

Conclusions: Long-term results after switching from TDF to TAF in an OLT recipient population with a high rate of renal dysfunction show sustained improvements in key bone and renal safety parameters.
SAT369
Functional cure based on pegylated interferon alpha therapy in nucleoside analog-suppressed HBeAg negative chronic hepatitis B: a multicenter real-world study (Everest Project in China)-3.5 years data update
Chun Xi1, Dongyiing Xie1, Lei Fu2, Wen-hua Zhang3, Jia Wei4, Guojun Li5, Jiahong Yang6, Xinyue Chen7, Jia-bin Li8, Jia Shang9, Yu-juan Guan10, Yongfang Jiang11, Ying Guo12, Yi-jian Zeng13, Jiabo Chang14, Yanzhong Peng15, Minghua Lin16, Guangyu Huang17, Jia Li18, Shengwang Gu19, Jia-wei Geng20, Zhiliang Gao21. 1First Affiliated Hospital of Sun Yat-sen University, Department of Infectious Diseases, Guangzhou, China; 2Xiangya Hospital Central South University, Changsha, China; 3Cansu Wuwei Cancer Hospital, Wuwei, China; 4Affiliated Hospital of Yunnan University, Kunming, China; 5The Third People's Hospital of Shenzhen, Shenzhen, China; 6People's Hospital of Deyang City, Deyang, China; 7Beijing Youan Hospital, Capital Medical University, Beijing, China; 8The First Affiliated Hospital of Anhui Medical University, Hefei, China; 9Henan Provincial People's Hospital, Zhengzhou, China; 10Guangzhou Eighth People's Hospital, Guangzhou, China; 11The Second Xiangya Hospital of Central South University, Changsha, China; 12The third people's hospital of Taiyuan, Taiyuan, China; 13Chengdu Public Health Medical Center, Chengdu, China; 14The Second Hospital of Nanjing, Nanjing, China; 15Peking University First Hospital, Beijing, China; 16Guangzhou First People's Hospital, Guangzhou, China; 17The Fourth People's Hospital of Shenzhen, Shenzhen, China; 18Tianjin Second People's Hospital, Tianjin, China; 19Huaxia Medical District of General Hospital of Eastern Theater Command, Huaian, China; 20The First People's Hospital of Yunnan Province, Kunming, China; 21The Everest Project is a multicentre real-world study in China which focused on functional cure of CHB (NCT04035837). Patients who had NA therapy for more than one year, HBV DNA<100 IU/ml, HBeAg negative and HBSag ≤1500 IU/ml were recruited since 2018. “Add-on” or “switch to” pegIFN alpha strategy for 48 weeks or up to 96 weeks was decided by doctor and patients. Data on those who have completed 48 weeks of treatment were analysed. mITT population included 5648 patients and PP population included 3988 patients.

Background and aims: Add-on or switch to pegylated interferon alpha (PegIFN alpha) in nucleoside analog (NA) treated chronic hepatitis B (CHB) patients is effective strategies to improve functional cure (HBSAg loss) rate. We aimed to investigate the efficacy and safety of “add-on” or “switch to” therapy in large scale real-word and the predictors for HBSAg loss by pegIFN alpha.

Method: The Everest Project is a multicentre real-world study in China which focused on functional cure of CHB (NCT04035837). Patients who had NA therapy for more than one year, HBV DNA<100 IU/ml, HBeAg negative and HBSag ≤1500 IU/ml were recruited since 2018. “Add-on” or “switch to” pegIFN alpha strategy for 48 weeks or up to 96 weeks was decided by doctor and patients. Data on those who have completed 48 weeks of treatment were analysed. mITT population included 5648 patients and PP population included 3988 patients.

Results: In the PP analysis, 81% patients were male, the mean age was 40.9 years and the mean baseline of HBSAg was 380.6 IU/ml. The HBSAg loss rate were 9.5%, 22.0%, 29.0% and 33.2% at 12, 24, 36 and 48 weeks, respectively (figure 1A). HBSAg baseline level, ALT flare are predictors for functional cure of CHB (NCT04035837). Patients achieved HBSAg < 500 IU/ml at 24 weeks had significantly higher HBSAg loss rate than those with HBSAg ≥500 IU/ml (36.7% vs. 1.3%, p < 0.0001, figure 1C). For patients with HBSAg decline >1 log10 IU/ml from baseline to 24 weeks, the 48-week HBSAg loss rate was 58.6%, while 10.0% for those HBSAg decline ≤1 log10 IU/ml (p <0.0001) (figure 1C). Patients with higher ALT level at 12 weeks (≥5×ULN) had a higher 48-week HBSAg loss rate (46.3%) (figure 1D). There are 1006 patients (68.4%, 1006/1470) achieved HBSAg ≤100 IU/ml at 48 weeks, although they did not achieved HBSAg loss. Those patients might achieve functional cure for further prolonged therapy of PegIFN alpha. There were no severe adverse events during this project.

Conclusion: Functional cure could be well achieved in NA-suppressed HBeAg negative CHB patients by pegIFN alpha strategy. Lower HBSAg at baseline, lower HBSAg at 24 weeks, a rapid decline of HBSAg and ALT elevations at 12 weeks are predictors for functional cure at 48 weeks. There are still good chances of functional cure by prolonged treatment for patients who had not achieved HBSAg loss in 48 weeks course. PegIFN alpha therapy was well-tolerated.

SAT370
Understanding the dynamics of HBSAg decline through model-informed drug development (MIDD) of JNJ-3989 and JNJ-6379 for the treatment of chronic hepatitis B virus infection (CHB)

Background and aims: JNJ-3989 is an N-acetylgalactosamine-conjugated siRNA, consisting of 2 triggers JNJ-3976 and JNJ-3924, designed to target hepatitis B virus (HBV)-derived RNAs, thereby reducing all viral proteins. JNJ-6379 is a capsid assembly modulator inducing formation of empty HBV capsids. The phase 2b study REEF-1 assessed the combination of 40, 100, and 200 mg JNJ-3989 as Q4W subcutaneous injections with or without 250 mg QD oral JNJ-6379 on a background of nucleos (t)ide analogue (NA) (AASLD 2021). The relationship between exposure to JNJ-3989 + NA ± JNJ-6379 and HBSAg decline was assessed using mechanism-based pharmacokinetic-pharmacodynamic (PK-PD) modeling (see Figure).

Figure: TMDD-IRM model developed based on Phase 1 and 2 PK and PD data for JNJ-3989.
Method: This PK-PD model, a Transporter-Mediated Drug Disposition (TMDD) with Indirect Response Model (IRM), was developed based on plasma PK of JNJ-3989 obtained from pooled Phase 1 and 2 studies in healthy, hepatically impaired, and CHB subjects, the latter also providing PD biomarker (HBsAg) data. Asialoglycoprotein (ASGPR)-mediated liver uptake was incorporated by leveraging information from plasma and liver [JNJ-3989 concentrations collected in a HBV mouse study. The IRM described the relationship between estimated human liver concentrations and the inhibition of HBsAg production leading to observed HBsAg decline in patients, taking into account the treatment status at baseline [not currently treated (NCT) or virologically suppressed (VS)], and baseline HBcAg status (+ or -). A covariate analysis was performed to investigate treatment- and/or subgroup-specific HBsAg dynamics.

Results: JNJ-3989 liver uptake is saturable through ASGPR resulting in a decreased fraction of the dose that reaches the liver as the dose increases. The dynamics of HBsAg decline were governed by the accumulation of JNJ-3989 in liver, the exposure-dependent inhibition of HBsAg production, and the estimated HBsAg half-life. Covariate analysis indicated that (i) NCT HBsAg+ patients had faster and more pronounced HBsAg decline compared to other subgroups, (ii) combination treatment with JNJ-6379 led to a less pronounced decline in HBsAg, and (iii) JNJ-3989 activity is inversely associated to body weight.

Conclusion: JNJ-3989 showed a non-linear concentration-dependent liver uptake, mediated by ASGPR. HBsAg levels decreased in a dose-dependent manner up to 48 weeks of JNJ-3989 treatment in REEF-1. Covariate analysis identified that HBsAg dynamics display treatment- and subgroup-specific behavior.

SAT371 Serum HBsAg and ddPCR HBV-DNA as predictive parameters of HBsAg loss after nucleo(s)tide analogue (NA) treatment discontinuation in non-cirrhotic patients with chronic hepatitis B
Anna Francesca Guerrì1, Giovanni Tomassoli1, Lorenzo Piermatteo2, Stefano D’Anna2, Romina Salpini2, Valentina Scivieri2, Paolo Ventura1, Gian Luca Abbati1, Antonello Pietrangelo1, Reggio Emilia, Internal Medicine, Modena, Italy; 2University of Rome “Tor Vergata”, Italy
Email: anna.f.guerra@hotmail.it

Background and aims: According to international guidelines, stopping nucleo(s)tide analogue (NA) treatment in selected non-cirrhotic Chronic Hepatitis B (CHB) patients may promote sustained serological and virological off treatment response. Nevertheless, this approach often leads to virus-induced flares, which may result to life-threatening liver failure. Therefore, in order to assure a safe discontinuation of treatment, reliable predictors of post-NAs remission need to be identified. Here, we aimed to identify predictive parameters of off-NA response at the end of treatment and, specifically, their association with HBsAg loss or HBsAg <100 IU/ml (known to be predictive of subsequent HBsAg loss).

Method: 38 non-cirrhotic CHB patients, with complete virological suppression (>4 years), were prospectively monitored after suspending NA treatment for a median (IQR) of 16 (10–19) months. For each patient, a plasma sample at suspension date (baseline, BL) was collected and used to quantify serum HBV-DNA by highly sensitive droplet digital PCR (ddPCR). HBsAg was quantified by the ARCHITECT HBsAg assay at BL, every 2 weeks from suspension in the first month, followed by every month until the sixth month, then every 3 months, in order to assess the achievement of HBsAg <100 IU/ml or HBsAg loss.

Results: At BL, ddPCR revealed that 28 (73.7%) patients had detectable serum HBV-DNA (median [IQR] 5 [2–11] IU/ml), while 10 (26.3%) were completely negative to HBV-DNA. After NA suspension, 7 (18.4%) achieved HBsAg <100 IU/ml (median [IQR]: 43 [35–53] IU/ml) and 8 (21.1%) lost HBsAg at last follow-up.

As expected, patients achieving HBsAg loss had lower HBsAg levels at BL (140 [70–480] IU/ml with vs 1162 [439–3135] without HBsAg loss, p = 0.014).

Notably, the negativity to HBV-DNA by ddPCR at BL strongly correlated with the achievement of HBsAg <100 IU/ml or HBsAg loss after NA suspension (outcome observed in 70% [7/10] with vs 28.6% [8/28] without negative BL HBV-DNA; OR [95% CI]: 5.8 [1.3–23.6], p = 0.03). Even more, the combination of HBsAg <500 IU/ml + negativity HBV-DNA by ddPCR at BL was the best predictor for achieving HBsAg <100 IU/ml or HBsAg loss (outcome observed in 85.7% with vs 27.6% without this combination; OR [95% CI]: 15.8 [1.6–152.2]; p = 0.008; PPV = 86%; NPV = 72%).

Conclusion: NA suspension can be an effective strategy to constrain or silence intrahepatic HBV reservoir in accurately selected patients. Residual HBV replicative activity at NA suspension, measured by highly sensitive assays, provides an added value in identifying patients more prone to achieve HBV functional cure.

SAT372 Exploring hepatitis B virus as an immunotherapeutic target for clinical trials of adoptively transferred T cells
Suhasini Lulla1, Tsung-Yen Chang1, Spyridoulas Vasileiou1, Manik Kuvalekar2, Ayumi Watanabe1, Rovana Velazquez2, Jenny Stanton2, Ann Leen1, 1Center for Cell and Gene Therapy, Baylor College of Medicine, Houston Methodist Hospital, Texas Children's Hospital, Houston, United States; 2AlloVir Inc
Email: AMLEEN@texaschildrens.org

Background and aims: Patients chronically infected with hepatitis B virus (HBV) have endogenous T cell deficits including dysfunctional and exhausted HBV-reactive cells, which may be addressed by the adoptive transfer of HBV-reactive T cells from healthy immune individuals. HBsAg-positive, allogeneic, hematopoietic cell transplant (HCT) recipients who received stem cells (and lymphocytes) from donors that were positive for HBC and HBs antibodies have shown high rates of functional cure post-transplant. We explored the feasibility of extending this benefit to all patients with chronic HBV infection by generating a bank of HBV-specific T cells (HBVSTs) from healthy donors that are suitable for off-the-shelf clinical use.

Method: HBVSTs were produced using peptide libraries spanning immunodominant antigens to expand reactive cells. Following a single in vitro stimulation, we achieved a 7.3 ± 0.6 (p = 9) fold increase, representing a >6000-fold enrichment of HBV-reactive T cells. The phenotypic profile of these cells was assessed by flow cytometry with antibodies to: CD3, CD4, CD8, CD25, CD69, CD45RO, CD16, CD56. The effector profile of reactive cells was assessed using intracellular cytokine staining (ICS), luminecx and/or IsoPlexis. In vitro cytolytic capacity was evaluated in a short-term killing assay using antigen-loaded autologous targets and partially HLA-matched HbP2.15 cells.

Results: Reactive cells were polyclonal and dominated by CD4+ T cells (mean 72 ± 4%) with a minor CD8+ (21 ± 2%) component. The cells expressed markers associated with central (CD45RO+CD26+: 59 ± 3%) or effector memory (CD45RO+CD62L-: 30 ± 3%) potential and were activated based on expression of CD25 (59 ± 5%) and/or CD69 (21 ± 3%). Post-expansion, these HBVSTs were Th1-polarized and polyfunctional based on their ability to simultaneously produce TNF, IFNγ, IL-2, GM-CSF, granzyme B, MIP-1α and MIP-1β. Finally, these cells were able to selectively kill virus-expressing autologous targets (40:1 E:T 36% specific lysis) and partially HLA-matched HBV-infected HepG2 cells (71%) with no specific lysis each).

Conclusion: This study establishes the feasibility of developing banks of ex vivo expanded HBV-specific T cells that are suitable for clinical use. Further evaluation of these HBVSTs using in vivo models and in chronic HBV patients is warranted.
Background and aims: BLV monotherapy as well as combination with PEG-interferon α 2a (PEG-IFNα) for 48 weeks induced HDV RNA declines in HDV patients included in the French ATU early access program started in September 2019. To date, there is no data available evaluating the efficacy and safety of BLV 2 mg at 18 months. The aim of this study was to evaluate 18-month safety and virological response in HBV/HDV patients receiving 2 mg BLV with or without PEG-IFNα 2a included in the French BLV ATU (real-life study).

Method: 145 patients (male gender 99, mean age 41, 3 years, cirrhosis 90) with chronic HBV/HDV co-infection, with cirrhosis or moderate fibrosis and elevated ALT levels, without liver decompensation, were included in the French early access program. Patients received 2 mg BLV qd sc alone (group A) or in combination with PEG-IFNα once weekly (group B), according to physician’s choice.

Results: Among these 145 patients, 19 patients switched BLV 2 mg to BLV 10 mg (reason: no response observed after at least 3 months of treatment with 2 mg), 43 patients stopped BLV for many reasons (lost to follow-up, no response, side-effects related to the disease, patient’s wish) and 83 always received BLV 2 mg. At M12, HDV-RNA was undetectable in 39% and 85% of patients treated with BLV and BLV + PEG-IFNα, respectively. In October 2021, M18 data were already available in 38 patients. Among them, no new severe side-effect was reported. Undetectable HDV-RNA and combined response (HDV-RNA decrease ≥2 log_{10} or undetectable and normal ALT <40 IU/L) were observed in 17 (44.7%) and 14 patients (36.8%), respectively. Details are indicated in the table. Among 7 patients treated with BLV 2 mg alone for at least 18 months, HDV-RNA was undetectable in 3 and HDV-RNA decrease >2 log_{10} or undetectable and normal ALT <40 IU/L was observed in 2.

Characteristics of patients according to response at month 18.

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Undetectable HDV-RNA</th>
<th>Normal ALT &lt;40 IU/L</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cirrhosis</td>
<td>YES (N = 17)</td>
<td>NO (N = 21)</td>
</tr>
<tr>
<td>BLV associated with PEG-IFNα</td>
<td>10 (58.8%)</td>
<td>12 (57.1%)</td>
</tr>
<tr>
<td>Stop BLV 2 mg before M13</td>
<td>12 (70.6%)</td>
<td>8 (38.1%)</td>
</tr>
<tr>
<td>Stop PEG-IFN before M13</td>
<td>2 (11.8%)</td>
<td>14 (66.7%)</td>
</tr>
<tr>
<td>Switched to BLV 10 mg during the 12 months</td>
<td>8 (47.6%)</td>
<td>6 (28.6%)</td>
</tr>
<tr>
<td>HDV-RNA decrease ≥2 log_{10} or undetectable and normal ALT &lt;40 IU/L</td>
<td>YES (N = 14)</td>
<td>NO (N = 24)</td>
</tr>
<tr>
<td>Cirrhosis</td>
<td>8 (57.1%)</td>
<td>14 (58.3%)</td>
</tr>
<tr>
<td>BLV associated with PEG-IFNα</td>
<td>10 (71.4%)</td>
<td>10 (41.7%)</td>
</tr>
<tr>
<td>Stop BLV 2 mg before M13</td>
<td>3 (21.4%)</td>
<td>14 (58.3%)</td>
</tr>
<tr>
<td>Stop PEG-IFN before M13</td>
<td>7 (50%)</td>
<td>7 (29.2%)</td>
</tr>
<tr>
<td>Switched to BLV 10 mg during the 12 months</td>
<td>0</td>
<td>7 (29.2%)</td>
</tr>
</tbody>
</table>

Conclusion: In this first real-world cohort and long-term follow-up, daily BLV 2 mg monotherapy is safe and well tolerated during 18 months. Strong antiviral responses against HDV in real-life were observed. Final results (month 18) will be presented during the meeting.
Mean BMD (Hip T-score) did not change significantly from TAF onset (-2.1) to mo-12 (-1.8, P = 0.164) but improved at mo-24 (-1.4, P = 0.016).

Conclusion: In most NA experienced CHB pts with renal and/or BMD disorders/risks, two-year TAF therapy is safe and effective achieving or maintaining virological suppression and improving ALT, eGFR and serum phosphate levels. eGFR improvement can be achieved in up to 60% of all pts and 75% of those with baseline eGFR 30–60.

SAT375
Treatment of chronic hepatitis B in sub-Saharan Africa: 5-year results of a pilot program in Ethiopia
Stian Magnus Stauring Orlien1,2, Hailemichael Desalegn3, Hanna Aberra2, Eyerusalem Mamo1, Benon Amare1, Sine Grude4, Kristina Hommersand5, Nega Berhe2,5, Kristina Johannessen2,6.
1Vestfold Hospital Trust, Department of Paediatrics, Norway; 2Oslo University Hospital Ullevål, Regional Advisory Unit for Imported and Tropical Diseases, Norway; 3St. Paul’s Hospital Millennium Medical College, Ethiopia; 4University of Oslo, Faculty of Medicine, Norway; 5Addis Ababa University, Akilu Lemma Institute of Pathobiology, Ethiopia; 6Vestfold Hospital Trust, Department of Infectious Diseases, Norway
Email: stian@orlien.no

Background and aims: The World Health Organization has set an ambitious goal of eliminating viral hepatitis as a major public health threat by 2030. In sub-Saharan Africa, however, antiviral treatment of chronic hepatitis B (CHB) is virtually unavailable in the public sector. Experiences from real-life CHB cohorts are needed to inform treatment guidelines and policy makers. Here we present 5-year results from one of the first and largest CHB treatment programs on the continent.

Method: Adults with CHB were enrolled in a cohort study at St. Paul’s Hospital Millennium Medical College, Addis Ababa, from 2015. Liver function tests, viral markers and transient elastography was assessed at baseline and thereafter at 6-monthly intervals. Tenofovir disoproxil fumarate (TDF) was initiated based on the European Association for the Study of the Liver (EASL) criteria, with some modifications. Changes in laboratory markers were analyzed using Wilcoxon rank-sum tests. Adherence to therapy was measured by pharmacy refill data.

Results: In total, 1303 patients were included in the program; 533 (40.9%) were women and the median age was 31 years (interquartile range 26–40). Co-infections were rare: 29 patients (2.2%) were anti-HCV positive, and 19 (1.5%) were anti-HDV positive. Overall, 294 individuals (22.6%) started TDF therapy within the first five years of follow-up. Thirty-nine (13.3%) of these patients died, of whom 36 (92.3%) had compensated cirrhosis at baseline. Eight individuals (2.7%) developed hepatocellular carcinoma. Liver stiffness declined steadily in patients on TDF therapy; median change from baseline after 1, 3 and 5 years was –2.9 kPa, –5.2 kPa and –5.6 kPa, respectively. Among patients in care, 141 of 149 (94.6%) had suppressed viroemia (<69 IU/ml). In patients with available pharmacy refill data, 253 of 290 (87.2%) had ≥80% adherence.

Conclusion: This pilot program demonstrated that CHB therapy is feasible in Ethiopia with excellent long-term clinical and virological results. Our findings support rolling out large-scale treatment programs in sub-Saharan Africa.

SAT376
Decrease in the burden of integrated hepatitis B virus DNA in chronic hepatitis B patients with minimally elevated alanine aminotransferase on tenofovir disoproxil fumarate as revealed by long-read DNA-sequencing
David Pan1, Cameron Soulette1, Dong Han1, Ricardo Ramirez2, Nicholas Van Buuren1, Jaw-Town Lin3, Cheng-Hao Tseng4, Li Li4, Simon Fletcher1, Hongmei Mo1, Becket Feierbacher1, Vithika Suri1, Yao-Chun Hsu4,1 Gilead Sciences, Inc., Foster City, United States; 2China Medical University, Digestive Medicine Center, Taichung, Taiwan; 3E-Da Cancer Hospital, Division of Gastroenterology and Hepatology, Kaohsiung, Taiwan; 4National Yang Ming Chiao Tung University, Institute of Biomedical Bioinformatics, Taipei, Taiwan
Email: david.pan3@gilead.com

Background and aims: Treatment with tenofovir disoproxil fumarate (TDF) was recently shown to reduce the number of distinct, transcriptionally active hepatitis B virus (HBV) integrations in chronic hepatitis B (CHB) patients with mild alanine aminotransferase (ALT) elevation. This short-read RNA-Sequencing (RNA-Seq) analysis was limited to the identification of expressed HBV integrations and hence did not measure the complete burden of integrated HBV DNA. Here, we use targeted long-read DNA Sequencing (DNA-Seq) to enable comprehensive analysis of the effect of TDF treatment on HBV integrations.

Method: A phase 4, randomized, double-blind, placebo-controlled study was conducted to evaluate the efficacy of TDF in CHB patients with mild ALT elevation (≥1 fold but <2-fold of the upper limit normal (ULN)) without hepatocellular carcinoma (HCC) (NCT01522625). Targeted long-read DNA-Seq was performed on paired liver biopsies (baseline and year 3 post-treatment) from TDF (n = 28) and placebo (n = 27) treated patients. The average on-target read length for the long-read DNA-Seq was 5.5 kilobases (kb). The long-read DNA-Seq data was analyzed using the ViraAL Integrations AND Translocations (VALLIANT) bioinformatics workflow.

Results: All patients had evidence of integrated HBV DNA at baseline with integrations detected near (±5 kb) 2, 165 genes including 13 genes in the Catalogue Of Somatic Mutations In Cancer (COSMIC) database. Of the patients with integrated HBV DNA, 98% (n = 54/55) had ≥1 integrated HBV sequence (s) flanked by the same human chromosome and 80% (44/55) of patients contained ≥1 integrated HBV sequence (s) flanked by two different human chromosomes, indicating an inter-chromosomal translocation. Consistent with our previous short-read RNA-Seq analysis, there was a significant decrease in integration burden at year 3 post-treatment in TDF-treated (p = 0.0076) but not placebo-treated (p > 0.05) patients.

Conclusion: Targeted long-read DNA-Seq analysis revealed pervasive integrated HBV DNA in CHB patients with minimally elevated ALT, with ≥80% individuals having evidence of HBV-related chromosomal translocation. In line with our previous analysis, TDF treatment significantly decreased the integrated HBV DNA burden.
significantly decreased the integrated HBV DNA burden in these patients. Together, these results suggest that early treatment of CHB patients with TDF may play a role in reducing the burden of integrated HBV DNA, which is commonly associated with hepatocarcinogenesis.

SAT377
Serum HBV RNA levels are associated with risk of hepatitis flare after stopping NA therapy in HBeAg-negative patients
Kathy Jackson1, Kumar Visvanathan2, Samuel Hall2, Gareth Burns3, Sara Bonanzinga4, Despina Anagnostou4, Paul Desmond4, Dilip Ratnam4, William Sievert4, Miriam Levy4, Amanda Nicoll5, John Lubel5, Peter Angus5, Marie Sinclair5, Simone Strasser5, Meng Ngu5, Christopher Meredith5, Gail Matthews5, Peter Revill5, Vijaya Sundararajan6, Sara Vogr6, Alison Kuchta6, Jesse Canchola7, Jason Torres7, Jasmine Lau7, Alexander Thompson7, Victoria Infectious Diseases Laboratory and the Doherty Institute, Australia; 2St Vincent’s Hospital and the University of Melbourne, Gastroenterology, Fitzroy, Australia; 3Western Health, Gastroenterology, Footscray, Australia; 4Monash Health, Gastroenterology, Australia; 5Monash Health and Monash University, Australia; 6Liverpool Hospital and South Western Sydney Clinical School UNSW, Australia; 7Eastern Health and Monash University, Australia; 8Monash University and the Alfred Hospital, Australia; 9Austin Hospital and the University of Melbourne, Australia; 10Royal Prince Alfred Hospital and UNSW, Australia; 11Concord Hospital and the University of Sydney, Australia; 12Bankstown-Lidcombe Hospital, Sydney, Australia; 13The Kirby Institute UNSW and St Vincent’s Hospital Sydney; 14Latrobe University and the University of Melbourne, Australia; 15Roche Molecular Systems, Inc., Pleasanton, CA, United States
Email: alexander.thompson@svha.org.au

Background and aims: Among HBeAg-negative chronic hepatitis B (CHB) patients on long-term nucleos (t)ide analogue (NA) therapy, treatment discontinuation has been associated with HBsAg loss and durable virological suppression, but also hepatitits flares requiring NA therapy to be restarted. The prediction of clinical outcomes after stopping NA therapy remains challenging. Quantification of circulating HBV RNA is a promising biomarker in CHB patients. We have evaluated the role of serum HBV RNA levels to predict clinical outcomes in a large cohort of patients enrolled in a prospective NA-STOP study.

Method: The Melbourne HBV-STOP study was a prospective multicentre study of NA discontinuation in 110 HBeAg-negative non-cirrhotic patients who had achieved long-term virological suppression on treatment. All patients were followed for 96 weeks. In a subset, we performed an exploratory analysis of serum HBV RNA levels for predicting clinical outcomes after stopping NA therapy. HBV RNA levels were measured at baseline and longitudinally using the automated Roche cobas® HBV RNA Investigational Assay. Clinical outcomes of interest included rates hepatitis flare (ALT>5xULN); disease remission (HBV DNA<2000 IU/ml and ALT<2xULN) and HBsAg loss, as well as rates of NA re-treatment.

Results: HBV RNA levels were tested at baseline and off-treatment in 65 patients. At baseline, the median age was 56 yrs, 54% were male, and 75% were Asian. Median HBsAg level was 701 (1.6–19912) IU/ml. Following treatment withdrawal, virological reactivation occurred in all participants, 38% experienced a hepatitits flare (ALT>5xULN), 26% restarted NA therapy and 6% (n = 4) lost HBsAg by 96 weeks. At baseline, serum HBV RNA was detectable in 16/65 (25%). The detection of HBV RNA in serum at baseline was positively associated with risk of hepatitis flare [ALT >5 xULN, 63% vs 31%, OR = 3.8, 95% CI = (1.2, 12.3), p value = 0.03], as well as lower likelihood of sustained disease remission as well as HBsAg loss. HBV RNA levels were undetectable at baseline in all patients who achieved HBsAg loss. Of patients HBV RNA negative at baseline, HBV RNA levels became detectable in 47/49 patients during follow-up. The time to detection of HBV RNA was shorter for patients stopping TDF than ETV (median 49 vs 90 days, p = 0.02). The detection of HBV RNA over time was associated with rising HBVDNA levels>10^4 IU/ml. HBV RNA levels>10^3 cp/ml off-treatment were associated with increased risk of hepatitis flare (ALT>5xULN).

Conclusion: Serum HBV RNA was detectable in a minority of HBeAg-negative patients on long-term NA therapy. The detection of any serum HBV RNA prior to stopping NA therapy, and rising HBV RNA off-treatment, were associated with risk of subsequent hepatitis flare, as well as lower likelihood of HBsAg loss. HBV RNA levels show promise as a biomarker for predicting clinical outcomes after stopping NA therapy in patients with HBeAg-negative CHB.

SAT378
Efficacy and safety of tenofovir alafenamide versus tenofovir disoproxil fumarate in treatment-naive patients with chronic hepatitis B
Jihye Lim1, Won-Mook Choi1, Ju Hyun Shim1, Danbi Lee1, Kang Mo Kim1, Young-Suk Lim1, Han Chu Lee1, Jongji Choi1, 1Asan Medical Center, University of Ulsan College of Medicine, Gastroenterology, Korea, Rep. of South
Email: jkchoi0803@gmail.com

Background and aims: We aimed to evaluate the efficacy and safety of tenofovir alafenamide (TAF) compared with tenofovir disoproxil fumarate (TDF) in treatment-naive patients with chronic hepatitis B (CHB) based on real world data.

Method: We analyzed 2,747 patients with CHB under TAF (n = 502) or TDF (n = 2,245) treatments. Virological response (VR: HBV DNA <15 IU/ml), on-treatment ALT normalization, the incidence of HCC, renal function, and lipid profiles were compared between these groups. Propensity score matching of 495 pairs was also conducted for these comparisons.

Results: The mean age of the total cohort was 48.6 years and 58.2% were male. Cirrhosis had a 33.3% prevalence in this study population. VRs at 12-, 24-, and 36 months were achieved in 70.3%, 81.2%, and 83.3% of the TAF and 67.9%, 84.3% and 86.1% of the TDF cases, respectively (p >0.05 for all). Normalized ALT, as determined by local laboratory criteria (<40 U/L), occurred in 79.7%, 90.6%, and 86.2% of the TAF group and 78.2%, 85.8%, and 85.7% of the TDF group at 12-, 24-, and 36 months, respectively (p >0.05 for all). The HCC risk did not statistically differ across the entire cohort (TAF: 0.80/100 person-years [PYs] vs TDF: 1.45/100 PYs, P = 0.30) or in the PS-matched cohort (TAF: 0.82/100 PYs vs TDF: 0.90 PYs, P = 0.60). The TAF group showed a lower median increase in serum creatinine from baseline during the early study period. Compared with the TAF group, the TDF group showed significant decreases in total cholesterol, triglyceride, and HDL, but not in LDL.

Conclusion: Real-world data indicate that TAF has comparable efficacies to TDF in terms of VR and ALT normalization, with no higher risk of HCC.
SAT379

Bulevirtide 2 mg/day monotherapy in patients with chronic hepatitis delta with or without cirrhosis: a multicenter European cohort real-life study

Alessandro Loglio¹, Peter Ferenci², Katja Deterding³, Sara Colonia Uceda Renteria⁴, Dana Sambarino⁵, Mathias Jachs⁶, Caroline Schwarz⁷, Marta Borghi⁸, Kerstin Port⁹, Riccardo Perbellini¹, Floriana Facchetti¹, Elisabetta Degasperi¹, Benjamin Maasoumy³, Thomas Reiberger², Markus Cornberg³, Heiner Wedemeyer⁴, Pietro Lampertico¹,², Foundation IRCCS Ca’ Granda Ospedale Maggiore Policlinico, Division of Gastroenterology and Hepatology, Milan, Italy;¹²Medical University of Vienna, Division of Gastroenterology and Hepatology, Vienna, Austria;³Hannover Medical School, Germany;²Foundation IRCCS Ca’ Granda Ospedale Maggiore Policlinico, Clinical Laboratory, Milan, Italy; Klinik Ottakring, Department of Internal Medicine IV, Vienna, Austria; University of Milan, CRC “A. M. and A. Migliavacca” Center for Liver Disease, Department of Pathophysiology and Transplantation, Milan, Italy

Email: ale.loglio@gmail.com

**Background and aims:** Bulevirtide (BLV) has been recently approved for the treatment of HDV-related chronic hepatitis but its ‘real-life’ effectiveness and safety—especially in patients with cirrhosis—are still poorly known. This study aimed to describe the early virological and biochemical responses in a large European cohort.

**Method:** All consecutive HDV patients who started BLV 2 mg/day in three EU countries were enrolled in this study. Demographic, clinical and virological features were collected at baseline and during therapy. Primary end point was virological response (≥2 Log decline or undetectable HDV-RNA), secondary end points included virological non-response (<1 Log decline), biochemical response (normal ALT), combined response, and safety at week 24. HDV-RNA was quantified by Robogene 2.0 (LOQ 6 IU/ml), in-house RT-PCR (LOQ 100 cp/ml) and Robogene 1.0 (LOQ 80 IU/ml).

**Results:** 58 patients were enrolled: 47 (25–79) years, 62% males, 97% Caucasian, 78% cirrhotics, 67% varices, spleen diameter 17 (8–25) cm, platelets 88 (28–288)×10⁹/mm³, transient elastography: 16.3 (1.7–57.8) kPa, CAP 203 (100–320) dB/m; 69% previous interferon therapy, 97% under NA therapy, 2 patients with HCC. At baseline (BLV start): ALT 60 (7–691) U/L (83% >ULN), albumin 4.1 (2.8–4.9) g/dL, HBsAg 3.7 (1.7–4.8) Log IU/ml, 91% HBeAg negative, 87% HBV-DNA undetectable, Baseline HDV-RNA levels were 4.9 (3.3–6.6) Log IU/ml, 4.7 (2.0–7.3) Log cp/ml and 5.8 (1.9–7.5) Log IU/ml, respectively in the three countries. By week 24, ALT levels declined to 34 (18–70) U/L and normalized in 77% of patients. HDV-RNA showed an overall 2.0 (0–3.9) Log decline; virological response was observed in 54% of patients (10% with HDV-RNA <LOQ), while 46% achieved a combined (virological and biochemical) response. A virological non-response (<1 Log decline at week 24) was observed in 27% of patients, even if 60% of them normalized ALT levels. HBeAg levels remained unchanged. BLV was well tolerated, with no significant injection site reactions, including in patients with active HCC or clinically significant portal hypertension.

**Conclusion:** This real-life multicenter EU cohort study demonstrated the early effectiveness and safety of BLV 2 mg monotherapy even in difficult-to-treat cirrhotic HDV patients. However, the rate of virological non-response at week 24 was higher than previously estimated. The week 48 data will be presented at the meeting.

**SAT380**

The orally available sodium/taurocholate co-transporting polypeptide inhibitor A2342 blocks hepatitis B and D entry in vitro

Britta Bonn¹, Ellen Stränsberg¹, Ivaana Uzelac¹, Michael Kirstgern², Nora Goldmann³, Dieter Glebe³, Joachim Geyer³, Erik Lindström¹

¹Alibero Pharma, Inc., Boston, MA, United States; ²Institute of Pharmacology and Toxicology, Justus Liebig University of Giessen, Giessen, Germany; ³Institute of Medical Virology, Justus Liebig University Giessen, Giessen, Germany

Email: britta.bonn@alibero-pharma.com

**Background and aims:** A2342 is a novel small molecule, orally available, selective inhibitor of hepatic transporter Na+/taurocholate co-transporting polypeptide (NTCP). NTCP mediates uptake of bile acids into hepatocytes and acts as a host receptor for hepatitis B and D viruses (HBV/HDV). The preS1 domain of the large envelope protein of HBV/HDV is essential for binding of these virus particles to NTCP. We previously demonstrated that A2342 lowers HBV DNA viral load in infected human hepatocytes in vitro and also attenuates HBV viral load and HBV antigens in infected humanized mice in vivo. Here, we aim to provide more detail on the NTCP inhibitory mechanism.

**Method:** Human NTCP-expressing HEK293 cells were used to evaluate inhibition of 1 µmol/L [³H]taurocholic acid transport and [³H]preS1 peptide binding as surrogate parameters for virus binding. Human NTCP-expressing HepG2 cells were used to evaluate entry inhibition of HDV and HBV via immunostaining against hepatitis D antigen (HDAg) and hepatitis B core antigen (HBcAg), respectively, and measuring hepatitis B e antigen (HBeAg) levels in supernatant of HBV-infected cells. Cryopreserved human hepatocytes infected with a clinical isolate of HBV were used for infection experiments; HBV DNA levels in supernatant were analysed. The peptides preS1 (genotype D) and myrcludex B or tenofovir disoproxil fumarate (TDF) were used as positive controls.

**Results:** A2342 inhibited [³H]taurocholic acid uptake (half-maximal inhibitory concentration [IC₅₀], 186 nmol/L) and [³H]preS1 peptide binding (IC₅₀, 149 nmol/L) in a concentration-dependent manner. In infection experiments, A2342 (range, 100–400 nmol/L) inhibited numbers of HBeAg-positive cells by 75%–90% and HDAg-positive cells by 40%–60%. HBeAg levels in supernatant were reduced with A2342 by >90% at all concentrations. In cryopreserved human hepatocytes, A2342 reduced HBV DNA levels in a concentration-dependent manner when given 18 h before infection. A2342 was not effective when given 18 h post-infection. Additive antiviral effects were evident when A2342 was given together with TDF. A2342 was devoid of cellular toxicity in hepatocytes and cell lines.

**Conclusion:** A2342 inhibits NTCP-mediated bile acid uptake and HBV preS1 peptide binding in similar manners and blocks entry of HBV and HDV. These data further support A2342 as the first orally bioavailable molecule able to inhibit HBV/HDV entry via NTCP in the nanomolar range.

**SAT381**

Comparative performance analysis between manual and automatic RNA extraction to quantify HDV RNA by RoboGene 2.0 kit in untreated and bulevirtide-treated HDV patients

Sara Colonia Uceda Renteria¹, Alessandro Loglio², Marta Borghi³, Dana Sambarino², Riccardo Perbellini², Floriana Facchetti², Sara Monico², Elisabetta Degasperi², Ferruccio Ceriotti³, Pietro Lampertico²,³ Foundation IRCCS Ca’ Granda Ospedale Maggiore Policlinico, Clinical Laboratory, Milan, Italy; Foundation IRCCS Ca’ Granda Ospedale Maggiore Policlinico, Division of Gastroenterology and Hepatology, Milan, Italy; University of Milan, CRC “A. M. and A. Migliavacca” Center for Liver Disease, Department of Pathophysiology and Transplantation, Milan, Italy

Email: sara.ucedarenteria@policlinico.mi.it

**Background and aims:** Diagnosis and management of Chronic Delta Hepatitis (CHD) requires highly sensitive and reliable tests for HDV
RNA quantification coupled with automated lab procedures to optimize time and resources. Aim of the study was to compare two different extraction methods to quantify HDV RNA levels in untreated and Bulevertide (BLV)-treated HDV patients.

**Method:** This is a single-center retrospective study, evaluating frozen sera from consecutive untreated and BLV-treated HDV patients. HDV RNA levels were quantified by Robogene HDV RNA quantification kit 2.0 (Roboscreen GmbH, Leipzig, Germany; LOQ 6 IU/ml, linear range 5 to 10^8 IU/ml, panenotypic) by using two different extraction methods: manual method, i.e., INSTANT Virus RNA/DNA kit (Analytik Jena AG, Jena, Germany) versus automatic method, i.e., EZ1 DSP Virus Kit (Qiagen, Hilden, Germany).

**Results:** 96 frozen sera collected from 18 Caucasians patients with CHD either untreated (baseline) or BLV treated were analyzed. The main baseline features of the patients were the following: 48 (29–77) years, 67% males, 100% HDV-GT1, 100% cirrhosis, all without TDF or ETF treatment; 67% previously interferon-exposed; ALT 106 (32–222) U/L, HBsAg 3.7 (2.5–4.3) Log IU/ml; 94% HBeAg negative, 72% HBV DNA undetectable. Overall, HDV-RNA levels were 3.61 (0.70–6.60) vs 2.66 (0.70–5.52) Log IU/ml, by manual vs automated extraction. Viremia tested undetectable in 0 (0%) vs 1 (1%), while <LOQ in 3 (3%) vs 14 (15%) patients, respectively. Compared to the automated method, manual RNA extraction reported higher HDV-RNA levels in 90 samples [median 0.80 (0.07–2.11) Log IU/ml], similar levels in 3 [two <LOQ samples, and one 197 IU/ml], and lower levels in 3 [0.11 (0.09–0.17 Log IU/ml). In 15 samples tested “undetectable” or <LOQ by the automated method, HDV-RNA was <LOQ in 3, and positive low-titer [30 (7–92) IU/ml] in 12 samples tested with manual one. During the first 6 months of BLV monotherapy, HDV-RNA progressively declined using both manual [baseline 4.29–3.76–3.52–2.74–2.26 Log IU/ml] and automated extraction [3.59–3.41–2.64–1.61–0.85 Log IU/ml], achieving <LOQ result in 11% vs 47% at month six, respectively.

**Conclusion:** Quantification of HDV RNA by Robogene 2.0 is significantly influenced by the extraction method, the manual extraction being more sensitive although more time consuming. Therapeutic trials with new anti-HDV therapeutics should consider this important information.

**SAT382**  
Combination therapy in HBeAg-negative chronic hepatitis B patients with low-level viremia to nucleos (tide) analogues

Xin-Yue Chen1,2, Shan Ren1,2,3, Junfeng Lu1,2, Lina Ma2, Sujun Zheng2, Zhongjie Hu2.

**Background and aims:** Considering that the ultimate goals of treatment are to decrease the morbidity and mortality related to chronic hepatitis B (CHB), the recently updated guidelines of liver disease recommend that people with low-level viremia (LLV) to nucleos (tide) analogues (NAs) should switch or add another drug for people with a suboptimal virological response. To compare and evaluate the efficacy and safety of pegylated interferon (peg-IFNα) in combination with NAs and NAs in combination with NAs in HBeAg-negative CHB patients with LLV to NAs, so as to investigate optimal treatment regimen with end point of therapy.

**Method:** Totally 240 HBeAg-negative CHB patients with LLV to NAs were enrolled in the study, and divided into 2 groups receiving Peg-IFNα+NAs (IFN group) or NAs+NAs (NA group) according to administration of NAs. Complete virological response (HBV DNA concentration of less than 20 IU/ml or 100IU/ml) rate, HBsAg loss/seroconversion rate at 48 weeks of treatment were compared between the 2 groups.

**Results:** There were 178 patients in IFN group and 89 patients in NA group, and 162 patients in the IFN group and 78 patients in NA group received 48-week treatment. At 12 weeks of treatment, the complete virological response rate was 51.1% (40/78) in the NA group, which was seemed higher than that in the PegIFN group (45.1%, 73/162), but the difference was not statistically significant (X^2 = 0.52, P = 0.47). At 48 weeks, the complete virological response rates of PegIFNα group and NA group were 97.50% (158/162) and 85.90% (67/78), respectively, with statistically significant differences (X^2 = 10.56, P = 0.001). There was no significant difference in HBsAg levels at baseline between the PegIFN group and NA group (823.97 vs. 988.50, t = 0.80, P = 0.43). In the PegIFNα group, HBsAg titer decreased significantly from baseline to week 12 (823.97 vs. 527.7, t = 2.31, P = 0.02), and then it decreased slowly from week 12 to week 24 (399–324.9IU/ml). While in the NA group, HBsAg titer did not change significantly from baseline to week 48, there was no statistically significant difference (988.5 vs. 847.1, t = 0.84, P = 0.41). At week 48, the HBsAg loss/seroconversion rate in PegIFNα group (50/162, 30.9%) was higher than that in NA group (4/78, 5.1%), and the difference was statistically significant (X^2 = 19.89, P < 0.001).

**Conclusion:** The treatment regimens of Peg-IFNα+NAs and NAs+NAs are effective in suppression of HBV replication in HBeAg-negative CHB patients with LLV to NAs, but Peg-IFNα+NAs is superior to NAs+NAs in. Combination therapy with IFN as the basis will achieve reliable end point of therapy in HBeAg-negative CHB patients with LLV to NAs.

**SAT383**

ABI-4334, a novel inhibitor of hepatitis B virus core protein, promotes formation of empty capsids and prevents covalently closed circular DNA formation by disruption of incoming capsids

Nuruddin Unchwanimala1, William Delaney1, Kathryn M Kitrinos1.

1Assembly Biosciences, Inc., South San Francisco, United States

Email: kkitrinos@assemblybio.com

**Background and aims:** Core inhibitors (CIs) are a novel class of antivirals with the potential to improve cure rates in patients with chronic hepatitis B virus infection (CHBV). CIs have demonstrated potent antiviral activity in Phase 1 clinical studies and additive antiviral activity when combined with nucleos (t)ide reverse transcriptase inhibitors (NtRs) compared to NtRs alone in Phase 2 studies. CIs have multiple mechanisms of action, including inhibition of pre-genomic RNA (pgRNA) encapsidation, preventing assembly and release of infectious viral particles and disruption of incoming capsids, preventing covalently closed circular DNA (cccDNA) formation. ABI-4334 (4334) is a novel CI with single digit nM potency against pgRNA encapsidation and cccDNA formation. Here we further characterize the preclinical profile of 4334.

**Method:** CI binding pocket variants and NtR-resistant mutants were assessed for 4334 sensitivity in a HepG2 transient transfection assay. Specificity of 4334 for HBV inhibition was assessed using a panel of 7 different viruses. Effects on pgRNA encapsidation were determined by inducing AD38 cells in the presence of 10x EC50 4334 for 4 days. Intracellular levels of core protein, HBV DNA, and HBV pgRNA were measured by Western, Southern, and Northern blots, respectively. Intracellular capsid levels were measured by native gels. 4334 effects on cccDNA formation were determined by infecting HepG2–NTCP cells with HBV, treating with 4334 for 3 hours (capsid DNA) or 4 days (cccDNA), and then measuring HBV DNA species by Southern blot.

**Results:** 4334 demonstrated broad antiviral activity with activity comparable to wild-type for 14/16 CI binding pocket variants and 7/7 NtR mutants. The antiviral activity of 4334 was specific to HBV, with no activity against any other viruses, including HIV and HCV. 4334 did not impact intracellular core protein levels but inhibited pgRNA encapsidation resulting in empty capsid formation, thus acting as a class II CI. Addition of 4334 also resulted in premature melting of incoming capsids during early infection stages, resulting in significantly lower levels of total HBV DNA deposition and cccDNA formation.
Effect of 4334 on pgRNA Encapsulation

- % Relative to DMSO
- ETV
- 4334

Core Protein Capsids DNA RNA Encapsitated

Conclusion: 4334 is a potent CI with broad coverage across CI binding pocket variants and Nrt1 mutants. The activity of 4334 against pgRNA encapsidation is consistent with a class II CI. 4334 treatment results in melting of cytoplasmic HBV capsids, which prevents cccDNA formation. A Phase 1a first-in-human study with 4334 is planned for 2022.

SAT384
Real-world high adherence to hepatitis B antiviral treatment practices in Israel
Yana Davidov1, Fadi Abu Baker2, Ariel Israel1, Ziv Ben Ari1,2, Sheba Medical Center, Liver Diseases Center, Tel Aviv-Yafo, Israel; 2Hillel Yaffe Medical Center, Department of Gastroenterology and Hepatology, Hadera, Israel; 3Leumit Health Services, Leumit Research Institute and Department of Family Medicine, Israel; 4Tel Aviv University, Sackler School of Medicine, Tel Aviv-Yafo, Israel
Email: y.davidov@gmail.com

Background and aims: Epidemiologic data regarding chronic hepatitis B virus (CHB) infections in Israel are limited as large population-based studies have not been performed. This work aimed to evaluate adherence to European Association for the Study of the Liver (EASL) practice guidelines to antiviral treatment in Israel.

Method: Clinical and demographic data of HBsAg-positive patients registered in the Leumit-Health-Service database (one of the four major health maintenance organizations in Israel) between 2000-2019, were retrieved. Patients were compared according to eligibility to antiviral treatment, and type of nucleos (t)ide analogue (NA) treatment.

Results: In total, 1216 patients had documented HBsAg positivity (Israel born: 95.8%, males: 58.6%, mean age: 40.2 ± 14.2 years), 90.6% of whom were HBsAg negative. Cirrhosis was documented for 6% of the patients. Antiviral therapy eligibility was met by 37% of patients, among whom 89% received antiviral therapy. Antiviral therapies include NA with a high barrier to resistance (HBR) (64.5%) (entecavir 36.3% and tenofovir 28.2%) and NA with a low barrier to resistance (LBR) (35.5%) (adefovir 17.1% and lamivudine 33.8%). Compared to patients who received LBR NA, patients receiving HBR NA had shorter treatment (68.7 ± 50 months vs. 161.5 ± 42.6 months, p < 0.0001) and follow-up duration (125 ± 68 months vs. 188 ± 48 months, p < 0.0001); at the end of follow-up ALT levels and APRI score were higher among patients on LBR NA compared to patients on HBR NA.

Conclusion: Most of the patients infected with HBV were born in Israel and were HBsAg-negative. The majority of the patients received antiviral treatment according to the international practice guidelines. However, one-third of them were treated with a less potent NA probably due to their lower cost. These findings should encourage optimization of HBV care and full compliance with the professional practice guidelines recommendations.

SAT385
No detectable resistance to bulevirtide in participants with chronic hepatitis D (CHD) through 24 weeks of treatment
Julius Hollnberger1,2, Yang Liu3, Ross Martín3, Savrina Manhas3, Thomas Aeschbacher2, Silvia Chang4, Simin Xu3, Bin Han3, Tahmineh Yazdii3, Lindsey May3, Dong Han3, Katrin Schöneweis3, John F. Flaherty3, Vithika Suri1, Dmitry Manuilov1, Roberto Mateo3, Evguenia S Sravovskaja3, Hongmei Mo3, Stephan Urban1,4,1University Hospital Heidelberg, Department of Molecular Virology, Heidelberg, Germany; 2German Center for Infection Research (DZIF), Heidelberg; 3Gilead Sciences, Inc., Foster City, United States; 4German Center for Infection Research (DZIF), Heidelberg, Germany
Email: stephan.urban@med.uni-heidelberg.de

Background and aims: Bulevirtide (BLV) blocks entry of HDV into hepatocytes via inhibition of the interaction between the HBV preS1 domain and the sodium taurocholate cotransporting polypeptide (NTCP) receptor. Previous studies show that treatment with BLV alone leads to a substantial HDV RNA reduction. Here, we present results from a comprehensive virologic analysis in HDV-infected participants who received BLV at doses of 2 mg, 5 mg, or 10 mg subcutaneously once daily for 24 weeks across two studies (MYR202 [Phase 2] and MYR301 [Phase 3]).

Method: Resistance analysis was performed for participants who experienced a suboptimal response to BLV (virologic non-responder [VNR]; defined as a decline in HDV RNA <1 log10 IU/ml from baseline [BL] at week 24) or virologic breakthrough (VB, defined as two consecutive increases in HDV RNA ≥2 log10 IU/ml from nadir or two consecutive HDV RNA values ≥LOD if previously <LOD). Virologic partial responder (VPR) and virologic responder (VR) were defined as HDV RNA decline ≥1 but <2 log10 IU/ml and decline ≥2 log10 IU/ml or HDV RNA <LOD at Week 24 respectively. Resistance testing included deep sequencing of the HBV PreS1 BLV region and HDV HDAg region. Additionally, in vitro phenotypic testing was performed for clinical isolates at baseline and Week 24 for VNRs and those with VB. For the analysis control, sequencing and/or phenotypic analysis were performed for all available BL samples in the two studies.

Results: Overall, resistance analyses were performed for 26 VNRs and 1 participant with VB representing 13/77 (17%), 9/32 (28%), and 5/80 (6%) participants receiving daily BLV at 2 mg, 5 mg, and 10 mg groups, respectively. No amino acid substitutions at HBV PreS1 BLV region or HDV HDAg associated with resistance to BLV were identified from any (6%) participants receiving daily BLV at 2 mg, 5 mg, and 10 mg groups, respectively. No amino acid substitutions at HBV PreS1 BLV region or HDV HDAg associated with resistance to BLV were identified from any participants at BL and Week 24. Clinical isolates carrying the amino acid substitutions remained sensitive to BLV in vitro; all the amino acid substitutions were seen in the participants achieving a virologic response. Importantly, by phenotypic analysis, BLV medium EC50 values obtained from 117 baseline samples were similar across VNRs (EC50 = 0.42 nM), VPR (EC50 = 0.38 nM) and VR (EC50 = 0.27 nM) regardless of the presence of HBV and HDV polymorphisms.

Conclusion: This is the largest resistance analysis to date to demonstrate that no genotypic and phenotypic resistance to BLV has been detected through 24 weeks of treatment.
Background and aims: Currently approved therapies for chronic hepatitis B (CHB) infrequently achieve a functional cure in patients, which requires a sustained loss of hepatitis B surface antigen (HBsAg). In CHB patients, HBV targeted small interfering RNAs (siRNAs) have significantly reduced HBsAg, indicating a potential for their use in a curative therapeutic regimen. Here we evaluate the antiviral activity of ALG-125755, a N-acetylgalactosamine (GalNAc)-conjugated siRNA, in the adeno-associated virus (AAV)–HBV mouse efficacy model and its pharmacokinetic (PK) and safety profile in rats and monkeys.

Method: In the AAV–HBV mouse model, various doses of ALG-125755 or vehicle were administered subcutaneously (SC) once, biweekly for 10 weeks (6 doses), or monthly for 8 weeks (3 doses). For 24 weeks during dosing and follow-up, blood and liver samples were collected for plasma HBsAg and hepatitis B e antigen (HBeAg) assessments and liver ALG-125755 concentrations. The plasma samples were analyzed by LC-hybridization whereas the liver samples were analyzed by LC-MS for ALG-125755 concentration. For PK and toxicity studies, rat and monkey were given single or weekly subcutaneous doses of ALG-125755 and plasma, liver and kidney were collected at various timepoints and analyzed for ALG-125755 concentrations by LC-MS. The plasma samples were analyzed for plasma HBsAg and hepatitis B e antigen (HBeAg) assessments and liver ALG-125755 concentrations. The plasma samples were analyzed by LC-hybridization whereas the liver samples were analyzed by LC-MS for ALG-125755 concentration. For PK and toxicity studies, rat and monkey were given single or weekly subcutaneous doses of ALG-125755 and plasma, liver and kidney were collected at various timepoints and analyzed for ALG-125755 concentrations by LC-MS. The plasma samples were analyzed for plasma HBsAg and hepatitis B e antigen (HBeAg) assessments and liver ALG-125755 concentrations. The plasma samples were analyzed by LC-hybridization whereas the liver samples were analyzed by LC-MS for ALG-125755 concentration. For PK and toxicity studies, rat and monkey were given single or weekly subcutaneous doses of ALG-125755 and plasma, liver and kidney were collected at various timepoints and analyzed for ALG-125755 concentrations by LC-MS. The plasma samples were analyzed for plasma HBsAg and hepatitis B e antigen (HBeAg) assessments and liver ALG-125755 concentrations. The plasma samples were analyzed by LC-hybridization whereas the liver samples were analyzed by LC-MS for ALG-125755 concentration. For PK and toxicity studies, rat and monkey were given single or weekly subcutaneous doses of ALG-125755 and plasma, liver and kidney were collected at various timepoints and analyzed for ALG-125755 concentrations by LC-MS. The plasma samples were analyzed for plasma HBsAg and hepatitis B e antigen (HBeAg) assessments and liver ALG-125755 concentrations. The plasma samples were analyzed by LC-hybridization whereas the liver samples were analyzed by LC-MS for ALG-125755 concentration. For PK and toxicity studies, rat and monkey were given single or weekly subcutaneous doses of ALG-125755 and plasma, liver and kidney were collected at various timepoints and analyzed for ALG-125755 concentrations by LC-MS. The plasma samples were analyzed for plasma HBsAg and hepatitis B e antigen (HBeAg) assessments and liver ALG-125755 concentrations. The plasma samples were analyzed by LC-hybridization whereas the liver samples were analyzed by LC-MS for ALG-125755 concentration. For PK and toxicity studies, rat and monkey were given single or weekly subcutaneous doses of ALG-125755 and plasma, liver and kidney were collected at various timepoints and analyzed for ALG-125755 concentrations by LC-MS. The plasma samples were analyzed for plasma HBsAg and hepatitis B e antigen (HBeAg) assessments and liver ALG-125755 concentrations. The plasma samples were analyzed by LC-hybridization whereas the liver samples were analyzed by LC-MS for ALG-125755 concentration. For PK and toxicity studies, rat and monkey were given single or weekly subcutaneous doses of ALG-125755 and plasma, liver and kidney were collected at various timepoints and analyzed for ALG-125755 concentrations by LC-MS. The plasma samples were analyzed for plasma HBsAg and hepatitis B e antigen (HBeAg) assessments and liver ALG-125755 concentrations. The plasma samples were analyzed by LC-hybridization whereas the liver samples were analyzed by LC-MS for ALG-125755 concentration. For PK and toxicity studies, rat and monkey were given single or weekly subcutaneous doses of ALG-125755 and plasma, liver and kidney were collected at various timepoints and analyzed for ALG-125755 concentrations by LC-MS. The plasma samples were analyzed for plasma HBsAg and hepatitis B e antigen (HBeAg) assessments and liver ALG-125755 concentrations. The plasma samples were analyzed by LC-hybridization whereas the liver samples were analyzed by LC-MS for ALG-125755 concentration. For PK and toxicity studies, rat and monkey were given single or weekly subcutaneous doses of ALG-125755 and plasma, liver and kidney were collected at various timepoints and analyzed for ALG-125755 concentrations by LC-MS. The plasma samples were analyzed for plasma HBsAg and hepatitis B e antigen (HBeAg) assessments and liver ALG-125755 concentrations. The plasma samples were analyzed by LC-hybridization whereas the liver samples were analyzed by LC-MS for ALG-125755 concentra...
infection (cHBV). In vitro, VBR is not a potent inhibitor of CYP450 s or drug transporters. Here we describe the clinical evaluation of VBR’s drug-drug interaction (DDI) potential from Phase 1 and Phase 2a studies.

**Method:** Studies 201 (NCT03577171; N = 73) and 202 (NCT03576066; N = 25) were Phase 2a, double-blind, placebo-controlled studies evaluating VBR and NrtIs in patients with cHBV in which sparse PK samples were collected. Study 103 was a 3-part Phase 1 DDI study in healthy subjects. Part 1 (N = 20) investigated the potential of VBR to inhibit CYP2C9, 2C19, 2D6, and 2C8 through use of the index substrates tolbutamide, omeprazole, dextromethorphan, and repaglinide, respectively. Parts 2 (N = 18) and 3 (N = 20) evaluated CYP3A4 and 2B6 inhibition/induction, respectively, using midazolam and bupropion. Intensive PK samples were collected, and PK analysis was conducted by non-compartmental methods.

**Results:** In Studies 201 and 202, there were no clinically significant differences in mean trough VBR or NrtI concentrations following combination therapy in patients with cHBV (Figure 1a/1b). In Study 103 (Part 1), co-administration of VBR did not change the exposure of omeprazole, dextromethorphan, or repaglinide, suggesting VBR is not an inhibitor of CYPs 2C19, 2D6, or 2C8. Tolbutamide exposure was increased by approximately 30% with VBR co-administration, indicating VBR is a weak inhibitor of CYP2C9. In Part 2, midazolam exposure was reduced by 33% following co-administration with VBR, with no concomitant change in 1-hydroxymidazolam exposure, indicating VBR is not an inhibitor/inducer of CYP3A4. In Part 3, co-administration of VBR did not change the exposure of bupropion, indicating VBR is not an inhibitor/inducer of CYP2B6.

**Conclusion:** The results in Phase 2a studies suggest no clinically significant DDI between VBR and NrtIs. Based on the Phase 1 study, VBR is a weak inhibitor of CYP2C9, but is not an inhibitor of CYP2C19, 2D6, or 2C8. Overall, VBR shows a favorable DDI profile for use in combination treatments including NrtIs and other concomitant medications.

**SAT389**

**Improving the pharmacokinetic profile of the hepatitis B virus core inhibitor ABI-H3733 following oral administration: results from new formulation activities**

Michael Shen1, Zhixin Zong1, Naqqi Mohammed1, Katie Zomorodi1, Luisa M Stamm1, William Delaney1, Nicole White1. 1Assembly Biosciences, Inc., South San Francisco, United States

Email: mshen@assemblybio.com

**Background and aims:** ABI-H3733 (3733) is a novel orally administered inhibitor of the hepatitis B virus (HBV) core protein, a viral structural protein essential for HBV replication. 3733 targets multiple aspects of the viral replication cycle and has the potential to enhance cure rates for patients with chronic HBV infection (cHBV). 3733 is in Phase 1 development and has demonstrated favorable systemic exposure with a half-life of 21 hours using a liquid formulation (LF) in healthy subjects. An initial prototype tablet formulation (T1) only achieved 30% exposure compared to the LF with predicted trough concentrations (Cmin) approximately 28- and 5.5-fold higher than the protein-adjusted EC50 (paEC50) for pgRNA encapsidation and cccDNA formation, respectively, providing the opportunity to improve formulation for future clinical studies.

**Method:** The initial LF and T1 formulations of 3733 were tested in dog pharmacokinetic (PK) studies (at a dose of 50 mg) and assessed in healthy subjects at doses ranging from 100 to 500 mg. Due to the low exposure of T1 in both dogs and humans, a new tablet formulation (T2) was designed to improve the absorption and achieve comparable exposure as the LF. The pharmacokinetics of T2 and LF were evaluated in 6 male beagle dogs at 100 mg (3 dogs with T2 and 3 dogs with LF).

**Results:** In the initial dog PK study, T1 showed 36.7% AUC compared to the LF at 50 mg dose (human equivalent dose of approximately 150 mg). Human PK data were comparable with the dog PK data indicating the dog is a predictive model to evaluate the relative exposure for different formulations. T2 was subsequently tested in the dog PK model at 100 mg dose (predicted human equivalent dose 300 mg) and showed equivalent AUC compared to the LF.

**Conclusion:** Based on the relative PK data in the dog model, T2 formulation is expected to have similar 3733 exposure as the LF in humans, with predicted Cmin approximately 150- and 29-fold higher than the paEC50 for pgRNA encapsidation and cccDNA formation, respectively. The improved T2 formulation will be used in an upcoming Phase 1b study conducted with cHBV patients.

**Figure:** Mean Plasma Concentration-time Profiles of 3733 After Single Oral Doses of LF and T2 in Male Beagle Dogs

**Conclusion:** The results in Phase 2a studies suggest no clinically significant DDI between VBR and NrtIs. Based on the Phase 1 study, VBR is a weak inhibitor of CYP2C9, but is not an inhibitor of CYP2C19, 2D6, or 2C8. Overall, VBR shows a favorable DDI profile for use in combination treatments including NrtIs and other concomitant medications.
Background and aims: EDP-514, a novel class II HBV core inhibitor, demonstrated nanomolar potency in vitro, and a 4- to 4.4-log viral load reduction in an HBV mouse model. Here, we present the safety, pharmacokinetic (PK) and antiviral activity from a phase 1b study of multiple ascending doses (MAD) of EDP-514 in nucleo(-tide) (nuc)-suppressed chronic hepatitis B (CHB) patients.

Method: This phase 1/2, randomized, double-blind, placebo-controlled study was conducted in two parts. In Part 1, healthy adult subjects received single or multiple ascending doses of EDP-514 or placebo. In Part 2, noncirrhotic, HBeAg (+) or (-) subjects virologically suppressed on nuc therapy received EDP-514 or placebo in a 3:1 ratio of 24 subjects in 3 cohorts: 200 mg, 400 mg, 800 mg) for 28 days.

Results: The 24 subjects enrolled were mostly male (63%), Asian (67%), HBeAg (+) or (-) (88%), treated with tenofovir (92%), with a mean age of 45 years and a mean BMI of 27 kg/m². All T2EAEs (n = 20) were mild except for 1 moderate event (200 mg) of abdominal pain that led to drug discontinuation, and 1 severe allergic reaction to aloes cream (800 mg). There were no other grade 3 T2EAEs or any SAEs. No clinically significant laboratory abnormalities, liver function tests elevations or clinically relevant ECG or vital signs changes were observed. EDP-514 exhibited PK support of once-daily (QD) dosing, with trough concentrations up to ~21-fold above the EC50. HBV DNA remained undetectable and no virologic failures or breakthroughs were reported through 28 days of treatment. At Day 28, a maximum HBV RNA reduction of 2.3 log in HBeAg (+) and 2.8 log in HBeAg (+) patients was observed in EDP-514 arms compared to 1.2 log in placebo. There were no discernible changes in HBeAg, HbcAg, and HBsAg.

Conclusion: EDP-514 was safe and well tolerated through 28 days of treatment in CHB nuc-suppressed patients, showed time-linear PK supportive of QD dosing with concentrations of up to ~21-fold above the paEC50, and resulted in a higher log reduction in HBV RNA; up to a maximum of 2.8 log, was observed in HBeAg (+) patients receiving EDP-514.

SAT391
Preclinical activity of small-molecule oral PD-L1 checkpoint inhibitors capable of reinvigorating T cell responses from chronic hepatitis B patients

Emily P. Thi1, Andrew G. Cole1, Gavin Heffernan1, Christina Jott1, Seyma Ozturk1, Sharie C. Ganchua1, Dan Nguyen1, Ingrid Graves3, Vijay Ahuja4, Kim Stever1, Kristi Fan1, Jorge C. Quintero1, Steven G. Kultgen1, Maria Shubina1, Boya Liu1, Sunny Tang1, Troy O. Harasym5, Angela M Lam1, Michael J. Sofia1, Michael Child4, Gaston Picchio4, Karen Sims4, Man-Fung Yuen6

Background and aims: T cell tolerance is a critical driver in maintaining chronic hepatitis B (CHB) infection. The PD-1/PD-L1 checkpoint axis plays a key role in tolerization and inhibition of this axis by antibody approaches has been associated with loss of hepatitis B surface antigen and seroconversion in CHB patients. Oral small-molecule inhibitors of PD-L1 can enable tuneable on-target engagement with potential for better tissue penetration and improved efficacy. Here we report the preclinical in vitro activity of these compounds, as well as in vivo efficacy and ability to reinvigorate HBV-specific T cells from CHB patients.

Method: In vitro activity was assessed in a Jurkat T cell NFAT reporter assay and PD-L1 reduction was confirmed in CHO-K1 cells expressing human PD-L1 (CHO-K1-hPD-L1) and in peripheral blood mononuclear cells (PBMCs) from healthy donors. T cell activation assays were conducted with PBMCs from healthy donors and CHB patients. Non-specific cytokine release was evaluated in human whole blood. Pharmacokinetic (PK) evaluations were conducted in rodents and non-human primates (NHP). In vivo efficacy was evaluated in a MC38 tumor humanized PD-L1 and PD-1 mouse model.

Results: Two optimised PD-L1 inhibitor compounds were evaluated which mediated potent activation of T cells in a Nfat reporter assay (EC50s of 13 and 18 nM). Compound treatment resulted in reduction of PD-L1 expression on the cell surface through a novel internalization mechanism, with EC50 ranging from 1.9–24 nM in CHO-K1-hPD-L1 and primary human myeloid cells. Dose responsive elevations in IL-2 production occurred upon compound treatment of PBMCs stimulated with staphylococcal enterotoxin B. Compound treatment did not elicit non-specific cytokine release in human whole blood, supportive of favourable immune safety. PK profiles showed low systemic clearance in rodents and NHP. In a MC38 tumor model, oral administration of compounds at 10 and 30 mg/kg once daily resulted in profound tumor reduction with T cell activation comparable to anti-PD-L1 antibody. PD-L1 inhibitor treatment of PBMCs from CHB patients ex vivo resulted in HBV-specific T cell reinvigoration.

Conclusion: Novel oral small molecule PD-L1 inhibitors able to mediate activation and reinvigoration of HBV-specific T cells from CHB patients were identified. These compounds display in vivo anti-tumor efficacy comparable to anti-PD-L1 antibody and possess favourable preclinical profiles for further development.

SAT392
Safety, tolerability, pharmacokinetics (PK), and antiviral activity of the 3rd generation capsid inhibitor AB-836 in healthy subjects (HS) and subjects with chronic hepatitis B (CHB)

Edward J Gane1, Alina Jucov2, Liudmyla Kolomichuk3, Timothy Eley4, Joanne Brown4, Yele King4, Elina Medvedeva5, Maksym Chernyakhovskyj6, Nagraj Mani5, Andrew G. Cole5, Steven G. Kultgen5, Reddy Pamulapati5, Emily P. Thi1, Troy O. Harasym5, Ravi Dugyala5, Sabin Chaudhuri5, Michael J. Sofia5, Michael Child4, Gaston Picchio4, Karen Sims4, Man-Fung Yuen6,7

Background and aims: AB-836 is an ongoing 3-part study evaluating safety, PK and antiviral activity of AB-836 in HS (Parts 1 and 2) and CHB subjects (Part 3). Preliminary data from Parts 1, 2 and the first 2 cohorts of Part 3 are presented.

Method: In Part 1, HS enrolled into two 8-subject cohorts and were randomized to single doses of AB-836 or placebo (6:2) in 5 alternating dose panels from 10mg-175 mg fasted, and a 6th panel of 125 mg with food. In Part 2, 3 unique cohorts of 10 HS were randomized to 50 mg, 100 mg or 150 mg or placebo (8:2) once daily (QD) for 10 days. In Part 3, 2 ongoing cohorts of 12 HBV DNA+, HBeAg
(-) or (-) CHB subjects will randomize to 50 mg or 100 mg or placebo (10:2:QD for 28 days. Samples are collected for PK in all subjects and antiviral activity in CHB subjects. Safety and tolerability are monitored throughout.

**Results:** HS (N = 47) were mean age 29 years, mean BMI 24.7 kg/m², all male and 57% white. CHB subjects (N = 10) were mean age 44 years, mean BMI 23.5 kg/m², 60% male, 70% white, 60% HBeAg (-) with mean 5.2 log₁₀ IU/ml HBV DNA at baseline (BL). Preliminary safety data showed AB-836 was well-tolerated in HS. No deaths or serious adverse events (AEs) were observed. One HS (50 mg QD) discontinued on Day 13 due to an AE of agitation. All but 3 AEs were mild (Grade 2 headache, agitation, and bronchitis); only 1 was assessed as related to AB-836 (Grade 1 rash). In ongoing Part 3, there have been no AEs; 1 CHB subject (100 mg) had a transient increase in ALT from BL Grade 1 to Grade 3 at a single visit that resolved with continued dosing. There were no clinically significant abnormalities in clinical laboratory tests in HS and no clinically significant abnormalities in ECGs, vital signs or physical exams in any subject. Single and multiple dose AB-836 PK in HS were dose proportional and support QD dosing with/without food. Mean (SE) HBV DNA log₁₀ change from BL at Day 28 was −2.4 (0.3), −3.1 (0.8) and −0.0 (0.19) at 50 mg, 100 mg, and placebo, respectively. Updated data will be presented.

**Conclusion:** Single and multiple doses of AB-836 in HS and up to 100 mg QD for 28 days in CHB subjects have been generally safe and well-tolerated. Robust antiviral activity was observed at Day 28 of treatment. These results support further evaluation of AB-836 alone and in combination with other agents, including the GalNAc siRNA analogue withdrawal: 4.5 year follow-up of the Toronto STOP Study

**Background and aims:** Studies have found benefits in nucleos(t)ide analogues (NA) discontinuation in chronic hepatitis B (CHB) patients, but currently heterogeneous outcomes are observed with little understanding of the long-term implications of stopping therapy. This study prospectively evaluates clinical outcome comparisons in HBeAg negative patients who stop or continue NA, and those with eventual retreatment.

**Method:** 67 HBeAg negative patients in a randomized control study were allocated to stopping (n = 45) or continuing (n = 22) NA therapy and were evaluated over 4.5 years. Patients were retreated based on standardized protocol if they had HBV DNA >20, 000 IU/ml, HBeAg seroreversion, or HBV DNA>2000 IU/ml, virological relapse (HBV DNA >2000 IU/ml), clinical relapse (HBV DNA >2000 IU/ml and ALT>1.5xULN). HBeAg decline >0.5 IU/ml and HBsAg loss were compared.

**Results:** Mean duration of long-term follow-up (LTU) was 227 weeks. 23/45 (51%) stop patients were retreated, with median time to retreatment of 36 weeks. HBeAg loss was achieved by 2/45 (4%) patients who stopped and 1/21 (5%) continue patients at LTU. Virological relapse and clinical relapse in the stop group was observed in 41 (91%) patients and 32 (71%) patients, respectively. HBeAg decline >0.5 IU/ml at LTU was achieved by 12/22 (55%) not
retreated stop patients, 10/23 (43%) retreated stop patients, and 3/22 (14%) continue patients. Incidence of HBsAg decline >0.5 IU/ml was higher in the stop group than those in the continue group (p < 0.05). Higher mean HBsAg decline was also observed in the stop group (-0.67 IU/ml) compared to continue group (-0.15 IU/ml, p < 0.05) by end of follow-up. No patients experienced adverse outcomes, liver decompensation, or death.

Conclusion: CHB patients that stop NA have high prevalence of virological relapse and clinical relapse. However, despite a limited HBsAg loss, those that stop therapy exhibited higher HBsAg reduction compared to continued NA treatment.

S490 Pharmacodynamics of durable HBsAg suppression by AB-729 short interfering RNA correlates with pharmacokinetics of RNA-induced silencing complex (RISC) loading within liver
Emily P. Thi1, Maria Shubina1, Ingrid Graves1, Angela M Lam1, Michael J. Sofia1, Arbutus Biopharma, Warminster, United States

Background and aims: AB-729 is an N-Acetylgalactosamine (GalNAc)-conjugated short interfering RNA (siRNA), currently in Phase 2a clinical development in combination with other agents for treatment of CHB. AB-729 blocks all HBV RNA transcripts, resulting in durable suppression of viral replication and antigen production, including circulating HBV DNA and the hepatitis B surface antigen (HBsAg). This antiviral effect is mediated through association of AB-729 with the RNA-induced silencing complex (RISC), the RNA:protein complex responsible for mediating cleavage of HBV RNA. Here we investigate the mechanisms underlying the extent and duration of AB-729 activity through assessment of siRNA persistence in liver using an adenovirus-associated HBV (AAV-HBV) mouse model.

Method: Longitudinal serum, plasma, and liver samples from AAV-HBV mice receiving a single dose of either a non-HBV targeting control GalNAc siRNA or a surrogate GalNAc siRNA containing the AB-729 siRNA trigger (HBV-siRNA) (1 or 3 mg/kg, n = 8) were assessed for HBsAg and total and RISC-loaded siRNA by chemiluminescent immunoassay, Ago2 immunoprecipitation and stem-loop quantitative reverse-transcription polymerase chain reaction.

Results: A dose responsive decline in serum HBsAg occurred following single doses of 1 and 3 mg/kg of HBV-siRNA, with mean maximum declines of 0.9 log10 and 1.9 log10 at Day 14, respectively. The kinetics of HBsAg decline did not correlate with that of total intrahepatic concentrations of HBV-siRNA, which peaked at 4-hour post dose and rapidly declined over time. Instead, maximal HBsAg reduction coincided with an increase in the number of RISC-loaded complexes. A decline in the number of RISC-loaded complexes was observed following day 14, mirroring a rebound in HBsAg. HBsAg subsequently returned to baseline 112 days after single doses of HBV-siRNA, which correlated with the detection of only trace amounts of RISC-loaded complex.

Conclusion: HBsAg suppression mediated by AB-729 in CHB patients is characterized by durable responses which persist up to 48 weeks post-dosing. The mechanisms driving this long duration of activity have not yet been assessed. Our preclinical data reveals that HBsAg reduction coincides with the pharmacokinetics of siRNA RISC-loading. These data suggest that the direct-acting antiviral activity of AB-729, mediated by RNA interference activity, may be a key driver of the prolonged HBsAg suppression observed in CHB patients administered AB-729.

SAT396 Inhibition of hepatitis B surface antigen by RNA interference therapeutic AB-729 is associated with increased cytokine signatures in HBV DNA+ chronic hepatitis B patients
Sharie C Ganchua1, Bhavna Paratala1, Christina lott1, Man-Fung Yuen2, Edward J Gane2, Timothy Eley1, Karen Sims1, Kevin Gray1, Deana Antoniello1, Angela M Lam1, Michael J. Sofia1, Gasto Picchio1, Emily P. Thi1, Arbutus Biopharma, Warminster, United States; Queen Mary Hospital, Hong Kong; Auckland Clinical Studies, New Zealand

Background and aims: Therapeutic strategies aimed at reducing antigenemia, particularly hepatitis B surface antigen (HBsAg), may result in HBV-specific immune reawakening in chronic hepatitis B (CHB). AB-729 is a single trigger N-Acetylgalactosamine (GalNAc)-conjugated siRNA targeting all HBV transcripts, currently in clinical development in combination with other agents for CHB treatment. Here we report immunological assessment of cytokines and other soluble immune biomarkers in CHB subjects not currently on nucleos(t)ide analog (NA) therapy (HBV DNA+) and compare these profiles to NA-suppressed (HBV DNA-) CHB subjects receiving a single dose of AB-729.

Method: Longitudinal plasma samples from subjects receiving a single dose of AB-729 (90 mg, n = 5 HBV DNA+, n = 6 HBV DNA-) were assessed for cytokines and other soluble immune biomarkers using multiplex Luminex assays.

Results: Following a single dose of AB-729, transient elevations of 2 to 38-fold over pre-dose baseline levels in at least one of IFNg, CXCL1, IP-10, sBTLA, sLAG3, sLR2, sGITRL, sPD-L1, sCD80, and sCD86 were observed in 5/5 HBV DNA+ subjects. In HBV DNA- subjects, transient elevations of 2 to 7-fold over pre-dose baseline were observed in at least one of IFNg, IL-17a, CXCL9, CXCL13 and CD163 (3/6 subjects). In HBV DNA+ subjects, transient increases in IFNg (4/5 subjects) and CXCL1 (3/5 subjects) were associated with transient ALT elevations in the period up to 12 weeks post-dose. In contrast, in HBV DNA- subjects ALT elevation was accompanied by IFNg increase in only 1/6 subjects. All ALT elevations were mild (Grade 1) and no liver safety markers were considered adverse by the investigators.

Conclusion: We believe this is the first data comparing immunological responses of HBV DNA+ and DNA- CHB subjects undergoing HBsAg reduction following GalNAc-siRNA treatment. Our findings suggest that following AB-729 dosing, a greater breadth of cytokine and soluble immune biomarker responses with IFNg and T cell activation signatures are observed in HBV DNA+ subjects compared to NA-suppressed CHB patients. Transient elevations in point-related markers in HBV DNA+ patients were also observed, which were accompanied by mild ALT elevations. These results suggest that HBV DNA+ CHB patients are more immunologically responsive following AB-729 dosing. Assessment of responses following AB-729 repeat dosing in HBV DNA+ subjects with concomitant initiation of NA therapy is ongoing.
SAT397
Reduction of hepatitis B surface antigen mediated by RNA interference therapeutic AB-729 in chronic hepatitis B patients is associated with T cell activation and a decline in exhausted CD8 T cells
Sharie C Ganchua1, Bhavna Paratala1, Christina Iott1, Edward J Gane2, Man-Fung Yuen1, Timothy Eley1, Karen Sims1, Kevin Gray1, Deana Antoniello1, Angela M Lam1, Michael J. Sofía1, Gaston Picchio1, Emily P. Thi1, 1Arbutus Biopharma, Warminster, United States; 2Auckland Clinical Studies, New Zealand; 3Queen Mary Hospital, Hong Kong
Email: ethi@arbutusbio.com

Background and aims: AB-729 is a GalNAc-conjugated RNA interference (RNAi) therapeutic, currently in Phase 2 clinical development in combination with other agents for the treatment of chronic hepatitis B (CHB). Reduction of antigenemia in CHB, particularly hepatitis B surface antigen (HBsAg), may result in HBV-specific immune reawakening. Here we report immunological assessments in CHB subjects receiving repeat doses of AB-729 after 48 weeks (wks) of treatment and 12 wks of follow-up.

Method: Longitudinal plasma and peripheral blood mononuclear cell (PBMC) samples from virologically suppressed subjects undergoing repeat dose dosing of AB-729 60 mg every 4 weeks (Q4W, n = 5 for PBMC; n = 6 for plasma assays) or every 8 weeks (Q8W, n = 7 for plasma assays; n = 2 for PBMC) were assessed using Luminex, IFN gamma (IFNg) T cell fluoro-spot, immunophenotyping by flow cytometry and thymidine-based T-cell proliferation assays.

Results: By EOT, 5/5 subjects receiving AB-729 Q4W exhibited increases in IFNg-producing HBV-specific T cells. 3/5 subjects had increases in IFNg-HBV-specific T cells between wks 16–28 which coincided with a plateau in HBsAg response, mild to moderate transient serum alanine aminotransferase (ALT) elevations (Grade 1–2), and was preceded by T cell proliferation. 2/5 subjects experienced pronounced increases in IFNg-HBV-specific T cells at EOT or at 12 wks follow-up. HBV-specific T cell IFNg production was also observed in subjects receiving AB-729 Q8W dosing (2/2). A decline in exhausted CD8 T cells was observed beginning at wk 28 and was present at EOT and at 8–12 wks of follow-up (AB-729 Q4W cohort; 4/6 subjects, Figure). This decline in exhausted CD8 T cells coincided with a plateau in HBsAg response. No significant increases in plasma cytokine/chemokine levels were observed. Mild increases in sBTLA, sCD86, sCTLA-4, sPTHA, sCTLA4. No changes in adverse events related to liver safety markers were noted in either cohort.

Conclusion: Our findings suggest that HBsAg reductions, as a result of treatment with repeat doses of AB-729 every 4 or 8 weeks, is accompanied by HBV-specific T cell activation and proliferation with mild to moderate ALT elevations. A decline in exhausted CD8 T cells at the end of treatment and at 8–12 weeks of follow-up suggest that HBV-specific T cell immune restoration (reawakening) may be durable.

SAT398
Characterizing of hepatitis B virus serum RNA kinetics during TDF plus pegylated interferon alfa-2a with and without nucleic acid polymers
Leeor Hershkovich1, Louis Shekhtman1, Michel Bazinet2, Mark Anderson3, Mary Kuhrns3, Gavin Cloherty3, Scott Cotler1, Andrew Vaillant2, Harel Dahari1, 1Program for Experimental and Theoretical Modeling, Division of Hepatology, Department of Medicine, Stritch School of Medicine, Loyola University Chicago, Maywood, United States; 2Replicor Inc., Montreal, Quebec, Canada; 3Abbott Diagnostics, Abbott Park, IL, United States
Email: harel.dahari@gmail.com

Background and aims: Serum HBV RNA (RNA), and HBV core-related antigen (HbcAg) are markers of cccDNA activity. Little is known about the serum RNA response during tenofovir disoproxil fumarate (TDF), and pegylated interferon alpha-2a (pegIFN) with and without nucleic acid polymer (NAP) treatment. Here we aim to characterize RNA kinetics under TDF and pegIFN with and without NAP combination therapies.

Method: Forty participants with chronic HBV in the REP 401 study (Gastro 2020; 158:2180–94) received 48 weeks of triple combination therapy with NAPs, pegIFN, and TDF. In the experimental group (n = 20), triple combination therapy (TDF + pegIFN + NAPs) followed 24 weeks of TDF. In the control group (n = 20), triple combination therapy followed 24 weeks of TDF monotherapy and 24 weeks of dual therapy (TDF + pegIFN). Abbott RUO assay for RNA (LLOQ 1.65 log10 U/ml) was used every 4 weeks. The threshold for kinetic patterns was defined as a 3-fold change.

Results: Under dual therapy 10 (50%) participants experienced had RNA increase which was followed by a new elevated plateau (n = 6) or by a decline (transient increase, n = 4). All 6 participants establishing a new elevated RNA plateau level experienced a subsequent monophasic decline in RNA following the introduction of NAPs in the control group (Table 1). Under triple therapy in the experimental group 11 (55%) participants had a transient increase. The timing of RNA flares was significantly (p < 0.02) correlated with ALT flares.
Conclusion: TDF + pegIFN induces transient increases in serum HBV RNA which either self-resolve or resolve in the presence of NAPs. The correlation of serum HBV RNA elevations with ALT flares suggests release of HBV RNA containing virus subsequent to cytolytic clearance of infected hepatocytes. The mechanism by which pegIFN or NAPs lead to an RNA increase may not indicate an increase in cccDNA activity and requires further research.

SAT399
Early antiviral efficacy of tenofovir alafenamide fumarate in the initial treatment of chronic hepatitis B patients with normal ALT

Background and aims: Patients were screened according to antiviral treatment indications recommended by China Guidelines for the prevention and treatment of chronic hepatitis B, some patients (over 30 years old or have a family history of liver cancer) will have ALT in normal range (An upper limit of normal for ALT is 50 U/L for males and 40 U/L for females). This study was designed to investigate the therapeutic effect of tenofovir alafenamide fumarate (TAF) on chronic hepatitis B (CHB) patients with normal alanine transaminase (ALT).

Method: A total of 79 treat-naive CHB patients treated with TAF antiviral therapy alone in Beijing Ditan Hospital, Capital Medical University from November 2018 to May 2021 were reviewed, including 39 patients in normal ALT group and 40 patients in abnormal ALT group. The clinical data of patients at baseline and 24 weeks after treatment were collected, and the changes of HBV DNA, serum hepatitis B virus e antigen (HBsAg) and hepatitis B virus surface antigen (HBsAg) were compared between the two groups before and after treatment.

Results: After 24 weeks of treatment, in the normal ALT group, HBV DNA decreased significantly from (5.0 ± 2.1) log10 IU/ml to (2.0 ± 1.5) log10 IU/ml (p = 0.000), in abnormal ALT group, HBV DNA decreased from (6.7 ± 1.9) log10 IU/ml to (1.8 ± 1.0) log10 IU/ml (p = 0.000). After 24 weeks of treatment, the rate of complete viremia resolution (CVR) (HBV DNA <20 IU/ml) was 64.1% (25/39) in the normal ALT group, and 50.0% (20/40) in the abnormal ALT group. There was no significant difference between the two groups (p = 0.206). The CVR rates of normal ALT group and abnormal ALT group were 100% at baseline of low viral load (HBV DNA <10^3). At 24 weeks, the proportion of HBV DNA target not detected (TND) in the normal ALT group was 43.6% (17/39), significantly higher than that in the abnormal ALT group [12.5% (5/40)] (p = 0.003). Subgroup analysis was performed for the normal ALT group according to the reference upper limit of normal (ULN) recommended by AASLD 2016 (male ≤30 U/L, female ≤19 U/L). In normal ALT group (AASLD 2016), the CVR is 92.3% (12/13), in 30 U/L < ALT ≤50 U/L (male) and 19 U/L < ALT < 40 U/L (female) group, the CVR at 24 w is 50% (13/26), respectively, the difference was statistically significant (p = 0.013).

Conclusion: Tenofovir alafenamide fumarate can obtain better antiviral efficacy in CHB patients with normal ALT, and the efficacy is not lower than that in CHB patients with abnormal ALT.

SAT400
Viral and ALT kinetics after nucleos (t)ide analogue withdrawal among patients who remain off-therapy: results from a global, multi-ethnic cohort of chronic hepatitis B patients (RETRACT-B study)

Grishma Hirote1,2,3, Bettina Hansen1,3, Chien-Hung Chen4, Tung-Hung Su5, Margarita Papatheodoridi5, Sabela Lens7, Stijn Van Hees8, Sylvia Brakenhoff9, Hannah S.J. Choi1, Rong-Nan Chien10, Wai-Kay Seto11, Grace Wong12, Jordan Feld1,2,3, Henry LY Chan12, Man-Fung Yuen13, Milan Sonneveld9, Thomas Vanwolleghem8, Xavier Forns7, George Papatheodoridis6, Jia-Horang Kao1, Yao-Chun Hsu13, Markus Cornberg4, Rachel Wen-Juei Jeng10, Harry Janssen1,2,3, Toronto General Hospital, University Health Network, Toronto Centre for Liver Disease, Toronto, Canada; 1University of Toronto, Institute of Medical Science, Toronto, Canada; 2The Toronto Viral Hepatitis Care Network (VIRCAN), Toronto, Canada; 3KaoHSiang Chang Gung Memorial Hospital, Taiwan; 4National Taiwan University Hospital, Taiwan; 5Medical School of National and Kapodistrian University of Athens, Greece; 6Hospital Clinic Barcelona, University of Barcelona, IDIBAPS and CIBEREHD, Barcelona, Spain; 7Antwerp University Hospital, Department of Gastroenterology and Hepatology, Antwerp, Belgium; 8Erasmus MC University Medical Center, Department of Gastroenterology and Hepatology, Rotterdam, Netherlands; 9Chang Gung Memorial Hospital Linkou Medical Center, Chang Gung University, Department of Gastroenterology and Hepatology, Linkou, Taiwan; 10The University of Hong Kong, Hong Kong, Department of Medicine and State Key Laboratory of Liver Research, Hong Kong; 11The Chinese University of Hong Kong, Hong Kong; 12E-DA Hospital-I-Shou University, Kaohsiung, Taiwan; 13Centre for Individualized Infection Medicine (CiIM), Hannover Medical School, Department of Gastroenterology, Hepatology and Endocrinology, Hannover, Germany.

Background and aims: Recent studies have analyzed the best candidates for nucleos (t)ide analogue (NA) cessation with respect to HBsAg loss. However, whether patients remain off-therapy is often dependent on local reimbursement policies. Patients who remain off-therapy, with/without HBsAg loss, have not been well characterized. We aim to describe this group and analyze early viral and biochemical kinetics after NA cessation.

Method: Virally suppressed, non-cirrhotic CHB patients who were HBsAg negative at NA cessation were included. Patients with coinfection, prior interferon therapy, or prior HCC diagnoses were excluded. We used mixed-effects regression to analyze HBsAg, HBV DNA, and ALT kinetics among patients who remained off-therapy at the end of 1 yr after NA cessation; only patients with follow-up ≥1 yr were included.
Conclusion: Early kinetics were good indicators of outcomes following NA cessation among patients who remain off-therapy. Patients without HBsAg loss showed increases in HBV DNA and ALT with worse clinical outcomes and only nominal decreases in HBsAg compared to those who achieved HBsAg loss.

SAT401
Discovery of oral PDL1 small molecule inhibitors specifically designed for the treatment of chronic hepatitis B
Tongfei Wu1, Sarah Stevens2, Cheng Liu2, Kristina Rekstyte-Matiene3, Elke Behaeghel1, Sucheta Mukherjee2, Sandra Chang2, Ruchika Jaisinghani2, Antissa Stoycheva2, Andreas Jekle2, Qingling Zhang2, Kusum Gupta2, Jerome Deval2, Julian Symons2, Lawrence Blatt2, Leonid Beigelman2, Pierre Raboisson1, Francois Gonzalez2, 1Aligos Belgium BVBA, Leuven, Belgium, Belgium; 2Aligos Therapeutics, Inc., South San Francisco, CA, Belgium; 3Novelix, Leuven, Belgium.
Email: fgonzalvez@aligos.com

Background and aims: Chronic hepatitis B (CHB) is characterized by high viral replication and exhaustion of virus-specific T cells. In CHB patients, upregulation of PD1 on HBV-specific T cells and PD1 on liver cells cause T-cell exhaustion and persistent viral infection. Therefore, inhibiting the PD1/PDL1 pathway has recently emerged as an attractive therapeutic strategy to restore a virus-specific T cell response and reverse immune tolerance. Seven PD1/PDL1 antibodies are currently approved as cancer therapies and nivolumab (anti-PD1) has demonstrated some clinical efficacy in CHB patients. However, the systemic immune-related adverse effects associated with antibodies limit their therapeutic window and therefore, there is a need to develop better tolerated PDL1/PDL1 inhibitors for CHB patients. Here, we rationally designed oral PDL1 small molecule inhibitors to localize T cell activation to the liver and thereby mitigate systemic toxicity in CHB patients.

Method: Biochemical PD1/PDL1 interaction was assessed by AlphalISA®. Cellular activity was measured using a co-culture reporter assay in which NFAT activity of Jurkat T cells is constitutively inhibited by the engagement of PD1 by PDL1-expressing CHO cells. In vivo pharmacokinetic analyses and efficacy were assessed in humanized-PDL1 MC38 subcutaneous xenografts and in the AAV-HBV mouse model. HBV-specific T cell activation assays were performed in PBMCs from an HBV-infected patient and assessed by measuring IFNγ release.

Results: Using structure-based and rationale design, we identified a series of oral PDL1 small molecule inhibitors. In biochemical assays, our lead molecules inhibited PD1/PDL1 interaction with an IC50 value of 16 pM. In PD-1/PDL1 blockade cellular assays, these compounds increased TCR signaling with an EC50 value of 1.5 pM, a similar potency to nivolumab. In mice, our lead molecules displayed good oral bioavailability and high liver/plasma ratios. When dosed orally in MC38 tumor-bearing mice, our lead molecules were well tolerated. Importantly, these compounds showed similar in vivo efficacy to durvalumab in this tumor model that relies on systemic exposure. To test whether our compounds can release exhaustion of HBV-specific T cells, we stimulated PBMCs from an HBV-infected patient with HBV peptide antigens in presence of our lead compounds (Figure). ALG-093453 activated HBV-specific T cells in a dose dependent manner to similar or higher extend as nivolumab and durvalumab.

Conclusion: We designed oral PDL1 small molecule inhibitors specifically for CHB. Our lead molecules show similar in vitro potency and in vivo efficacy in systemic models to FDA-approved PD1/PDL1 antibodies, together with high liver/plasma exposure ratios. Our PDL1 small molecule inhibitors have the potential to activate HBV-specific T cells in the liver, while decreasing bystander T cell activation in the periphery.
ASOs target the open reading frames of the small HBsAg and the HBx protein respectively. Both ASOs contain next generation spirocyclopropyl Bridged Nucleic Acid (scp BNA) and nucleobase modified monomers that reduced hepatotoxicity while maintaining efficacy in AAV-HBV mouse model. In this study, we further explored additional BNAs such as guanidine-bridged nucleic acid (GuNA) and other proprietary BNAs in the sequences of ALG-020572 and ALG-020576. We demonstrated that further improvement of in vitro and in vivo activities could be achieved.

Method: ASOs with lNA and 3rd gen BNA chemistries were synthesized on MerMade 12 and MerMade 48 synthesizers. In vitro screening of ASOs was carried out in HepG2.2.15 cells or HBV infected primary human hepatocytes (PHH) using an HBsAg release assay. The AAV-HBV mouse model was used to test efficacy and hepatotoxicity of GalNAc-ASOs by analyzing HBsAg and ALT in mouse plasma.

Results: ALG-021682 and ALG-021639 are GalNAc 4 conjugated ASOs targeting the same site as ALG-020572. ALG-021682 contains GuNA and ALG-021639 contains a novel 3rd gen BNA. Unconjugated ALG-021682 showed a 5-fold lower EC50 than unconjugated ALG-020572 in HepG2.2.15 assay. In HBV infected PHH, the unconjugated ALG-021639 was 5-fold more potent than unconjugated ALG-020572. When tested in the AAV-HBV mouse model, both ALG-021682 and ALG-021639 exhibited a 2-fold lower HBsAg nadir than that of the ALG-020572 analog when dosed at a single dose of 5 mg/kg subcutaneously. None of the ASOs demonstrated ALT elevations. Finally, ALG-021618 is an ALG-020576 derived ASO with a novel structure. It was inactive in vitro due to the inability to be metabolically processed by HepG2.2.15 cells. However, in the AAV-HBV mouse model with 3 × 10 mg/kg repeat dosing on days 0, 3 and 7, ALG-021618 achieved a HBsAg nadir of − 1.8 log10 IU/ml vs. − 1.2 log10 IU/ml for ALG-020576. By day 60, ALG-020576 dosed animals reverted to baseline HBsAg levels but ALG-021618 still suppressed HBsAg by 1 log10 IU/ml.

Conclusion: GuNA and other novel BNAs improved the in vitro and in vivo activities of our lead ASO ALG-020572. Novel modifications of ALG-020576 significantly improved the in vivo depth and durability of HBsAg knockdown. Further investigations combining these chemistries are ongoing.

SAT404
Induction of pre-s antibodies in HBsAg negative chronic hepatitis B patients by therapeutich vaccination with the pre-s based subunit vaccine VXX001-interim analysis

Petra Munda1, Ina Tulaeva2, Rudolf E. Stauber3, Pia Gattringer2, Michael Trauner1, Helmut Brunar4,5, Rudolf Valenta2, Peter Ferenci2.
1Medical University of Vienna, Internal Medicine 3, Gastroenterology and Hepatology, Austria; 2Medical University of Vienna, Internal Medicine 3, Gastroenterology and Hepatology, Austria; 3Medical University of Graz, Internal Medicine 1, Graz, Austria; 4Vivaraxon AG, Austria
Email: peter.ferenci@meduniwien.ac.at

Background and aims: VXX001 is an HBV vaccine candidate based on a HBV-derived preS fused to grass pollen allergen peptides. The aim of this prospective double-blind, placebo-controlled trial (NCT03625934) was to investigate if VXX001 can induce preS-specific antibody and T cell responses in 4 different cohorts including patients with chronic hepatitis B.

Method: This is an interim analysis of non-cirrhotic patients with HBeAg-negative chronic hepatitis B on long-term treatment (>3 years) with nucleo (t)sides analogues (NUCs) (cohort 4a) treated either with 5 s.c. injections (visits 2, 3, 4, 5, 6) of either VX001 or placebo in 4-week intervals (randomized 3:1), respectively Inclusion criteria: HBV DNA <20 IU/ml (detection limit); HBsAg<1000 IU/ml. Thirteen verum patients (87%) remained HBV-DNA negative with normal ALT, and none of them required repeated NUC treatment. A longer follow-up is needed to evaluate the long-term impact of vaccination and stop of NUC therapy.

SAT404
HEC121120, a novel allosteric modulator of HBV core protein demonstrates potent antiviral activities in vitro and in vivo

Qingying Lai1, Pu Wang1, Xinchang Liu2, Qingyun Ren2, Baohua Gu1, Jing Li1, Yunfu Chen1. 1State Key Laboratory of Anti-Infective Drug Development (NO. 2014DQ780357), Sunshine Lake Pharma Co., Ltds, Pharmacology and toxicology division, Dongguan, China; 2State Key Laboratory of Anti-Infective Drug Development (NO. 2015DQ780357), Sunshine Lake Pharma Co., Ltds, Dongguan, China
Email: chenyunfu@hec.cn

Background and aims: Capsid assembly modulators (CAMS) represent a clinically validated strategy for the treatment of chronic hepatitis B. Here, we report on HEC121120, a novel class I CAM with improved antiviral activities in vitro and in vivo.

Method: Antiviral activities on HBV DNA were determined in HepG2.2.15 cells and in HBV-infected primary human hepatocytes (PHH) both in vitro and ex vivo using quantitative PCR. In vivo antiviral efficacy was assessed in the AAV-HBV mouse model with 8 weeks of treatment and 4-week off-treatment follow-up period.

Results: HEC121120 showed potent antiviral activity on HBV DNA production (EC50 = 5.03 nM) in HepG2.2.15 cells with low cytotoxicity (CC50≥150 μM), similar to that of GLS4 (EC50 = 8.66 nM, CC50≥150 μM). However, significantly enhanced potency was demonstrated in HBV-infected PHH with EC50 150.3 nM and 724 nM for HEC121120 and GLS4, respectively. In PHH isolated from chronically infected
humanized liver mouse, 14 days of GLS4 (5 μM) and HEC121120 (2 μM) treatment resulted in suppression of HBV DNA, HBsAg and HBeAg while entecavir (ETV) had no effect on either viral antigen. To compare with similar compounds in AA V-HBV mouse model, treatment with ETV (0.1 mg/kg, QD, p.o.) and JNJ-632 (200 mg/kg, QD, s.c.) resulted in potent reduction of serum HBV DNA but no significant impact on serum HBsAg and HBeAg level. In contrast, both GLS4/RTV (25/20 mg/kg, BID, p.o.) and HEC121120 (12.5 mg/kg or 50 mg/kg, BID, p.o.) potently suppressed HBsAg and HBeAg in addition to HBV DNA. At the end of treatment, HBV DNA declined 3.6, 1.7, 3.5, 4.2, 5.5 log10 for ETV, JNJ-632, GLS4/RTV, HEC121120 (12.5 mg/kg dose) and HEC121120 (50 mg/kg dose), respectively. The mean decline for HBsAg was 1.0, 0.9, 1.4 log10 and the mean decline of HBeAg was 0.6, 0.8, 1.2 log10 for GLS4/RTV, HEC121120 low dose and HEC121120 high dose. There was no significant rebound of viral antigens in GLS4/RTV and HEC121120 treated animals during the 4-week follow-up period. Furthermore, liver IHC showed HBcAg positive hepatocytes were significantly reduced in HEC121120 treated groups compared to control. Similar to GLS4, HEC121120 caused a dose dependent, self-limiting ALT elevations but at an earlier time and with increased magnitude in higher dose group of HEC121120. Concomitantly, the decrease of HBsAg correlated well with the timing and magnitude of ALT, indicative of ALT flare as a therapeutic effect.

Conclusion: HEC121120 is a novel class I CAM, which demonstrated improved antiviral properties both in vitro and in vivo, further clinical study will be conducted to evaluate the antiviral potency in CHB patients.

SAT405
Evaluation of quantitative HBsAg levels in chronic hepatitis B—a targeted literature review
Anadi Mahajan1, Saifuddin Kharawala1, Nitesh Singh1, Supriya Desai1, Stuart Kendrick2, Emily Lloyd2, Vera Gielien2. 1Bridge Medical Consulting, London, United Kingdom; 2GlaxoSmithKline, Research and Development, United Kingdom
Email: anadimahajan@bridgemedical.org

Background and aims: A targeted literature review (TLR) was conducted in patients with chronic hepatitis B (CHB). Objective 1: Hepatitis B surface antigen (HBsAg) titres across disease phases, and their cross-sectional relationship with clinical, biochemical and treatment characteristics. Objective 2: Association between HBsAg titres and long-term disease outcomes (cirrhosis, hepatocellular carcinoma [HCC], liver transplant, mortality). Objective 3: Change in HBsAg titres and their relationship with the above characteristics.

Method: Structured searches were performed in MEDLINE® and Embase® (January 2000 to March 2021), with bibliographic searches, hand searches of relevant congress abstracts (2019–2021) and grey literature searches.

Results: Of all studies identified, 59 were selected for reporting, of which 46% were retrospective-cohort and 25% prospective-cohort. HBsAg titres were generally higher in initial Hepatitis B e-antigen (HBeAg)-positive phases than in later HBeAg-negative phases. Cross-sectionally, higher HBsAg titres were consistently associated with higher Hepatitis B Virus (HBV) DNA levels (moderate-to-strong in HBeAg-positive phases; weak-to-moderate in HBeAg-negative phases) and lower age (moderate). Greater decline in HBsAg was consistently associated with subsequent HBsAg seroclearance (hazard ratio [HR]: 1.95 to 43.83) and with lower HBV DNA levels (odds ratio [OR]: 2.82 to 26.52 for virological response). HBsAg titres predicted development of HCC and cirrhosis in treatment-naïve CHB patients by multivariate analysis. Data were limited for prediction of cirrhosis.

Conclusion: HBsAg titres are associated with HBV DNA and age across CHB phases. Decline in HBsAg titres is associated with HBsAg seroclearance and lower HBV DNA levels. HBsAg titres can predict the development of long-term outcomes.

Funding: GlaxoSmithKline (Study 217135).

Conflicts of interest: SKh, AM, NS and SD are employees of Bridge Medical.

SAT406
Nucleoside/nucleotide analogoues monotherapy is safe and efficient for the prevention of HBV flare-ups after liver transplantation in the long term
Orly Sneh Arbib1, Assaf Issachar1,2, Marius Braun1,2, Michal Cohen-Naftaly1,2, Yael Harif1, Evelin Oxtrud1. 1Beilinson, Petah
Background and aims: The recurrence rate of HBV after transplantation decreased dramatically due to prophylactic therapy including hepatitis B immunoglobulin (HBlg) and nucleoside/nucleotide (Nuc) analogues. Published data on cessation of HBlg after transplantation and treatment with Nuc analogues as monotherapy are scarce especially in western world.

In 2013 we decided to stop HBlg in liver transplant patients with undetectable HBV DNA in serum during follow-up, more than 2y post LT with good compliance, normal liver function tests that were HBeAg negative and with viral load less than 2000IU/ml at transplantation. Lamivudine was switched to entecavir or tenofovir, before stopping HBlg. Due to excellent results we decided in 2018 stop HBlg as soon as possible after transplantation in patients who fulfill the other criteria.

We aimed to determine the long-term efficacy of Nuc analogues monotherapy for prevention of HBV seroconversion and flare-up of hepatitis. Overall graft and patient were assessed.

Method: This is a retrospective study on a prospectively maintained data base of transplanted patients in the largest transplant center in Israel. All patients that required LT due to HBV and its complications are followed up by biannual liver function tests, HBV serology, HBV DNA, AFP and ultrasound.

Results: 630 liver transplants were performed in our center since 1995, 420 patients are in active follow-up. HBV related disease was the reason for LT in 84 patients, and 25 were eligible for monotherapy (Table 1). The patients were treated with dual therapy for an median time of 7.2 years (IQR 3.4–12.7 years). During a follow-up of median 6.8 years (IQR 4.2–7.4 years) after HBlg discontinuation there were no hepatitis flares, however, two patients treated with entecavir had detectable HBsAg in serum (one of them also temporarily exhibited low titre HBV DNA in serum during follow-up). Two patients had detectable HBsAb, two years after the HBlg was discontinued. There was no recurrence of HCC. There was no graft failure. Five patients received active immunization.

Conclusion: The Long term follow-up reiterates the safety and efficacy of monotherapy with Nuc analogous in carefully selected Caucasian patients including HCC patients and HBV/HDV co-infected patients.

SAT407
A new method to identify co-variation in hepatitis B virus whole genome sequences identifies networks of polymorphisms associated with drug resistance
Sheila Lumley1, Steven Lin2, Louise Downs1, Cori Campbell1, Anna McNaughton3, Azim Ansari1, Philippa Matthews4, 1Peter Medawar Building for Pathogen Research; 2Wellcome Trust Centre for Human Genetics; 3University of Bristol; 4The Francis Crick Institute
Email: sheila.lumley@trinity.ox.ac.uk

Background and aims: We developed a model to identify coevolving amino acid (aa) sites within or between hepatitis B virus (HBV) proteins with the aim of identifying structural or functional protein interactions while accounting for the population structure among the isolates (founder effect). Here we present a computationally efficient method to identify co-varying sites across the HBV genome in the context of its phylogeny. We examine the trends in covariation across the genome and apply this to the study of drug resistance associated mutations (RAMs).

Method: We downloaded 9313 genotype A, B, C and D whole genome HBV sequences from HBVdb. We aligned, deduplicated and translated them into a sequences. We built a phylogeny for each genotype and

Figure 1: (abstract: SAT407): Network analysis highlighting covarying pairs in which one or more amino acids are Lamivudine or Tenofovir RAMs. Each node represents an amino acid. Node colour indicates the protein: p = reds, C = greens, S = blues, X = yellow. Line width is inversely proportional to the adjusted harmonic mean p value.
reconstructed the ancestral state for each polymorphic site. We used Fisher exact test to investigate covariance between a changes on the tree between two sites. We combined p values using harmonic mean p value and used false discovery rate to account for multiple testing.

**Results:** We identified 1066 co-varying aa pairs across the genotypes; 547 (51%) pairs involved core protein, 532 (50%) polymerase, 351 (33%) surface, and 87 (8%) X. Core protein was enriched in the proportion of covarying sites relative to other proteins. Within-protein covariations were enriched across all genotypes. Of the 615 within-protein covarying pairs, 53 (9%) were adjacent, and 60 (10%) were ≤3 a apart. For genotypes B, C and D, most co-variaying sites were linked in a dominant network, the largest of which included 131/186 (70%) covarying amino acids (genotype B). Identification of known primary/secondary RAM pairs in this dataset validated our method; previously reported RAMs were enriched among the covarying sites (OR 2.1, p <0.05). 136 pairs were identified where one or more sites was a known RAM. RAMs co-varied in networks spanning all four proteins (Fig 1), demonstrating the global epistatic connectivity of RAMs.

**Conclusion:** Covariation analysis reveals a complex, genotype-specific network of a substitutions in HBV. We have shown how this method can describe networks of RAMs, and it could further provide evidence of sites of clinical relevance pertinent to understanding viral evolution and phylogeny, immune escape, and therapeutic vaccine design.

SAT408

Baseline bile acid levels but not bile acid increases during bulevirtide treatment of hepatitis D are associated with HDV RNA decline

Katja Deterding1, Cheng-Jian Xu1,2, Kerstin Port1.

1 Hannover Medical School, Gastroenterology, Hepatology and Endocrinology, Hannover, Germany; 2 Center for Individualized Infection Medicine, CiIM, a joint venture between Hannover Medical School and the Helmholtz Center for Infection Research, Hannover, Germany

**Background and aims:** Bulevirtide is an entry inhibitor blocking entry of HBsAg into hepatocytes by interfering with Na+-taurocholate cotransporting polypeptide (NTCP), the HBV/HDV receptor. As NTCP is a bile acid transporter, one would expect an increase of bile salts during bulevirtide treatment. Still, there is no data available if the increase in bile acids reflect antiviral efficacy.

**Method:** We studied 14 patients (11 male, 3 female) with compensated HDV infection receiving bulevirtide 2 mg subcutaneously once daily for at least 12 weeks. The median age of the patients was 48 years (±12, 44) and all of the patients had liver cirrhosis or advanced fibrosis and 7 were previously treated with pegylated interferon alfa.

**Results:** ALT levels improved in all patients over time with 7/14 patients showing normal ALT values at treatment week 12. An HDV RNA drop of at least 50% was evident in 12/14 patients at week 12 including 8 patients with a more than 1log IU/ml and 2 patients achieving a fast response with more a than 2 log HDV RNA decline. Total serum bile acids showed a heterogeneous pattern before and during treatment. Bile salts levels were above the limit of normal already before treatment in 6 patients and increased during bulevirtide administration with different kinetics in most patients. Of note, no patient reported systemic itching. Baseline bile acids were associated with higher transient elastography values (p = 0.01) but liver stiffness was not associated with bile acid changes during treatment.

**Bile acid levels before the start of treatment were associated with HDV RNA declines at treatments weeks 2, 8 and 12 (rho = −0.70 and p = 0.005, rho = −0.75 and p = 0.002, rho = −0.61 and p = 0.02, respectively; see figure).** However, bile acid increases during treatment were not associated with subsequent HDV RNA declines at neither time point (p = 0.73; p = 1, p = 0.28, respectively).

**Conclusion:** In conclusion, we demonstrate that the bileviritide-induced increase in bile salts does not correlate with HDV RNA decline in patients with hepatitis D. Thus, blocking HBsAg entry and interfering with the bile acid transporter function of NTCP occur at different concentrations. Thus, in clinical practice, regular measurement of bile salts during bulevirtide treatment does not predict virological response to bulevirtide treatment.

SAT409

Low levels of qHBsAg and tenofovir therapy are associated with successful treatment withdrawal in HBeAg negative chronic hepatitis B: results from spanish multicentric study

Anna Pocurull1,2,3,4, Elena Hoyas5, Manuel Rodríguez6, Mireia Miquel1, Clara Amiama Roig1, Sergio Rodriguez-Tajes1,2,3,4, Francisco Javier García-Samaniego Rey5, Emilio Suarez6, Sabela Lenz1,2,3,4, Anna Pocurull1,2,3,4, Elena Hoyas5, Manuel Rodríguez6, Mireia Miquel1, Clara Amiama Roig1, Sergio Rodriguez-Tajes1,2,3,4, Francisco Javier García-Samaniego Rey5, Emilio Suarez6, Sabela Lenz1,2,3,4, 1Hospital Clínic de Barcelona, Liver Unit; 2University of Barcelona; 3IDIBAPS; 4CIBEREHD; 5Hospital Universitario Virgen de Valme, Sevilla; 6Hospital Universitario Central de Asturias, Oviedo; 7Hospital Parc Taulí, Sabadell; 8Hospital La Paz, Madrid

**Background and aims:** Clinical guidelines suggest that nucleos(t)ide analogues (NA) discontinuation in HBeAg negative chronic hepatitis B (CHB) may increase functional cure rates. However, information about predictive factors in Caucasian patients is still limited also influenced by different re-treatment criteria. We aimed to analyze baseline factors and outcomes after NA withdrawal in 5 Spanish Centers with homogeneous re-treatment criteria.

**Method:** Prospective inclusion of 96 non-cirrhotic patients with HBeAg-negative CHB in complete viral suppression after >3 years. The re-treatment criteria after NA withdrawal were: ALT >10 upper limit normal (ULN) and bilirubin >2 mg/dl, ALT >5 ULN during 1 month, or ALT >2 ULN and DNA-VHB >2,000 IU/ml >6 months.

**Results:** The median age of the cohort was 55 (IQR: 46–63) years old and 68% were male. Fibrosis values assessed by Fibroscan® were low in all cases (4, 9 (4–6) kPa). At the time of NA withdrawal, 72% received tenofovir and 28% entecavir [median treatment duration of 11 (7–15) years, similar in both groups]. qHBsAg levels (n = 89) were 904 (305–2416) IU/ml. After a median follow-up of 28 (24–47) months after NA withdrawal, Twenty-two patients (23%) achieved HBeAg loss. Previous treatment with tenofovir (p < 0.05) and low levels of qHBsAg (<1000 IU/ml) before stopping treatment (p < 0.05) were associated to a higher rate of functional cure. Twenty-six patients (27%) accomplished re-treatment criteria due to ALT >5 ULN (n = 5) or >10 ULN (n = 7) of which 5 also had bilirubin >2 mg/dl. One patient required liver transplantation due to a fulminant hepatitis.
**SAT410**  
**Preliminary results of the effectiveness and safety of Tenofovir Alafenamide Fumarate prophylaxis in HBV-infected individuals, who received chemo/immunosuppressive therapy**

Feyza Gunduz1, Serdar Durak2, Yasemin Unsal3, Mehmet Demir4, Zeynep Melekgolu Elik5, Abdullah Emre Yildirim6, Shahin Mehdiyev7, Haydar Adanir7, Coskun Ozer Demirtas1, Enver Ucbilek8, Yasemin Balaban9, Elif Sitre Koç10, Ayse Batirel11, Gulten Unlu12, Ozgur Gunal13, Levent Gorenek1, Fatma Sirmatel12, Alper Senere1, Emin Parlak14, Fehmi Tabak16, Ankara City Hospital, Turkey; Istanbul Training and Research Hospital, Turkey; Sakarya University School of Medicine, Turkey; Ege University Faculty of Medicine, Turkey; Hittti University Faculty of Medicine, Turkey; Istanbul Bagcilar Training and Research Hospital, Turkey; Duzce University Faculty of Medicine, Turkey; Recep Tayyip Erdogan University Faculty of Medicine, Turkey; Sisli Hamideye Etfal Training and Research Hospital, Turkey; Bezmii Alem Vakif University Faculty of Medicine, Turkey; Ankara University School of Medicine, Turkey; Istanbul University Faculty of Medicine, Turkey; Fatih University Faculty of Medicine, Turkey; Istanbul University Faculty of Medicine, Turkey; Gaziantep University School of Medicine, Turkey; Akdeniz University School of Medicine, Turkey; Mersin University School of Medicine, Turkey; Hacettepe University School of Medicine, Turkey; Acibadem University School of Medicine, Turkey; Baskent University School of Medicine, Turkey; Health Sciences University, Umraniye Training and Research Hospital, Turkey; Ankara City Hospital, Turkey  

**Background and aims:** There are very limited data regarding the efficacy and safety of tenofovir alafenamide fumarate (TAF) prophylaxis to prevent HBV reactivation in HBV-infected individuals undergoing chemo/immunosuppressive therapy. The aims of the present study were to determine the effectiveness and safety of TAF prophylaxis in HBV-infected individuals, who receive chemo/immunosuppressive therapy.

**Method:** This is a multicenter, observational study. Data were entered in a standardized electronic case report form (CRF) from each center and collected from the CRF. TAF was administered at a dose of 25 mg/day at the initiation of the chemo/immunosuppressive therapy. The mean follow-up period was 17.1 ± 7.8 months.

**Results:** A total of 326 HBV-infected individuals with benign and malign diseases received TAF prophylaxis. Among these patients, 158 patients (57.0%: 83/158) with at least 6 months of follow-up were included into analysis. Mean age was 59.55 ± 12.2 years. Thirty patients had detectable HBV DNA and 5% were HBeAg positive. Solid tumors were the most common primary disease (33.5%), followed by rheumatic diseases (32.9%) and myeloproliferative diseases (32.2%). Of these patients, 48% received cytotoxic chemotherapy, 17% received B cell depletion therapy, 13% received anti-TNF therapy, 8% were received glucocorticoid therapy, and 12% patients were received other treatments. During the follow-up period, none of the patients had clinical, biochemical, and serological evidence of HBV reactivation under TAF prophylaxis. No HBV-related morbidity and mortality was observed. HBV DNA became negative in 77% of the patients with detectable HBV DNA. All patients maintained their chemo/immunosuppressive therapy without interruption. TAF prophylaxis was well tolerated. The renal function tests and lipid profiles, except triglyceride level did not significantly change from the baseline to the end of the follow-up period (Table 1). No serious adverse events were reported.

**Conclusion:** Based on the results of the study, TAF prophylaxis prevents chemo/immunosuppressive therapy-induced HBV reactivation in HBV-infected individuals receiving chemo/immunosuppressive therapy. TAF is safe and tolerable in such individuals.

**Keywords:** HBV reactivation, HBV prophylaxis, Tenofovir Alafenamide Fumarate
Turkey. We studied TAF use in chronic hepatitis B patients in a real life setting across the country.

Method: Treatment-experienced chronic HBV patients were included. Twenty-five sites from 15 cities were enrolled. Patients’ demographics, laboratory studies before TAF and during TAF treatment were recorded. Data at baseline, in 6th month and in 12th month were compared.

Results: The study included 509 treatment-experienced patients. Among patients, median age was 53 years, male 302 (59.3%), HBeAg-negative 348 (68.1%), median ALT 23 U/L, median fibrosis score 2, and HAI 7. They were previously using TDF (83.9%), entecavir (6.8%), lamivudine (5.5%), telbivudine (3.0%), and adefovir (0.8%). Before TAF, treatment duration <6 months 13 (2.9), 6–12 months 29 (5.6), >12 months 403 (90.6). Indications to switch were osteoporosis 206 (40.5%), blood phosphate level 108 (21.2%), physicians decision 65 (12.8), glomerular filtration rate (GFR) 62 (12.2%), drug affecting bone mineral density 59 (11.6%), proteinuria/albuminuria 49 (9.6%), transplantation 11 (2.2%), steroids 6 (1.2%), fracture history 2 (0.4%), and hemodialysis 2 (0.4%).

Among all patients with HBV-DNA <20 IU/ml was 76.0% at baseline (during switch), 88.0% in 6th month and 84.1% in 12th month (p < 0.05). ALT normalization was 72.3% at baseline, 76.9% in 6th month and 81.0% in 12th month (p < 0.05). Creatinine levels and estimated (eGFR) remained stable from baseline to 6th and 12th months (0.82 mg/dl, 0.86 mg/dl, and 0.88 mg/dl (p > 0.05); 95 ml/min, 14 IU/ml, horizontal dotted line in Fig. 1). Six patients were excluded.

Conclusion: Although the majority of the patients were using potent nucleos (t)ide analogs, switching to TAF was associated with improved virologic and biochemical responses. Renal functions and lipid parameters remained stable and the drug was well tolerated. Real life data confirmed the efficacy and safety of TAF in treatment-experienced chronic hepatitis B patients.

SAT412
Mathematical modeling of HDV RNA kinetics suggests high peginterferon Lambda efficacy in blocking viral production: insights from the LIMT-1 study

E Fabian Cardozo-Ojeda, Sarah Duehren, Saeed Sadiq Hamid, Yoav Lurie, Edward J Gane, Anat Nevo-Shor, David Yardeni, Scott Cotler, Ingrid Choong, Jeffrey Glenn, Harel Dahari, Ohad Etzion, Program for Experimental and Theoretical Modeling, Department of Medicine, Stritch School of Medicine, Loyola University Chicago, Maywood, United States; 2Program for Experimental and Theoretical Modeling, Department of Medicine, Stritch School of Medicine, Loyola University Chicago, Maywood, United States; 3Aga Khan University, Karachi, Pakistan; 4Shaare Zedek, Jerusalem, Israel; 5Auckland Hospital, Auckland, New Zealand; 6Soroka University Medical Center, Beer-Sheba, Israel; 7Eiger BioPharmaceuticals, Inc., Palo Alto, United States; 8Stanford University, Stanford, United States

Email: harel.dahari@gmail.com

Background and aims: We previously reported 5 HDV RNA kinetic patterns under peginterferon-lambda (Lambda) monotherapy therapy (The Liver Meeting, AASLD 2019 #LP12). Here we sought to provide insights into HDV-host dynamics and Lambda efficacy using a mathematical modeling approach.

Method: Thirty-three chronic HDV infected patients participated in a randomized, open-label, Phase 2 clinical study (LIMT-1) of Lambda 120 µg (n = 19) or 180 µg (n = 14), administered once weekly by subcutaneous injections for 48 weeks, with 24 weeks of follow-up. All subjects were on tenofovir or entecavir. Kinetic data was obtained at Week 1 and every four weeks during and post Lambda therapy. HDV RNA was measured by Robogene®2.0 (limit of quantification of 14 IU/ml, horizontal dotted line in Fig. 1). Six patients were excluded from HDV kinetic analysis. The remaining 27 patients were previously categorized into 4 HDV kinetic patterns: monophasic, MP (Fig. 1a), biphasic, BP (Fig. 1b), flat-partial response, FPR (Fig. 1c) and triphasic/staircase, TP (Fig. 1d). We used a mathematical model of virus dynamics with or without proliferation of HDV-susceptible and HDV-infected hepatocytes to recapitulate the 4 HDV kinetic patterns and assess the impact of Lambda in blocking viral production. We fitted the models to the HDV data using a population, nonlinear mixed-effects approach. HDV clearance rate was fixed to 0.43 day⁻¹ as previously estimated under lonafarnib (Lancet Infect Dis 2015:15: 1167–74).

Figure 1. (a-d) Represenative modeling calibration (curves) with patients’ HDV RNA (symbols) during 48-week Lambda monotherapy. Horizontal lines represent HDV RNA limit of quantification. (‘%T0’) is the estimated percentage of non-infected susceptible start at the Lambda monotherapy and the hepatitis virus production rate distribution. The estimated eGFR and %RSE (and) using the best model fits.

Results: We found that only a model with hepatocyte proliferation of HDV-susceptible and HDV-infected cells is able to recapitulate all the 4 HDV kinetic patterns (Fig. 1a-d). The model predicts that population median half-life of HDV-infected hepatocytes is 9 days (equivalent to death/loss rate of 0.08 day⁻¹ [%RSE = 38%]), and that Lambda blocks virus production with population median efficacy of 99% [%RSE = 0.5%]. The model predicts that participants with monophasic (Fig. 1a) and biphasic (Fig. 1b) HDV kinetic patterns have a high fraction of noninfected hepatocytes at the start of treatment compared to those with TP and FPR (Fig. 1e). Those with BP kinetics had a ~3.5-fold faster hepatocyte proliferation compared to MP (Fig. 1f). However, hepatocyte proliferation in those with BP was ~2-fold slower than those in the TP and FPR (Fig. 1f).

Conclusion: This study provides, for the first time, a dynamic description of HDV response under Lambda monotherapy. Modeling results predict that Lambda blocks viral production (as estimated under pegylated IFN-α therapy) with high efficacy. The model predicts that the HDV kinetic patterns depend on Lambda efficacy, the fraction of noninfected hepatocytes at the beginning of treatment and their proliferation rates. Further theoretical and experimental efforts are needed to verify and/or refine our understanding of Lambda mode of action against HDV.
SAT413
Heterologous prime-boost immunotherapy circumvents tolerance and induces broadly neutralizing antibodies that protects against hepatitis B and D co-infection and hepatitis D super-infection
Lars Frelin1, Panagiota Maravelia1, Rani Burm2, Yi Ni1, Gustaf Ahlén1, Lieven Verhoye2, Freya Van Houtte2, Anna Pasetto1, Stephan Urban1, Philip Meuleman2, Matti Sällberg1, Karolinska Institutet, Department of Laboratory Medicine, Huddinge, Sweden; 2University of Gent, Laboratory of Liver Infectious Diseases, Belgium; 3University of Heidelberg, Department of Molecular Virology, Germany
Email: lars.frelin@ki.se

Background and aims: Chronic hepatitis B and D virus (HBV/HDV) infections are a major cause of severe liver disease and cancer that generally require lifelong therapy. A hallmark of chronic HBV infection is the profound T cell dysfunction/tolerance to viral proteins, and strategies to break this tolerance may therefore contribute to achieving functional cures. The HDV antigen acts as a heterologous antigen and supports HBV-specific immunactivation, leading to enhanced anti-HBV antibody and T cell responses. Its incorporation into an immunotherapeutic approach to enhance neutralizing antibody and T-cell responses to HBV preS1 is therefore being investigated.

Method: Plasmid DNA and fusion proteins containing HBV preS1 and HDAg sequences were expressed in E. coli. Antibody and T-cell responses directed against preS1 and HDAg after DNA-prime protein boost immunization were assessed in rabbits and in wild type and HBsAg-transgenic mice. Protection against HBV/HDV co-infection, and HDV super-infection was assessed in uPA-Scid mice repopulated with human hepatocytes against in vivo.

Results: A DNA prime protein boost immunization resulted in superior anti-preS1 and anti-HDAg antibody and T-cell responses in mice and rabbits compared to repeated immunization with DNA or protein alone (Figure 1). Antibody titres resulting from immunization were similar across HBV genotypes A-H. The induced antibodies also had broadly neutralizing activity against both HBV and HDV in vitro. Immunization of wild-type and HBsAg transgenic C57BL/6 mice resulted in equivalent antibody titres, supporting the role of HDAg in circumventing T cell tolerance to HBV. Passive transfer of antisera from immunized wild-type mice resulted in protection against HBV/HDV co-infection in 3/3 mice with humanized livers compared to 0/4 control animals that received serum from un-immunized mice. Passive transfer of antisera from immunized wild-type mice resulted in protection against HDV superinfection in 3/3 mice with humanized livers that had been infected with HBV 8 weeks previously, compared to 0/4 control animals that received serum from un-immunized mice.

Conclusion: This novel prime-boost immunotherapy circumvents immune tolerance and induces endogenous production of high levels of broadly neutralizing preS1 antibodies and T cells against preS1 and HDAg. Our results merits further investigation as a curative strategy for HBV mono-infection and HBV/HDV co-infection.

SAT414
Real-world data on treatment with bulevirtide in patients with chronic hepatitis B and D coinfection
Toni Heria1, Magdalena Hahn1, Melanie Maier2, Johannes Niemeyer1, Florian Gerhardt1, Jonas Schumacher1, Janett Fischer1, Johannes Wiegand1, Thomas Berg1, Florian van Bommel1, Leipzig University Medical Center, Division of Hepatology, Department of Medicine II, Leipzig, Germany; 2Leipzig University Medical Center, Institute of Medical Microbiology and Virology, Leipzig, Germany
Email: florian.vanboemmel@medizin.uni-leipzig.de

Background and aims: The hepatitis B and D virus (HBV/HDV) hepatocyte entry inhibitor bulevirtide (BVL) is available in Europe since July 2020. Real-world data on efficacy and safety of BVL in patients with chronic hepatitis delta (CHD) are sparse. We report efficacy and tolerability of BVL treatment in patients with CHD.

Method: CHD patients were treated with BVL 2 mg/day in combination with tenofovir disoproxil fumarate (TDF) 245 mg/day. HDV RNA and HBV DNA were quantified by real-time PCR based assays (HDV: Roche Diagnostics, lower limit of detection (LLD) 150 genome equivalents (GEQ)/ml; HBV: Abbott Molecular, LLD 10 IU/m), and HBV surface antigen (HBsAg) by the ARCHITECT assay (Abbott Molecular, sensitivity 0.05 IU/ml).

Results: 7 patients were recruited (4 male, age 41 ± 8.1 years, 5 Caucasians, 2 Asians, 4 with cirrhosis Child-Pugh A); Before BVL treatment initiation, median serum HDV RNA levels were 3.9 × 10⁶ ± 4.96 × 10⁶ [range 1.36 × 10⁷ to 1.57 × 10⁸] GEQ/ml, median serum HBV DNA 27 ± 203 [range 600] IU/ml, median serum HBsAg 1100 ± 16230 [range 47470] IU/ml and median elevation of alanine aminotransferase (ALT) levels 2.27 ± 1.81 [range 5.13] above upper limit of normal (ULN).

After a mean follow-up of 6.7 months, improvement >50% or normalization of ALT was observed in 5/7 patients, suppression of HDV RNA below the detection limit in 2/7, reduction of HDV RNA >2 log GEQ/ml in 2/7, reduction of HDV RNA <2 log GEQ/ml in 2/7 and HBV rebound in 1 patient. Complete virological responders (n = 2, both with cirrhosis) had low HDV RNA levels at baseline (3.22 × 10³ and 3.24 × 10³ GEQ/ml) and showed a normalization of ALT after 9 or 10 months of treatment. Partial virological responders >2 log GEQ/ml (n = 2, 1 with cirrhosis) presented with higher baseline HDV RNA (1.57 × 10⁶ and 1.36 × 10⁸ GEQ/ml) and showed a reduction of ALT >50% after 5 or 9 months of treatment. Virological non-responders <2 log GEQ/ml (n = 2, 1 with cirrhosis) presented with initial HDV RNA levels of 3.9 × 10⁶ and 3.5 × 10⁵ GEQ/ml, and showed no or <50% reduction of ALT after 3 or 7 months of treatment. 1 patient (no cirrhosis, baseline HDV-RNA 1.9 × 10⁷ GEQ/ml) showed a rebound of serum HDV RNA to 1.48 × 10⁶ GEQ/ml after initial complete response (5 months of treatment), while ALT normalized. HBV DNA was undetectable in 6/7 patients at the end of observation. No BVL related adverse effects were recorded in all individuals.

Conclusion: BVL is well tolerated and leads to a biochemical response in the majority of patients, but the virological response is variable, depending on the viral load at baseline. Further studies should evaluate BVL dose adjustments or peginterferon alfa-2a combination treatments in patients showing insufficient virologic responses.
Background and aims: Whether hepatitis B e antigen (HBeAg) status at the start of nucleos (t)ide analogue (NA) therapy is associated with differential outcomes following NA withdrawal remains unclear. We aimed to compare rates of virological and clinical relapse, ALT flares, and hepatitis B surface antigen (HBsAg) loss in chronic hepatitis B (CHB) patients who were HBeAg-positive versus negative at the start of the most recent NA therapy (SOT).

Method: We investigated outcomes in CHB patients who stopped NA therapy from centres across North America, Europe, and Asia. All included patients were HBeAg-negative and non-cirrhotic at NA discontinuation. Rates of virological (HBV DNA ≥2, 000 IU/ml) or clinical (HBV DNA ≥2, 000 IU/ml and ALT ≥2 × ULN) relapse, ALT flares (≥5 or 10 × ULN), and HBsAg loss were compared between SOT HBeAg-positive and -negative patients, using race-stratified Cox regression adjusting for age, sex, NA therapy duration, treatment history, and ALT and HBsAg levels at the end of therapy (EOT).

Results: Of 1, 360 CHB patients included, 1, 142 were HBeAg-negative and 218 HBeAg-positive at SOT. The HBeAg-negative group was older (54 vs 43 years) and had a higher proportion of males (73% vs 65%), fewer patients previously treated with interferon (8% vs 14%), and lower HBsAg levels at EOT (2.6 vs 3.1 log_{10} IU/ml), all p < 0.05. The duration of NA therapy and racial composition were comparable between the two groups. HBeAg-negativity versus positivity at SOT was significantly associated with a higher rate of virological relapse (adjusted hazard ratio [aHR] 1.9, p < 0.01) but not clinical relapse (aHR 1.2, p = 0.14). Other significant predictors of virological relapse included higher HBsAg levels at EOT (log_{10} IU/ml, aHR 1.7), TDF versus ETV treatment (aHR 1.6), and prior use of other NA (aHR 1.2), all p < 0.05. For clinical relapse, higher HBsAg (log_{10} IU/ml, aHR 1.9) and ALT (× ULN, aHR 1.4) levels at SOT, TDF versus ETV treatment (aHR 1.6), prior use of other NAs (aHR 1.5), and male sex (aHR 1.6) were identified as predictors, all p < 0.01. No differences in rates of ALT flares (≥5 or 10 × ULN) or HBsAg loss were observed.

Conclusion: CHB patients who were HBeAg-negative versus positive at SOT experienced higher rates of virological relapse, despite having longer time spent in the HBeAg-negative phase of infection. Off-therapy ALT elevations and HBsAg loss were not associated with HBeAg status at SOT.

Background and aims: We aimed to determine the real-life efficacy and tolerability of tenofovir alafenamide fumarate in liver transplant recipients: a multicenter study

Method: This a multicenter retrospective study. A total of 196 recipients were enrolled into the study. The primary end points were virological and biochemical response at week 24 and 48 of the treatment, the secondary end point was tolerability of TAF. Median duration of the TAF treatment was 11.6 months (range: 0–60 months).

Results: A total of 108 recipients who had at least 6 months follow-up were included in the analysis. Mean age was 58 ± 10 years, 74% were male. Of these, 80% were on tacrolimus-based and 38% on everolimus-based treatments. Median duration from LT to TAF initiation was 24.5 months (range: 0–252 months). Seventeen patients received TAF treatment as first-line therapy, whereas 91 patients switched to TAF treatment. Renal dysfunction and osteoporosis were the most common indications for TAF treatment. Baseline median serum ALT level was 25 IU/L (range: 10–96 IU/L) and baseline median HBV DNA level was 890 IU/ml, respectively. Virological and biochemical response were 90% and 71% at week 24.
24, and 100% and 92% at week 48, respectively. From baseline to the last follow-up, improvement in ALT at every 24 weeks compared by linear mixed model was significant; −3.226 IU/mL [95% CI: (−5.62) to (−0.84); p = 0.009]. After the switch to TAF treatment, none of the patients experienced HBV reactivation.

TAF treatment was well tolerated. Renal functions and lipid profile remained stable during TAF treatment (Figure 1). No serious adverse events were reported. No graft rejection was observed.

Conclusion: The present study indicates that TAF is effective and tolerable in liver transplant recipients.

SAT417

Impact of patient-related factors on the pharmacokinetics of Bulevirtide

Renu Singh1, Parag Kumar1, Rory Leisegang1, Francesco Bellanti2, Craig Comisar2, Kishore Poliredy2, Vithika Suri1, Dmitry Manuilov1, John F. Flaherty1, Sandhya Girish1, Gilead Sciences, Foster City, United States; 2Cellectar Inc, Princeton, United States

Email: renu.singh16@gilead.com

Background and aims: Bulevirtide (BLV) is a novel, first-in-class, potent, highly selective hepatocyte entry inhibitor of the hepatitis delta virus (HDV) that binds to and inactivates sodium taurocholate cotransporting polypeptide (NTCP), an essential HDV entry receptor. BLV is a 47-amino acid lipopeptide, recommended at a 2 mg dose by cotransporting polypeptide (NTCP), an essential HDV entry receptor. BLV is a 47-amino acid lipopeptide, recommended at a 2 mg dose by cotransporting polypeptide (NTCP), an essential HDV entry receptor. BLV is a 47-amino acid lipopeptide, recommended at a 2 mg dose by cotransporting polypeptide (NTCP), an essential HDV entry receptor. BLV is a 47-amino acid lipopeptide, recommended at a 2 mg dose by cotransporting polypeptide (NTCP), an essential HDV entry receptor.

Method: Comprehensive PK data from participants in 2 Phase 1 studies (N = 48), 3 Phase 2 studies (N = 314), and 1 Phase 3 study (N = 101) were analysed using nonlinear mixed-effects modeling (NONMEM®) software. Individual BLV PK parameter estimates were generated and the impact of patient-specific covariates (eg, baseline BLV weight (WT), age, sex, race, BLV dose, health status, BL HDV viral load, creatinine clearance, presence of anti-drug antibodies, liver function tests, comedictions (oral antivirals and pegylated interferon alpha) were evaluated.

Results: Nonlinear PK was observed with greater than dose proportional increase in BLV exposure. The final BLV model was described by a 2-compartment model with sequential zero-first order absorption and first-order elimination from the central compartment. An absolute SC bioavailability of 53.4% was estimated with a dose effect on clearance adequately characterizing the nonlinear PK.

Conclusion: Across a wide range of participants, BLV exposures were inversely correlated with WT along with slightly higher exposures in patients with cirrhosis. These changes in BLV exposures were not considered clinically meaningful. These data support the use of the recommended 2 mg once daily dose across the spectrum of participants with varied patient-related factors.

SAT418

Reduction of liver stiffness in chronic hepatitis B patients treated with tenofovir disoproxil fumarate: a prospective observational study

Heejin Cho1, Yun Bin Lee1,2, Yeonjuang Ha2, Young Eun Chon2, Mi Na Kim2, Joo Ho Lee2, Seong Gyu Hwang2. 1Department of Internal Medicine and Liver Research Institute, Seoul National University College of Medicine, Seoul, Korea, Rep. of South; 2Department of Internal Medicine, CHA Bundang Medical Center, Seongnam, Korea, Rep. of South Email: yblee@snu.ac.kr

Background and aims: Regression of hepatic fibrosis during antiviral therapy in patients with chronic hepatitis B has been demonstrated, but data about influence of long-term treatment with tenofovir disoproxil fumarate (TDF) on liver stiffness (LS) measured by transient elastography are scarce. We aimed to investigate changes in LS values during 144-week antiviral therapy with TDF in patients with chronic hepatitis B.

Method: A total of 48 treatment-naïve patients with chronic hepatitis B who initiated TDF therapy were enrolled and followed up for 144 weeks. Laboratory tests and LS measurements were performed at baseline and repeated at weeks 12, 24, 48, 96 and 144. A significant decline of LS was defined as ≥30% drop of LS value from the baseline to week 96.

Results: Among the 48 enrolled patients, 11 patients were lost to follow-up before 96 weeks and 37 patients were included in the analysis (median age, 45 years [interquartile range, 35 – 55.5 years]; 20 men [54.1%]). During antiviral therapy with TDF, the median LS value decreased from 14.1 kPa to 8.6 kPa, 6.5 kPa, and 6.2 kPa at weeks 48, 96 and 144, respectively (all P < 0.001; Figure 1). At week 96, virologic and biochemical response were achieved in 34 patients (91.9%) and 33 patients (89.2%), respectively. Moreover, 21 of 36 patients (58.3%) in whom the 96-week LS values were measured showed a significant decline of LS and higher baseline LS value was a single independent predictor of a significant decline of LS (odds ratio, 1.212; 95% confidence interval, 1.027–1.431; P = 0.023).
Conclusion: During the long-term antiviral therapy with TDF, LS values declined significantly in treatment-naïve patients with chronic hepatitis B.

SAT419
Toll-like receptor 8 agonism activates monocytes and induces antiviral cytokine production by T-cells in HIV and chronic hepatitis B co-infection
Lydia Tang1,2, Natarajan Ayitian1,2, Shyamasundaran Kottili1,2.
1University of Maryland, Baltimore, Baltimore, United States; 2Institute of Human Virology, Baltimore, United States

Background and aims: In people with HIV/CHB co-infection, progression and mortality from liver disease is worse than among people without HIV. There is no effective cure for CHB. Immune-targeting therapy aimed at recovering HBV-specific immunity is a strategy for CHB cure. Toll-like receptors (TLRs) are a group of pattern recognition receptors identified as immunomodulatory targets for CHB treatment. TLRs activate antigen presenting cells, priming the adaptive immune system. In clinical trial, TLR8 agonism was shown to induce antiviral cytokine production and enhanced HBV-specific B-cell responses in CHB. The aim of this study is to evaluate the effect of HIV co-infection with CHB on HBV-specific immune responses to TLR8 agonism.

Method: CD14+ monocytes and CD3+ T cells were isolated from autologous peripheral blood mononuclear cell samples by pan T cell negative selection (Miltenyi Biotec) or FACSAria sorting from people without HIV. There is no effective cure for CHB. Immune-targeting therapy aimed at recovering HBV-specific immunity is a strategy for CHB cure. Toll-like receptors (TLRs) are a group of pattern recognition receptors identified as immunomodulatory targets for CHB treatment. TLRs activate antigen presenting cells, priming the adaptive immune system. In clinical trial, TLR8 agonism was shown to induce antiviral cytokine production and enhanced HBV-specific B-cell responses in CHB. The aim of this study is to evaluate the effect of HIV co-infection with CHB on HBV-specific immune responses to TLR8 agonism.

Results: Samples from 7 patients with CHB and 7 with HIV/CHB were analyzed. At baseline, monocyte population was larger in CHB compared to HIV/CHB (p = 0.03) with higher HLA-DR, CD11c and IL6 expression and induced stronger HBV-specific CD8T cell responses than HIV/CHB with higher induction of TNF alpha (p = 0.01), IFN gamma (p = 0.002), IL-2 (p = 0.003), and IL-21 (p = 0.03). In vitro treatment of monocytes with ssRNA40, a TLR8 agonist, then pulsed with HBV peptide and co-cultured with autologous T cells. Activation of monocytes by TLR8 stimulation was evaluated by flow cytometry immunophenotyping and compared with unstimulated monocytes. Activation of HBV-specific CD8 T cells by TLR8 stimulated monocytes was then evaluated by measuring (by intracellular staining and flow cytometry) production of pro-inflammatory cytokines. For statistical analysis student’s t-test was used with p < 0.05 considered significant.

Results: Samples from 7 patients with CHB and 7 with HIV/CHB were analyzed. At baseline, monocyte population was larger in CHB compared to HIV/CHB (p = 0.03) with higher HLA-DR, CD11c and IL6 expression and induced stronger HBV-specific CD8 T cell responses than HIV/CHB with higher induction of TNF alpha (p = 0.01), IFN gamma (p = 0.002), IL-2 (p = 0.003), and IL-21 (p = 0.03). In vitro treatment of monocytes with ssRNA40, a TLR8 agonist, then pulsed with HBV peptide and co-cultured with autologous T cells. Activation of monocytes by TLR8 stimulation was evaluated by flow cytometry immunophenotyping and compared with unstimulated monocytes. Activation of HBV-specific CD8 T cells by TLR8 stimulated monocytes was then evaluated by measuring (by intracellular staining and flow cytometry) production of pro-inflammatory cytokines. For statistical analysis student’s t-test was used with p < 0.05 considered significant.

Results: Samples from 7 patients with CHB and 7 with HIV/CHB were analyzed. At baseline, monocyte population was larger in CHB compared to HIV/CHB (p = 0.03) with higher HLA-DR, CD11c and IL6 expression and induced stronger HBV-specific CD8 T cell responses than HIV/CHB with higher induction of TNF alpha (p = 0.01), IFN gamma (p = 0.002), IL-2 (p = 0.003), and IL-21 (p = 0.03). In vitro treatment of monocytes with ssRNA40, a TLR8 agonist, then pulsed with HBV peptide and co-cultured with autologous T cells. Activation of monocytes by TLR8 stimulation was evaluated by flow cytometry immunophenotyping and compared with unstimulated monocytes. Activation of HBV-specific CD8 T cells by TLR8 stimulated monocytes was then evaluated by measuring (by intracellular staining and flow cytometry) production of pro-inflammatory cytokines. For statistical analysis student’s t-test was used with p < 0.05 considered significant.

Conclusion: TLR8 agonism activated monocytes. These, in turn, were able to activate HBV-specific antiviral CD8 T cell functions. In HIV/CHB samples, this effect on T cells was seen despite the absence of significant changes in the monocytes with TLR8 treatment, supporting further study of toll-like receptor agonism for CHB treatment in people with HIV/CHB.

SAT420
Comparison of body weight and lipid profiles following tenofovir disoproxil fumarate or entecavir switching to tenofovir alafenamide—an interim analysis
Pin-Nan Cheng1, Chun-Jen Liu2, Jyh-Jou Chen3, I-Cher Feng4, Hsing-Tao Kuo3, Pei-Lun Lee3, Ming-Lung Yu5, Yencheng Chiu1, Chiu Hung-Chih1, Shih-Chieh Chien1, Pei-Jer Chen2.
1National Cheng Kung University Hospital, Department of Internal Medicine, Tainan, Taiwan; 2National Taiwan University Hospital, Department of Internal Medicine, Taipei, Taiwan; 3Chi-Mei Medical Center, Liouying, Tainan, Taiwan, Department of Internal medicine, Tainan, Taiwan; 4Kaohsiung Medical University Hospital, Kaohsiung, Taiwan, Department of Internal Medicine, Kaohsiung, Taiwan

Background and aims: Body weight (BW) and lipid profiles changes have been reported in HIV infected patients treated with tenofovir alafenamide (TAF) containing regimens. Tenofovir disoproxil fumarate (TDF) treated chronic hepatitis B (CHB) patients exhibited lower lipid profiles in phase III study. The impact of TAF, as a new drug for CHB treatment, on BW and lipid profiles remains unclear and needs to investigate.

Method: This was a prospective, multi-center, observational study. CHB patients from five hospitals in Taiwan treated with TDF or entecavir for at least 1 years and then switched to TAF were enrolled. Measurement of biochemical, virological, and atherosclerotic cardiovascular disease (ASCVD) risk score at baseline and then at an interval of 12 weeks or 48 weeks by items. Primary end point was the body weight changes following switching to TAF or entecavir. Secondary end points included ASCVD score changes, and changes of lipid and sugar profiles following switching to TAF.

Results: At the end of October 2021, 99 patients, including 63 males with a mean age of 54.3 years, completed a 48 weeks follow-up were enrolled for analysis. Of them, 65 and 34 patients treated with TDF or entecavir before switching to TAF, respectively. At baseline, significantly lower TG, Chol, and LDL (all p < 0.05) in TDF switch group than entecavir switch group. Figure 1 shows the BW changes during 48 weeks of TAF treatment. Following switching to TAF, significant BW gain was present from 12 weeks and maintained thereafter until 48 weeks in TDF switch group comparing with baseline BW. In contrast, BW remained unchanged in entecavir switch group during 48 weeks of observation. In TDF switch group but not entecavir switch group, all of the lipid profiles including TG (88.6 ± 48.3 vs. 104.4 ± 66.6 mg/dL, p = 0.014), Chol (160.3 ± 33.1 vs. 188.1 ± 38.9 mg/dL, p < 0.001), LDL (104.9 ± 28.9 vs. 121.9 ± 34.2 mg/dL, p < 0.001), and HDL (48.2 ± 11.7 vs. 58.2 ± 13.2 mg/dL, p = 0.015) were significantly increased following 48-week TAF treatment. ASCVD risk score had a trend toward a significant increase in TDF switch group (6.3 ± 9.5 vs. 7.0 ± 9.4, p = 0.051), but not in entecavir switch group (12.5 ± 16.7 vs. 13.2 ± 18.5, p = 0.343).

Conclusion: TLR8 agonism activated monocytes. These, in turn, were able to activate HBV-specific antiviral CD8 T cell functions. In HIV/CHB samples, this effect on T cells was seen despite the absence of significant changes in the monocytes with TLR8 treatment, supporting further study of toll-like receptor agonism for CHB treatment in people with HIV/CHB.
SAT421
Real life efficacy and tolerability of Tenofovir Alafenamide Fumarate in patients with hepatitis-B virus-related cirrhosis
Suna Yapali1, Hale Gökcan2, Serdar Durak3, Zeynep Melekoğlu Elik2, Fatih Güzelbutlu4, Sezgin Vatansever2, Derya Ari5, Shahnin Mehdiyev7, Haydar Adanir8, Elif Şirte Koç1, Feyza Gunduz7, Mehmet Arslan5, Kamil Özdiş3, Dinc Dincer6, Ramazan İdlıman2.  Acibadem University, Turkey; 2 Ankara University Medical School, Turkey; 3 KTU Faculty of Medicine, Turkey; 5SBÜ Haydarpaşa Numune Eğitim ve Araştırma Hastanesi, Turkey; 6 Kâtip Çelebi Üniversitesi, İzmir, Turkey; 7 Ankara Şehir Hastanesi, Turkey; 8 Marmara University Research And Education Hospital, Turkey; 9 Akdeniz University, Turkey; 10 Sağlık Bilimleri Üniversitesi Ümraniye Eğitim ve Araştırma Hastanesi, Turkey
Email: sunayapali@gmail.com

Background and aims: We aimed to determine the real-life efficacy and tolerability of tenofovir alafenamide fumarate (TAF) in patients with hepatitis B virus (HBV)-related cirrhosis

Method: This multicenter study included a total of 91 patients with HBV-related cirrhosis who received TAF treatment as first line treatment or switched to TAF. The primary end points were virological and biochemical response at week 24 and 48 of the treatment, the secondary end point was the assessment of safety and tolerability of TAF. Median follow-up on TAF treatment was 13.7 (range 6–26) months.

Results: Of the 91 patients with cirrhosis, 43 patients who had at least 6 months of follow-up were included in the analysis. Mean age was 64 ± 11 years and %63 was male. Baseline median MELD score was 10 (range: 9–14), and 4 (9.3%) were decompensated. Six (14%) patients received TAF treatment as first line therapy. Baseline median serum ALT and HBV DNA levels were 25 IU/L (range: 10–96 IU/L) and 51000 IU/ml, respectively. Thirty-seven (86%) patients switched to TAF treatment. Renal dysfunction and hypophosphatemia were the most common indications for TAF treatment.

Virological and biochemical responses were 67% and 67% at week 24 and 100% and 83% at week 48, respectively. Serum HBV DNA was undetectable at week 36 among all patients with detectable HBV DNA at baseline. From baseline to the last follow-up, improvement in ALT was at every 24 weeks compared by linear mixed model was significant: −1.13 IU/ml [95% CI: (−1.8)–(−0.45), P = 0.005]. None of the patients experienced HBV reactivation. During TAF treatment, renal functions and lipid profile were stable (Figure 1). No serious adverse effect was observed.

Conclusion: Following TDF switch to TAF, BW increased shortly and the lipid-lowering effects of TDF diminished.Combining BW gain and increase of lipid profiles, CVD risk may need to monitor closely.

SAT422
Effects of the siRNA JN-3989 and/or the capsid assembly modulator (CAM-N) JN-6379 on viral markers of chronic hepatitis B (CHB): results from the REEF-1 study
Man-Fung Yuen1, Tarik Asselah2, Ira M Jacobson3, Maurizia Brunetto4, Harry Janssen5, Tetsuo Takehara6, Jinlin Hou7, Thomas Kakuda8, Tom Lambrecht9, Ronald Kalmeyer9, Carine Guinard-Azadian10, Cristina Mayer10, John Jerzorwski10, Thierry Verbinnen2, Oliver Lenz9, Unesh Shukla6, Michael Biermer9.
1 Queen Mary Hospital, Department of Medicine and State Key Laboratory of Liver Research, The University of Hong Kong, Hong Kong, China; 2 Université de Paris, INSERM UMR1149 and Hôpital Beaujon, APHP, Clichy, France; 3 New York University Grossman School of Medicine, New York, New York, United States; 4 University of Pisa, Pisa, Italy; 5 University of Toronto, Toronto, Canada; 6 Osaka University Graduate School of Medicine, Osaka, Japan; 7 Nanfang Hospital, Southern Medical University, Guangzhou, China; 8 Janssen Research and Development, United States; 9 Janssen Research and Development, Belgium; 10 Janssen Research and Development, France; 11 Janssen Research and Development, Germany
Email: mfyuen@hku.hk

Background and aims: JN-3989 is an siRNA targeting all hepatitis B virus (HBV) RNAs thereby reducing viral proteins. JN-6379, a CAM-N, prevents the formation of infectious viral genome-containing capsids. The REEF-1 study (NCT03982186) assessed the efficacy and safety of monthly s.c. injections of JN-3989 (40, 100, and 200 mg) and/or 250 mg daily oral JN-6379 versus placebo in combination with daily oral NA in not currently treated (NCT) or virologically suppressed (VS) HBeAg positive (HBeAg+) or negative (HBeAg-) CHB patients.

Method: In this Phase 2b, multicenter, active-controlled study, CHB patients (N = 470) were randomized and dosed for a 48-week double-blind placebo-controlled treatment period. Changes in viral markers were assessed. Data from week 24 follow-up (FU W24) are presented.

Results: JN-3989 reduced HBsAg in a dose dependent manner with the greatest decline at the 200 mg dose (mean [SD] reduction of 2.6 [0.10] log10 IU/ml at week 48 (W48) versus control (0.22 [0.85] log10 IU/ml; P < 0.001). By FU W24, 47.0% of patients in the JN-3989 200 mg group had HBsAg < 100 IU/ml. HBsAg reduction from baseline (BL) remained ≥ 1 log for 84.3% and ≥ 2 log for 37.3% of patients in the JN-3989 200 mg group at FU W24. 19.1% and 29.7% of patients met NA stopping criteria ([ALT < 3x ULN, HBV DNA < LLOQ, HBsAg < 10 IU/ml] with JN-3989 200 mg at W48 and until FU W24, respectively. Only 3 of 66 (4.5%) patients who met NA stopping criteria met NA re-starting criteria during the follow-up. Declines in HBeAg and HBcAg were generally dose dependent and greater in patients with higher baseline (BL) levels, thus reductions were most pronounced in NCT HBeAg+ patients with mean (SD) change from BL at W48 of − 2.22 (1.14) log10 IU/ml for HBeAg and − 2.56 (0.93) log10 IU/ml for HBcAg in the 200 mg JN-3989 group.
Safety, pharmacokinetics and antiviral activity of GST-HG141, a hepatitis B virus capsid assembly modulator, in subjects with chronic hepatitis B

Jiajia Mai1, Hong Zhang1, Min Wu1, Yanhua Ding1, Junqi Niu1, Vadim Bichko2, Yanao He2, John Mao2, Dong Zhang2, Wenqiang Wu2, Hong Ren2, George Zhang2, Hongming Li2, Shuhui Chen3.

1The First Hospital of Jilin University, Changchun, China; 2Fujian Cosunter Pharmaceutical Co., Ltd., Fuzhou, China; 3Domestic Hepatitis B Research Center, Shanghai, China

Background and aims: Hepatitis B virus (HBV) capsid assembly modulators (CAMs) are clinically validated agents for the chronic HBV drug development, with a potential for HBV cure. Safety, tolerability, and pharmacokinetics of GST-HG141, a novel CAM, in healthy subjects (NCT04386915) has been reported previously [Li et al., Antimicrob Agents Chemother. 2021;65(10)]. The aim of this study was to evaluate safety, PK and antiviral activity of multiple doses of GST-HG141 in patients with chronic hepatitis B (CHB).

Method: A multi-center, randomized, double-blind, placebo-controlled multiple ascending-dose phase Ib study (NCT04386981). Patients with CHB, who were not treated with interferon or nucleoside (≥12 or >6 months, respectively), HBeAg-positive or negative (serum HBV DNA ≥2x10^5 or ≥2x10^6 IU/ml, respectively) received oral BID doses of GST-HG141 (25, 50 and 100 mg) for 28 days. Ten patients in each cohort were randomized to receive a drug or placebo (1:1). An unblinded LC-MS/MS method was used to quantify GST-HG141 in plasma. The PK parameters were calculated with WinNonlin 8.3 software. Serum HBV DNA and HBV pgRNA were determined using quantitative Real-Time PCR, serum HBV antigens by ELISA methods.

Results: Administration of 25, 50 or 100 mg of GST-HG141 BID for 28 days was well tolerated. No SAEs or dose-related increase in number of AEs was reported. No TEAEs leading to discontinuation of treatment. A rapid and robust decline in serum HBV DNA was observed (median 2.9, 3.3 and 3.5 log_{10} IU/ml for 25, 50 and 100 mg dose cohorts, respectively). Serum HBV pgRNA levels decreased by median 2.2 log_{10} U/ml in all dose cohorts, with a maximum median decrease of 2.40 log_{10} U/ml in the 100 mg dose cohort at day 29 of treatment. No virus breakthrough was noted. No statistically significant decline in serum HBsAg, HBeAg or HbcAg was observed. However, there was a trend of serum HBeAg and HbcAg decrease in patients, receiving the drug. Plasma GST-HG141 exposure increased relatively proportionally with the dose. Moderate accumulation (mean values 1.67–2.38) was seen with dosing for 28 days.

Conclusion: GST-HG141 is well tolerated, safe and effective in CHB patients. Further development of GST-HG141 for CHB is warranted. Phase II drug combination study with GST-HG141 and nucleoside analogs is underway.

SAT424

Predictors of sustained response in hepatitis B surface antigen-negative patients after peginterferon therapy: an observational study

Jun Chen1, Yan Huang1, Xiaoyu Hospital Central South University, Department of Infectious Diseases, Changsha, China

Email: drhyan@126.com

Background and aims: Hepatitis B surface antigen (HBsAg) clearance is considered the functional cure and recommended as the optimal end point of antiviral therapy for chronic hepatitis B (CHB) patients. Although patients could achieve HBsAg clearance after pegferferon treatment, HBsAg reversal occurred in some patients. This study aimed to investigate predictors of sustained response in HBsAg-negative patients after peginterferon therapy.

Method: CHB patients with HBsAg clearance after pegferferon therapy were enrolled from 2018 to 2021. Patients were followed up for 48 weeks after functional cure. Patients with sustained negative HBsAg were non-recurrence group and patients with HBsAg reversal were recurrence group.

Results: A total of 176 patients achieved HBsAg clearance after pegferferon treatment. 113 patients were included at the 48-week follow-up (104 in non-recurrence group, 9 in recurrence group). The cumulative rates of HBsAg reversion at 12 weeks, 24 weeks, 36 weeks, and 48 weeks after achieving functional cure were 2.89%, 3.85%, 6.72%, and 7.92%, respectively. HBsAb at the end of treatment was significantly higher in non-recurrence patients compared with recurrence patients at week 48 (p <0.001).

Table: Analysis of potential predictors for sustained response

<table>
<thead>
<tr>
<th>Variables</th>
<th>Non-recurrence (N = 104)</th>
<th>Recurrence (N = 9)</th>
<th>p value</th>
</tr>
</thead>
<tbody>
<tr>
<td>HBeAg at baseline (S/CO)</td>
<td>0.36 [0.32, 0.42]</td>
<td>0.35 [0.27, 0.36]</td>
<td>0.171</td>
</tr>
<tr>
<td>HBsAb at baseline (mIU/ml)</td>
<td>4.53 [1.65, 18.76]</td>
<td>9.26 [7.24, 30.79]</td>
<td>0.359</td>
</tr>
<tr>
<td>HbcAg at baseline (S/CO)</td>
<td>7.64 ± 1.54</td>
<td>7.94 ± 1.27</td>
<td>0.567</td>
</tr>
<tr>
<td>HBeAg at the end of treatment (mg)</td>
<td>0.46 ± 0.60</td>
<td>7.94 ± 1.27</td>
<td>0.397</td>
</tr>
<tr>
<td>HBsAb at the end of treatment (mg)</td>
<td>416.50 ± 13.43</td>
<td>8.32 &lt;0.001</td>
<td></td>
</tr>
<tr>
<td>HbcAg at baseline (S/CO)</td>
<td>386.61</td>
<td>8.32</td>
<td>0.382</td>
</tr>
<tr>
<td>HbcAg at the end of treatment (S/CO)</td>
<td>7.89 ± 1.38</td>
<td>8.50 ± 0.65</td>
<td>0.382</td>
</tr>
<tr>
<td>Consolidation treatment time, n (%)</td>
<td>0.644</td>
<td></td>
<td></td>
</tr>
<tr>
<td>0–12 weeks</td>
<td>15 (14.42)</td>
<td>2 (22.22)</td>
<td></td>
</tr>
<tr>
<td>12–24 weeks</td>
<td>29 (27.89)</td>
<td>1 (11.11)</td>
<td></td>
</tr>
<tr>
<td>24–36 weeks</td>
<td>27 (25.96)</td>
<td>2 (22.22)</td>
<td></td>
</tr>
<tr>
<td>36–48 weeks</td>
<td>33 (31.73)</td>
<td>4 (44.44)</td>
<td></td>
</tr>
</tbody>
</table>

Conclusion: HBsAb level at the end of treatment is a potential predictor of sustained response. Evaluating HBsAb level when pegferferon discontinued can improve sustained functional cure.
Background and aims: Tenofovir Alafenamide (TAF) is a novel prodrug of tenofovir (TFV) with non-inferior efficacy and greater plasma stability resulting in enhanced delivery of TFV and reduced plasma concentrations leading to an improved bone and renal safety profile over tenofovir disoproxil fumarate (TDF). TAF is approved for use in adult patients with Chronic Hepatitis B (CHB). However, safety and efficacy data in pediatric CHB patients are lacking. In a multicenter, randomized, double-blind, placebo-controlled trial we evaluated the safety and efficacy of TAF in children 6 years and older weighing ≥ 25 kg.

Method: Males or females aged 12 to <18 years weighing ≥35 kg (Cohort 1), and 6 to <12 years weighing ≥25 kg (Cohort 2, Group 1), with HBV DNA ≥2 x 10^5 IU/ml, ALT ≥1.5 x ULN, and creatinine clearance (eGFR; Schwartz method) ≥80 ml/min were randomized (2:1) to TAF 25 mg or PBO daily for 24 weeks, after which all patients ≥1.5 × ULN, and creatinine were randomized to TAF 25 mg or PBO daily for 24 weeks, after which all patients 35 kg were re-randomized to double blind treatment; however, no patient had eGFR <90 ml/min/1.73m² at Week 24. Mean % increases from BL to Week 24 in BMD were +1.9% vs. +2.0%; [p = 0.83]). Viral resistance was not detected through Week 24. TAF and TFV plasma exposures were similar between the two treatment groups, with TAF having lower renal clearance.

Results: 88 patients were randomized and treated (Cohort 1: TAF 47, PBO 23; Cohort 2 group 1: TAF 12, PBO 6). Baseline (BL) characteristics were similar; overall mean (range) age and mean (SD) weight were 14 (7–17) years and 50.9 (12.9) kg, respectively; 58% were male, 66% Asian, 68% had HBV DNA ≥8 log10 IU/ml and mean (SD) ALT 107 (118) U/L. 99% were HBeAg-positive, with genotypes D (44%), C (24%), and B (23%) being most common. Overall, at Week 24, 11/59 (19%) TAF and 9/59 (15%) PBO patients had HBV DNA <20 IU/ml (p = 0.0137); mean (SD) HBV DNA change from BL TAF vs PBO was −4.98 (1.52) log10 IU/ml and −0.10 (0.64) log10 IU/ml (p < 0.0001), respectively. High BL viral load and genotype D were associated with lower rates of viral suppression. A higher proportion of TAF vs PBO patients had ALT normalization (TAF 67%, PBO 4%; p < 0.0001), while the rate of HBeAg seroconversion was similar (TAF 7%, PBO 3%). Grade 3 or 4 AEs and SAEs related to study treatment were similar for TAF vs PBO. Slight fluctuations in eGFR were noted for both treatment groups during double blind treatment; however, no patient had eGFR <90 ml/min/1.73m² at Week 24. Mean % increases from BL to Week 24 in BMD were similar in the TAF vs PBO (spine: +1.6% vs. +1.9%; [p = 0.77]; whole body: +1.9% vs. +2.0%; [p = 0.83]). Viral resistance was not detected through Week 24. TAF and TFV plasma exposures were similar between the two treatment groups, with TAF having lower renal clearance.

Conclusion: In pediatric CHB patients, viral suppression and ALT normalization were superior to placebo, while safety results, including changes in BMD, were similar for TAF and PBO at Week 24.
Conclusion: Taken together, these data support that AMS-I-1274 is a novel class II capsid inhibitor with high anti-HBV potency and a favorable preclinical profile for clinical advancement.

SAT427
Viral nucleic acids suppression activity of RO7049389 plus NUC with/without Peg-IFN in virologically-suppressed and naive chronic hepatitis B patients: 48-week treatment and post-treatment follow-up
Man-Fung Yuen1, Rozalina Balabanska2, Jinlin Hou3, Edward J Gane4, Tien Huey Lim5, WenHong Zhang6, Qing Xie7, Piyawat Komolmit8, Apinya Leerapun9, Sheng-Shun Yang10, Chau-Ting Yeh11, Wen Zhang11, Xue Zhou12, Zenghui Xue13, Miriam Triyatni14, Ethan Chen13, Rui Li12, Qingyan Bo13. 1Queen Mary Hospital, The University of Hong Kong, Hong Kong, China, China; 2Acibadem City Clinic Tokuda Hospital EAD, Sofia, Bulgaria; 3Nanfang Hospital, Southern Medical University, Guangzhou, China; 4New Zealand Liver Transplant Unit, The University of Auckland, Auckland, New Zealand; 5Middlemore Hospital, Auckland, New Zealand; 6Huashan Hospital, Fudan University, Shanghai, China; 7Ruijin Hospital, Shanghai Jiaotong University School of Medicine, Shanghai, China; 8King Chulalongkorn Memorial Hospital, Bangkok, Thailand; 9Maharaj Nakorn Chiang Mai Hospital, Chiang Mai, Thailand; 10Taichung Veterans General Hospital, Taichung, Taiwan; 11Chang Gung Memorial Hospital, Linkou Branch, Taoyuan, Taiwan; 12Roche Pharma Research and Early Development, Roche Innovation Centre Shanghai, Shanghai, China; 13Roche (China) Holding, Shanghai, China; 14E. Hoffmann-La Roche, Basel, Switzerland
Email: qingyan.bo@roche.com

Background and aims: RO7049389 is a Class I HBV core protein allosteric modulator that induces abnormal capsid assembly, leading to depletion of functional core protein thereby inhibiting HBV DNA replication and cccDNA formation. Here we report antiviral and safety results following 48 weeks of RO7049389 plus NUC with/without Peg-IFN-alpha and 24 weeks of follow-up (NCT02952924).

Method: The ongoing open-label study enrolled NUC-suppressed patients to receive RO7049389+NUC (Cohort A, n = 32), and treatment naïve patients to receive RO7049389+NUC without (Cohort B, n = 10) or with (Cohort C, n = 30) Peg-IFN alpha for 48 weeks. At Week 48, all patients except for 5 Cohort C patients who met NUC stopping criteria (HBV DNA <LLOQ and HBsAg <100 IU/ml) entered a 24-week NUC-alone follow-up period.

Results: In Cohort A (11/32 HBeAg+; baseline HBV DNA <LLOQ), 30/32 patients completed the 72-week study with HBV DNA maintained <LLOQ. In all patients with quantifiable HBV RNA at baseline, HBV RNA declined to <LLOQ (10 copies/ml) by Week 4, but rebounded to approximately the baseline level during NUC-alone follow-up. In Cohort B (6/10 HBeAg+; mean baseline HBV DNA 5.7 log10IU/ml) and Cohort C (19/30 HBeAg+; mean baseline HBV DNA 6.9 log10IU/ml), a total of 37 patients (10 and 27 respectively) completed the 72-week study. All patients achieved HBV DNA <LLOQ except for four Cohort C HBeAg+ patients who had detectable HBV DNA below 150 IU/ml by Week 48. During 24-week follow-up with NUC treatment, except for 2 patients with non-compliance issue, all other patients maintained HBV DNA <LLOQ or at low levels (below 250 IU/ml) and two further patients achieved <LLOQ by Week 72. In 30/33 treatment naïve patients with quantifiable HBV RNA at baseline, HBV RNA decreased <LLOQ at Week 48, and remained an average of >2 log10 copies/ml below baseline at the end of follow-up. RO7049389+NUC ± Peg-IFN was safe and well tolerated up to 72 weeks. No RO7049389-related SAEs occurred; two early terminations in each cohort of A and C were due to non-safety reasons. Most common Grade 2–4 lab abnormalities (ALT elevations) were mainly observed in treatment-naïve patients and were accompanied by a decline in viral markers. ALT elevations resolved spontaneously and were not accompanied by significant changes in liver function.

Conclusion: RO7049389+NUC ± Peg-IFN demonstrated potent effect on viral nucleic acids suppression even in treatment naïve patients. HBV DNA was suppressed and maintained <LLOQ in the majority of treatment-naïve patients. Mean HBV RNA levels remained >2 log10 copies/ml below baseline after the cessation of RO7049389, which may suggest a certain level of suppression in cccDNA level/transcriptional activity in treatment naïve patients. RO7049389 plus current standard of care for 48 weeks was safe and well tolerated, supporting further development in viremic patients.
SAT428

Phase 1b/2a study of heterologous ChAdOx1-HBV/MVA-HBV therapeutic vaccination (VTP-300) combined with low-dose nivolumab (LDN) in virally-suppressed patients with CHB on nucleos (t)ide analogues

Tom Evans1, Eleanor Barnes2, 1Vaccitech, Oxford, United Kingdom; 2Oxford University, Nuffield Department of Medicine, Oxford, United Kingdom
Email: tom.evans@vaccitech.co.uk

**Background and aims:** Induction of a CD8+ T cell response to HBV may be required to achieve a functional cure of chronic hepatitis B (CHB). The highest magnitude CD8+ T cell responses achieved to date in man have been induced by replication incompetent adenoviral vectors followed by attenuated poxvirus boosts.

**Method:** Vaccitech with Oxford University is developing a therapeutic HBV vaccine (VTP-300) using a chimpanzee adenoviral vector (ChAdOx1-HBV) and a Modified vaccine Ankara boost (MVA-HBV), that encode the inactivated polymerase, core, and the entire large S (ChAdOx1-HBV) and a Modified vaccine Ankara boost (MVA-HBV), respectively. Responses were enhanced from baseline in 13 patients (32–4.3) log IU/ml, HDV RNA 4.9 (3.3–6.6) log IU/ml. During 48 weeks of BLV monotherapy, HDV RNA declined by 3.1 (0.2–4.6) log IU/ml, becoming undetectable in 6 (33%) patients and <100 IU/ml in 9 (50%). A virological response, defined as HDV RNA undetectability or ≥2 log IU/ml decline, was observed in 14 (78%) patients, while 2 (11%) were non-responders. Median ALT declined to 34 (15–76) U/L; a biochemical response (ALT normalization) was observed in 89% of patients while a combined response (virological and biochemical) was observed in 72%. AST, GGT, AFP, albumin, IgG and gammaglobulin levels improved (p < 0.001), while HBsAg, HBV RNA, HBcAg, platelets and bilirubin did not significantly change. While Child-Pugh Turcotte (CPT) score remained unchanged in all patients with CPTA5 at baseline, 4 out of 5 patients with baseline CPT A6 improved their liver function to CPT A5. No liver-related complications occurred during treatment. BLV was well tolerated: the only adverse event observed was a fully asymptomatic increase of serum bile acids; no site injection reactions were observed. No patient discontinued treatment.

**Conclusion:** A 48-week course of BLV 2 mg/day monotherapy is safe and effective even for difficult-to-treat HDV patients such as those with compensated cirrhosis and CSPH. Virological response is associated with an improvement of liver function tests and CPT score.
SAT430
Bulevirtide avoids future clinical events and related costs compared to pegylated-interferon alpha in chronic hepatitis D in Spain
Maria Buti1, José Luis Calleja Panero2, Miguel Ángel Rodríguez Sagrado3, Helena Cantero4, Ana de las Heras5, Raquel Domínguez–Hernández6, Miguel Ángel Casado5, 1Hospital Universitari Vall d’Hebron, Hepatology and Internal Medicine, Barcelona, Spain; 2Puerta de Hierro Majadahonda University Hospital, Gastroenterology and Hepatology, Majadahonda, Spain; 3Hospital Ramón y Cajal, Pharmacy, Madrid, Spain; 4Gilead Sciences, Market Access, Madrid, Spain; 5Pharmacoeconomics and Outcomes Research Iberia (PORIB), Pozuelo de Alarcón, Spain Email: rdominguez@porib.com

Background and aims: Chronic Hepatitis D (CHD) is the most severe form of all chronic viral hepatitis. Although it is not approved, pegylated-interferon alpha (PEG-IFN-α) is the most used treatment for patients with CHD. Bulevirtide (Hepcludex®) is a novel, first-in-disease and first-in-class entry inhibitor with the European Medicine’s Agency conditional approval to treat adults with compensated CHD. The aim of the study was to evaluate the avoided clinical events and their costs of bulevirtide compared to PEG-IFN-α, in patients with CHD in Spain.

Method: The course of the disease was simulated, for a lifetime horizon, through a decision-tree model integrated into a Markov model in order to predict the number of clinical events and derived costs of using bulevirtide in comparison to PEG-IFN-α in CHD patients. A cohort of 3, 882 patients was assumed (national prevalence figures), from which 46.90% were cirrhotic at baseline. “Response to bulevirtide” was defined as achieving the combined response end point (hepatitis D virus–RNA undetectable or ≥2log decline and alanine aminotransferase normalisation) at 24–48 weeks, and “non-response” was considered when the combined response end point was not reached. For bulevirtide, responders remained under treatment beyond 48 weeks, except for patients with HBsAg seroclearance or progression, whereas non-responders stopped treatment at week 48. For PEG-IFN-α, patients were treated until week 48. The parameters of the analysis (patient characteristics, efficacy of bulevirtide and PEG-IFN-α, disease progression and unitary event costs) were extracted from the literature. Only clinical event direct costs were evaluated in the model, from the National Health System perspective (€, 2021). Results were described as avoided events of decompensated cirrhosis (DC), hepatocellular carcinoma (HCC), liver transplant (LT) and liver-related death, and their avoided costs.

Results: In a cohort of 3, 882 patients during a lifetime period, treatment with bulevirtide could avoid 202 DC events, 105 HCC, 15 LT and 407 liver-related deaths in comparison to PEG-IFN-α, resulting in a 16%, 7%, 14% and 13% event reduction, respectively. This would imply a total cost reduction related to events of 12.5 million € with bulevirtide vs PEG-IFN-α (2.3 million € for DC, 1.3 million € for HCC, 7.5 million € for LT and 1.4 million € for liver-related deaths).

Conclusion: Bulevirtide for CHD could avoid a significant number of clinical events compared to PEG-IFN-α, leading to a slower disease progression and cost savings originated by the reduction in the number of negative liver-related events.

SAT431
Quantitative HBsAg (qHBsAg) as an end point to stop nucleos (t) ide analogues in chronic hepatitis B: a meta-analysis with meta-regression
Seng Gee Lim1, Ada Ee Der Teo1, Edwin Shih-Yen Chan2, Wah Wah Phyo1, David Hsing Yu Chen3, Carol Anne Hargreaves3
1National University Health System, Division of Gastroenterology and Hepatology, Singapore, Singapore; 2Singapore Clinical Research Institute, Singapore; 3National University of Singapore, Data Analytics Consulting Centre, Faculty of Science, Singapore
Email: mdclims@nus.edu.sg

Background and aims: Guidelines differ on recommendations for stopping nucleoside analogue (NA) therapy in HBeAg-negative Chronic Hepatitis B (CHB) as the risk-benefit trade-off is unclear. An end-of-treatment quantitative HBsAg (EOTqHBsAg) <1000IU/ml or <100IU/ml has been proposed as criterion to stop NA. We assessed this by meta-analysis and meta-regression.

Method: We searched PubMed, EMBASE and abstracts of major liver conferences for studies of HBeAg-negative CHB NA discontinuation. Risk of bias was assessed by Newcastle-Ottawa tool (modified). Random-effects meta-analysis and meta-regression was performed with covariates of ethnicity (ETHN), EOTqHBsAg (<1000IU/ml [EOT_1000] and as an ordinal variable [EOT_ORD]), duration of NA therapy (TDUR); dichotomised at 24months[EOT_24] and 36 months[EOT_36]) and duration of follow-up (FUP) after stopping NA. We assessed pooled risk, with 95% confidence intervals (95%CI) of HBsAg loss, virological (VR) and biochemical relapse (BR). Heterogeneity was reported as I². Multivariate meta-regression models examined covariates to explain the heterogeneity.

Results: A total of 42 studies were included (34papers, 8 abstracts). The pooled risks of HBsAg loss, VR and BR for stopping therapy at EOTqHBsAg<1000IU/ml were 41.2% (95% CI30.6–52.7%), 43.4% (95% CI30.6–57.2%) and 21.4% (95% CI14.3–30.9%) respectively compared 5.8% (95% CI3.6–9.4%), 75.5% (95% CI64.7–83.8%) and 48.1% (95% CI35.9–60.6%) respectively for those with EOTqHBsAg≥1000IU/ml. The pooled risks of HBsAg loss, VR and BR for stopping therapy at EOTqHBsAg<1000IU/ml were 21.5% (95% CI11.8–36.0%), 69.0% (95% CI43.2–86.8%) and 14.9% (95% CI7.6–27.1%) respectively, compared to 4.0% (95% CI1.8–8.9%), 66.7% (95%CI41.8–84.8%) and 34.0% (95% CI20.3–51.1%) respectively for those with EOTqHBsAg≥1000IU/ml. ETHN significantly contributed to HBsAg heterogeneity. In Asians, EOTqHBsAg<1000IU/ml had HBsAg loss of 33.9% while in Caucasian studies, EOTqHBsAg<1000IU/ml had HBsAg loss of 34.6%, hence a difference in threshold between ethnicities is advocated. Multivariate analysis showed TDUR (continuous) was significant for VR and BR but subgroup analysis of TDUR_24 or TDUR_36 showed no difference.

Conclusion: This meta-analysis provides level 1 evidence to adopt EOTqHBsAg as a criterion to stop NA in HBeAg-negative CHB patients; in Asians EOTqHBsAg<1000IU/ml can be advocated, while in Caucasians, EOTqHBsAg<1000IU/ml is appropriate.

Journal of Hepatology 2022 vol. 77(S1) | S665–S939

S869
SAT432
Low level of HBcrAg is beneficial to functional cure obtained with pegylated interferon therapy in inactive HBsAg carriers
Hong Li1, Li Li1, Ling Qin2, Yali Liu1, Zhang Jing1, Xin-Yue Chen1, Zhenhuan Cao1,1 Beijing Youan Hospital, Capital Medical University, The Third Unit, Department of Hepatology, Beijing, China; 2Beijing Youan Hospital, Capital Medical University, Biomedical Information Center, Beijing, China; 3Beijing Youan Hospital, Capital Medical University, The First Unit, Department of Hepatology, Beijing, China
Email: caozhenhuanyu@mail.ccmu.edu.cn

Background and aims: HBsAg clearance, represented functional cure, is extremely difficult to obtain clinically. Our and other recent studies have shown that IHCs treated with pegylated-interferon (PEG-IFN) results in high HBsAg clearance rates of 44.7% to 65%. Recent study showed that hepatitis B core-related antigen (HBcrAg) could be used as a valuable marker for HBV replication. However, the predictive value of HBcrAg for HBsAg clearance is unclear. This study aims to identify HBcrAg associated with functional cure in IHCs with PEG-IFN therapy.

Method: IHCs received PEG-IFN 135 ug weekly for 96 weeks. Subjects who achieved clearance of HBsAg were considered as responders (R group), and those who did not were considered as non-responders (NR group). To evaluate the factors in predicting HBsAg clearance, univariate and multivariate logistic regression analyses were performed. The receiver operator characteristic curves and the area under the receiver operator characteristic curve (AUROC) were used to evaluate prognostic values.

Results: Our results showed that 39 cases obtained HBsAg clearance (group R), while 21 cases did not (group NR). There was no significant difference in age, ALT, and AST levels between two groups. HBcrAg were all significantly lower in R group than NR group at baseline, 12 and 24 weeks. HBsAg quantification were lower in the R group than in the NR group at 12 and 24 weeks (Table 1). Univariate logistic regression analysis showed that HBcrAg at baseline (OR 10.763, p = 0.001), and at 12 weeks (OR 12.511, p < 0.001), and 24 weeks (OR 5.468, p = 0.019) and 24 weeks (OR 10.719, p = 0.001). A multifactor logistic regression analysis was performed with Y = 219.2277 + 1.269*BaselineHBcrAg-0.994*12weekHBcrAg-0.825*24weekHBcrAg. AUROC was up to 0.916 with 93.5% sensitivity and 85.7% specificity.

Table: Characteristics of R and NR groups at baseline, 12 and 24 weeks of treatment

<table>
<thead>
<tr>
<th>Parameter</th>
<th>R group n = 39</th>
<th>NR group n = 21</th>
<th>p</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gender (M/F)</td>
<td>27/12</td>
<td>16/5</td>
<td>0.568</td>
</tr>
<tr>
<td>Age (years)</td>
<td>38.05 ± 11.25</td>
<td>40.62 ± 11.26</td>
<td>0.368</td>
</tr>
<tr>
<td>Baseline</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ALT (U/L)</td>
<td>30.88 ± 14.62</td>
<td>33.17 ± 14.36</td>
<td>0.570</td>
</tr>
<tr>
<td>AST (U/L)</td>
<td>27.97 ± 6.89</td>
<td>28.17 ± 8.32</td>
<td>0.946</td>
</tr>
<tr>
<td>Lg HBsAg (IU/ml)</td>
<td>1.61 ± 0.97</td>
<td>2.08 ± 0.73</td>
<td>0.067</td>
</tr>
<tr>
<td>HBcrAg (mU/ml)</td>
<td>5.45 ± 1.09</td>
<td>6.71 ± 1.16</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>12week</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ALT (U/L)</td>
<td>82.56 ± 89.52</td>
<td>66.05 ± 49.14</td>
<td>0.681</td>
</tr>
<tr>
<td>AST (U/L)</td>
<td>64.89 ± 74.50</td>
<td>47.71 ± 28.05</td>
<td>0.545</td>
</tr>
<tr>
<td>Lg HBsAg (IU/ml)</td>
<td>0.67 ± 1.21</td>
<td>1.70 ± 0.98</td>
<td>0.001</td>
</tr>
<tr>
<td>HBcrAg (mU/ml)</td>
<td>5.79 ± 0.95</td>
<td>7.17 ± 1.31</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>24week</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ALT (U/L)</td>
<td>54.77 ± 50.70</td>
<td>54.45 ± 48.95</td>
<td>0.728</td>
</tr>
<tr>
<td>AST (U/L)</td>
<td>46.39 ± 28.24</td>
<td>46.65 ± 45.28</td>
<td>0.636</td>
</tr>
<tr>
<td>Lg HBsAg (IU/ml)</td>
<td>−0.29 ± 1.14</td>
<td>1.22 ± 1.27</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>HBcrAg (mU/ml)</td>
<td>5.33 ± 0.93</td>
<td>6.63 ± 1.61</td>
<td>0.003</td>
</tr>
</tbody>
</table>

Conclusion: This study provides evidence supporting serum HBcrAg as a clinical predictor of HBsAg clearance, which has a higher predictive value compared to the conventional predictors of HBsAg and ALT.

SAT433
Comparative risk of hepatocellular carcinoma in patients with chronic hepatitis B receiving tenofovir- or entecavir-based regimens: a meta-analysis using individual patient data
Won-Mook Choi1, Terry Cheuk-Fung Yip2, Grace Wong2, W. Ray Kim3, Leland Yee4, Craig Brooks-Rooney5, Tristan Curtes6, Harriet Cant6, Chien-Hung Chen7, Chi-Yi Chen8, Yi-Hsiang Huang8,9,10, Young-Joo Jin11, Dai Won Jun12, Jin-Wook Kim13,14, Neung Hwa Park15,16, Cheng-Yueng Peng17,18, Hyun Phil Shin19, Jungwoo Shin11, Yao-Hsu Yang20,21, Young-Suk Lim1,1 University of Ulsan College of Medicine, Department of Gastroenterology, Liver Center, Asan Medical Center, Seoul, Korea, Rep. of South; 2The Chinese University of Hong Kong, CUHK Medical Data Analytics Centre, Department of Medicine and Therapeutics, Hong Kong SAR, Hong Kong; 3Stanford University School of Medicine, Division of Gastroenterology and Hepatology, Stanford, United States; 4Gilead Sciences, Foster City, United States; 5Costello Medical Consulting Ltd, United States; 6Costello Medical Consulting Ltd, Cambridge, United Kingdom; 7Kaohsiung Chang Gung Memorial Hospital and Chang Gung University College of Medicine Kaohsiung, Division of Hepatogastroenterology, Department of Internal Medicine, Taiwan; 8Ditmanson Medical Foundation Chia-Yi Christian Hospital Chia-Yi, Division of Hepatogastroenterology, Department of Internal Medicine; 9Division of Gastroenterology and Hepatology, Department of Medicine, Taipei Veterans General Hospital, Taipei, Taiwan; 10National Yang Ming Chiao Tung University, Institute of Clinical Medicine, Taipei, Taiwan; 11Digestive Disease Center, Department of Internal Medicine, Inha University Hospital, Inha University School of Medicine, Incheon, Korea, Rep. of South; 12Hanyang University College of Medicine, Department of Internal Medicine, Hanyang University Hospital, Seongnam, United States; 13Seoul National University Bundang Hospital, Department of Medicine, Seongnam, Korea, Rep. of South; 14Seoul National University College of Medicine, Department of Internal Medicine, Seoul, Korea, Rep. of South; 15Ulsan University Hospital, Department of Internal Medicine, University of Ulsan College of Medicine, Ulsan, Korea, Rep. of South; 16Ulsan University Hospital, Biomedical Research Center, University of Ulsan College of Medicine, Ulsan, Korea, Rep. of South; 17China Medical University Hospital, Center for Digestive Medicine, Department of Internal Medicine, Taichung, Taiwan; 18China Medical University, School of Medicine, Taichung, Taiwan; 19Kyung Hee University School of Medicine, Department of Gastroenterology and Hepatology, Kyung Hee University Hospital at Gangdong, Seoul, Korea, Rep. of South; 20Chiai Chang Gung Memorial Hospital, Department of Traditional Chinese Medicine, Chiayi, Taiwan; 21Chang Gung Memorial Hospital, Health Information and Epidemiology Laboratory, Chiayi, Taiwan
Email: limys@amc.seoul.kr

Background and aims: Chronic hepatitis B (CHB) is associated with a long-term risk of hepatocellular carcinoma (HCC), which can be mitigated by nucleo (s) tide analogue therapies such as tenofovir disoproxil fumarate (TDF) and entecavir (ETV). Aggregate data meta-analyses have been unable to reach a consensus on the relative effectiveness of TDF and ETV to reduce the risk of HCC due to challenges with heterogeneity and different methodologies of included studies. To account for these challenges, this meta-analysis used individual patient data (IPD) to compare the risk of HCC in patients receiving TDF or ETV and identify any subgroup of patients who may benefit more from one treatment than the other.

Method: A literature review identified 20 observational studies from East Asia reporting HCC incidence in patients receiving TDF or ETV, 11 agreed to participate in this study. Eligible patients were adults with CHB who were treatment-naive before receiving TDF or ETV monotherapy and completed at least 1 year of treatment. After adjustment for potential confounding variables and multiple imputation to account for missing data, a one-stage IPD meta-analysis
evaluated the hazard ratio (HR) of treatment with TDF versus (vs) ETV to reduce HCC risk using a multivariable Cox proportional hazards model. Subgroup analyses for age, sex, HBeAg positivity, cirrhosis status and diabetes status were also conducted.

Results: Data from 42,939 eligible patients (6,979 TDF and 35,960 ETV) were included. The treatments were similar in terms of baseline age (TDF: 48.32 years [yrs] vs ETV: 52.26 yrs), sex (female: 38.64% vs 34.13%), follow-up time (3.71 yrs vs 3.97 yrs) and presence of cirrhosis (38.01% vs 33.69%). Patients receiving TDF were associated with a significantly lower risk of developing HCC: adjusted HR (95% confidence interval [CI]) = 0.77 (0.61–0.98), p = 0.03. In all subgroup analyses, TDF showed a lower risk of HCC than ETV (HR <1.0), with the risk difference most pronounced in the HBeAg positive subgroup (Figure).

Figure: Analyses for cumulative incidence of HCC in patients with CHB treated with TDF or ETV

*Statistically significant results are in bold. For the ‘50 years or older’ and ‘non-diabetic’ subgroups, the upper bound of each CI is <1.00, but each has been rounded up to 1.00 when reported to two decimal places.

Conclusion: The risk of developing HCC was significantly lower in CHB patients receiving TDF than ETV. TDF was consistently associated with lower HCC risk across all subgroups, but most notably in HBeAg positive patients.

SAT434

**Safety, pharmacokinetics, and antiviral activity of the S-antigen Transport Inhibiting Oligonucleotide Polymers (STOPS) drug candidate ALG-010133 in subjects with chronic hepatitis B**

Edward J Gane1, Kosh Agarwal2, Man-Fung Yuen3, Alina Jucov4, Christian Schwabe5, Kha Le6, Stanley Wang7, Christopher Westland8, Kim Steel9, Qingling Zhang7, Vikrant Gohil10, Felix Lai11, Meenakshi Venkatraman12, Lawrence Blatt13, Leonid Beigelman14, Tse-I Lin1, Sushmita Chanda7, Matt McClure12, John Fry13, University of Auckland, Auckland, New Zealand; 2King’s College Hospital, Institute of Liver Studies, London, United Kingdom; 3The University of Hong Kong, Queen Mary Hospital, Department of Medicine, School of Clinical Medicine, Hong Kong, Hong Kong; 4ARENSIA Exploratory Medicine, Republican Clinical Hospital and Nicolaie Testemitanu State University of Medicine and Pharmacy, Chisinau, Moldova; 5New Zealand Clinical Research, Auckland, New Zealand; 6Aligos Therapeutics, Inc.; 7SARPO Consulting, Melbourne, Australia

Background and aims: To evaluate the safety, pharmacokinetics (PK) and antiviral activity of ALG-010133, a STOPS molecule designed to reduce hepatitis B S-antigen (HBsAg) in chronic hepatitis B (CHB) patients.

Method: This was a 3-part, multicenter, double-blind, randomized, placebo-controlled study. In Parts 1 and 2, single and multiple subcutaneous (SC) doses of ALG-010133 were generally well tolerated in healthy volunteers (Gane et al, EASL 2021). Part 3 evaluated weekly SC doses of ALG-010133 or placebo × 12 weeks in virologically suppressed Hepatitis B e-antigen (HBeAg) negative CHB subjects (N = 10); (cohort; 8 active; 2 placebo). Reported here are preliminary
POSTER PRESENTATIONS

blinded Part 3 safety, PK, and antiviral data; unblinded data will be presented at the conference.

**Results:** 31 CHB subjects completed dosing and follow-up in Cohorts 1 (120 mg; N = 10), 2 (200 mg; N = 10), and 3 (400 mg; N = 11). Most subjects were male (61%) and 48% were white, with mean age 48 years, mean BMI 26.1 kg/m² and baseline HBsAg across cohorts of 3.6 to 3.7 log₁₀ IU/ml. There was 1 unrelated serious treatment emergent adverse event (TEAE) (hospitalization for orchiitis) and 1 unrelated TEAE (COVID-19 infection) resulting in premature study drug discontinuation. All TEAEs were Grade 1 or 2 in severity, except for 1 Grade 3 TEAE of injection site erythema (severity based only on surface area criteria of ≥100 cm²); required no treatment and resolved despite continued study drug dosing and the aforementioned TEAE of orchitis (Grade 3). There was no dose relationship to severity or frequency for any TEAE. The most common (≥3 subjects) TEAEs were injection site erythema (n = 5), increased ALT (n = 4), injection site bruising (n = 4), increased AST (n = 3), and injection site pruritus (n = 3); none were assessed as clinically concerning. Although treatment-emergent ALT and AST elevations (n = 13) were observed, all were Grade 1 (<2.5x upper limit of normal [ULN]) or 2 (<2.5 to <5x ULN) and none led to premature study drug discontinuation or were associated with symptoms or evidence of liver dysfunction. There were no other clinically significantly lab abnormalities. No clinically significant physical examinations, vital signs, or ECG abnormalities were reported. Plasma ALG-010133 exposures increased more than dose proportionally between the 120 to 400 mg dose levels, with moderate variability and minimal accumulation. Compared to baseline, the magnitude of HBsAg decline at Week 12 was <0.1 log₁₀ IU/ml for placebo and across all ALG-010133 dose levels, including the projected efficacious dose level of 400 mg (estimated to maintain total liver exposures >3x EC₉₀ for HBsAg inhibition).

**Conclusion:** ALG-010133 was safe and well tolerated with predictable PK properties when given to CHB subjects as multiple SC doses of up to 400 mg. No meaningful HBsAg reduction was observed across all cohorts. Further clinical development of ALG-010133 has been discontinued.

**SAT436**

Ccostimulation of CD40 and type-I interferon immune pathways by a bifunctional molecule in HBV infection models and healthy non-human primates

Xavier Marniquet1, Marion Dajon1, Julie Montegut1, Maria Elena Giusepponi2, Michela Pecoraro2, Elena Vicentini2, Francesca Morandini2, Floriana Zanderigo2, Denise Federico2, Othée Bonnin3, Gregory Neveu1, Charlotte Blanc1, Christelle Marcou1, Juliette Lavaux1, Michel Didier4, Galina Boldina5, Jacques Dumas3, Thomas Bouquin1, Annabelle Milla1, Hugh Watson1, Kara Carter1, Antoine Alam11, Evotec ID (Lyón), Antiviral Research Unit, Lyon, France; 2Aptuit (Verona) Srl, Verona, Italy; 3Sanofi, Vitry-sur-Seine, France Email: xavier.marniquet@evotec.com

**Background and aims:** Type-I interferons (IFN-I) have shown limited ability to cure patients with chronic hepatitis B (CHB). New strategies that enable safe elimination of hepatocytes harbouring HBV genomes are needed. Immune-mobilising monoclonal TCR against viruses (ImmTAV®) are unique bispecific soluble proteins designed to redirect polyclonal T cells, regardless of their specificity, to eliminate virus-infected cells. IMC-I109V-101 is an open-label Phase 1/2 study evaluating IMC-I109V in HLA-A*02:01 positive patients with CHB who are non-cirrhotic, HBsAg-negative and virally suppressed on nucleos (t)ide analogues. Part 1 is a single ascending dose to identify a safe and pharmacologically active dose. Part 2 is a multiple ascending dose to evaluate safety and anti-HBV activity of repeated doses over 24 weeks. Secondary objectives include PK and effects on serum HBsAg, HbcAg and HBV RNA levels.

**Results:** Three patients each received a single dose of 0.8 mcg, based on the minimum anticipated biological effect level (MABEL). Doses were well tolerated and not associated with adverse events in any subject. Preliminary PK, HbsAg and liver enzymes were available for the first two participants. PK analysis showed that the maximum serum concentrations were consistent with the dose level. By 12 hours, serum concentrations declined below the lower limit of quantification. Serum HBsAg levels transiently decreased by 11–15% during Days 3–15 post infusion, before returning to baseline within 3 weeks (Figure 1). The decreases coincided with small, transient elevations in ALT, albeit within the normal range.

**SAT437**

IMC-I109V, a novel T cell receptor (TCR) bispecific (ENVxCD3) designed to eliminate HBV-infected hepatocytes in chronic HBV patients: initial data from a first-in-human study

Stefan Bourgeois1, Young-Suk Lim2, Edward J Gane3, Hyun Woong Lee1, Wendy Cheng4, Jeong Heo5, Won Kim1, Maria Buti6, Alexander Thompson7, Gail Matthews18, Ewa Janczewska1, Stephen Ryder1, Raul J. Andrade3, Yuan Yuan14, Adel Benlahrech15, Jay Wustner16, Lucy Dorrell16, Man-Fung Yuen17, Ziekenhuis Netwerk Antwerpen, Belgium; 2Asan Medical Centre; 3University of Auckland; 4Gangnam Severance Hospital; 5Royal Perth Bentley Group; 6Pusan National University Hospital; 7SMC-SNU Boramae Medical Centre; 8Hospital Universitario Valle Hebron; 9St Vincent’s Hospital Melbourne; 10St Vincent’s Hospital Sydney; 11ID Clinic Arkadiusz Psuła; 12Nottingham University Hospitals NHS Trust; 13Hospital Universitario Virgen de la Victoria-IBIMA; 14Immunocore plc; 15Immunocore Ltd; 16Immunocore Ltd, United Kingdom; 17The University of Hong Kong Email: lucy.dorrell@immunocore.com

**Background and aims:** HBsAg clearance is the treatment goal for chronic hepatitis B (CHB). New strategies that enable safe elimination of hepatocytes harbouring HBV genomes are needed. Immune-mobilising monoclonal TCR against viruses (ImmTAV®) are unique bispecific soluble proteins designed to redirect polyclonal T cells, regardless of their specificity, to eliminate virus-infected cells. IMC-I109V is an affinity-enhanced HBV-specific TCR fused to an anti-CD3 scFv T cell activating moiety, that redirects non-exhausted effector T cells to eliminate hepatocytes presenting HLA-bound HBsAg (Env)-derived peptide. Since the mechanism results in hepatocyte lysis, transient liver enzyme increases are expected, necessitating a conservative dosing schedule in our first-in-human study.

**Method:** IMC-I109V-101 is a first-in-human Phase 1/2 study evaluating IMC-I109V in HLA-A*02:01 positive patients with CHB who are non-cirrhotic, HBsAg-negative and virally suppressed on nucleos (t)ide analogues. Part 1 is a single ascending dose to identify a safe and pharmacologically active dose. Part 2 is a multiple ascending dose to evaluate safety and anti-HBV activity of repeated doses over 24 weeks. Secondary objectives include PK and effects on serum HBsAg, HbcAg and HBV RNA levels.

**Results:** Three patients each received a single dose of 0.8 mcg, based on the minimum anticipated biological effect level (MABEL). Doses were well tolerated and not associated with adverse events in any subject. Preliminary PK, HbsAg and liver enzymes were available for the first two participants. PK analysis showed that the maximum serum concentrations were consistent with the dose level. By 12 hours, serum concentrations declined below the lower limit of quantification. Serum HBsAg levels transiently decreased by 11–15% during Days 3–15 post infusion, before returning to baseline within 3 weeks (Figure 1). The decreases coincided with small, transient elevations in ALT, albeit within the normal range.
SAT438
Long-term outcomes after cessation of antiviral therapy in HBeAg negative patients
Rachel Wen-Juei Jeng1, 2, Yen-Chun Liu1,2, Chien-Wei Peng1,2,2, Rong-Nan Chien1, 2, Yun-Fan Liaw1,3, 1Linkou Chang Gung Memorial Hospital, Gastroenterology and Hepatology, Taoyuan, Taiwan; 2Chang Gung University, College of Medicine, Taoyuan, Taiwan; 3Linkou Chang Gung Memorial Hospital, Liver Research Unit, Taoyuan, Taiwan
Email: rachel.jeng@gmail.com

Background and aims: We reported a cohort of 691 HBeAg negative chronic hepatitis B patients who had stopping Nuc (Hepatology 2018) with a median follow-up duration about 3 years. We have extended the follow-up to a median of 6.6 (Q1-Q3: 5–8.2) years and to examined the long-term outcome of these patients.

Method: The 691 HBeAg negative CHB patients were followed-up till Dec 2021. Virological relapse (VR) was defined as HBV DNA >2000U/ml and clinical relapse (CR) as VR plus ALT >2X ULN. Retreatment decision was made according to the Taiwan reimbursement criteria: cirrhosis with detectable HBV DNA or non-cirrhosis with CR prolonged over 3 months or CR with serum bilirubin level >2 mg/dL or INR >1.5 or by joint physician/patient discussion. According to the clinical outcome and management, these patients were categorized into 4 groups: A: no CR and no retreatment (retx); B: no CR but retx; C: CR and no-retx; D: CR and retx.

Results: During a median of 6.6 years follow-up of this observational cohort, 180 (26%) were group A, 27 (4%) were group B, 103 (15%) were group C and 381 (55%) were group D. The cumulative VR, CR, retreatment rate are listed in Table. The annual HBsAg decline in group C and 381 (55%) were group D. The cumulative VR, CR, CR/no Retx; C: CR and no-retx; D: CR and retx.

Conclusion: The concomitant HBsAg declines and ALT elevations indicate that a single, very low dose of IMC-I109V elicited on-target activity consistent with the TCR bispecific (ENVxCD3) mechanism of action, without adverse events. These results are encouraging for the prospect of identifying a tolerable and active treatment regimen with higher and repeat dosing. Enrolment in Part 1 dose escalation continues to evaluate this novel mechanism designed to eliminate HBV-positive hepatocytes. (Eudract no. 2019–004212-64).

SAT439
Bepirovirsen, antisense oligonucleotide (ASO) against hepatitis B virus (HBV), harbors intrinsic immunostimulatory activity via Toll-like receptor 8 (TLR8) preclinically, correlating with clinical efficacy from the Phase 2a study
Shihyun You1, Jared Delahaye1, Megan Ermel1, Jennifer Singh1, William Jordan1, Avijit Ray1, Nicholas Galwey2, Daren Austin3, Dickens Theodore4, Melanie Paff1. 1GlaxoSmithKline, Collegeville, PA, United States; 2GlaxoSmithKline, Stevenage, United Kingdom; 3GlaxoSmithKline, Brentford, United Kingdom; 4GlaxoSmithKline, Research Triangle Park, NC, United States
Email: shihyun.k.you@gsk.com

Background and aims: Bepirovirsen (BPV) is a modified ASO targeting HBV RNAs including pregenomic RNA; GS3389404 (GSK404) is GalNac conjugated BPV. Phase 2a studies (NCT02981602 and NCT03020745) showed more robust dose-related HBsAg reductions and ALT flares with BPV than GSK404, prompting a hypothesis that preferential distribution of BPV to nonparenchymal cells may confer immune activity. To investigate the mechanism of BPV immunostimulatory effect, this post-hoc analysis evaluated changes in soluble proteins measured in study NCT02981602; preclinical models were used to validate the activity.

Method: This study analyzed plasma and serum from 30 patients receiving placebo (PBO) or BPV administered on Days 1, 4, 8, 11, 15 and 22 (treatment naïve: PBO n = 6, BPV 150 mg n = 6, 300 mg n = 12; nucleos[t]ide-treated: PBO n = 2, BPV 300 mg n = 4). Soluble proteins from plasma (only treatment-naïve groups) collected at 0.5, 4, 6 and 24 hours post dose were evaluated with the Olink 1536 Explore panel for pathway analysis; soluble proteins from serum on Days 1, 2, 8, 15, 22, 23, 29, 36, 57 and 85 were evaluated with the Olink 96 Inflammation panel for correlation analysis. A generalized linear mixed effects model compared changes from baseline at each time point. Mean fold changes and p values were used to select analytes for pathway analyses (Enrichr). A subset of proteins was used in principal component analysis (PCA). BPV was tested in a panel of pattern recognition receptor (PRR)-overexpressing cell lines (InvivoGen) in vitro and TLR8 activity was validated in human TLR8 (hTLR8) transgenic mice in vivo.

Results: Within 6- and 24-hour post BPV dosing, the most significant change was observed in the epithelial mesenchymal transition pathway (p = 2.75E-10) and in the inflammatory response pathway (p = 4.13E-8), respectively. Notably, induction of IL12B, IFNg, and IL1Ra, but not type I IFNs were detected, suggestive of TLR8

Table: Summary of cumulative events of these 691 HBeAg negative CHB patients

<table>
<thead>
<tr>
<th>Event</th>
<th>1-year</th>
<th>2-year</th>
<th>3-year</th>
<th>5-year</th>
<th>10-year</th>
</tr>
</thead>
<tbody>
<tr>
<td>Virological relapse</td>
<td>72%</td>
<td>84%</td>
<td>86%</td>
<td>88%</td>
<td>89%</td>
</tr>
<tr>
<td>Clinical relapse</td>
<td>42%</td>
<td>60%</td>
<td>65%</td>
<td>70%</td>
<td>72%</td>
</tr>
<tr>
<td>Retreatment</td>
<td>21%</td>
<td>39%</td>
<td>48%</td>
<td>57%</td>
<td>63%</td>
</tr>
<tr>
<td>HBsAg loss</td>
<td>1%</td>
<td>3%</td>
<td>6%</td>
<td>10%</td>
<td>27%</td>
</tr>
<tr>
<td>No CR/no Retx</td>
<td>4%</td>
<td>11%</td>
<td>18%</td>
<td>27%</td>
<td>57%</td>
</tr>
<tr>
<td>CR/no Retx</td>
<td>0%</td>
<td>2%</td>
<td>3%</td>
<td>13%</td>
<td>38%</td>
</tr>
<tr>
<td>No CR/Retx</td>
<td>0%</td>
<td>0%</td>
<td>0%</td>
<td>0%</td>
<td>6%</td>
</tr>
<tr>
<td>CR/Retx</td>
<td>0%</td>
<td>1%</td>
<td>1%</td>
<td>3%</td>
<td>11%</td>
</tr>
<tr>
<td>HCC</td>
<td>4%</td>
<td>6%</td>
<td>1%</td>
<td>2%</td>
<td>2%</td>
</tr>
<tr>
<td>Non-cirrhosis</td>
<td>1%</td>
<td>2%</td>
<td>8%</td>
<td>11%</td>
<td></td>
</tr>
<tr>
<td>Cirrhosis</td>
<td>8%</td>
<td>11%</td>
<td>8%</td>
<td>11%</td>
<td>3%</td>
</tr>
<tr>
<td>Liver-related mortality (due to HCC, hepatic decompensation or cirrhotic complication)</td>
<td>2%</td>
<td>3%</td>
<td>2%</td>
<td>3%</td>
<td></td>
</tr>
<tr>
<td>Non-cirrhosis</td>
<td>0%</td>
<td>0%</td>
<td>0%</td>
<td>0%</td>
<td>6%</td>
</tr>
<tr>
<td>Cirrhosis</td>
<td>3%</td>
<td>6%</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Conclusion: The finite therapy does much increase the functional cure rate, especially in those remain untreated. The HBsAg loss rate accelerated along with follow-up time, especially after year 3.
**Background and aims:** Bulevirtide (BLV) was recently approved for treatment of hepatitis D in Europe. Theory predicts that drugs like BLV that block virus infection should lead to a monophasic viral decline that is driven by the rate of loss/death of HDV-infected cells (Shekhtman et al. PMID: 34995688). The current study is the first to characterize HDV and ALT kinetics under BLV monotherapy in patients with advanced compensated cirrhosis.

**Method:** Eighteen patients with HDV-related advanced compensated cirrhosis were treated with BLV 2 mg/day monotherapy. All were receiving TDF or ETV for HBV. Blood samples were collected at treatment initiation, weeks 4 and 8, and every 8 weeks thereafter. HDV RNA was measured by Robogene 2.0 (lower limit of quantification, LLoQ = 6 IU/ml). ALT normalization was defined as 41 U/L and 59 U/L for women and men, respectively.

**Results:** Median baseline HDV and ALT were 4.9 log IU/ml [IQR 4.4–5.8] and 106 U/L [IQR 81–142], respectively. During therapy, patients fit into 6 interim HDV kinetic patterns (Fig. 1): monophasic, MP (n = 3, Fig. 1a), biphasic, BP (n = 7, Fig. 1b), flat-partial response, FPR (n = 4, Fig. 1c), FPR followed by decline (n = 1, Fig. 1d), FPR followed by breakthrough (n = 1, Fig. 1e), and non-responder, NR (n = 2, Fig. 1f). MP patients had significantly (p = 0.039) longer median HDV t1/2 of 46 days [range:41–60] compared to BP/FPR patients (26 days [range:11–49]) during the first viral decline phase, suggesting two distinct HDV-infected cell population turnovers. There was no difference (p > 0.18) in HDV t1/2, length (median 11 weeks [range 3–22]) and magnitude (median 2.0 log U/ml [range 1.1–3.3]) of first viral decline phase from baseline between BP and FPR patients. The 2nd slower phase slope of viral decline in BP patients was not significantly different (p = 0.18) than the first phase slope of viral decline in MP patients, suggesting similar HDV-infected cell population turnover. ALT normalization was achieved in 14 (78%) patients at a median of 8 weeks (range: 4 to 16) from initiation of BLV therapy. MP patients had a significantly (p = 0.048) lower median ALT decline slope of 1.4 U/wk [range:0.6–8.9] compared to BP/FPR patients (10.1 U/wk [range:4.5–28.5]), supporting, in part, the theory that HDV decline under BLV reflects the loss/death rate of HDV-infected cells.

**Conclusion:** While theory predicts a MP viral decline under BLV, this pattern was only identified in 3 patients (17%). In 7 patients (39%) the first rapid phase observed in patients with BP suggests that an additional HDV-infected cell population with a shorter t1/2 might exist compared to patients with MP decline. Six patients (33%) experienced a FPR kinetic pattern suggesting suboptimal BLV dosage, which should be further investigated. The current findings will help to develop theoretical models to explain the observed viral dynamics and develop response guided therapy strategies.

---

**Figure 1. HDV kinetic patterns under BLV monotherapy in patients with advanced liver cirrhosis.** (a) monophasic, MP, i.e., a single phase of viral decline (n=3), (b) biphasic, BP, viral decline consisting of a first phase decline that was 2-fold larger than the second phase decline rate (n=7), (c) flat-partial response, FPR, defined as a first phase viral decline followed by a plateau that was not significantly (p>0.05) different from slope=0 (n=4), (d) FPR followed by decline (n=1), (e) FPR followed by breakthrough (n=1), and (f) non-responder, NR, defined as having < ~1.0 log IU/mL decline from baseline (n=2). Solid lines for HDV reflect modelling using piecewise linear regression and dashed lines between ALT markers are shown only to highlight the trajectory.

---

**Funding:** GSK (NCT02981602)
SAT441
Mechanistic pharmacokinetics/pharmacodynamics modelling of the simultaneous effects of bepirovirsen on hepatitis B surface antigen and alanine transaminase changes in chronic hepatitis B patients: phase 2b analysis to inform phase 3 decision-making
Amir Youssef1, Mohamed Ismail2, Mindy Magee1, Dickens Theodore3, Melanie Paff4, Robert Elston5, Ahmed Nader1. 1GlaxoSmithKline, Clinical Pharmacology Modeling and Simulation, Collegeville, PA, United States; 2Enhanced Pharmacodynamics LLC, Buffalo, NY, United States; 3GlaxoSmithKline, Development, Clinical Sciences Hepatology/GI, Research Triangle, NC, United States; 4GlaxoSmithKline, Development, Collegeville, PA, United States; 5GlaxoSmithKline, Development, Clinical Sciences Hepatology/GI, Stevenage, Hertfordshire, United Kingdom
Email: amir.s.youssef@gsk.com
This abstract is under embargo until the start of the Late Breaker session on Saturday 25 June 2022, 14:00 BST. It will be made publicly available on the congress website once the embargo has lifted.

SAT442
Improved treatment response and bone density in patients with chronic hepatitis B (CHB) switched to tenofovir alafenamide (TAF) from other nucleos(t)ide analogue: 96-week results from a prospective multinational study
Eiichi Ogawa1, Dae Won Jun2, Hidenori Toyoda3, Yao-Chun Hsu4, Eileen Yoon5, Sang Bong Ahn6, Son Do7, Huy Trinh8, Hirokazu Takahashi9,10, Masaru Enomoto11, Satoshi Yasuda3, Cheng-Hao Tseng5, Ming-Lun Yeh12,13, Keigo Kawashima14, Han Ah Lee15, Kaori Inoue16, Hiroaki Haga17, Ai-Thien Do7, Mayumi Maeda15, Joseph Hoang16, Ramsey C. Cheung18,19, Yoshiyuki Ueno15, Yuichiro Eguchi20, Norihiro Furusyo1, Ming-Lung Yu12,13, Yasuhiro Tanaka14,19, Mindie Nguyen20. 1Kyushu University Hospital, Department of General Internal Medicine, Japan; 2Hanyang University, Department of Gastroenterology, Korea, Rep. of South; 3Ogaki Municipal Hospital, Department of Gastroenterology, Japan; 4E-Da Hospital, Division of Gastroenterology and Hepatology, Department of Internal Medicine, Kaohsiung, Taiwan; 5Inje University Sanggye Paik Hospital, Department of Internal Medicine, Korea, Rep. of South; 6Nowon Eulji Medical Center, Eulji University College of Medicine, Department of Internal Medicine, Korea, Rep. of South; 7Osaka City University Graduate School of Medicine, Department of Hepatology, Osaka, Japan; 8Saga University Hospital, Liver Center, Saga, Japan; 9Saga University Faculty of Medicine, Division of Metabolism and Endocrinology, Saga, Japan; 10Osaka City University Graduate School of Medicine, Department of Hepatology, Osaka, Japan; 11Gastroenterology and Hepatology Department, Graduate School of Medicine, Hokkaido University, Sapporo, Japan; 12Kakugakai Medical University Hospital, Hepatobiliary Division, Department of Internal Medicine, Izumi, Japan; 13Kagoshima Medical University, Hepatitis Research Center, College of Medicine and Hepato-Cancer Research Center, Kagoshima, Japan; 14Nagoya City University Graduate School of Medical Sciences, Department of Virology and Liver Unit, Nagoya, Japan; 15Yamagata University Faculty of Medicine, Department of Gastroenterology, Yamagata, Japan; 16Stanford University Medical Center, Division of Gastroenterology and Hepatology, Department of Medicine, Palo Alto, United States; 17Veterans Affairs Palo Alto Health Care System, Division of Gastroenterology and Hepatology, Palo Alto, United States; 18Locomedical Eguchi Hospital, Locomedical General Institute, Saga, Japan; 19Kumamoto University Graduate School of Medical Sciences, Department of Gastroenterology and Hepatology, Kumamoto, Japan; 20Stanford University, Department of Epidemiology and Population Health, Palo Alto, United States
Email: mindiehn@stanford.edu

Background and aims: Prior studies comparing TAF with TDF have shown similar efficacy and improved renal/bone safety, but outcome data for patients switched to TAF after other nucleos(t)ide analogues (NA) are limited. We aimed to assess treatment and safety outcomes of CHB patients switched to TAF after at least 1 year of another NA regimen.

Method: We prospectively enrolled adult CHB patients who switched from any NA to TAF at 14 centers in Japan, Korea, Taiwan, and the U.S.
All patients gave written informed consent. Primary outcomes were complete viral suppression (CVS, HBV DNA<20 IU/ml), biochemical response (BR, ALT<35/25 U/L men/women), and complete response (CVS+BR). Safety assessments included changes in estimated glomerular filtration rate (eGFR) and bone T-scores.

Results: We enrolled 270 eligible patients. Mean age was 58.1 ± 10.6, 58.2% were male, 99.6% were Asian, 12.2% had cirrhosis, and 7.8% had chronic kidney disease (CKD). 73.7% switched from entecavir monotherapy, 23% from TDF/adevovir-based therapy (7.8%: combination therapy), 3.3% from another nucleoside analogue, and mean duration of NA treatment prior to TAF was 7.5 ± 4.0 years. Between switch and week 96 follow-up, the proportions of patients with CVS (95.2% to 98.8%), BR (75.2% to 78.7%), and complete response (72.6% to 77.9%) significantly increased (all p < 0.001). As shown in Figure, comparing levels at switch vs. week 96 of follow-up, there was no significant difference in mean eGFR (88.4 ± 16.9 vs. 89.3 ± 16.3, p = 0.13) or the distribution of CKD stage (p = 0.10). In contrast, between switch and week 96 follow-up, mean T-scores significantly improved (from −1.43 ± 1.36 to −1.17 ± 1.38, p < 0.001), more patients had normal bone density (47% vs. 35%) and fewer patients had osteoporosis/osteopenia (53% vs. 65%) or osteoporosis (14% vs. 20%) (p = 0.019, Figure). In multivariable analysis, significant factors associated with worsening eGFR were age (adjusted odds ratio [aOR] 1.09, p = 0.004) and baseline eGFR, while male sex was associated with lower risk of developing osteopenia/osteoporosis (aOR 0.29, p = 0.020). Twelve patients (4.4%, 15/270) did not complete week-96 follow-up. There were 15 SAEs (5.6%, 15/270) and none were related to TAF.

Conclusion: At 96-week following switch to TAF after an average of 7.5 years of treatment with other NA regimen, complete treatment response rated increased while renal function remained stable and bone density significantly improved.

SAT443
Long-term suppression maintained after cessation of AB-729 treatment and comparable on-treatment response observed in HBeAg+ subjects
Man-Fung Yuen1, Elina Berliha2, Wattana Sukkepamsarinjaroen3, Jacinta Holmes4, Apinya Leerapun5, Piseit Tangkijvanich6, Simone Strasser7, Alina Jucov2, Edward J Gane8, Emily P. Thi9

Background and aims: AB-729 is an N-Acetylglucosamine (GalNAc)-conjugated single trigger RNA interference therapeutic that targets all HBV RNA transcripts, including HBx, resulting in suppression of viral replication and viral antigens. AB-729 is in Phase 2 clinical development for the treatment of chronic hepatitis B (CHB). Here we report additional on treatment and follow-up data from AB-729–001 including a dedicated HBeAg+ cohort.

Method: In AB-729–001 Part 3, 41 non-cirrhotic, CHB subjects received AB-729 60 mg every 4 weeks (Q4W, Cohort E, N = 7), 60 mg every 8 weeks (Q8W, Cohort F, N = 7), 90 mg Q8W (Cohorts I (N = 6), G (N = 7) and K (N = 7)), or 90 mg every 12 weeks (Q12W, Cohort J, N = 7). Cohort G was HBV DNA+ and initiated tenofovir disoproxil fumarate on Day 1; all other cohorts were virologically suppressed on stable nucleos (t)ide analogue (NA) therapy. Cohort K was all HBeAg+ at baseline. Eligible subjects could continue AB-729 through Week 48. Subjects are followed 48 weeks or more after AB-729 discontinuation.

Results: 40/41 eligible subjects consented to treatment extension. Complete on-treatment data for Cohorts E and F have been reported; at Weeks 32 and 36 post last dose, respectively, mean HBsAg change in Cohorts E and F was −1.0 log10 or more and 4/11 subjects with data remained <100 IU/ml. One subject in Cohort E underwent HBsAg seroconversion after AB-729 discontinuation while still on NA. The mean HBsAg declines for the 90 mg Cohorts I, J, K and G were similar (Table). In Cohorts I, J, G, 12/17 subjects with data were <100 IU/ml and 6 were <10 IU/ml at Week 48. At 20 Weeks post last dose, 11/18 subjects with data were <100 IU/ml and 3 were <10 IU/ml. The mean (SE) log10 change in HBsAg was −0.71 (0.44) at Week 32 in Cohort K. There were no deaths or discontinuations due to AEs. There were 2 unrelated SAEs; all other AEs were Grade 1 or 2.

Baseline and Preliminary Mean (SE) log10 Change in HBsAg

<table>
<thead>
<tr>
<th>Nominal Visit</th>
<th>Cohort I N=6</th>
<th>Cohort J N=7</th>
<th>Cohort G N=7</th>
<th>HBeAg+ only Cohort K N=7</th>
</tr>
</thead>
<tbody>
<tr>
<td>Baseline IU/ml</td>
<td>3.36 (0.23)</td>
<td>3.37 (0.28)</td>
<td>3.14 (0.14)</td>
<td>3.23 (0.14)</td>
</tr>
<tr>
<td>Week 12</td>
<td>−1.37 (0.22)</td>
<td>−1.11 (0.35)</td>
<td>−1.56 (0.32)</td>
<td>−1.63 (0.39)</td>
</tr>
<tr>
<td>Week 24</td>
<td>−1.80 (0.23)</td>
<td>−1.56 (0.25)</td>
<td>−1.82 (0.29)</td>
<td>−1.99 (0.35)</td>
</tr>
<tr>
<td>Week 36</td>
<td>−2.06 (0.28)</td>
<td>−1.70 (0.39)</td>
<td>−2.08 (0.32)</td>
<td>−2.28 (0.43)</td>
</tr>
<tr>
<td>Week 48</td>
<td>−1.91 (0.32)</td>
<td>−1.80 (0.41)</td>
<td>−2.16 (0.34)</td>
<td>−2.32 (0.40)</td>
</tr>
<tr>
<td>20 Weeks Post Last Dose</td>
<td>−1.42 (0.26)</td>
<td>−1.63 (0.39)</td>
<td>−1.50 (0.13)</td>
<td>−1.63 (0.39)</td>
</tr>
</tbody>
</table>


Conclusion: AB-729 repeat dosing continues to be generally safe and well tolerated with robust and sustained declines in HBsAg that are comparable across treatment regimens. Neither HBeAg status nor DNA+ at baseline appear to affect response. In 17/31 subjects with data across all cohorts, HBsAg <100 IU/ml was maintained at least 20
Background and aims: Chronic hepatitis delta (CHD) is the most severe form of chronic viral hepatitis with major clinical challenges. HDV tight dependence on its helper virus, Hepatitis B Virus (HBV) and the host cell machinery for its life cycle limits the development of drugs directly acting on HDV, while its therapeutic management remains unsatisfactory. We aim to identify compounds that block HDV replication by targeting HDV ribozymes (Rz), specific viral RNA sequences that undergo self-cleavage and ensure an efficient viral replication. We performed a high throughput screening (HTS) of FDA approved drug libraries to identify novel antivirals against HDV infection.

Method: We generated stable Huh7 human hepatoma cells expressing a reporter gene (secreted Gaussia luciferase, Gluc) either downstream (2xRz-Gluc) or upstream (Gluc-2xRz) of two HDV antigenomic Rz sequences. The cis-acting HDV Rz is self-cleaved leading to mRNA degradation and no detection of the secreted luciferase, whereas in the case of its inhibition, the detection of Gluc was monitored. Constrict with Gluc alone was used as control. Validation of the assay was performed using a morpholino antisense nucleotide (GeneTools) as a positive control. We performed HTS of FDA approved drug libraries and measured the secreted luciferase as a readout of Rz inhibition after the addition of the molecules. Each plate with Z factor>0.4 was considered valid. Dose-response effect and toxicity evaluation of the hits with Z-score >5 was calculated. Analyses and statistic calculations were performed using an excel macro based on Genedata and ActivityBase softwares (IDBS). All data were generated from two independent experiments.

Results: No effect in the luciferase induction was observed in 2xRz-Gluc transfected cells treated with the antisense morpholino, whereas a dose dependent induction of the luciferase expression was detected in Gluc-2xRz transfected cells, implying the efficient inhibition of HDV antigenomic Rz autocatalytic cleavage (EC50 = 27.3 µM). We thus performed HTS on Gluc-2xRz. Gluc cells were included to ensure the specific induction of Gluc due to the inhibition of the HDV antigenomic Rz. The compounds with a Z-score>5 were selected as positive hits with potentially promising inhibitory effect. We identified six compounds, namely APE000283, APE000286, APE000283, APE000283, APE000286, APE000283, APE000916 and APE000445 that showed a specific inhibitory effect on HDV antigenomic Rz in the Gluc-2xRz cells. No sign of toxicity was observed.

Conclusion: Six out of 6644 screened compounds showed a specific inhibitory effect on HDV antigenomic Rz. Further studies investigating the antiviral effect in a relevant cell culture infection model and the mechanism of action are currently ongoing. Drug combinatorial studies and resistance emergence studies will be additionally performed in the future.

SAT445
Generation and functional analysis of spacer modified HBV-specific chimeric antigen receptors that harbor a Fab fragment as binding domain
Zhe Xie1, Oliver Quitt1, Lisa Wolff1, Elfriede Nößner1, Ulrike Protzer1,2.
1Institute of virology, Technical University of Munich/Helmholtz Zentrum München, München, Germany; 2German Center for Infection Research (DZIF), partner site Munich, Munich, Germany
Email: protzer@tum.de

Background and aims: Chimeric antigen receptor (CAR) T-cell therapy is a promising novel therapeutic approach for cancer, but has recently also been explored in the context of chronic viral infection. CARs are synthetic receptors designed to drive antigen-specific activation of T-cells upon binding to cognate antigen, however, some of these artificial receptors have been found to elicit different levels of ligand-independent constitutive signaling. Our study aimed at generating novel CARs using antibody Fab fragments that target the hepatitis B virus envelope protein (HBVenv) on the membrane of HBV-infected cells and to study how their specificity can be guaranteed and which role different spacer lengths play.

Method: We constructed novel CARs that contain the HBVenv-specific human B cell-derived antibody fragment (4D06) as binding domain and CD3- as well as CD28 signaling domains (FabCAR). To determine the impact of spacer length on constitutive signaling, we employed several human immunoglobulin G (IgG) spacers with different lengths (IgG1C1H2C2H3 (225aa), IgG4C1H2C2H3 (226aa), IgG4CH3 (116aa) or IgG4Hinge (9aa)) and studied the activation of FabCAR-engrafted T-cells in the presence and absence of target antigen. T-cell activation was assessed by quantification of pro-inflammatory cytokines and elimination of HBVenv-transgenic hepatoma cells.

Results: T-cells from healthy donors were successfully engrafted with 4D06 FabCARs and efficiently eliminated HBVenv-transgenic Huh7S and HepG2 SML cells. Elimination of target cells was accompanied by secretion of interferon gamma, tumor necrosis factor alpha and granzyme B. However, T-cells expressing FabCARs with a long spacer showed high levels of antigen-independent cytokine release and eliminated antigen-negative control cells. This constitutive, ligand-independent T-cell activation correlated with the spacer length and limiting spacer length allowed for antigen-specific T-cell activation. Employing the shortest spacer domains (IgG4 Hinge) completely abolished the constitutive T-cell activation and rendered the FabCAR-engrafted T-cells HBV specific.

Conclusion: Our findings demonstrate that the spacer region of a CAR construct can significantly influence ligand-independent signaling and indicate that spacer length modification is an interesting strategy to improve efficacy and safety of CAR T-cells. T-cells stably transduced with 4D06 FabCARs containing a short spacer efficiently eliminated HBVenv-positive cells in an antigen-dependent manner and represent an interesting novel means to treat chronic hepatitis B and HBV-associated hepatocellular carcinoma.

SAT446
Randomised double-blind study of nitazoxanide for virologically suppressed HBeAg negative chronic Hepatitis B
Yong Chuan Tan1,2, Liang Shen1, Htet Htet Toe Wai Khine1, Yuh Ling Amy Tay1, Celina Adraneda1,2, Jean-Francois Rossignol4, Celine Rossignol4, Seng Gee Lim1,2.
1National University of Singapore, Singapore, Department of Medicine, of Gastroenterology and Hepatology, Singapore, Singapore; 2National University Hospital, Singapore, Division of Gastroenterology and Hepatology, Singapore, Singapore; 4Romark L C, United States School of Medicine, National University of Singapore, Singapore, Biostats Unit, Singapore, Singapore; 5National University of Singapore, Singapore, Division of Gastroenterology and Hepatology, Singapore, Singapore; 3Yong Loo Lin School of Medicine, National University of Singapore, Singapore, Biostats Unit, Singapore, Singapore; 4Romark L C, United States
Email: mdcv341@nus.edu.sg

Background and aims: Nitazoxanide (NTZ) is a potential HBV therapeutic agent. NTZ disrupts Hepatitis B X protein (HBx) and host DNA-binding protein 1 (DBB1) interaction and prevents the formation of HBx-DBB1 protein complex responsible for the degradation of host restriction factor-structural maintenance of chromosomes 5/6 (SMC5/6). Restoration of SMC5/6 level after NTZ treatment suppresses Hepatitis B covalently closed circular DNA expression in vivo. (Sekiba, Otsuka et al. 2019) A subsequent pilot study demonstrated good anti-viral efficacy with 33% of patients (3 of
9 patients) achieving HBsAg loss (Rossignol and Brechot 2019). Consequently, this randomized controlled trial was designed to test NTZ efficacy.

**Method:** We conducted a phase 2, double-blinded, placebo-controlled, dose-finding, randomized control trial for Hepatitis B e antigen (HBeAg) negative Chronic Hepatitis B patients on long-term (>1 year) nucleos (t)ide analogues (NUCs) (Tenofovir disoproxil fumarate, Tenofovir alafenamide, or Entecavir). Participants were randomized (1:1:1:1) to receive either placebo (Group 1), NTZ 600 mg once daily (Group 2), NTZ 600 mg twice daily (Group 3), or NTZ 900 mg twice daily (Group 4), in addition to their NUC therapy. Primary efficacy end point was defined by the mean change in quantitative Hepatitis B surface antigen (qHBsAg) from baseline to week 48. Secondary end points included sustained off-treatment Hepatitis B surface antigen (HBsAg) loss, qHBsAg reduction, Hepatitis B DNA suppression, and change in baseline Fibroscan and/or Fibrosis-4 score.

**Results:** In total, 48 patients were enrolled. 12, 13, 10, and 13 patients were randomized to Group 1, 2, 3, and 4 respectively. There were no statistical differences in the key baseline patient characteristics (age, gender, presence of fatty liver, cirrhosis, Fibroscan score, Fibrosis-4 score, previous PEG-IFN exposure) between treatment groups. Overall, 4 patients who received NTZ and 1 patient who received placebo experienced severe adverse events (SAEs). 4 cases of grade 3 SAEs were deemed to be unrelated to NTZ (hepatoocellular carcinoma (n = 2); gastroesophageal reflux (n = 1); perianal abscess (n = 1)). Grade 4 SAE for alanine transaminase and aspartate aminotransferase elevation occurred in 1 patient (group 4) before resolving uneventfully with NTZ dose reduction. The primary and secondary efficacy end points were not met in all groups. No statistical difference in qHBsAg reduction or mean qHBsAg was detected between groups at all study time-points. Analysis of individual patient quantitative HBsAg kinetics did not identify any NTZ responder. The study was terminated early because of the lack of efficacy.

**Conclusion:** NTZ is safe and tolerable in CHB. Regrettably, the addition of NTZ to NUC therapy did not increase anti-viral efficacy.

**SAT447**

**Low-level viremia in patients with chronic hepatitis B receiving entecavir, tenofovir and tenofovir alafenamide**

Xiaohao Wang1, Dachuan Cai1, Zhang Juan1. The Second Affiliated Hospital, Chongqing Medical University, Infectious Diseases, Chongqing, China

Email: cqmucdc@cqmu.edu.cn

**Background and aims:** Low-level viremia (LLV) has been reported to be associated with unfavourable outcomes in patients with chronic hepatitis B (CHB). The aims are to evaluate the effect of therapeutic drugs including entecavir (ETV), tenofovir (TDF) and tenofovir alafenamide (TAF) on LLV in CHB patients.

**Method:** We conducted a phase 2, double-blinded, placebo-controlled, dose-finding, randomized control trial for Hepatitis B e antigen (HBeAg) negative Chronic Hepatitis B patients on long-term (>1 year) nucleos (t)ide analogues (NUCs) (Tenofovir disoproxil fumarate, Tenofovir alafenamide, or Entecavir). Participants were randomized (1:1:1:1) to receive either placebo (Group 1), NTZ 600 mg once daily (Group 2), NTZ 600 mg twice daily (Group 3), or NTZ 900 mg twice daily (Group 4), in addition to their NUC therapy. Primary efficacy end point was defined by the mean change in quantitative Hepatitis B surface antigen (qHBsAg) from baseline to week 48. Secondary end points included sustained off-treatment Hepatitis B surface antigen (HBsAg) loss, qHBsAg reduction, Hepatitis B DNA suppression, and change in baseline Fibroscan and/or Fibrosis-4 score.

**Results:** In total, 48 patients were enrolled. 12, 13, 10, and 13 patients were randomized to Group 1, 2, 3, and 4 respectively. There were no statistical differences in the key baseline patient characteristics (age, gender, presence of fatty liver, cirrhosis, Fibroscan score, Fibrosis-4 score, previous PEG-IFN exposure) between treatment groups. Overall, 4 patients who received NTZ and 1 patient who received placebo experienced severe adverse events (SAEs). 4 cases of grade 3 SAEs were deemed to be unrelated to NTZ (hepatoocellular carcinoma (n = 2); gastroesophageal reflux (n = 1); perianal abscess (n = 1)). Grade 4 SAE for alanine transaminase and aspartate aminotransferase elevation occurred in 1 patient (group 4) before resolving uneventfully with NTZ dose reduction. The primary and secondary efficacy end points were not met in all groups. No statistical difference in qHBsAg reduction or mean qHBsAg was detected between groups at all study time-points. Analysis of individual patient quantitative HBsAg kinetics did not identify any NTZ responder. The study was terminated early because of the lack of efficacy.

**Conclusion:** NTZ is safe and tolerable in CHB. Regrettably, the addition of NTZ to NUC therapy did not increase anti-viral efficacy.

**SAT448**

**Continued suppression of viral markers observed following discontinuation of nucleos (t)ide analogue therapy in chronic hepatitis B subjects with low hepatitis B surface antigen levels after 48 weeks of treatment with AB-729**

Man-Fung Yuen1, Simone Strasser2, Wattana Sukeepaisarnjaroen3, Varun Sharma2, Deana Antoniello2, Elina Medvedeva4, Emily P. Thi5, Gaston Picchio6, Timothy Eley7, Karen Sims4. The University of Hong Kong, Division of Gastroenterology and Hepatology, Hong Kong, Royal Prince Alfred Hospital, AW Morrow Gastroenterology and Liver Centre, Australia; 1Khon Kaen University, Department of Medicine, Thailand; 2Arbus Biopharma, Clinical Development, Warnminster, United States; 3Arbus Biopharma, Discovery, Warnminster, United States

Email: ksims@arbusbio.com

**Background and aims:** AB-729 is an N-Acetylgalactosamine (GalNAc)-conjugated single trigger RNA interference therapeutic that targets all HBV RNA transcripts, including HBx, resulting in suppression of viral replication and all viral antigens. AB-729 is currently in Phase 2 clinical development in combination with other antiviral agents for the treatment of chronic hepatitis B (CHB). Study AB-729-001 assessed up to 48 weeks of AB-729 in combination with nucleos (t)ide analogue (NA) therapy. Here we report early follow-up data for subjects who met protocol eligibility criteria and elected to stop NA therapy at least 24 weeks after their last dose of AB-729.

**Method:** Subjects participating in study AB-729-001 who received 60 mg or 90 mg of AB-729 every 4 (Q4W), 8 (Q8W), or 12 (Q12W) weeks for 48 weeks were assessed for eligibility to stop NA therapy at least 24 weeks after their last dose of AB-729. Stopping criteria included ALT <2 × ULN, HBeAg negative, HBV DNA undetectable, and HBsAg <100 IU/ml on two separate measurements. Safety and PD endpoints were not met in all groups. No statistical difference in qHBsAg reduction or mean qHBsAg was detected between groups at all study time-points. Analysis of individual patient quantitative HBsAg kinetics did not identify any NTZ responder. The study was terminated early because of the lack of efficacy.

**Conclusion:** Compared with ETV, TDF and TAF are superior in reducing the risk of LLV in CHB patients.

**SAT4448**

**Continued suppression of viral markers observed following discontinuation of nucleos (t)ide analogue therapy in chronic hepatitis B subjects with low hepatitis B surface antigen levels after 48 weeks of treatment with AB-729**

Man-Fung Yuen1, Simone Strasser2, Wattana Sukeepaisarnjaroen3, Varun Sharma2, Deana Antoniello2, Elina Medvedeva4, Emily P. Thi5, Gaston Picchio6, Timothy Eley7, Karen Sims4. The University of Hong Kong, Division of Gastroenterology and Hepatology, Hong Kong, Royal Prince Alfred Hospital, AW Morrow Gastroenterology and Liver Centre, Australia; 1Khon Kaen University, Department of Medicine, Thailand; 2Arbus Biopharma, Clinical Development, Warnminster, United States; 3Arbus Biopharma, Discovery, Warnminster, United States

Email: ksims@arbusbio.com

**Background and aims:** AB-729 is an N-Acetylgalactosamine (GalNAc)-conjugated single trigger RNA interference therapeutic that targets all HBV RNA transcripts, including HBx, resulting in suppression of viral replication and all viral antigens. AB-729 is currently in Phase 2 clinical development in combination with other antiviral agents for the treatment of chronic hepatitis B (CHB). Study AB-729-001 assessed up to 48 weeks of AB-729 in combination with nucleos (t)ide analogue (NA) therapy. Here we report early follow-up data for subjects who met protocol eligibility criteria and elected to stop NA therapy at least 24 weeks after their last dose of AB-729.

**Method:** Subjects participating in study AB-729-001 who received 60 mg or 90 mg of AB-729 every 4 (Q4W), 8 (Q8W), or 12 (Q12W) weeks for 48 weeks were assessed for eligibility to stop NA therapy at least 24 weeks after their last dose of AB-729. Stopping criteria included ALT <2 × ULN, HBeAg negative, HBV DNA undetectable, and HBsAg <100 IU/ml on two separate measurements. Safety and PD endpoints were not met in all groups. No statistical difference in qHBsAg reduction or mean qHBsAg was detected between groups at all study time-points. Analysis of individual patient quantitative HBsAg kinetics did not identify any NTZ responder. The study was terminated early because of the lack of efficacy.

**Conclusion:** Compared with ETV, TDF and TAF are superior in reducing the risk of LLV in CHB patients.
Tenofovir alafenamide fumarate (TAF) is among the main drugs for long-term antiviral therapy. Long term administration of TAF can lead to dyslipidemia in HIV patients. Dyslipidemia is associated with arteriosclerosis and hepatocarcinogenesis. Therefore, this study prospectively investigates the effects of TAF on blood lipids after 24 weeks in chronic hepatitis B (CHB) patients.

Method: Forty CHB patients with normal blood lipids were treated with TAF for 24 weeks among them there are 19 female and 21 male patients, 13 patients treated with ETV switching to TAF, 13 patients treated with TDF switching to TAF, 14 patients treated with initial TAF, and 7 patients with fatty liver. The serum level of cholesterol (TC), low density lipoprotein (LDL), high density lipoprotein (HDL-C), and triglyceride (TG) at baseline and 24 weeks treatment were analyzed.

Results: After TAF treatment for 24 weeks, the HDL, LDL and TC levels showed a trend of increasing, and the TC level increased significantly (p = 0.006). Typically, the TC level increased significantly in female patients (p = 0.041) and in patients with TDF switching (p = 0.036). Compared with the non-fatty liver patients, the TG levels increased significantly in the patients with fatty liver (p = 0.006). In addition, the dyslipidemia rate increased after TAF treatment, and the LDL abnormal rate (LDL ≥2.5 mmol/L) was up to 20% (p < 0.005).

Background and aims: Tenofovir alafenamide fumarate (TAF) is one of the new antiretroviral drugs that is widely used in clinical practice. Dyslipidemia after switching from tenofovir disoproxil fumarate (TDF) to TAF treatment has been reported, but limited data exist for female patients. The purpose of this study was to observe the changes in lipid indices after switching from TDF to TAF treatment in female patients.

Conclusion: After switching from TDF to TAF treatment, the LDL abnormal rate increased significantly in female patients, and the TC level showed a trend of increasing, which is consistent with previous reports.
SAT450
Off-therapy cure of hepatitis delta after 3 years of bulevirtide monotherapy in a patient with compensated advanced cirrhosis
Maria Paola Anolli1, Elisabetta Degasperi1, Colonia Sara Uceda Renteria2, Dana Sambarino3, Marta Borghi1, Riccardo Perbellini1, Alessandro Loglio1, Caroline Scholtes3,4, Floriana Facchetti1, Mirella Fraggioli3, Andrea Costantino5, Ferruccio Ceriotti2, Fabien Zoulüm1,4, Pietro Lampertico1,6
1Foundation IRCCS Ca' Granda Ospeda Ob Maggiore Policlinico, Division of Gastroenterology and Hepatology, Milan, Italy; 2Foundation IRCCS Ca' Granda Ospeda Ob Maggiore Policlinico, Virology Unit, Milan, Italy; 3Hospices Civils de Lyon (HCL) and Université Claude Bernard Lyon 1 (UCBL1), Hepatology Department, Lyon, France; 4INSERM UI1052, Centre de Recherche sur le Cancer de Lyon (CRCL), Lyon, France; 5Foundation IRCCS Ca' Granda Ospeda Ob Maggiore Policlinico, Division of Gastroenterology and Endoscopy, Milan, Italy; 6University of Milan, CRC “A. M. and A. Migliavacca” Center for Liver Disease, Department of Pathophysiology and Transplantation, Milan, Italy
Email: maria.anolli@unimi.it

Background and aims: Bulevirtide (BLV) has been recently approved for the treatment of chronic hepatitis Delta (CHD) in Europe, yet the rates of the off-therapy sustained responses following long-term BLV based treatment are currently unknown.

Method: A 54-year Caucasian male with HDV related compensated cirrhosis and clinically significant portal hypertension (CSPH) was treated with BLV monotherapy for 3 years and then followed for 48 weeks off-therapy. Clinical and virological characteristics were collected every 2 months after BLV withdrawal. HDV RNA was quantified by Robogene 2.0 (LOD 6 IU/ml), HBcAg by LUMIPULSE® G (LOQ 3 Log U/ml), HBV RNA by cobas® 6800 (LOQ 10 cp/ml).

Results: At the end of the 3 years of BLV monotherapy, ALT were within the normal range, HDV RNA <6 IU/ml and liver function was preserved (CPT score A). During 48 weeks of post-BLV follow-up, HDV RNA levels remained undetectable (HDV RNA <6 IU/ml) and liver function tests within the normal range at all timepoints. While no changes were observed for HBV DNA (always <10 IU/ml) and HBV RNA (always <10 cp/ml) levels, HBsAg and HBcAg levels declined (4 changes were observed for HBV DNA (always <10 IU/ml) and HBV function tests within the normal range at all timepoints. While no RNA levels remained undetectable (HDV RNA <6 IU/ml) and liver

Conclusion: At the end of the 3 years of BLV monotherapy, ALT were within the normal range, HDV RNA <6 IU/ml and liver function was preserved (CPT score A). During 48 weeks of post-BLV follow-up, HDV RNA levels remained undetectable (HDV RNA <6 IU/ml) and liver function tests within the normal range at all timepoints. While no changes were observed for HBV DNA (always <10 IU/ml) and HBV RNA (always <10 cp/ml) levels, HBsAg and HBcAg levels declined (4 changes were observed for HBV DNA (always <10 IU/ml) and HBV function tests within the normal range at all timepoints. While no RNA levels remained undetectable (HDV RNA <6 IU/ml) and liver

SAT451
Combination treatment of a PAPD5/7 inhibitor with an antisense oligonucleotide bepirovirsen with concurrent dosing shows additive HBsAg decreases in the A/A-HBV mouse model
Jared Delahaye1, Edward Long1, Chi Lau1, Jacob Parsons1, Bo Wen1, Zhiyi Cui1, Melanie Paff1, Shibyun You1, Martin Leivers1
1GlaxoSmithKline, Collegeville, PA, United States
Email: martin.t.leivers@gsk.com

Background and aims: Achieving high levels of functional cure of chronic hepatitis B virus infection not on stable nucleos (i) tides analogue therapy: interim results from the randomised phase 2b B-Clear study
Seng Gee Lim1, Cristina Pojoga2,3, Harry Janssen4, Denis Gusev5, Robert Plesniak6, Keiji Tsuji7, Ewa Janczewska8, Corneliu Petru Popescu9, Pietro Andreone9, Jinlin Hou10, Manuela Arbune11, Adrian Gadano12, Diana Petrova14, Jun Inoue15, Teeraha Piratvisuth16, Young-Suk Lim17, Apinya Leerapun18, Masanori Atsukawa19, Ji-Dong Jia20, Eternity Labio21, Teerha Piratvisuth16, Young-Suk Lim17, Apinya Leerapun18, Masa

Conclusion: Combinations of a PAPDS5/7 inhibitor (GSK193) and antisense oligonucleotide (bepirovirsen) provide additional reductions in HBsAg when dosed concurrently in the A/A-HBV mouse model of HBV. Concurrent dosing of these compounds is also superior in terms of maximal HBsAg suppression to sequential dosing preclinically.

SAT452
Efficacy and safety of bepirovirsen in patients with chronic hepatitis B virus infection not on stable nucleos (i) tides analogue therapy: interim results from the randomised phase 2b B-Clear study
Seng Gee Lim1, Cristina Pojoga2,3, Harry Janssen4, Denis Gusev5, Robert Plesniak6, Keiji Tsuji7, Ewa Janczewska8, Corneliu Petru Popescu9, Pietro Andreone9, Jinlin Hou10, Manuela Arbune11, Adrian Gadano12, Diana Petrova14, Jun Inoue15, Teeraha Piratvisuth16, Young-Suk Lim17, Apinya Leerapun18, Masanori Atsukawa19, Ji-Dong Jia20, Eternity Labio21, Teerha Piratvisuth16, Young-Suk Lim17, Apinya Leerapun18, Masanori Atsukawa19, Ji-Dong Jia20, Eternity Labio21, Teerha Piratvisuth16, Young-Suk Lim17, Apinya Leerapun18, Masanori Atsukawa19, Ji-Dong Jia20, Eternity Labio21, Teerha Piratvisuth16, Young-Suk Lim17, Apinya Leerapun18, Masanori Atsukawa19, Ji-Dong Jia20, Eternity Labio21, Teerha Piratvisuth16, Young-Suk Lim17, Apinya Leerapun18, Masanori Atsukawa19, Ji-Dong Jia20, Eternity Labio21, Teerha Piratvisuth16, Young-Suk Lim17, Apinya Leerapun18, Masanori Atsukawa19, Ji-Dong Jia20, Eternity Labio21, Teerha Piratvisuth16, Young-Suk Lim17, Apinya Leerapun18, Masanori Atsukawa19, Ji-Dong Jia20, Eternity Labio21, Teerha Piratvisuth16, Young-Suk Lim17, Apinya Leerapun18, Masanori Atsukawa19, Ji-Dong Jia20, Eternity Labio21, Teerh
Efficacy and safety of bepirovirsen in patients with chronic hepatitis B virus infection on stable nucleos (t)ide analogue therapy: interim results from the randomised phase 2b B-Clear study

Man-Fung Yuen1, Robert Plesniak2, Seng Gee Lim3, Keiji Tsuji4, Gheorghe Diaconescu5, Adrian Gadano6, Ju Hyun Kim7, Tarik Asselah8, Jinhoo Yim9, Jeong Heo10, Giuliano Rizzardini11, Harry Janssen12, Nevin Indriz16, Jennifer Cremer21, Robert Elston22, Tamara Lukic23, Lauren Maynard22, Fiona Campbell22, Melanie Paff22.

1Queen Mary Hospital, China; 2University of Rzeszow, College of Medicine, Centrum Medyczne w Lancucie Sp. z o.o., Poland; 3National University Health System, Singapore; 4Hiroshima Red Cross Hospital, Japan; 5Sf.Cuv. Parascheva Infectious Diseases Clinical Hospital, Bulgaria; 8Hôpital Beaujon, France; 9Korea University Ansan Hospital, Korea, Rep. of South; 10College of Medicine, Pusan National University and Biomedical Research Institute, National University Hospital, Korea, Rep. of South; 11Luigi Sacco Hospital, Italy; 12Dr Victor Babes Clinical Hospital of Infectious and Tropical Diseases, Carol Davila University of Medicine and Pharmacy, Romania; 13Dr Victor Babes Clinical Hospital of Infectious and Tropical Diseases, Carol Davila University of Medicine and Pharmacy, Romania; 14Alexandrovska, Bulgaria; 15Department of Medicine, University of Saskatchewan, Canada; 16UMHAT Sofiamed, Bulgaria; 17Regional Institute of Gastroenterology and Hepatology, Romania; 18Kumamoto University, Japan; 19Center for Prevention and Control of AIDS and Infectious Diseases, Russian Federation; 20ID Clinic, Poland; 21GlaxoSmithKline, United States; 22GlaxoSmithKline, United Kingdom; 23GlaxoSmithKline, United Arab Emirates

Email: jennifer.x.cremer@gsk.com

This abstract is under embargo until the start of the Late Breaker session on Saturday 25 June 2022, 14:00 BST. It will be made publicly available on the congress website once the embargo has lifted.

Violation of the embargo will be taken seriously. Individuals and/or sponsors who violate EASL’s embargo policy may face sanctions relating to current and future abstract submissions, presentations, and visibility at EASL Congresses. The EASL Governing Board is at liberty to ban attendance and/or retract data.

Copyright for abstracts (both oral and poster) on the website and as made available during The International Liver Congress™ 2022 resides with the respective authors. No reproduction, re-use or transcription for any commercial purpose or use of the content is permitted without the written permission of the authors. Permission for re-use must be obtained directly from the authors.
EVALUATION OF INTERLEUKIN-6 FOR STEPSWISE DIAGNOSIS OF MINIMAL HEPATIC ENCEPHALOPATHY IN PATIENTS WITH LIVER CIRRHOSIS

Simon Johannes Gairing1,2, Julian Anders1, Leonard Kaps1,2, Michael Nagel1,2,3, Maurice Michel1,2, Wolfgang Maximilian Kremer1,2, Max Hilscher1,2,3, Peter Galle1,2, Jörn Schattenberg1,4, Marcus-Alexander Wörns1,2,3, Christian Labenz1,2. 1University Medical Center of the Johannes Gutenberg-University, Department of Internal Medicine I, Mainz, Germany; 2University Medical Center of the Johannes Gutenberg-University, Cirrhosis Center Mainz (CCM), Mainz, Germany; 3Dortmund Hospital, Department of Gastroenterology, Hematology, Oncology and Endocrinology, Dortmund, Germany; 4University Medical Center of the Johannes Gutenberg-University, Metabolic Liver Research Program, Mainz, Germany

Email: sgairing@uni-mainz.de

Background and aims: Minimal hepatic encephalopathy (MHE) is associated with poor quality of life and dismal prognosis. Psychometric testing is time consuming and therefore often neglected in routine clinical practice. Thus, predictive biomarkers are urgently needed to stratify patients at risk for MHE. This study aimed to evaluate the diagnostic accuracy of interleukin-6 (IL-6) serum levels as part of a stepwise diagnostic algorithm to detect MHE in patients with liver cirrhosis.

Method: The development cohort comprised 197 prospectively recruited patients without evidence of HE grade 1–4. A total of 52 patients served as the independent validation cohort. The Psychometric Hepatic Encephalopathy Score (PHES) was used for MHE diagnosis.

Results: In total, 50 (25.4%) patients of the development cohort were diagnosed with MHE. Serum IL-6 levels were more than twice as high in patients with MHE as in patients without MHE (16 vs 7 pg/ml, p <0.001). In logistic regression analysis, elevated IL-6 levels remained independently associated with MHE (OR 1.036, 95%CI 1.009–1.064, p = 0.008) after adjusting for other variables such as MELD, albumin, CRP and history of ascites. Using a cut-off value of IL-6 ≥7 pg/ml would have avoided subsequent time-consuming psychometric testing in 38% of all patients (sensitivity 90%, 95%CI 77%-96%; negative predictive value 93%, 95%CI 84%-98%). These results were confirmed in the validation cohort (sensitivity: 94%, NPV: 93%).

Figure: Discriminative ability of Interleukin-6 to detect minimal hepatic encephalopathy in the development cohort of patients with liver cirrhosis. AUC = 0.751, 95% CI 0.675–0.827, p <0.001.
Conclusion: IL-6 serum levels may serve as biomarker in a stepwise diagnostic algorithm reducing the number of patients requiring elaborate testing with PHES. In particular, IL-6 would be helpful in patients being incapable of performing other tests e.g., due to language barriers.

SAT487
Evaluation of statins as a new therapy to alleviate chronotropic dysfunction in cirrhotic rats
Qamar Niaz1,2, Sania Mehreen3, Mahmoud Ghazi-Khansari1, Farahnaz Jazaeri1. 1Department of Pharmacology, School of Medicine, Tehran University of Medical Sciences, Tehran, Iran; 2Department of Pharmacology and Toxicology, Faculty of Bio-Sciences, University of Veterinary and Animal Sciences, Lahore, Pakistan; 3Department of Zoology, Faculty of Fisheries and Wildlife, University of Veterinary and Animal Sciences, Lahore, Pakistan
Email: fjazaeri@yahoo.com

Background and aims: Liver cirrhosis defines by regenerative nodules and fibrotic septa which causes cirrhotic cardiomyopathy (CCM) with chronotropic hypo-responsiveness. Statins have been reported to decrease inflammation, fibrosis, and portal pressure (PP) in liver cirrhosis through inhibition of Ras homolog family member A (RhoA) and stimulation of endothelial nitric oxide synthase (eNOS). Therefore, we studied the effect of atorvastatin on chronotropic hypo-responsiveness in biliary cirrhotic rats.

Method: Male duct ligation (BDL) or sham surgery performed on Wistar (Rattus norvegicus) male rats and grouped as BDL/Saline, BDL/Ator-7d (days) (Atorvastatin 15 mg/kg/day), and BDL/Ator-14d groups or Sham/Saline, Sham/Ator-7d, and Sham/Ator-14d groups for cirrhosis or control groups respectively. Corrected QT (QTc) interval, chronotropic responses, serum brain natriuretic peptides (BNP), and heart tumour necrosis factor-alpha (TNF-alfa), nuclear factor erythroid 2-related factor 2 (Nrf2), and malondialdehyde (MDA) levels were studied along with liver histopathology, and atrial RhoA and eNOS genes expression.

Results: The chronotropic responses were decreased in BDL/Saline and increased in BDL/Ator-7d group. QTc interval, BNP, TNF-alpha, and MDA levels were elevated in BDL/Saline and reduced in BDL/Ator-14d group. The Nrf2 level raised non-significantly in BDL/Saline and significantly in BDL/Ator-14d group. The liver inflammation and fibrosis increased in BDL/Saline and were not affected in BDL/Ator-7d and BDL/Ator-14d groups. The RhoA expression down-regulated in BDL/Saline, BDL/Ator-7d, and BDL/Ator-14d groups while the eNOS expression up-regulated non-significantly in BDL/Saline and down-regulated in BDL/Ator-14d group.

Figure: Average atrial beating rates of sham (control) and BDL (cirrhotic) rats after treatment with saline or atorvastatin (15 mg/kg/day for 7 and 14 days). The atrial beating rates were recorded before, and after stimulation with 10−10 to 10−5 M cumulative concentrations of isoproterenol. The data represent the mean ± SEM. At least, 6–8 rats were included per experimental group. (4B): [*P < 0.05, **P < 0.01, ***P < 0.001 and ****P < 0.0001 BDL/Saline group compared to Sham/Saline group, and **P < 0.05 BDL/Ator-7d group compared to BDL/Saline group]

Conclusion: Atorvastatin alleviates the chronotropic hypo-responsiveness, and down-regulates the RhoA and eNOS expressions along with anti-inflammatory, anti-oxidant, and anti-stress effects in CCM.

SAT488
The effect of sarcopenia on survival of patients with cirrhosis: a systematic review and meta-analysis
Xinxing Tantai1, Yi Liu2, Yee Hui Yeo3, Michael Praktiknjo4, Ezequiel Mauro5, Yuhei Hamaguchi6, Cornelius Engelmann7, Peng Zhang8, Jae Yoon Jeong9, Jeroen van Vught10, Huijuan Xiao11, Huan Deng12, Xu Gao13, Qing Ye14, Jiayuan Zhang15, Longbao Yang13, Yaqin Cai13, Yixin Liu16, Na Liu17, Zongfang Li12, Tao Han14, Toshimi Kaido18, Joo Hyun Sohn19, Christian Strassburg20, Thomas Berg21, Jonel Trebicka21, Yao-Chun Hsu22, Jan Ijzermans23, Jinhai Wang23, Grace Su23, Fanpu Ji24, Mindie Nguyen25, 1The Second Affiliated Hospital of Xi’an Jiaotong University, Department of Gastroenterology, China; 2The Second Affiliated Hospital of Xi’an Jiaotong University, Department of Infectious Diseases, China; 3Cedars-Sinai Medical Center, Division of General Internal Medicine, United States; 4University Hospital Bonn, Department of Internal Medicine I, Germany; 5Hospital Italiano de Bs. As., Liver Transplant Unit, Liver Unit, Argentina; 6Japanese Red Cross Osaka Hospital, Department of Gastrointestinal Surgery; 7Department of Medicine II, Leipzig University Medical Center, Division of Hepatology, Germany; 8University of Michigan Medical School, Department of Surgery, United States; 9National Medical Center, Department of Gastroenterology and Hepatology, Korea, Rep. of South; 10Erasmus MC University Medical Centre, Department of Surgery, Division of Hepatobiliary and Transplant Surgery, Netherlands; 11The Third Central Hospital of Tianjin, Department of Nutrition, China; 12The Second Affiliated Hospital of Xi’an Jiaotong University, National and Local Joint Engineering Research Center of Biodiagnosis and Biotherapy, China; 13The Second Affiliated Hospital of Xi’an Jiaotong University, Department of Gastroenterology, China; 14The Third Central Hospital of Tianjin, Department of Gastroenterology and Hepatology, China; 15Xi’an Jiaotong University, Xi’ an Jiaotong University Library, China; 16The Second Affiliated Hospital of Xi’an Jiaotong University, Department of Gastroenterology, China; 17the Second Affiliated Hospital of Xi’an Jiaotong University, Department of Gastroenterology, China; 18St Luke’s International Hospital, Department of Gastroenterological and General Surgery, Japan; 19Hanyang University Guri Hospital, Department of Internal Medicine, Korea, Rep. of South; 20Leipzig University Medical Center, Division of Hepatology, Department of Medicine II, Germany; 21Goethe University Clinic Frankfurt, Department of Internal Medicine I, Germany; 22Fu Jen Catholic University Hospital, Division of Gastroenterology and Hepatology; 23University of Michigan Medical School, Department of Medicine, United States; 24The Second Affiliated Hospital of Xi’an Jiaotong University, Department of Infectious Diseases, China; 25Stanford University Medical Center, Division of Gastroenterology and Hepatology, United States
Email: jifanpu1979@163.com

Background and aims: The association between sarcopenia and prognosis in patients with cirrhosis remains to be determined. In this study, we aimed to quantify the association between sarcopenia and the risk of mortality in patients with cirrhosis, by sex, underlying liver disease etiology, and severity of hepatic dysfunction.

Method: PubMed, Web of Science, EMBASE, and major scientific conference sessions were searched without language restriction through 13 January 2021 with additional manual search of bibliographies of relevant articles. Cohort studies of ≥100 patients
Conclusion: Sarcopenia was highly and independently associated with higher risk of mortality in patients with cirrhosis.

SAT489 Effectiveness of probiotics in the secondary prevention of hepatic encephalopathy among cirrhotic patients

Muhammad Farooq Hanif1, Abdul Rehman2, Raja Omar Fiaz3, Khalid Mahmud Khan1, Pakistan Kidney And Liver Institute And Research Centre, Gastroenterology and Hepatology, Lahore, Pakistan; 2Mayo Hospital, Gastroenterology and Hepatology, Lahore, Pakistan; 3Central Park Medical College, Gastroenterology and Hepatology, Lahore, Pakistan; 4Jinnah Hospital, Lahore, Gastroenterology and Hepatology, Lahore, Pakistan

Email: farooqdr@hotmail.com

Method: Patients with known chronic liver disease admitted with hepatic encephalopathy, were randomized to group A (Lactulose alone) and group B (Lactulose + Probiotics). Probiotic used was Cap. Ecotec 180 mg, 1 trillion CFU (Lactobacillus, Bifidobacterium, S. thermophilus, Lbculgaricus). After discharge each patient was followed for six months for hepatic encephalopathy recurrence. The absence of hepatic encephalopathy at the end of six months treatment for each patient was considered as effective treatment response. Compliance to the treatment and side effects were also noted during this time period.

Results: 166 patients included in the study. Mean age was 55.84 ± 7.82 and 52.37 ± 6.95 in group A and B respectively. Majority of patients were of child class B (75.90%), whereas 6% were child class C and 18% were child class A. Overall encephalopathy occurred in 51.80% and 36.14% of patients in group A and B respectively (p = 0.02). Encephalopathy was more common among relatively older females and patients with advanced child class with baseline ammonia more than 80ug/dl. Abdominal bloating, distaste and diarrhea were the common side effects in both groups with no significant difference in the side-effect profile. Patients were compliant to the treatment in both groups.

Conclusion: In our cohort of cirrhotic patients, combination of lactulose and probiotics showed better response compared to lactulose alone in the long term secondary prevention of hepatic encephalopathy.

SAT490 Sarcopenia as a predictor of mortality and complications in cirrhosis patients-A prospective cohort study

Nidhiin Devadas1, K Sandesh1, K SunilKumar1, 2Government Medical College, Kozhikode, Medical Gastroenterology, Kozhikode, India

Email: niddas@gmail.com

Background and aims: Sarcopenia is a promising tool for prognostication of cirrhosis.EWGSOP2 guidelines define sarcopenia based on muscle strength, muscle quantity or quality and physical performance. Many previous studies didn’t use a standardized definition of sarcopenia and was based on skeletal muscle measurement by CT or MRI. Ultrasound guided thigh muscle thickness (TMT) measurement is a validated, cost effective and easy method for assessment of sarcopenia and was based on skeletal muscle measurement by CT or MRI. Ultrasound guided thigh muscle thickness (TMT) measurement is a validated, cost effective and easy method for assessment of muscle quantity. There is paucity of Indian studies analysing prognostic role of sarcopenia in cirrhosis.

To study the predictive role of sarcopenia on mortality and complications in cirrhosis patients.

Method: This was a prospective cohort study with 120 consecutive patients each in sarcopenia and no sarcopenia groups. Sarcopenia was diagnosed based on EWGSOP2 guidelines using ultrasound guided measurement of TMT. They were followed up for 6 months. Kaplan-Meier analysis with LogRank test was used to compare survival and

Conclusion: Sarcopenia was one of its complication is 10–14% in general, 16–21% with decompenated cirrhosis and 30–40% are of those with cirrhosis at some time during their clinical course. The risk for first bout of overt hepatic encephalopathy is 5–25% within 5 years after cirrhosis. This study compared the effectiveness of lactulose alone versus combination of lactulose plus probiotics for secondary prevention of hepatic encephalopathy in cirrhotic patients. SAT490

with cirrhosis and ≥12 months of follow-up that evaluated the association between sarcopenia, muscle mass and the risk of mortality were included.

Results: 22 studies with 6965 patients with cirrhosis were included. The pooled prevalence of sarcopenia in patients with cirrhosis was 37.5% overall (95% CI 32.4–42.8), higher in male patients (41.9%), patients with alcohol associated liver disease (ALD) (49.6%), patients with CTP grade C (46.7%), and when sarcopenia was defined in patients by lumbar 3- skeletal muscle index (L3-SMI) (44.4%). Sarcopenia was associated with the increased risk of mortality in patients with cirrhosis (adjusted-hazard ratio [aHR] 2.30, 95% CI 2.01–2.63), with similar findings in sensitivity analysis of cirrhosis patients without HCC (aHR 2.33, 95% CI 1.95–2.83) and in subgroup analysis by sex, liver disease etiology, and severity of hepatic dysfunction (Figure). The 1-, 3-, and 5-year cumulative probabilities of survival in patients with sarcopenia were 76.6%, 64.3%, and 45.3%, compared to 93.4%, 82.0%, and 74.2%, respectively in patients without sarcopenia (all P < 0.001). The association between quantitative muscle mass index and mortality further supports the poor prognosis for patients with sarcopenia (aHR 0.95, 95% CI 0.93–0.98).
Cox proportional hazards model was used for multivariate analysis to determine risk factors of mortality.

Results: Cirrhosis patients with sarcopenia (N1 = 120, M:F = 80:40, Median age-58yrs [51–64]) and without sarcopenia (N2 = 120, M:F = 93:27, Median age-54yrs [46.25–60]) were enrolled. Six month cumulative survival was 56.7% and 76.7% in sarcopenia and no sarcopenia groups respectively (p = 0.001). Six month cumulative survival in severe and non-severe sarcopenia was 23.9% and 70% respectively (p = 0.001). Age, sex, nutritional status, sarcopenia status, CTP score, MELD score, Bilirubin, Albumin, INR and Sodium were significantly associated with survival. A multivariate analysis showed sarcopenia (HR = 1.283, 95%CI 1.092–2.130, p = 0.031), female sex (HR = 1.851, 95%CI 1.106–3.097, p = 0.019), CTP class C (HR = 1.447, 95%CI 1.252–1.794, p = 0.002) and MELD score>15 (HR = 1.116, 95%CI 1.056–2.203, p = 0.05) as independent predictors of mortality. Development of complications like ascites, HE, Covid infection and UGI bleed were significantly higher in sarcopenia group, while SBP, AKI, cellulitis, UTI, HCC and ACLF were not statistically significant between two groups.

Conclusion: Sarcopenia is an independent prognostic marker of mortality in cirrhosis and is associated with increased risk of complications like ascites, HE, Covid infection and UGI bleed. Severe sarcopenia has even poorer outcome. It appears that addition of sarcopenia to existing scoring systems of cirrhosis will improve prognostication of patients.

Key Words: Sarcopenia, Cirrhosis, Thigh muscle thickness, Prognostic tool

SAT491 Diagnosis and pathophysiological analysis of sarcopenia using liver MR in chronic liver disease
Atsushi Nakamura1.1 Kawasaki, Japan
Email: naka2722@gmail.com

Background and aims: There are a few studies of sarcopenia (SP) diagnosed by magnetic resonance imaging (MRI), and paraspinal muscle area (PSMA) measurement at the level of superior mesenteric artery (SMA) has been reported to be useful (Hepatology 2018). However, there are racial differences in body size, and there is no standard for Asians in MRI. The other hand, in liver cirrhosis (LC), adipopenia (AP) is also associated with worse prognosis, and MRI proton density fat fraction (PDFF) has been shown to reflect body fat mass closely. The aim of this study was to develop SP criteria for MRI based on the GLIM criteria, which are global diagnostic criteria for malnutrition, and to clarify the relationship with patient prognosis. In addition, we analyzed the significance of AP assessment.

Method: This is a retrospective study using imaging data from 506 patients with chronic liver disease (CLD) who underwent MR elastography (mean age 62 years, 60% male, LC 119, HCC 47). The etiologies was HBV/HCV, 241; NAFLD, 153; alcohol, 53; and others, 59. SP was diagnosed by determining the cut off value of PSMI (PSM index: PSMA/Height²) for each gender based on ROC analysis of body mass index (BMI) against the criteria for malnutrition (in Asian population). AP was also diagnosed by setting the cut off value of MRI-PDFF according to the GLIM criteria by ROC analysis.

Results: 1) SP in CLD: BMI and PSMI were correlated in patients without ascites (M/F: T = 0.477/0.534, p < 0.001), and the cut off value of SP in males and females was 12.62 and 9.77 cm²/m², respectively (AUC: 0.91/0.77, p < 0.001). The prevalence of SP in CLD was 25%, and there was no difference by sex; the prevalence of SP was significantly higher in LC and HCC cases (p < 0.05). Furthermore, by MRE fibrosis stage (F0/1/2/3/4), SP increased from F3 and was inversely correlated with steatosis grade (p < 0.01). On the other hand, PDFF was significantly correlated with subcutaneous fat area at the SMA level (M/F: r = 0.558/0.628, p < 0.001) and AP (PDFF<2.2%) was 17%. In multivariate analysis of factors contributing to SP, age (OR 1.05), Alb (0.23), and PDFF (0.91) were extracted (p < 0.05 for each).

2) Prognosis of LC: Child-Pugh classification (A/B/C) was 66/35/18 cases, prevalence of SP was 32/58/82%, AP was 26/33/76%, and SP and AP was 17/42/79%. During the observation period (25 ± 16 m), there were 22 liver-related deaths. The 3-year survival rate by Kaplan-Meier method was 96% in the non-SP group, 55% in the SP group, and 23% in the SP/AP group (log-rank test p < 0.01). In the Cox proportional hazard model, Child-Pugh score (HR 1.34) and SP and AP (5.60) were independent prognostic factors (p < 0.01).

Conclusion: We demonstrated the validity of new SP diagnostic criteria assessed by SMA levels on MRI in Asians. Our results indicate that the combination of SP and AP is a new phenotype of severe SP, and suggest the need to screen for SP in CLD from the pre-cirrhotic stage.

SAT492 Use of a cirrhosis database can positively impact patient care in United Kingdom practice
Jessica Sheare1, Dianne Backhouse1, Lynsey Corless1.1 Hull Royal Infirmary, Department of Gastroenterology, Hepatology and Endoscopy, Kingston upon Hull, United Kingdom
Email: lynsey.corless@nhs.net

Background and aims: Screening for oesophageal varices and surveillance for hepatocellular carcinoma (HCC) are advised for patients with cirrhosis but adherence to recommendations is poor. The study aimed to provide descriptive analysis of a new cirrhosis database.

Conclusion: The database was able to identify patients with cirrhosis who were not being screened for varices or HCC.
database, and evaluate rates of surveillance in a large teaching hospital.

**Method:** All patients diagnosed with advanced fibrosis/cirrhosis in our centre entered the database sequentially from April 2018. The service covers a population of 600,000, with expected prevalence of 600 cirrhotic patients. The database—rather than clinic visits—became the primary means to monitor HCC surveillance/endoscopic screening requests. Subsequent adherence to recommendations was measured in 2021.

**Results:** 841 patients entered the database over 3 years, with only 200 at inception—less than the predicted cirrhosis prevalence. 36 people died during follow-up and 5 left the area. Of the remaining 800 patients, median age was 60 years; 40% female. 46% of patients had alcohol related disease, 21% non-alcoholic fatty liver disease, 14% viral hepatitis. 63% of the cohort had Childs-Pugh (CP) A or advanced fibrosis, 14% CP-B, 3% CP-C. 21% had no stage recorded. 157 patients (20%) were on primary prophylaxis for variceal bleeding. Of the remaining 643 patients, 237 (37%) were on active endoscopic surveillance and a further 100 (16%) had attended endoscopy in the past 3 years. 43 patients (7%) were overdue, 40 (6%) declined, and 30 (5%) had documented clinical decision not to proceed. 191 patients (24%) had no documentation about screening. 603 (78%) of appropriate patients were up to date with HCC surveillance with a further 105 (14%) awaiting scan, significantly more than our historically reported adherence of 50% (p < 0.0001).

**Conclusion:** The database improved our knowledge of clinical characteristics of our patient population, and provided a way to readily monitor surveillance intervals. Most had appropriate HCC surveillance, surpassing our previous (or nationally reported) adherence rates. A quarter of patients had no documentation of variceal screening, highlighting an area for improvement. Given the rapid rise in cohort size, it is likely the database also reduces numbers lost to follow-up/surveillance in the event of clinic non-attendance, which may be particularly valuable in the post-Covid era of delayed appointments. This study shows the potential of a registry to improve care and outcomes in people with cirrhosis.

**SAT493**

**Psychomotor speed from minimal hepatic encephalopathy testing is associated with physical frailty in patients with end-stage liver disease**

Andres Duarte Rojo¹, Rachel K. Grubbs¹, Randi Wong², Pamela M. Bloomer¹, Robert Rahimi¹, Alexa Steinberg⁴, Jennifer Lai². ¹University of Pittsburgh Medical Center; ²University of California San Francisco; ³Baylor University Medical Center; ⁴Accellra Therapeutics

**Background and aims:** The Stroop EncephalApp (StE) is a neuro-psychological test assessing psychometric speed and cognitive processing and has been validated to diagnose minimal hepatic encephalopathy (HE). Frailty, as measured by the Liver Frailty Index (LFI), is highly prevalent in end-stage liver disease (ESLD), particularly among patients with HE. While the LFI comprises tests of physical function, it might conceivably also capture the contributions of cognitive impairment to physical frailty in ESLD. This study assessed the relationship between cognitive function (StE) and physical function (LFI) in ESLD.

**Method:** Patients with ESLD underwent LFI, StE and overt HE testing using modified orientation log (MO-log) and Clinical Hepatic Encephalopathy Staging Scale (CHESS) at 3 centers. Expected StE values were obtained from www.encephalapp.com. Pearson correlation and multivariable linear regression models were used to investigate StE variability. Stroop On, Stroop Off, and their combinations were analyzed separately to characterize StE contribution in terms of cognitive processing (On+Off) versus psychomotor speed (Off).

**Results:** Of 172 subjects (58 ± 10 years; 59% male; 93% white; 37% alcohol, 25% NASH), 68% had Child-Pugh B/C cirrhosis, and 69% had prior overt HE. On testing, 97% had normal mentation (MO-log ≥ 23), none had overt HE (CHESS ≥ 3) and 81% had minimal HE. Cognitive function in terms of StE On+Off increased across frailty categories and showed a fair linear relationship with LFI (Fig.), of similar magnitude to that observed for age (rho = 0.29, p < 0.001) and education (rho = − 0.24, p < 0.002). However, StE and LFI correlation weakened from Off (rho = 0.37, p < 0.001) to On (rho = 0.20, p = 0.008) and On-Off (rho = − 0.05, p = 0.5) modalities, suggesting that psychomotor speed was the main factor driving the association between cognitive and physical function. On multivariable analysis, adjusted for age, education and sex, only StE On+Off (β = 15.38, p < 0.02) and StE Off (β = 8.95, p < 0.001) remained associated with LFI.

**Conclusion:** Using StE and LFI, an association between cognitive and physical function in ESLD was found, likely attributable to psychomotor speed over cognitive processing. Our findings suggest that the comprehensive assessment of minimal HE should include frailty metrics, and vice versa. Also, such brain-muscle relationship further supports investigating interventions targeting both physical and cognitive function in ESLD.

**SAT494**

**A multistrain probiotic increases serum glutamine/glutamate ratio in patients with cirrhosis. A metabolomic analysis**

German Soriano¹,², Eva Roman²,³,⁴, Luca Laghi⁵, Juan Camilo Nieto⁶, Qiuyu Lan⁷, María Poca⁷, Edilmar Alvarado-Tapia⁷,², Berta Cuyàs⁷, Silvia Vidal⁷,¹, Candido Juárez⁷, Carlos Guainer¹,², Anges Escorsell¹, ¹Hospital de la Santa Creu i Sant Pau, Department of Gastroenterology, Barcelona, Spain; ²Instituto de Salud Carlos III, CIBERehd, Madrid, Spain; ³School of Nursing EUI-Sant Pau, Barcelona, Spain; ⁴Universitat Autònoma de Barcelona; ⁵University of Bologna, Italy; ⁶Research Institute IB-B Sant Pau, Spain; ⁷Hospital de la Santa Creu i Sant Pau, Department of Immunology, Spain

**Background and aims:** Probiotics can improve gut dysbiosis, intestinal barrier, ammonemia and proinflammatory state, as well as cognitive function and risk of falls in patients with cirrhosis. To explore the potential mechanisms underlying these effects, we aimed to analyze the changes in the blood metabolome of patients with cirrhosis after probiotic treatment.

**Method:** We performed untargeted metabolomics using ¹H-NMR spectroscopy in serum samples from 32 patients with cirrhosis and cognitive dysfunction [Psychometric hepatic encephalopathy score (PHE)≤4] or previous falls. These patients were included in a previous double-blind placebo-controlled trial (Román, Hepatol Commun 2020) and were randomized to receive the multistrain probiotic (brand name Vivomixx in Europe and Visbiome in USA), 450 × 10⁶ cfu bid for 12 weeks, or placebo. Baseline and end of treatment blood samples were analyzed. A false discovery rate (FDR)
5% correction for multiple testing was applied using the Benjamin-Hochberg method.

Results: Patients treated with the probiotic (n = 17) presented a statistically significant improvement in cognitive function and risk of falls (evaluated by the PHES and gait speed, respectively), proinflammatory state (C-reactive protein and TNF-α) and intestinal barrier (fatty acid binding protein [FABP]-6) at the end of treatment. No changes were observed in the placebo group (n = 15). After analyzing 54 metabolites, the main findings were an increase in blood glutamine (FDR p = 0.007), a decrease in glutamate (FDR p = 0.03) and an increase in the glutamine/glutamate ratio (FDR p = 0.01), while glutamate increased (FDR p = 0.02) and the glutamine/glutamate ratio decreased (FDR p = 0.03) in the placebo group. There was a correlation between the change in the ratio glutamate/glutamine and the change in the PHES (r = 0.34, p = 0.05), change in gait speed (r = 0.47, p = 0.008), and change in FABP-6 (r = −0.37, p = 0.04).

Conclusion: Our results suggest an influence of the multistrain probiotic Vivomixx on the glutamine/glutamate metabolism, and therefore in the capacity of ammonia detoxification, that could contribute to explain the beneficial effects observed in patients with cirrhosis.

SAT495
The composition of the bile acid pool is closely associated with fibrosis in the heart and liver of patients with cirrhosis
Signe Wiese¹, Jens Hove², Henriette Ytting¹, Svend Home Hansen³, Søren Møller⁴, Flemming Bendtsen⁵. ¹Hvidovre Hospital, Gastro Unit, Medical Division, Denmark; ²Hvidovre Hospital, Dept. Cardiology, Denmark; ³Rigshospitalet, Dept. Clinical Biochemistry; ⁴Hvidovre Hospital, Centre of Functional Imaging and Research, Denmark
Email: signewiese@gmail.com

Background and aims: The role of bile acids (BA) in relation to liver fibrosis and signs of heart disease in chronic liver disease are areas of increasing interest. We have previously reported a close association between increased total BA (tBA) concentrations and myocardial fibrosis in patients with cirrhosis, and a strong relationship between the extent of fibrosis in the liver and the heart. These fibrotic changes can accurately be determined by MRI with assessment of myocardial and liver extracellular volume (ECV). Our aim was to identify specific groups or individual BA related to fibrosis in the liver and heart of patients with cirrhosis.

Method: We prospectively included 52 cirrhotic patients. All patients underwent contrast-enhanced MRI with T1-mapping and ECV quantification, and assessments of tBA, a panel of 15 specific BA and C4, a biomarker of de novo BA synthesis.

Results: The BA composition of cirrhotic patients with myohepatic fibrosis was altered with increased conjugated BA levels (44 umol/l (21;87) vs. 14 umol/l (10;40), p = 0.02), predominantly glycine-conjugated BA (p = 0.01). The specific BA were markedly increased: glyco-chenodeoxycholic acid (GCDCA) (p = 0.016), glyco-ursodeoxycholic acid (GUDCA) (p = 0.005), glyco-cholic acid (GCA) (p = 0.04) and tauro-ursodeoxycholic acid (TUDCA) (p = 0.026). Similarly, patients with a high liver ECV indicating the most advanced liver fibrosis had increased tBA levels (p <0.001) and the BA pool consisted predominantly of primary BA (p <0.001) and conjugated BA (p <0.001) both glycine- and taurine-conjugated BA (p <0.001).

In these patients the following specific BA were increased: GCDCA (p <0.001), GCA (p <0.001), tauro-chenodeoxycholic acid (TCDDCA) (p = 0.001), tauro-cholic acid (TCA) (p = 0.001), GUDCA (p = 0.006) and TUDCA (p = 0.001). Moreover, C4 levels were reduced (p <0.005). When we assessed the relation to disease severity, we found the highest levels of tBA, primary BA and conjugated BA in Child Pugh C patients (p = 0.002, p = 0.003, p = 0.003, respectively).

Conversely, C4 levels decreased with disease severity (p <0.001). MELD also correlated with BA levels (r = 0.62, p <0.001) and C4 levels (r = −0.89, p <0.001).

Conclusion: The strong associations between myocardial fibrosis and in particular conjugated BA suggest a potential role of BA in the development of structural cardiac abnormalities in cirrhosis. Moreover, the composition of the BA pool is markedly altered in patients with advanced liver fibrosis and is closely related to disease severity.

SAT496
SBP vs. non-SBP bacterial infections at admission have comparable outcomes in a multi-center cohort of inpatients with cirrhosis
Jacqueline O’Leary¹, K. Rajender Reddy², Puneeta Tandon³, Patrick S. Kamath⁴, Guadalupe Garcia-Tsao⁵, Florence Wong⁶, Jennifer C. Lai⁷, Ram Subramanian⁸, Paul J. Thuluvath⁹, Benedict Malaiakkal¹⁰, Hugo E. Varma¹¹, Scott Biggins¹², Leroy Thacker¹³, Jasmohan S Bajaj¹³, ¹Dallas VA Medical Center, Dallas, United States; ²University of Pennsylvania, Philadelphia, United States; ³University of Alberta, Edmonton, Canada; ⁴Mayo Clinic Rochester, MN, Rochester, United States; ⁵Yale University, New Haven, United States; ⁶University of Toronto, Toronto, Canada; ⁷University of California San Francisco, San Francisco, United States; ⁸Emory University, Atlanta, United States; ⁹Mercy Medical Center; ¹⁰University of Tennessee, Knoxville, United States; ¹¹Mayo Clinic, Scottsdale, United States; ¹²University of Washington, Seattle, United States; ¹³VCU, Richmond, United States
Email: dr.jackieo@yahoo.com

Background and aims: Infections in cirrhosis lead to high rates of morbidity and mortality. While there are clear guidelines for diagnosis, treatment and prophylaxis for SBP, non-SBP infections are managed per local standards of care. We hypothesized that admission SBP would have a better prognosis compared to non-SBP bacterial infections in hospitalized patients with cirrhosis. Define outcomes in SBP vs. non-SBP infections in a large inpatient multi-center cohort adjusted for clinically relevant factors.

Method: NACSELD (North American Consortium for study of End-stage Liver Disease) included patients with cirrhosis without HIV or transplant admitted non-electively and followed for 30 days post-discharge. Demographics, cirrhosis details, admission reasons, hospital course and outcomes (ACLF, death, transplant) were recorded. We included patients admitted with bacterial infections (SBP vs others) diagnosed within 48 hours per IDSA guidelines. We excluded those with multiple admission infections, fungal or viral infections. Outcomes of SBP vs non-SBP patients were compared for transplant censored in-hospital mortality, transplant-censored 30-day mortality, transplant and 2nd infections after adjustment for admission factors (MELD, Na, HE, Albumin).

Results: 2, 062 total patients were included: 458 had admission infections (103 SBP and 354 non-SBP bacterial infections) and 1605
had no admission infection. No differences were seen between the 2 infected groups with respect to ACLF/organ failures, medications and outcomes (Table 1). The adjusted analysis found no difference between the SBP and Non-SBP groups for transplant censored inpatient mortality, transplant, risk for 2nd infection, ACLF and transplant-censored 30-day mortality (Table 2).

Table: Summary of Study Cohort

<table>
<thead>
<tr>
<th>SBP Non-SBP No Infection</th>
<th>(n = 103)</th>
<th>(n = 354)</th>
<th>(n = 1605)</th>
<th>p value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age</td>
<td>56.9</td>
<td>56.5</td>
<td>57.5</td>
<td>0.33</td>
</tr>
<tr>
<td>Gender (Male)</td>
<td>68%</td>
<td>59%</td>
<td>64%</td>
<td>0.16</td>
</tr>
<tr>
<td>MELD</td>
<td>22</td>
<td>19</td>
<td>18</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>Prior HE</td>
<td>65%</td>
<td>64%</td>
<td>57%</td>
<td>0.01</td>
</tr>
<tr>
<td>Hospital course</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ICU Transfer</td>
<td>28%</td>
<td>30%</td>
<td>18%</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>Brain failure</td>
<td>13%</td>
<td>17%</td>
<td>13%</td>
<td>0.11</td>
</tr>
<tr>
<td>Respiratory failure</td>
<td>15%</td>
<td>19%</td>
<td>9%</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>Circulatory failure</td>
<td>12%</td>
<td>14%</td>
<td>6%</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>AKI</td>
<td>60%</td>
<td>53%</td>
<td>36%</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>Renal failure</td>
<td>16%</td>
<td>11%</td>
<td>6%</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>Clinical Outcomes</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>In-Hospital Mortality</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Transplant</td>
<td>17%</td>
<td>8%</td>
<td>4%</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>30-day Mortality</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Transplant</td>
<td>19%</td>
<td>13%</td>
<td>8%</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>2nd Infection</td>
<td>11%</td>
<td>5%</td>
<td>3%</td>
<td>0.0001</td>
</tr>
<tr>
<td>2nd Infection</td>
<td>14%</td>
<td>19%</td>
<td>1%</td>
<td>&lt;0.0001</td>
</tr>
</tbody>
</table>

Table 2: Comparison of Adjusted OR of SBP vs. No-SBP

<table>
<thead>
<tr>
<th></th>
<th>OR</th>
<th>p value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Txp Censored In-Hospital Mortality</td>
<td>1.9</td>
<td>0.07</td>
</tr>
<tr>
<td>Txp Censored 30-day Mortality</td>
<td>1.3</td>
<td>0.43</td>
</tr>
<tr>
<td>Transplant</td>
<td>1.7</td>
<td>0.25</td>
</tr>
<tr>
<td>2nd Infection</td>
<td>0.7</td>
<td>0.20</td>
</tr>
<tr>
<td>ACLF</td>
<td>0.7</td>
<td>0.35</td>
</tr>
</tbody>
</table>

Conclusion: Patients with bacterial SBP and non-SBP infections were statistically similar with respect to development of 2nd infections, mortality, and transplant requirement after controlling for admission factors. Therefore, all patients with bacterial infections, not just SBP, should be monitored closely to prevent negative outcomes.

SAT497
Natural history of Hepatic Encephalopathy (HE) in a tertiary referral centre for hepatology
Chiara Mangini1, Chiara Formentin1, Alberto Biscontini1, Gianluca Giusti1, Paolo Angeli1, Lisa Zarantonello1, Sara Montagnese1.
1Department of Medicine, Padova, Italy
Email: sara.montagnese@unipd.it

Background and aims: The occurrence and recurrence of HE mark significant progression in the natural history of cirrhosis. While it is well known that HE is an unfavourable prognostic factor, few data on its evolution over time are available. Our aim was to study the evolution of HE (neuropsychological indices, also in relation to HE treatment and severity of liver disease) in patients with varying degree of HE on first assessment.

Method: 87 patients with cirrhosis (age 58 ± 11 years; 72 males) referred to the HE outpatient clinic of the Regional Centre for Liver Diseases at Padova University Hospital between June 2009 and January 2019 were included. They were evaluated from 2 up to 10 times (varying time-intervals), for purposes of liver transplantation selection, differential diagnosis or treatment optimization. The presence/severity of HE was assessed by clinical, neuropsychological (PHES) and neurophysiological (EEG) tools. The severity of liver disease was assessed by the MELD score. Treatment was instituted/modified according to both guidelines and local experience after each evaluation.

Results: On first assessment, 23 patients were classed as unimpaired, 32 as having covert and 32 as having overt HE. Amongst unimpaired patients, on second/third evaluation 56%/16% remained unimpaired, 35%/3% developed covert HE, 9%/0% developed overt HE. Amongst patients with covert HE, on second and third evaluation 25%/10% became unimpaired, 44%/19% remained covert, 31%/13% developed overt HE. Finally, amongst patients with overt HE, 19%/16% became unimpaired, 25%/13% became covert and 56%/25% remained overt. PHES results tended to improve over time in patients with overt HE and the EEG worsened over time (despite remaining within normal limits) in unimpaired patients. These trends were not confirmed after adjustment for HE history, HE treatment and MELD. Finally, in patients with multiple evaluations, HE evolution was manifold and difficult to predict (fig. 1).

Conclusion: While there is obvious HE risk associated with HE on first assessment, our data suggest that evolution over time is extremely variable and largely dependent on HE history/management and MELD. These data also support the concept that HE is an essentially reversible condition.

SAT498
Public knowledge and attitudes toward liver diseases and liver cancer in the brazilian population
Paulo Bittencourt1, Liana Codes2, Maria Lucia Ferraz1. 1Brazilian Liver Institute
Email: plbbr@uol.com.br

Background and aims: Cirrhosis, particularly viral hepatitis (VH) and alcoholic liver disease (ALD), are the 8th leading cause of death in Brazil. Hepatocellular carcinoma (HCC) was also shown to rank 11th among all cancers in terms of mortality. Despite the burden of liver diseases in Brazil, little is known about public awareness of the Brazilian population regarding screening and diagnosis of the most cirrhosis and HCC in the country. To investigate in a representative sample of the Brazilian population public knowledge, level of awareness and attitudes toward cirrhosis and HCC and their most frequent risk factors according to age, gender, average family income,
level of education and place of living. Method: Between September 8th to 15th 2021, 1,995 subjects ≥18 years (53% women, mean age 44 years and average family income of 654 USD per month) living in five Brazilian regions were prospectively interviewed using a questionnaire consisting of a set of nine questions regarding knowledge about the main causes of cirrhosis and HCC, clinical burden of non-alcoholic fatty liver disease (NAFLD) and information regarding current attitudes toward hepatitis B vaccination, hepatitis B and C testing, alcohol intake as well as previous assessment of liver health by any laboratory or imaging test.

Results: Most of the Brazilian subjects believe that alcohol abuse (63%–87%), NAFLD (29%–53%) and smoking (31%–47%) are the main causes of cirrhosis and HCC. On the contrary, VH were less often linked to either cirrhosis (23%) or HCC (15%). Unexpectedly, more than 2/3 of the Brazilians agreed that NAFLD is a risk factor for cirrhosis, cancer, diabetes and cardiovascular diseases. 55% of the Brazilians were alcohol drinkers and 32% of them claimed to drink more often than once a week. Nearly half of those drinkers use more than three doses of alcohol per day. Previous evaluation of liver disease was referred at least once by 41% of the subjects. Attitudes toward hepatitis B vaccination and hepatitis B and C testing was carried out by 66%, 48% and 40% of the subjects, despite the fact that 80% of them were aware of the availability free of charge of those tests in the public health system. The main reasons for not being tested for VH were perception that there is no need for testing or absence of symptoms. In general, knowledge and attitudes toward prevention of liver diseases were significantly higher in older people and subjects with higher level of education and income (p <0.05).

Conclusion: Despite its major association with liver disease, VH was not considered by the majority of the Brazilian population as the main cause of cirrhosis and HCC, leading a large proportion of those subjects to neglect hepatitis B vaccination and VH testing. Despite the large alcohol consumption and knowledge of its adverse impact in liver health, less than half of the Brazilians have been evaluated at least once for liver disease.

SAT499
The negative impact of the pandemic on hospital admissions, morbidity and 30-day mortality for acute cirrhosis decompensation: a tertiary care perspective
Kohilan Gananandan¹, Alexandra Phillips¹, Anmol Chikhla², Hannah Old³, Niharika Thakur³, Konstantin Kazankov⁴, Raj Mookerjee¹, Sharmaine Jia Ying Sim⁵, ¹The Liver Failure Group, Institute for Liver and Digestive Health, United Kingdom; ²Royal Free Hospital, United Kingdom; ³UCL Medical School, United Kingdom; ⁴Aarhus University Hospital, Aarhus, Denmark; ⁵University College London, London, United Kingdom

Background and aims: The global pandemic has inevitably diverted resources away from management of chronic diseases, including cirrhosis, where up to 40% of patients are readmitted with new cirrhosis decompensation events. Whilst there is increasing knowledge on COVID-19 infection in liver cirrhosis, little is described on the impact of the pandemic on decompensated cirrhosis admissions and outcomes, which was the aim of this study.

Method: A single-centre, retrospective study, evaluated decompensated cirrhosis admissions to a tertiary London hepatology and transplantation centre, from October 2018 to February 2021. Patients were included if they had an admission with cirrhosis decompensation defined as new onset jaundice or ascites, infection, encephalopathy, portal hypertensive bleeding or renal dysfunction. Admissions were excluded if they lasted <24 hours, were elective or occurred post liver-transplant.

Results: There were 351 admissions in the pre-COVID period (October 2018 to February 2020) and 240 admissions during the COVID period (March 2020 to February 2021), with an average of 20.4 admissions per month throughout. Patients transferred in from secondary centres had consistently higher severity scores during the COVID period (UKELD 58 versus 54; p = 0.007, MELD Na 22 versus 18; p = 0.006, AD score 55.0 versus 51.0; p = 0.055). The proportion of ITU admissions pre versus during-COVID stayed constant (22.9% versus 19.2%), but there was a trend towards increased ICU admissions with acute-on-chronic liver failure (ACLF) (73.9% versus 63.8% pre-pandemic). Of those admitted to the intensive care without ACLF, there was a significant increase in EF-CLIF acute decompensation (AD) scores during the COVID period (58 versus 48, p = 0.009). In addition, there was a trend towards increased hospital re-admission rates during the COVID period (29.5% versus 21.5%, p = 0.067). When censored at 30 days, time to death post discharge was significantly reduced during the COVID period (p < 0.05) with a median time to death of 35 days compared to 62 days pre-COVID.

Conclusion: This study provides a unique perspective on the impact that the global pandemic had on the clinical course and characteristics of decompensated cirrhosis admissions. The findings of increased early mortality and re-admissions, and higher AD scores, indicating increased disease morbidity, highlight the need to maintain resourcing on providing high-level hepatology care. Given that COVID-19 will likely be a chronic issue, alternative care pathways such as remote monitoring may need adoption to facilitate continuity of care post-discharge and to reduce readmission rates and morbidity in the future.
SAT500
Comparison of recommended daily energy intakes in people with cirrhosis, based on current guidelines, and their directly measured energy requirements: an individual patient data analysis

Clive Jackson1, Ana Limon-Miro2, Tannaz Esdamparast2, Hisami Yamanaka-Okumura3, Lindsay plank4, Christiani Jeyakumar Henry5, Angela Madden6, Livia Garcia Ferreira7, César Prieto de Frías8, Anne Wilkens Knudsen9, Evangelos Kalaitzakis10, Leah Gramlich11, Maitreyi Raman11, Cathy Alberda12, Dawn Belland13, Vanessa Den Heyer13, Puneeta Tandon14, Marsha Morgan14. 1Department of Clinical Neurophysiology, Royal Free Hospital, Royal Free NHS Foundation Trust, London, United Kingdom; 2Department of Medicine, University of Alberta, Edmonton, Canada; 3Department of Clinical Nutrition and Food Management, Institute of Biomedical Sciences, Tokushima University Graduate School, Tokushima, Japan; 4Department of Surgery, University of Auckland, Auckland, New Zealand; 5Department of Biochemistry, National University of Singapore, Singapore; 6School of Life and Medical Sciences, University of Hertfordshire, Hatfield, United Kingdom; 7Postgraduate Program in Nutrition and Health, Nutrition Department, Universidade Federal de Lavras, Brazil; 8Department of Gastroenterology, Clínica Universidad de Navarra, Pamplona, Spain; 9Medical Division, and Medical Unit, Nutritional Division, Copenhagen University Hospital Hvidovre, Hvidovre, Denmark; 10Department of Gastroenterology, University Hospital of Heraklion, University of Crete, Heraklion, Greece; 11Department of Medicine, Division of Gastroenterology, University of Calgary, Calgary, Alberta, Canada; 12Royal Alexandra Hospital, Alberta Health Services, Edmonton, Canada; 13University of Alberta Hospital, Alberta Health Services Nutrition Services, Edmonton, Canada; 14UCL Institute for Liver and Digestive Health, Division of Medicine, Royal Free Campus, University College London, London, University College London, London, United Kingdom
Email: marsha.morgan@ucl.ac.uk

Background and aims: Weight-based guidelines for the nutritional management of patients with cirrhosis have been formulated by EASL, ESPEN, AASLD and ISHEN. However, the guidance is discordant both in terms of recommended daily energy intakes, which range from 25 to at least 35 kcal/kg, and whether the reference for calculation should be actual, estimated dry or ideal body weight. This study aimed to compare recommended daily energy intakes with daily energy requirements based on direct measurement of resting energy expenditure (REE).

Method: REE was measured, using indirect calorimetry, in 900 patients with cirrhosis (mean [± SD] age 55.7±11.6 yr; 70% men); total daily energy requirements were determined, for individual patients, using 1.3 × REE. Daily energy intakes were calculated based on recommended intakes of 25, 30 and 35 kcal/kg referenced to actual body weight; ideal body weight calculated using the Hamwi, Devine, Robinson and Miller formulae, and, in patients with ascites, the estimated dry weight. The limits of agreement for each permutation of the recommended intakes and weight reference standards were compared with the calculated required intakes.

Results: Daily intakes of 25 kcal/kg would provide less energy than required and hence underfeeding in the majority of patients, irrespective of the weight standard used or the presence/absence of ascites. In contrast, daily intakes of 35 kcal/kg would provide more energy than required and hence overfeeding in the majority of patients. Daily intakes of 30 kcal/kg are closest to requirements but would still provide from 452 kcal less to 749 kcal more than required, based on actual body weight in patients without ascites, and from 833 kcal less to 767 kcal more than required based on estimated dry body weight in patients with ascites (Table).

Conclusion: The current weight-based guideline for determining daily energy intakes in patients with cirrhosis may pose a significant risk of under or overfeeding and need to be urgently reviewed.

SAT501
Rifaximin for the prevention and treatment of hepatic encephalopathy: a systematic review and meta-analysis of randomized clinical trials

Harry D Zacharias1, Jaclyn Yizhen Tan1, Fady Kamel1, Nina Kimer2, Lise Lotte Chuudi3, Marsha Morgan1. 1UCL Institute for Liver and Digestive Health, Division of Medicine, Royal Free Campus, University College London, London, University College London, London, United Kingdom; 2UCL, UCLH and Imperial College London, London, United Kingdom; 3GastroArmit Medical Division, Copenhagen University Hospital Hvidovre, Hvidovre, Denmark
Email: marsha.morgan@ucl.ac.uk

Background and aims: Rifaximin has been used for the treatment of hepatic encephalopathy (HE), in patients with cirrhosis, since the 1990s. However, whilst individual studies have shown benefit in acute/recurrent, chronic, and minimal HE, its main licensed indication remains the prevention of recurrent HE in combination with non-absorbable disaccharides (NAD). This systematic review and meta-analyses of randomised clinical trials (RCTs) for the prevention and treatment of HE, in patients with cirrhosis, compared (i) rifaximin vs. placebo/no intervention; (ii) rifaximin vs. NAD; and (iii) rifaximin co-administered with NAD vs. NAD alone.

Method: Electronic/manual searches of the literature were undertaken; further information was obtained from authors/pharmaceutical companies. Meta-analyses were conducted and results presented as relative risks (RR) and 95% confidence intervals (CI). Sources of heterogeneity and the influence of random and systematic errors were evaluated in subgroup/sensitivity analyses.

Results: A total of 38 RCTs involving 4376 people were included; individual patient data were available for 7 trials and additional information for a further 17; some trials included more than one comparison. Twelve studies compared rifaximin with placebo/no intervention minimal (n = 5) or chronic HE (n = 3) or for HE prevention (n = 4); meta-analysis showed no effects of rifaximin on mortality or serious adverse events (SAEs) but an overall beneficial effect on HE (RR = 0.58, 95% CI 0.56–0.91; NNTB = 5; participants = 969), confirmed in subgroup analyses in minimal HE but not in cirrhosis: no ascites (n = 770).
chronic HE or for HE prevention. Rifaximin was compared with NADs in 13 studies acute (n = 4); chronic (n = 4) and minimal HE (n = 2) and for HE prevention (n = 8); rifaximin plus lactulose had a beneficial effect on mortality (RR 0.69, 0.55–0.86; NNTB = 20; participants = 1836), subgroup analyses confirmed mortality benefit in acute HE (RR 0.65, 0.46–0.92; NNTB = 13; participants = 692) but not in HE prevention. Co-administration of the two drugs also had a beneficial effect on HE (RR 0.58, 0.48 to 0.71; n = 2306), with a NNTB of 5. Subgroup analyses confirmed benefit in both the treatment of acute HE (RR 0.62, 0.45 to 0.87) and in HE prevention (RR 0.54, 0.42 to 0.69) (Figure 1); there was no overall effect on SAEs; the evidence was of low to very low quality.

Figure: Random-effects meta-analysis of RCTs comparing the effect of rifaximin plus NAD vs. NAD alone

Conclusion: Rifaximin monotherapy does not convey benefit compared to NADs. However, rifaximin combined with lactulose is a safe and effective intervention for people with cirrhosis and acute HE, and for the prevention of recurrent HE. However, further high-quality studies are needed.

SAT502
Influence of cirrhotic cardiomyopathy defined according to the new multidisciplinary diagnostic criteria on overall mortality among cirrhotic patients
Simona Bota1, Marcel Razpotnik1, Philipp Wimmer2, Michael Hackl2, Gerald Lesnik3, Hannes Alber4, Markus Peck-Radosavljevic1, 1Klinikum Klagenfurt am Wörthersee, Department of Internal Medicine and Gastroenterology (IMuG) and Emergency Medicine (ZAE), Klagenfurt, Austria; 2Klinikum Klagenfurt am Wörthersee, Department of Internal Medicine and Cardiology (IMuk), Klagenfurt, Austria; 3Klinikum Klagenfurt am Wörthersee, Institut for diagnostic and interventional Radiology, Klagenfurt, Austria
Email: bota_simona1982@yahoo.com

Background and aims: New criteria of cirrhotic cardiomyopathy (CCM) were published from a multidisciplinary consortium (Izzy et al. Hepatology 2019 Nov 11. doi: 10.1002/hep.31034) and define systolic dysfunction of the left ventricle as ejection fraction (EF) ≤50% and/or global longitudinal strain (GLS) < -18%, while the diastolic dysfunction is diagnosed when three of the following conditions are present: average E/e' > 14, peak tricuspid regurgitation velocity > 2.8 m/s, septal e'< 7 cm/s, left atrial volume index > 34 ml/m². Our aim was to assess the influence of CCM defined according the new criteria on overall mortality among cirrhotic patients.

Method: Our prospective study included consecutive patients with liver cirrhosis without structural heart disease, arterial hypertension, HCC outside Milan criteria, portal vein thrombosis, presence of TIPS and with optimal acoustic echocardiography window. The patients were evaluated between 12/2018–11/2021 in our in- and out-patient Department. Conventional and speckle-tracking echocardiography (Vendor GE, EchoPAC PC software) were performed by a single investigator (EACVI TTE certified). The follow-up was performed until the patient was last seen or death.

Results: 412 cirrhotic patients were evaluated during the study period and 133 fulfilled the inclusion criteria and were included in the final analysis. The mean age of patients was 57.1 ± 10.2 years (60.1% males), 70.1% with alcoholic etiology and 48.1% with compensated liver cirrhosis.

CCM (systolic and/or diastolic dysfunction) was present on 15% of patients, only systolic dysfunction on 9.7% and only diastolic dysfunction on 7.5% of the cirrhotic patients. The median follow-up was 21 (0.5–36) months and 18/133 (13.5%) of cirrhotic patients died during the follow-up. The presence of diastolic dysfunction was associated with significantly higher mortality (p = 0.04) in our cohort of cirrhotic patients (Figure). The presence of CCM (systolic and/or diastolic dysfunction) tends also to increase mortality but did not achieve statistical significance.

Severity of liver disease, assessed by Child-Pugh and MELD score was not correlated with the presence of CCM: r = −0.0209, p = 0.73 and r = −0.010, p = 0.90.

Conclusion: Even if the follow-up was relatively short in our study, the presence of CCM (especially diastolic dysfunction) was associated with higher overall mortality among cirrhotic patients. Our data shows the importance of a cardiac (especially echocardiography with strain) evaluation of cirrhotic patients.

SAT503
Risk of herpes zoster infection in patients with cirrhosis: a nationwide population-based study in Korea
Dongsub Jeon1, Seon-Ok Kim2, Ye-Jee Kim2, Jonggi Choi1, 1Asan Medical Center, Department of Gastroenterology, Liver Center, Seoul, Korea, Rep. of South; 2Asan Medical Center, Biostatistics and Clinical Epidemiology, Seoul, Korea, Rep. of South
Email: j.choi@amc.seoul.kr

Background and aims: New criteria of cirrhotic cardiomyopathy (CCM) were published from a multidisciplinary consortium (Izzy et al. Hepatology 2019 Nov 11. doi: 10.1002/hep.31034) and define systolic dysfunction of the left ventricle as ejection fraction (EF) ≤50% and/or global longitudinal strain (GLS) < -18%, while the diastolic dysfunction is diagnosed when three of the following conditions are present: average E/e' > 14, peak tricuspid regurgitation velocity > 2.8 m/s, septal e'< 7 cm/s, left atrial volume index > 34 ml/m². Our aim was to assess the influence of CCM defined according the new criteria on overall mortality among cirrhotic patients.

Method: Our prospective study included consecutive patients with liver cirrhosis without structural heart disease, arterial hypertension, HCC outside Milan criteria, portal vein thrombosis, presence of TIPS and with optimal acoustic echocardiography window. The patients were evaluated between 12/2018–11/2021 in our in- and out-patient Department. Conventional and speckle-tracking echocardiography (Vendor GE, EchoPAC PC software) were performed by a single investigator (EACVI TTE certified). The follow-up was performed until the patient was last seen or death.

Results: 412 cirrhotic patients were evaluated during the study period and 133 fulfilled the inclusion criteria and were included in the final analysis. The mean age of patients was 57.1 ± 10.2 years (60.1% males), 70.1% with alcoholic etiology and 48.1% with compensated liver cirrhosis.

CCM (systolic and/or diastolic dysfunction) was present on 15% of patients, only systolic dysfunction on 9.7% and only diastolic dysfunction on 7.5% of the cirrhotic patients. The median follow-up was 21 (0.5–36) months and 18/133 (13.5%) of cirrhotic patients died during the follow-up. The presence of diastolic dysfunction was associated with significantly higher mortality (p = 0.04) in our cohort of cirrhotic patients (Figure). The presence of CCM (systolic and/or diastolic dysfunction) tends also to increase mortality but did not achieve statistical significance.

Severity of liver disease, assessed by Child-Pugh and MELD score was not correlated with the presence of CCM: r = −0.0209, p = 0.73 and r = −0.010, p = 0.90.

Conclusion: Even if the follow-up was relatively short in our study, the presence of CCM (especially diastolic dysfunction) was associated with higher overall mortality among cirrhotic patients. Our data shows the importance of a cardiac (especially echocardiography with strain) evaluation of cirrhotic patients.
Background and aims: Few data are available on the risk of herpes zoster (HZ) infection in patients with liver cirrhosis. We investigated whether patients with liver cirrhosis have an increased risk of HZ infection compared with general population and risk factors associated with HZ infection in patients with cirrhosis.

Method: We performed a nationwide population-based study, using the claim data of the Korean national health insurance database between 2009 and 2019. In total, 505,750 patients with liver cirrhosis were included, yielding 3,266,470 person-years of follow-up. We calculated the incidence rates and standardized incidence ratios (SIRs) of HZ infection in patients with liver cirrhosis to evaluate the risk of HZ infection compared with general population in the same sex and age group. Hazard ratios (HRs) for HZ infection and their 95% confidence intervals (CIs) were estimated using a Cox proportional hazard model for factors associated with increased risk for HZ infection.

Results: In this nationwide population-based study, the overall incidence rate of HZ infection was 21.6/1000 person-years and SIR was 1.09 (95% CI, 1.08–1.10) in patients with liver cirrhosis. Among the patients with liver cirrhosis, the incidence rate and SIR for HZ infection was significantly higher in female patients than male (incidence rate, 27.4 vs. 17.3; SIR, 1.11 vs. 1.06; p < 0.001 for both). The incidence rate of HZ increased with age (P trend <0.001), whereas the SIR of HZ infection showed U-shaped graph in the age curve showing incidence rate of HZ increased with age (P trend <0.001), whereas the SIR of HZ infection showed U-shaped graph in the age curve showing incidence rate of HZ infection compared with general population in the same sex and age group. Hazard ratios (HRs) for HZ infection and their 95% confidence intervals (CIs) were estimated using a Cox proportional hazard model for factors associated with increased risk for HZ infection.

Conclusion: In this nationwide population-based study in Korea, we found patients with liver cirrhosis have an increased risk for HZ infection, especially in female, with the peaks of SIR in both young patients under 50 and the elderly over 80. Therefore, zoster vaccination might be considered for patients with liver cirrhosis aged under 50 as well as the elderly.
Background and aims: Acute kidney injury (AKI) is a severe complication in patients with decompensated liver cirrhosis and is associated with a poor prognosis. Identifying and preventing the application of potential trigger substances for AKI is important in the management of these patients. In this context, only insufficient data regarding the nephrotoxic potential of CT-contrast media (CM-CT) is available. Here we investigate the nephrotoxic potential of CM-CT in patients with decompensated liver cirrhosis.

Method: In an exploratory analysis, patients with decompensated liver cirrhosis and ascites that received a paracentesis between 2012 and 2016 at Hannover Medical School (MHH) were included. Patients with AKI or relevant interventional procedures 7 days prior to baseline were excluded from this study. Propensity score matching (PPSM) was conducted, matching for MELD score, leukocyte count, intake of diuretics, presence of diabetes and age. Results were confirmed using data from a prospective registry that collects clinical data and biosamples from patients with liver cirrhosis and ascites that underwent a paracentesis between 2016 and 2020 (validation cohort) at MHH. Analyzed end points were 28-day incidence of AKI, severe AKI and liver transplant (LTx) free survival. Furthermore, measurement of neutrophil gelatinase-associated lipocalin (NGAL), an early marker for AKI, was conducted in plasma-samples from the prospective cohort.

Results: Overall, 140 patients were eligible for analysis in the retrospective cohort, of whom 61 patients received a CM-CT (43%). After PPSM, 51 patients with CM-CT were matched with 51 patients without CM-CT. Baseline parameters like MELD (CM-CT: 15 vs. No CM-CT: 16, p = 0.44), CRP values (CM-CT: 32 mg/dl vs. No CM-CT: 34 mg/dl, p = 0.80) and presence of infections at baseline (CM-CT: 35% vs. No CM-CT: 37%, p = 1.00) were comparable between both groups. The 28-day AKI incidence did not differ between both groups (p = 0.56). Furthermore, ITx-free survival and incidence of severe AKI was comparable (p = 0.37 and p = 1.00). In the validation cohort, CM-CT was noted in 13 patients (11%), while 105 patients had no CM-CT (89%). Incidence of AKI and severe AKI was comparable between the groups (p = 0.85 and p = 0.54). Finally, NGAL-levels did not differ significantly between CM-CT an no CM-CT patients (311 ng/ml vs. 266 ng/ml, p = 0.35).

Conclusion: CM-CT does not increase the risk for AKI in patients with decompensated liver cirrhosis.
Results: 152 patients (male: 72%; alcoholic liver disease: 35%; viral hepatitis: 22%; HCC 32%) were included in the study. 5-year survival was 68%. Sarcopenia pre-LT was present in 93 (62%) patients. Mean MELD did not differ between patients with and without sarcopenia (21 vs. 22; p = 0.4). Mean MRA pre-LT was 37 HU. Reduced MRA pre-LT was associated with higher BMI (p = 0.033), age (p < 0.001), male sex (p = 0.019), and a lower SMI (p = 0.041). Patients with hepatorenal syndrome or need of hemodialysis showed a lower MRA than those without (p = 0.018; p = 0.002). At short-term FU (11 months after LT) mean MRA was 35 HU and 35/50 (70%) fulfilled criteria of sarcopenia, whereas at long-term FU (56 months after LT) mean MRA was 34 HU and 35/52 (67%) were classified as sarcopenic. Neither MRA nor SMI was associated with higher BMI (p = 0.033), age (p < 0.001), male sex (21 vs. 22; p = 0.4). Mean MRA pre-LT was 37 HU. Reduced MRA pre-LT was associated with higher BMI (p = 0.033), age (p < 0.001), male sex (21 vs. 22; p = 0.4). Mean MRA pre-LT was 37 HU. Reduced MRA pre-LT was associated with higher BMI (p = 0.033), age (p < 0.001), male sex (21 vs. 22; p = 0.4). Mean MRA pre-LT was 37 HU. Reduced MRA pre-LT was associated with higher BMI (p = 0.033), age (p < 0.001), male sex (21 vs. 22; p = 0.4).

Conclusion: Neither SMI nor MRA as parameters of sarcopenia improved after transplantation. Besides the MELD score, MRA predicted short- and long-term survival after transplant. MRA and muscle quality should thus be defined prior to transplantation to stratify the patient's risk profile and should be validated in future studies. SATS08 Clinical and prognostic characterization of the patterns of decompensation of liver cirrhosis Marta Tonon1, Simone Incicco1, Valeria Calvino1, Alessandra Brocca1, Antonio Accetta1, Carmine Gabriele Gambino1, Marco Cola1, Daniel Salinas1, Salvatore Piano1, Paolo Angelii1. 1University of Padova, Unit of Internal Medicine and Hepatology, Department of Medicine, Padova, Italy Email: salvatorepiano@gmail.com

Background and aims: The clinical course of liver cirrhosis is characterized by two phases, compensated and decompensated cirrhosis, the latter characterized by the onset of complications (ascites, variceal bleeding, hepatic encephalopathy) and a worse prognosis. Recently, Acute Decompensation (AD), i.e. the development of complications that require hospitalization, has been characterized. However, complications of cirrhosis do not necessarily require hospitalization and can develop progressively. This type of decompensation has recently been defined as Non Acute Decompensation (NAD). At present time, there is no information regarding the incidence and prognostic impact of NAD. The aim of the study was therefore the evaluation of the incidence of NAD and AD in a group of outpatients with liver cirrhosis and the prognostic impact of these two decompensation patterns.

Method: 749 outpatients with cirrhosis were enrolled and consequently followed up until death, liver transplantation or the end of the study (August 2021). Clinical and biochemical data were collected, as well as the development of complications during follow-up, which were considered as AD if they resulted in hospitalization or NAD if they were managed at outpatient clinic.

Results: 379 patients (50.6%) did not develop any decompensation, 163 patients (21.8%) had NAD as first decompensation and 207 (27.6%) had AD. During follow-up, 216 patients (28.8%) died and 145 (19.4%) were transplanted. Survival at 10 years was significantly higher in patients who did not develop decompensations (79.6%) than in patients who developed NAD or AD (33.7% and 21.3%, respectively; p < 0.001, Fig. A). Eighty-three patients with NAD (50.9%) subsequently developed AD. There was no significant difference in 10-year survival between patients who developed AD after NAD and those who only had AD, while both of these groups showed shorter survival than patients who had only NAD. In multivariate analysis, age (HR 1.05, p < 0.001), MELD (HR 1.10, p < 0.001), varices at inclusion (HR 1.48, p = 0.03), albumin (HR 0.94, p < 0.001), MAP (HR 0.98, p = 0.006), effective etiological treatment (HR 0.38, p < 0.001) and NAD (HR 2.65, p < 0.001) or AD (HR 3.51, p < 0.001) were independent predictors of mortality.

Conclusion: In more than 20% of patients with cirrhosis the first decompensation is a NAD, which often precedes AD and is associated with a decreased survival. Patients who develop NAD must be monitored closely to prevent any development of AD.

SATS09 Safety, pharmacokinetics and pharmacodynamics of TNP-2092 capsule in Chinese liver cirrhosis patients with hyperammonemia: a randomized, double-blind, placebo-controlled, dose-escalation phase Ib/IIa study Jia Xu1, Jingrui Liu1, Jing Chen1, Zhenkun Ma1, Yanhua Ding1, Junqi Niu1. 1China Email: 747740607@qq.com

Background and aims: TNP-2092, a locally acting drug candidate, exhibits broad-spectrum antibacterial activity by inhibiting three essential drug targets RNA polymerase, DNA gyrase and topoisomerase IV. TNP-2092 has a lower propensity for the development of resistance than rifaximin.

Method: Thirty-six liver cirrhosis patients with fasting venous blood ammonia higher than normal were enrolled and received multiple ascending doses of TNP-2092 (100 mg 300 mg and 600 mg, BID for 14 days) or placebo under fed conditions. Patients with Child-Pugh

Figure: 120-month survival in patients according to the pattern of decompensation

Conclusion: In more than 20% of patients with cirrhosis the first decompensation is a NAD, which often precedes AD and is associated with a decreased survival. Patients who develop NAD must be monitored closely to prevent any development of AD.
grade C cirrhosis and grade 2 or above hepatic encephalopathy were excluded.

Results: TNP-2092 was safe and well tolerated in all treatment groups. The most commonly observed treatment emergent adverse events (TEAEs) were neutropenia (29.2%), leucopenia (16.7%) and lipase elevation (12.5%). The most of the TEAEs were mild and lack of dose relationships. The AUC and C max for TNP-2092 exhibited a dose-proportional increase. The systemic exposure of TNP-2092 increased 2- to 4-fold compared to that in healthy volunteers.

The blood ammonia level decreased in a dose-dependent fashion during and after the treatment (Table 1). TNP-2092 (600 mg BID) reduced the blood ammonia level by 24.03 ug/dL, compared to 15.43 ug/dL produced rifaximin (400 mg, TID) after 14 days of treatment as reported in literature.

Table 1: The change of blood ammonia before and after treatment:

<table>
<thead>
<tr>
<th>Dose (mg)</th>
<th>100 mg</th>
<th>300 mg</th>
<th>600 mg</th>
<th>placebo</th>
</tr>
</thead>
<tbody>
<tr>
<td>N=8</td>
<td>N=8</td>
<td>N=12</td>
<td>N=12</td>
<td></td>
</tr>
</tbody>
</table>

During the treatment (D2-D15), the proportion of blood ammonia measurements returned to normal:
- 13% 32% 32% 7.4% (p = 0.004)
- 47% 50% 69.4% 52.8% (p = 0.005)

After the treatment (D15), the reduction of blood ammonia level from pretreatment:
- 9.71 3.62 24.03 0.85 (p = 0.002)

Conclusions: TNP-2092 was safe and well tolerated with a linear pharmacokinetic and pharmacodynamic profile in liver cirrhosis patients with hyperammonemia. TNP-2092 showed potential to have a stronger effect on the blood ammonia level than rifaximin.

SAT510
Serological assessment of the collagen type III deposition predicts outcome in decompensated liver cirrhosis
Mette Juul Nielsen1, Robert Schierwagen2,3, Christian Jansen2, Frank Ushchern4,5, Sabine Klein4,5, Maximilian J Brol2,3, Michael Praktiknjo2, Chang Johannes2, Morten Karsdal1, Diana Leeming1, Jonel Trebicka2,4,5, 1Nordic Bioscience A/S, Denmark; 2University Hospital of Bonn, Department of Internal Medicine I, Bonn, Germany; 3University of Frankfurt, Department of Internal Medicine I, Frankfurt, Germany; 4European Foundation for Study of Chronic Liver Failure, Barcelona, Spain; 5University Clinic Odense, Department of Hepatology, Odense, Denmark
Email: mju@nordicbio.com

Background and aims: Fibrosis is the result of excessive collagen and extracellular matrix (ECM) accumulation, consequent to an imbalance in collagen formation and degradation. The balance between fibrogenesis and fibrolysis may be of importance for patient management and prognosis. Over time, the collagen fibrils become enzymatically cross-linked resulting in increased stiffness of the tissue. Here we investigated a novel fibrosis resolution biomarker, C-terminal cross-linked type III collagen degradation (CTX-III) in combination with the collagen formation biomarker PRO-C3, and their association with decompensation and predictors of mortality in patients with trans jugular intrahepatic portosystemic shunt (TIPS).

Method: In 83 patients with decompensated liver cirrhosis, plasma samples were taken from the hepatic vein at the time of TIPS insertion. Fibrogenesis was assessed using PRO-C3 and fibrolysis by the cross-linked collagen fragment CTX-III. The association between individual biomarkers and presence of ascites, Child-Pugh category, and MELD score was investigated. Patients with high fibrogenesis and low fibrolysis and vice versa were identified by CART analysis. The net type III collagen remodeling was defined as the ratio between fibrogenesis and fibrolysis, i.e., the PRO-C3:CTX-III ratio. Kaplan-Meier and Cox regression analyses were used to investigate the association of the balance between fibrogenesis and fibrolysis with 5-year transplant-free survival.

Results: At TIPS insertion, PRO-C3 was significantly elevated in patients with MELD score >11 (p = 0.014) and Child–Pugh Class C (p = 0.017). Interestingly, the degree of the type III collagen remodeling was not associated with disease severity, including MELD score, presence of ascites, and Child–Pugh class. When stratifying individual biomarkers according to their median, none of the biomarkers was associated with survival. Nevertheless, patients with excessive type III collagen deposition, defined by high fibrogenesis (PRO-C3) and low fibrolysis (CTX-III), at TIPS insertion had significantly shorter survival time compared to those with less type III collagen deposition (p = 0.020).

Conclusion: High level of fibrosis resolution is associated with less severe decompensation and better survival in liver cirrhotic patients with TIPS. The balance of collagen formation and collagen degradation provides additional information compared to each biomarker and is essential for the prediction of outcome in cirrhotic patients.

SAT511
Liver frailty index predicts poor outcomes in patients hospitalized for acute decompensation of cirrhosis
Simone Incicco1, Roberta Gagliardi1, Marta Tonon1, Valeria Calvino1, Nicola Zeni1, Alessandra Brocca1, Carmine Gabrielle Gambino1, Paolo Angeli1, Salvatore Piano1, 1Unit of Internal Medicine and Hepatology, Department of Medicine, University of Padova, Padova, Italy
Email: salvatorepiano@gmail.com

Background and aims: Physical frailty is highly prevalent in patients with end stage liver disease and has been associated with poor outcomes. Liver Frailty Index (LFI) is a standardized tool to assess frailty in patients with cirrhosis on liver transplant waiting list. However, there is a paucity of data on the prognostic value of LFI in patients hospitalized for acute decompensation (AD) of cirrhosis. We
evaluated LFI in patients hospitalized for AD and the association of LFI with complications occurred during hospitalization and 90-day survival.

**Method:** We enrolled 117 consecutive patients admitted for AD of cirrhosis from 2019 to 2021. LFI was performed at the time of hospital admission. Occurrence of complications (hepatic encephalopathy [HE], sepsis, organ failures, ACLF) during hospitalization was recorded. Patients were followed up until death, liver transplant or 90 days.

**Results:** Mean age and MELD-Na were 64 ± 10 and 20 ± 7, respectively. The majority of patients were male (71%) and had and alcohol-related cirrhosis (56%). Median LFI was 6.1 (IQR 5.0–6.5). LFI showed a weak, but significant, correlation with age (r = 0.202; p = 0.029), MELD-Na (r = 0.292; p = 0.001) and parameters of systemic inflammation such as C-Reactive Protein (r = 0.235; p = 0.014) and white blood cell (WBC) count (r = 0.207; p = 0.025).

LFI was significantly higher in patients developing hepatic encephalopathy, sepsis, renal failure, circulatory failure, respiratory failure and ACLF than in those who did not (Figure 1). Patients transferred to the ICU had significantly higher LFI than those who did not (Figure 1).

**Conclusion:** In patients with cirrhosis hospitalized for AD, LFI identifies patients at higher risk of worse outcomes and can be used for the assessment of frailty in these patients.
SAT513
Kidney transplant alone recipients with advanced liver disease have similar outcomes to those without advanced disease—a single-center study of 150 patients
Rohit Nathani1, Stephanie Rutledge2, Carolina Villarroel3,
Ron Shapiro1* Gene Im3. 1 Icahn School of Medicine at Mount Sinai
Morningside-West, Department of Medicine, New York, United States;
2 Icahn School of Medicine at Mount Sinai, Division of Gastroenterology,
Department of Medicine, New York, United States; 3 Icahn School of
Medicine at Mount Sinai Beth Israel, Department of Medicine, New York,
United States; 4 Icahn School of Medicine at Mount Sinai, Recanati/Miller
Transplantation Institute, Department of Surgery, New York, United States;
5 Icahn School of Medicine at Mount Sinai, Recanati/Miller Transplantation
Institute, Division of Liver Diseases, Department of Medicine, New York, United States
Email: rohit.nathani@mountsinai.org

Background and aims: The prevalence of concomitant liver disease (LD) in patients with end-stage renal disease is reported to be 7–40%.
The safety of kidney transplant alone (KTA) in those with advanced LD (F3–4) is controversial, with KDIGO guidelines recommending KTA consideration in compensated cirrhosis based on few small studies. The aim of this study was to compare outcomes in KTA patients with advanced LD to KTA patients with non-advanced LD.

Method: Retrospective analysis of all KTA patients at our center from 1/2012–12/2020 was performed. KTA patients with concomitant LD were identified by chart review. Advanced LD and cirrhosis status were determined by clinical criteria and if available, liver biopsy. Matched cohort analysis was performed using matching based on age, time on hemodialysis (HD), sex, and ethnicity. Primary outcome was mortality and secondary outcomes included serious infection (requiring intravenous antibiotics), allograft rejection, allograft failure, and liver decompensation.

Results: Over 8 years 1741 KTAs were performed, with 150 (8.6%) recipients having concomitant LD. KTA with LD cohort was mostly Over 8 years 1741 KTAs were performed, with 150 (8.6%) failure, and liver decompensation. (requiring intravenous antibiotics), allograft rejection, allograft was mortality and secondary outcomes included serious infection (76.5) months, hepatitis C virus infection as the most common etiology of LD (72%) and a mean follow-up of 1807 (SD ± 960) days. Transjugular liver biopsies were available for 62 (41%) patients with mean hepatic venous pressure gradient of 6.2 (SD ± 3.2) mmHg prior to KTA. We identified 29 (19%) patients with advanced LD at the time of KTA and 27/29 (93%) had compensated cirrhosis, mean MELD 21.8 (SD ± 3.8). The 1-, 3- and 5-year survival rates were 95.5%, 89.8% and 79.5% respectively. KTA patients without advanced LD (n = 46) were selected as a matched cohort. Kaplan-Meier survival analysis showed similar outcomes between KTA with LD subgroups (p = 0.09). On matched cohort analysis, 6 (21%) cases died compared to 9 (20%) controls (p = 0.9).

Mean time to death was 1645 (SD ± 939) days in cases compared to 689 (± 514) days in controls (p = 0.06). Secondary outcomes were similar between the 2 groups: serious infection 21% vs 28% (p = .51); allograft rejection 14% vs 13%, (p = .55); allograft failure 14% vs 4.3% (p = .2). Liver decompensation occurred in 4 (14%) cases after KTA vs 0 in control group (p = .6), mostly due to ascites (3/4), but also esophageal varices and hepatocellular carcinoma (causing death).

Conclusion: This is one of the largest single-center studies comparing outcomes in KTA patients with and without advanced LD. Although limited by small numbers, KTA patients with LD had excellent outcomes, with similar patient, graft, infection and liver decompensation outcomes between advanced LD and those without. This supports the practice of KTA in patients with concomitant LD, even with advanced fibrosis.

SAT514
Clinical features of exacerbation of portal vein thrombosis after discontinuation of anticoagulants
Takayuki Kondo1, Kisako Fujiwara1, Sae Yumita1, Takamasaha Ishino1,
Keita Ogawa1, Miyuki Nakagawa1, Hidemi Unoza1, Terunao Iwana1, Taka furumi Sakuma2, Naoto Fujita1, Keisuke Koroki1,
Hiroyuki Kanazaki1, Kazufumi Kobayashi1, Soichiro Kiyono1,
Masato Nakamura1, Naoya Kanogawa1, Tomoko Saito1,
Sadahisa Ogasawara1, Shingo Nakamoto1, Itsuhiro Chiba1, Kun Kato1,
Naoya Kato1. 1Graduate School of Medicine, Chiba University,
Department of Gastroenterology, Chiba, Japan
Email: takakondonaika@yahoo.co.jp

Background and aims: Portal vein thrombosis (PVT) is not a rare complication in cirrhosis. Currently, optimal management of PVT has been reported in the clinical guidelines. However, recommendations for the discontinuation of anticoagulants are not strictly defined. The present study aimed to clarify the clinical features of exacerbation of PVT after discontinuation of anticoagulants.

Method: This retrospective study included data from our institutional database between 2009 and 2020. This study enrolled 75 consecutive patients diagnosed with PVT by Doppler ultrasound (US) and contrast-enhanced computed tomography (CECT) who received anticoagulants and were followed up with at least one more CECT after diagnosis of PVT. Of the 75 patients, 50 patients discontinued anticoagulants at the physician's discretion. The PVT volume was measured using CECT images that included the whole spleno-portal-mesenteric axis. The outline of the PVT was traced manually in each slice and obtained at 5-mm intervals, and its volume was calculated by integrating all images. The sum of the diameter of portosystemic shunts diagnosed by Doppler US and CECT were calculated. The therapeutic assessment of the PVT was defined as complete response (0%), partial response (1–50%), slight response (51–75%), no response (76–100%), progression (≥101%).

Results: The PVT volume decreased significantly after anticoagulant therapy (pre-treatment 10.4 ± 10.8 cm3 vs. post-treatment 5.3 ± 7.5 cm3; p <0.01). Fifty-six patients (74.7%) achieved at least slight response (complete response 38.7%, partial response 26.7%, slight response 9.3%). Fifty patients discontinued anticoagulants, and 31 patients (62.0%) had the exacerbation of PVT after discontinuation of anticoagulants. The cumulative exacerbation rate of PVT was 24.0% at 3 months, 44.6% at 6 months, and 56.4% at 12 months. Multivariate
analysis showed that the sum of the diameter of portosystemic shunts (p = 0.02) and unknown cause of PVT (p = 0.02) were the significant predictive factors for the exacerbation of PVT after discontinuation of anticoagulants. A predictive model for the exacerbation of PVT after discontinuation of anticoagulants obtained by classification and regression tree analysis indicated the following subpopulations with distinct exacerbation rate: high risk (with unknown cause of PVT, exacerbation rate: 85%); intermediate risk (the sum of portosystemic shunts ≥12 mm and without unknown cause of PVT, exacerbation rate: 75%); and low risk (the sum of portosystemic shunts <12 mm and without unknown cause of PVT, exacerbation rate: 19%).

**Conclusion:** Patients with unknown cause of PVT or the development of portosystemic shunts should be monitored carefully after discontinuation of anticoagulants because of the high rate of exacerbation of PVT.

**SAT515**

**Systemic inflammatory response syndrome and renal resistive index as early predictors of treatment response to terlipressin in hepatorenal syndrome-acute kidney injury**

Vijay Narayanan¹, Avisek Chakravorty², Shivabrata Dhal Mohapatra², Rushil Solanki², Devika Madhur², Ravindra Pal², Krishnadas Devadas ³, ¹Government Medical College, Trivandrum, Medical Gastroenterology, Trivandrum, India; ²Government Medical College, Trivandrum, Medical Gastroenterology; ³Government Medical College, Trivandrum, Medical Gastroenterology, Trivandrum, India

**Background and aims:** A combination of terlipressin and albumin is the first-line pharmacologic treatment for Hepatorenal Syndrome-Acute Kidney Injury (HRS-AKI). The early identification of patients with a low likelihood of response to treatment is crucial, as they can be fast-tracked for liver transplantation. We assessed the response rates to terlipressin-albumin therapy in patients with decompensated cirrhosis and determined early predictors of treatment response. The mortality between treatment responders and non-responders was compared and predictors of six-month mortality were also assessed.

**Method:** This was a prospective observational study conducted in the Department of Medical Gastroenterology, Government Medical College, Trivandrum. Patients diagnosed to have HRS-AKI (based on the International Club of Ascites criteria) and treated with terlipressin-albumin were included. Univariate and multivariate logistic regression analysis was used to determine parameters that were predictive of HRS reversal. Best cut-offs of prediction were obtained from ROC curves.

**Results:** 84 patients with HRS-AKI were included. There was complete response to therapy in 54.8%, partial response in 14.3%, and no response in 31%. The factors associated with complete response to treatment were the presence of systemic inflammatory response syndrome (SIRS) at baseline (p <0.001), a rise in mean arterial pressure (MAP) ≥5 mmHg by day 3 of treatment (p <0.001), baseline serum creatinine ≤2.5 mg/dL (p <0.001), and a reduction in the renal resistive index (Delta-RRI) ≥5% by day 3 of treatment (p <0.001). On multivariate analysis, the independent predictors of complete response to treatment were the presence of SIRS at baseline (p = 0.016, OR = 6.19 (CI: 1.40–27)) and Delta-RRI ≥5% by day 3 (p = 0.001, OR = 24.2 (CI: 3.4–168.6)). The AUROC for predicting complete response to treatment was higher for SIRS Score (0.797) and Delta-RRI (0.803) than Child score (0.554) and MELD score (0.503) respectively. Non-responders had significantly higher mortality at 1 month (27% vs 9.5%, p = 0.04) and 6 months (74% vs 45%, p = 0.025).

**Conclusion:** SIRS and Delta-RRI are simple parameters to predict treatment response in HRS-AKI. Non-responders have higher mortality and should be identified early to expedite liver transplantation.

In HRS-AKI, the renal resistive index is a measure of the intrarenal vasoconstriction, and SIRS reflects the exaggerated systemic inflammation, both of which are reversed by terlipressin, leading to an enhanced treatment response.

**SAT516**

**A prospective study of global myocardial function in decompensated cirrhosis using advanced echocardiographic techniques and its clinical significance**

Jeyamani Ramachandran¹, Purendra Kumar Pati², Teresa Hecker³, Fahd Mohammadí, Libby John³, Vidyaaleha Chandran³, Matthew Chapman³, Yasmina Tashkent³, Rosemary McCormick³, Kylie Bragg³, Majo Joseph³, James Gunton³, Asif Chinnaratha³, Kate Muller³, Alan Wigg³, ¹Flinders Medical Centre, Flinders University, Australia; ²Lyell McEwin Hospital, Elizabeth Vale, Australia; ³Flinders Medical Centre, Bedford Park, Australia

**Background and aims:** Cirrhotic cardiomyopathy (CCM) is cardiac dysfunction due to cirrhosis without a primary cardiac cause. This study investigated CCM using global longitudinal strain (GLS) and global work index (GWI), sensitive measures of myocardial performance and their clinical significance over a 12-month follow-up. Assessed clinical events included acute kidney injury/hepatorenal syndrome (AKI/HRS), refractory ascites, cardiac failure, and death.

**Method:** Consecutively cirrhotic patients with ascites and those undergoing liver transplant (LT) assessment were studied prospectively after excluding those with prior cardiac diagnosis. Transthoracic echocardiography (TTE) and dobutamine stress echocardiogram (DSE) were performed. GLS by speckle tracking echocardiogram (STE) and GWI by combining STE and brachial artery blood pressure were calculated. CCM was defined according to 2019 criteria.

**Results:** Since January 2021, 65 cirrhotic patients were studied; Median (interquartile range, IQR) age 56 (13) years; 60% male; 72% related to alcohol misuse; 11 patients on beta-blockers; 28 in Child’s A combination of terlipressin and albumin is >23 was found to be an independent predictor of six mortality (p = 0.019, OR = 4.4 (CI: 1.3–15.4)).
class C, 30 in class B and 7 in class A; Median (IQR) MELD-Na 16 (12). CCM was diagnosed in 16 patients (25%) and was subclinical; systolic dysfunction (SD) in 9 patients, none with left ventricular ejection fraction (LVEF) <50%; Advanced diastolic dysfunction (DD) in 7 patients. If grade 2 DD seen in a further 16 patients were included, the prevalence of CCM reached 49%. A lower MELD-Na was associated with SD (mean MELD-Na 12 Vs 18 in patients with and without SD respectively, p = 0.015) with no significant association between DD and MELD Na. During the median follow-up of 181 days, 16 patients developed AKI/HRS and 33 patients experienced, refractory ascites, recurrent hydrothorax and or sepsis including peritonitis. No association was seen between SD, DD and CCM and these events. However, age (adjusted odds ratio = 1.018, 95%CI 1.037–1.185, p = 0.002) and AKI/HRS (adjusted odds ratio = 5.153, 95%CI 1.108–23.959, p = 0.037) emerged as independent predictors of CCM when grade 2 DD was included. Four patients died and three underwent successful LT. IVEF, GLS and GWI at baseline and on DSE were compared in 53 patients.

### Table 1: GLS, GWI, and IVEF values at rest and on DSE

<table>
<thead>
<tr>
<th>GLS (%)</th>
<th>GWI (mMg)</th>
<th>IVEF mean (standard deviation)</th>
</tr>
</thead>
<tbody>
<tr>
<td>21 (2)</td>
<td>1917 (370)</td>
<td>69 (7)</td>
</tr>
<tr>
<td>−20 (3)</td>
<td>1554 (396)</td>
<td>78 (7)</td>
</tr>
</tbody>
</table>

GLS and GWI were reduced or unchanged in 30 (57%) and 46 (87%) patients, on DSE. There was no association between this lack of augmentation and clinical events.

**Conclusion:** A quarter of patients with advanced cirrhosis had CCM as per the new criteria. Low GLS with preserved IVEF and lack of augmentation of GLS and GWI on DSE suggest that advanced cirrhosis is a negative inotropic state. Ongoing follow-up and repeat studies after LT could explore clinical impact and reversibility of CCM.

### SAT517

**Identification of overt hepatic encephalopathy precipitating factors: a pooled analysis of 3 clinical trials of rifaximin plus lactulose**

Arun Jesudian1, Arun Sanjay2, Robert Brown1, Zeev Heimanson3, Robert Israel1, Jasmohan S Bajaj1, 2, 4

1Weill Cornell Medicine, New York, United States; 2Virginia Commonwealth University, Richmond, United States; 3Salix Pharmaceuticals, Bridgewater, United States; 4McGuire VA Medical Center, Richmond, United States

Email: abj9004@med.cornell.edu

**Background and aims:** Hepatic encephalopathy (HE) is a cirrhosis-related complication and its occurrence has been linked with several precipitating factors (eg, infection). Guidelines recommend rifaximin as add-on therapy to lactulose for reduction in risk of overt HE (OHE) recurrence. The aim was to summarize precipitating factors associated with breakthrough OHE events, during 3 clinical trials, in patients who received rifaximin plus lactulose or lactulose alone.

**Method:** Data were pooled from 3 trials: a 6-month, randomized, double-blind, placebo-controlled trial; a 24-month, open-label maintenance trial; and a 6-month, randomized, open-label trial. Adults with cirrhosis who had a history of OHE and were currently in OHE remission (Conn score <2) and received rifaximin 550 mg twice daily plus lactulose or lactulose alone were included. For each OHE episode, investigators were asked to record any contributing factors or precipitating events if they could be identified. p values were determined using the Fisher’s exact test.

**Results:** 460 patients treated with rifaximin plus lactulose and 145 patients treated with lactulose alone were included. In the rifaximin plus lactulose group, 60.4% were male, the mean (SD) age was 57.1 (9.3); 38.9% were aged less than 55 y. In the lactulose alone group, 68.3% were male, the mean (SD) age was 56.6 (9.3); 37.2% were aged less than 55 y. The most commonly identified precipitating factors were infection, constipation, and dehydration, each observed in a similar percentage of patients in each group (p >0.05; Figure). Precipitating actors were not identified (ie, spontaneous) in a majority of patients in the rifaximin plus lactulose and lactulose alone groups (63.7% vs 82.8%; p <0.0001). Results were generally similar when subgrouped by male/female or by age (less than 55 y; at least 55 y).

**Conclusion:** Guidelines recommend identification and correction of precipitating factors to improve outcomes. In this analysis, the most commonly identified precipitating factors for OHE events in patients with a history of OHE were infection, constipation, and dehydration. A precipitating factor was not identified in a majority of cases; therefore, empiric therapy should be promptly initiated in the clinic, while factors are being identified. Prevention or early identification of OHE precipitating factors is an important part of cirrhosis disease management strategy to reduce the risk of OHE recurrence and related hospitalizations.

### SAT518

**Dementia frequently co-exists with hepatic encephalopathy but not other cirrhosis complications in US veterans with cirrhosis**

Adeyinka Adejumo1, Shari Roga12,3, Patrick Spoutz2, Linda Chia4, Jasmohan S Bajaj1, 2

1University of Pittsburgh, Medicine, Pittsburgh, United States; 2VA Pittsburgh Healthcare System, Center for Health Equity Research and Promotion, Pittsburgh, United States; 3Veterans Integrated Service Network 20, Pharmacy Benefits Management, Vancouver, United States; 4Veterans Integrated Service Network 8, Pharmacy Benefits Management, Bay Pines, United States; 5Virginia Commonwealth University and Richmond V AMC, Division of Gastroenterology, Hepatology, and Nutrition, Department of Medicine, Richmond, United States

Email: adeyinka.adejumo@yahoo.com

**Background and aims:** Dementia and hepatic encephalopathy (HE) can manifest similarly in patients with cirrhosis, though the treatments differ. The purpose of this study was to evaluate the prevalence of and risk factors for dementia among Veterans with cirrhosis.

**Method:** US Veterans with cirrhosis who received VA care between 2019 and 2021 were identified using ICD-10-CM codes. Factors associated with having a diagnosis of dementia were evaluated using multivariate logistic regression models, adjusting for demographic, clinical, and treatment characteristics.
comorbid illnesses, cirrhosis etiology, and cirrhosis complications (all defined by ICD-10-CM codes).

Results: The cohort included 71,552 veterans with cirrhosis, who were mostly men (96.2%) with a median age of 65.7 years (IQR 61–70). Ten percent (n = 7,295) of the overall cohort had a diagnosis of dementia overall, which increased to 12.4% among patients ≥65 years. Dementia was significantly associated with age (adjusted odds ratio and 95% confidence interval, AOR per 10 years: 1.64 [1.58–1.71]), white race (1.09 [1.01, 1.16]), urban residence (1.19 [1.11, 1.27]), alcohol-related cirrhosis (1.30 [1.18–1.44]), hepatitis B (1.39 [1.18–1.62]), alcohol use disorder (1.42 [1.29–1.61]), cerebral vascular disease, peripheral vascular disease, diabetes, chronic kidney disease, and chronic heart failure, and negatively associated with MELD-Na (0.95 [0.92–0.95] /5 points) in multivariate logistic regression (Figures 1A and 1B). Dementia was significantly positively associated with HE (2.87 [2.68–3.08]), but negatively associated with other cirrhosis complications in these models.

Conclusion: Diagnostic codes for dementia were found in 10% of Veterans with cirrhosis and most strongly associated with HE, but not other complications of cirrhosis. Furthermore, alcohol use disorder along with cardiovascular risk factors were associated with dementia, but not NASH itself. Further research is needed to determine strategies to differentiate between HE and dementia and manage this population with specific needs to prevent burden on families, patients and VHA system.

SAT59
Bacterial infections as a predisposing factor for the development of portal vein thrombosis in cirrhotic patients: a prospective study
Leonardo De Marco1, Filippo Cattazzo1, Michele Bevilacqua1, Anna Mantovani1, Andrea Dalbeni2, David Sacerdoti1.
1. Azienda Ospedaliera Universitaria Integrata Verona, Medicina interna C Liver Unit, Verona, Italy
Email: leonardo.demarco93@gmail.com

Background and aims: Non-malignant portal vein thrombosis (PVT) is one of the complications of liver cirrhosis. The predisposing factors for PVT in cirrhotic patients are not entirely clear. The aim of this study was to identify possible clinical risk factors related to the development of PVT in patients with liver cirrhosis.

Method: We prospectively collected data of 229 consecutive cirrhotic patients followed in our Liver Unit in Verona, enrolled from 2017 to 2020 with an median follow-up of 3.3 years. PVT was determined by ultrasound, computer tomography and/or magnetic resonance imaging. Malignant PVT was considered an exclusion criteria.

Results: Of the 229 patients with liver cirrhosis 26 (11%) developed non-malignant PVT. 17 (65%) were male, with a mean age of 67.3 ± 12.3 y. In patients with non-neoplastic PVT compared to the remaining population, we observed that the prevalence of bacterial infections (sepsis, pneumonia, urinary tract infections, cholangitis, gastroenteritis, bacteriemia, spontaneous bacterial peritonitis) that required hospitalization was significantly higher (50% vs 27.2%; p = 0.017). In the multivariate logistic regression analysis, when adjusted for age, sex, type 2 diabetes mellitus and chronic kidney disease, PVT was significantly and independently associated with bacterial infections (OR 2.72 [95% CI 1.12 to 6.57; p = 0.026]) and hepatocellular carcinoma (HCC) (OR 2.87 [95% CI 1.11 to 7.41; p = 0.029).

Conclusion: Our study showed that bacterial infections requiring hospitalization in patients with liver cirrhosis could be a predisposing factor for the development of PVT. Further studies will be needed to confirm this evidence.

SAT520
Impact of the COVID-19 pandemic on the incidence and type of infections in hospitalized patients with cirrhosis
Berta Cuyas1, Anna Huerta1, Maria Poca1,2, Edilmar Alvarado-Tapias1,3, Anna Brujats1, Eva Roman1,2,3, Carlos Guarnier1,2, Ángels Escorell1,2, German Soriano1,3, 1Hospital de la Santa Creu i Sant Pau, UAB, Gastroenterology, Barcelona, Spain; 2Centro de Investigación Biomédica en Red de Enfermedades Hepáticas y Digestivas (CIBEREHD), Spain; 3School of Nursing EUI-Sant Pau, Spain
Email: gsoriano@santpau.cat

Background and aims: Infections are a major cause of morbidity and mortality in patients with cirrhosis, especially those caused by multiresistant bacteria. Restrictive measures implemented due to the COVID-19 pandemic have changed hospital protocols: social distancing, hand washing, personal protective equipments. This situation may have changed the incidence and types of infections in patients with cirrhosis during the pandemic. We aimed to compare the infections in patients with cirrhosis hospitalized before the COVID-19 pandemic versus those hospitalized during the pandemic.

Method: We retrospectively analysed the infections in patients with cirrhosis hospitalized in the Gastroenterology department at a high complexity hospital, during the pre-pandemic period (3/2019–2/2020) and during the pandemic (3/2020–2/2021). Baseline characteristics, type of infections, type of bacteria, multiresistance and mortality were evaluated.

Results: A total of 421 episodes of hospitalization were analysed: 252 pre-pandemic and 169 during the pandemic (mean number of hospitalizations/month 210.5 ± 5.2 vs 141.1 ± 3.8, p = 0.001). Patients' baseline MELD was lower in the pre-pandemic group (9 ± 3.7 vs 12 ± 5, p < 0.001). A total of 223 infections were detected in 42% of hospitalizations (40.9% vs 43.8%, p = 0.55), and the percentage of nosocomial infections was 43.4% vs 42.6% (p = 0.89). Spontaneous bacterial peritonitis and respiratory infections were less frequent during the pandemic (24.8% of total infections in the pre-pandemic period vs 13.8% during the pandemic, and 22.5% vs 17%, respectively) and urinary tract infections were more frequent (22.5% vs 33%) (pNS). Culture positivity rate was similar (55% vs 60.6%, p = 0.40), and gram-negative bacteria were the most frequent bacteria isolated in both groups. We found a non-significant trend to a lower rate of multiresistant bacteria in the pandemic group (25.4% vs 19.3%, p = 0.41). ACLF incidence was 18.4% vs 12.9% (p = 0.27), and 30-day mortality was 14% vs 11.7% (p = 0.62).

Conclusion: There were less hospitalizations of patients with cirrhosis in the Gastroenterology department during the COVID-19 pandemic but they had worse baseline liver function. The incidence of infections and the rate of nosocomial infections were similar despite the restrictive measures. A non-significant trend to a lower rate of multiresistant bacteria and spontaneous bacterial peritonitis, and higher percentage of urinary infections were observed during the pandemic.
Increased expression of podoplanin, a marker of dilated lymphatic vessels in duodenal biopsies is an independent predictor of three-month mortality in patients with cirrhosis

Savneet Kaur1, Pinky Juneja1, S Muralikrishna Shastry2, Guresh Kumar2, Dinesh Mani Tripathi1, Vijayraghavan Rajan2, Archana Rastogi3, Shiv Kumar Sarin3, 1Institute of Liver and Biliary Sciences, New Delhi, India; 2Institute of Liver and Biliary Sciences, Molecular and Cellular Medicine, New Delhi, India; 3Institute of Liver and Biliary Sciences, Department of Hepatology, New Delhi, India

Email: shivsarin@gmail.com

Background and aims: The intestinal lymphatic capillaries (lacteals) and the mesenteric collecting vessels regulate gut immunity and fluid homeostasis. In cirrhosis, a dysfunction of the gut lymphatic vessels has been reported. We studied markers of lymphatic vessels in duodenal biopsies and investigated the performance of a highly expressed marker of lymphatic endothelial cells, podoplanin (pdpn), as a predictor of clinical outcomes in cirrhosis.

Method: A prospective, observational, single-centre cohort study was performed in consenting patients with cirrhosis of varying aetiology (n = 31) and matched healthy controls (n = 10). All subjects underwent an upper gastrointestinal tract endoscopy, during which duodenal biopsies were obtained. Gene expression of lymphatic channel markers, such as vascular endothelial growth factor 3 (vegfr3); pdpn and lymphatic vessel endothelial hyaluronan receptor 1 (lyv1) were studied in biopsies. Pdpn protein scores were calculated by the number and intensity of pdpn stained lymphatic channels/high power field. Gut inflammation was scored by counting the number of CD3-positive intraepithelial lymphocytes (IELs) in the biopsies and serum levels of TNF-alpha and IL-6 were studied by ELISA.

Results: Gene expression of lymphatic channel markers, vegfr3 and pdpn were enhanced in duodenal biopsies of cirrhosis patients compared to controls. Mean pdpn scores in patients with uncompensated cirrhosis (6.91 ± 1.26) were significantly higher than compensated cirrhosis (3.25 ± 1.60, P < 0.0001). Control biopsies showed a weak and minimal pdpn positivity. Pdpn scores were significantly correlated with serum albumin (r = −0.62, P < 0.0001), bilirubin (r = 0.69, P < 0.0001) and creatinine (r = 0.48, P = 0.005). In Cox regression analysis, pdpn score emerged as a significant and independent 3-month mortality predictor (HR: 5.61; 1.08–29.109; p = 0.04). Area under the curve for pdpn was 84.2 (70.6–97.8) and the cut-off value of pdpn score for predicting significant mortality was above 6.5 with a sensitivity of 100% and specificity of 75%. Although the number of IELs and TNF-alpha levels were not significantly different in patients with compensated and decompensated cirrhosis; IELs, serum TNF-alpha and IL-6 levels positively correlated with pdpn scores (p < 0.05 each). Pdpn score was also inversely associated with expression of gut permeability marker, zona occludin-1 (r = −0.46, p = 0.05).

Conclusion: An increased number of dilated lymphatic vessels characterized by high pdpn expression, in the duodenal biopsies are a characteristic feature of patients with decompensated cirrhosis and serve as an independent predictor of 3-month mortality. An increased gut permeability and inflammation in cirrhotic patients with dilated duodenal lymphatic channels might be contributing to enhanced systemic inflammatory responses and mortality.

Blood metabolomics unveils mitochondrial dysfunction as a potential key feature in the pathogenesis of hepatorenal syndrome

Ann T Ma1,2,3, Adria Juanola1,2, Martina Perez-Guasch1,2,3,4, Marta Carol1,2,3,4, Jordi Gratacós-Gines1,2,3, Laura Napoleon1,2,3, Ana Belén Rubio1,2, Emma Avitabile1,2,3, Anna Soria1,2,3, Marta Cervera2,3, Octavi Bassegoda1,2,3, Carlota Riba2,3, Núria Fabrellas1,2,3,4, Isabel Graupera2,3, Juango Lozano3, Elisa Pose1,2,3, Manuel Morales-Ruiz3,2,4, Elsa Solá1,2,3, Pere Ginés1,2,3,4 (Liver Unit, Hospital Clinic de Barcelona, Barcelona, Spain; 2Institut d’Investigacions Biomèdiques August Pi i Sunyer (IDIBAPS), Barcelona, Spain; 3Centro de Investigación Biomédica en Red de Enfermedades Hepática y Digestivas, Madrid, Spain; 4Facultat de Medicina-Universitat de Barcelona, Barcelona, Spain; 4Servei de Bioquímica i Genètica Molecular, Hospital Clinic de Barcelona, Barcelona, Spain)

Email: pgines@clinic.cat

Background and aims: Important hemodynamic changes occur in hepatorenal syndrome (HRS), including splanchnic vasodilation, decreased cardiac output, and resulting decreased renal perfusion. However, the exact metabolic pathways involved in HRS are unknown. Recently, studies using blood metabolomics have found distinct metabolic alterations in cirrhosis, but no specific studies on HRS have been reported. The aim of this study was to use blood metabolomics to unveil metabolic pathways involved in HRS, as well as identify potential biomarkers for diagnosis of HRS and prediction of treatment response.

Method: Untargeted metabolomics by liquid chromatography coupled to high-resolution mass spectrometry was performed in serum samples of patients with cirrhosis in different disease phases: severe HRS, meeting the definition of type 1 HRS (n = 28), acute tubular necrosis (ATN, n = 16) and acute decompensation of cirrhosis without acute kidney injury (AKI) (AD, n = 16). Of the patients with HRS, blood samples were collected prior to treatment with terlipressin and albumin, and 7–14 days post-treatment (available for 22/28; 17 treatment responders).

Results: Patients were predominantly male (90%), with a median age of 61. Principal component analysis revealed clear differences between AD and the other states (Figure). HRS was characterized by a significant upregulation of pentose and glucuronate interconversions pathways and by an accumulation of fatty acylcarnitines, both of which then decreased towards levels in AD after response to treatment. These findings are consistent with previous data in ACLF, and suggest the presence of mitochondrial dysfunction in HRS. Next, a regression analysis revealed that the combination of 3 metabolites could accurately differentiate HRS from ATN (AUROC of 0.94 (0.88–1.00)). Finally, we found that the combination of 2 metabolites predicted treatment response in HRS (AUROC 0.96 (0.89–1.00)).
**SATS23**

**Hyperammonaemia is an independent biomarker of liver-related complications and mortality in clinically stable outpatients with cirrhosis**

Tom H Tranah\(^1\), María Pilar Ballester\(^2\), Juan Antonio Carbonell-Asins\(^3\), Annarein Kerbert\(^4\), Gonçalo Alexandrino\(^5\), Maria Capilla\(^2\), Andra Caracostea\(^1\), Desamparados Escudero-García\(^2\), Karen Louise Thomsen\(^6\), Miguel Serra\(^2\), Debbie L. Shawcross\(^1\), Miguel Capilla\(^2\), Rajiv Jalan\(^4\), 1Institute of Liver Studies, Dept of Inflammation Biology, School of Immunology and Microbial Sciences, Faculty of Life Sciences and Medicine, King’s College London, London, United Kingdom; 2Hospital Clínico Universitario de Valencia, Digestive Disease Department, Valencia, Spain; 3UNIVERSIA Biomedical Research Institute, Valencia, Spain; 4Institute for Liver and Disease Health, University College London, Royal Free Campus, Liver Failure Group, London, United Kingdom; 5Hospital Prof. Doutor Fernando Fonseca, Amadora, Gastroenterology and Hepatology Department, Portugal; 6Aarhus University Hospital, Department of Hepatology and Gastroenterology, Denmark

**Background and aims:** Ammonia is important in the pathogenesis of hepatic encephalopathy (HE). Ammonia has also been implicated in the pathogenesis of liver-related complications such as liver cell death, sarcopenia, immune dysfunction and portal hypertension. We therefore, hypothesized that hyperammonaemia is a risk factor for the development of not only HE but also other liver-related complications and consequent mortality in clinically-stable outpatients with cirrhosis. We aimed to determine the role of ammonia in the risk of liver-related complications and/or mortality and derive a threshold value of ammonia that defines the risk. We also developed a prognostic model defining outcomes.

**Method:** A prospective observational cohort study of clinically stable cirrhotic outpatients followed-up in three tertiary hospitals was performed. Main outcomes were occurrence of liver-related complications and mortality. As normal ammonia varied across centres, it was normalized according to the upper limit of normality (A_ULN). Multivariable frailty competing risk modelling was performed with either liver-related complications or mortality as events of interest with liver transplantation as a competing risk. AUROC was calculated to compare prediction performance between A-ULN and severity scores at 1-year. Cut-off for A-ULN was calculated using maximally selected rank statistics. Fast unified random forests for survival with 500 trees using log-rank as splitting criteria was used to predict complications and mortality.

**Results:** 754 patients were included (66% males; mean 56 years) with median follow-up of 223 days (range: 2–2453). A total of 260 (35%) patients developed liver-related complications, infection being the most prevalent (16%). A_ULN was an independent predictor of both complications (HR = 2.27; 95CI = 1.97–2.61; p < 0.001) and mortality (HR = 1.59; 95CI = 1.33–1.89; p < 0.001). AUROC of A_ULN was 77.9% for 1-year complications; higher than traditional severity scores. Statistical differences in survival were found between high and low levels of A_ULN both for complications and mortality (p < 0.001) using 1.4 as cut-off from the training set. A_ULN remained the most important variable for the prediction of complications (Figure 1).

**Conclusion:** Ammonia is an independent predictor of liver-related complications and mortality in clinically stable outpatients with cirrhosis and performs better than traditional severity scores in predicting complications.

---

**SATS24**

**Prospective evaluation of the EASL clinical guidelines algorithm of management of acute kidney injury in cirrhosis**

Anna T Ma\(^1,2,3\), Cristina Solé\(^1,2,3\), Laia Escude\(^1\), Adria Juanola\(^1,2,3\), Laura Napoleone\(^1,2,3\), Emma Avitabile\(^1,2,3\), Martina Perez\(^1,2,3\), Marta Carol\(^1,2,3,4\), Ana Belén Rubio\(^1,2,3\), Marta Cervera\(^1,2,3\), Octavi Bassegoda\(^1,2,3,4\), Jordi Gratacós\(^1,2,3,4\), Anna Soria\(^1,2,3\), Nuria Fabrellas\(^1,2,3,4\), Isabel Grauera\(^1,2,3\), Elisa Posa\(^1,2,3,4\), Manuel Morales-Ruiz\(^1,2,3,4\), Esteban Poch\(^1,2,3,4\), Elsa Solà\(^1,2,3\), Pere Giné\(^1,2,3,4\), 1Liver Unit, Hospital Clinic de Barcelona, Barcelona, Spain; 2Institut d’Investigacions Biomèdiques August Pi i Sunyer (IDIBAPS), Barcelona, Spain; 3Centre de Investigación Biomèdica en Red de Enfermedades Hepática y Digestivas (CIBERHED), Madrid, Spain; 4Facultat de Medicina-Universitat de Barcelona, Barcelona, Spain; 5Biochemistry and Molecular Genetics Department, Hospital Clinic de Barcelona, Barcelona, Spain; 6Nephrollogy and Kidney Transplantation Department, Hospital Clinic de Barcelona, Barcelona, Spain

**Background and aims:** The EASL guidelines propose an algorithm for managing acute kidney injury (AKI) in cirrhosis. The effectiveness in clinical practice of this algorithm, based on expert opinion, has not been assessed. This study aimed to characterize the clinical outcomes of patients with AKI managed according to this algorithm.

**Method:** Single center prospective cohort study including consecutive patients admitted for acute decompensation of cirrhosis and AKI from 2019 to 2021. The management of patients followed the recommended EASL AKI algorithm, which includes categorization of patients according to AKI stage (1A or >1A) and albumin administration in the first 48 h for those with a stage >1A. Three crucial groups of patients were identified: 1/AKI 1A responders; 2/AKI>1A responders after albumin therapy; and 3/AKI>1A non-
responders after albumin therapy meeting AKI-HRS criteria. Response rates, defined as resolution of AKI in group 1, resolution or improvement to stage 1A in group 2, and resolution or improvement to a lower AKI stage in group 3, were calculated for each group. Three-month overall survival was also analyzed.

**Results:** A total of 203 AKI episodes in 138 patients were evaluated (median age 62, 76% male, 67% alcohol-related liver disease, Child-Pugh C 52%). Most patients with AKI-1A had resolution or persistent AKI-1A by day 3 (43% and 26% respectively), while only 31% progressed (Figure). Out of the 173 episodes with AKI>1A, 61 (35%) had resolution or improvement with albumin by day 3. Remarkably, most patients with persistent AKI-1A after albumin administration who met HRS-AKI criteria responded to vasoconstrictors (terlipressin) and albumin (73%). Three-month survival rate of patients in the 3 crucial groups were: 88%, 82%, and 50%, respectively. Non-responders to vasoconstrictor therapy had significantly lower 3-month survival compared to responders (17% vs 65% respectively).

### MELD 3.0

MELD 3.0 accurately predicts short term survival of patients with end-stage liver disease

Anna Vidovszky1, W. Ray Kim1, Allison Kwong1, Ajitha Mannalithara1.

1Stanford University, Division of Digestive Health, Redwood City, United States

Email: wrkim@stanford.edu

**Background and aims:** MELD 3.0 is the latest version of the Model for End-stage Liver Disease (MELD) which includes sex and albumin as new variables and updates all of its coefficients. We evaluated calibration of survival prediction of MELD 3.0.

**Method:** MELD 3.0 was developed based on data from liver transplant waitlist registrants in the US from Jan, 2016 and Dec, 2018. The entire cohort was randomly divided into model training and testing data sets. From the final Cox model for MELD 3.0 derived in the training set, we calculated survival function in mortality prediction. The model was then applied in the testing set to compare the predicted versus observed survival for the score quintiles.

**Results:** Out of the entire cohort (n = 29,410), a random 30% (n = 8,823) was set aside as the testing set. As reported previously, MELD 3.0 is calculated by the following formula: MELD 3.0 = 1.33 (if female) + 4.56 * loge (bilirubin) + 0.82 * (137-Na)-0.24 * (137-Na) - loge (creatinine)+9.09 * loge (INR)+11.14 * loge (creatinine) + 1.85 * (3.5-albumin)-1.83 * (3.5-albumin) * loge (creatinine) + 6 (online calculator available at medcalculators.stanford.edu/meld). Survival function for up to 90 days is shown below. The predicted and observed survival up to 30 days of the quintiles based on MELD 3.0 matched closely with no statistically significant difference between the two (GND test, p = 0.11), whereas the comparison based on MELD-Na was significantly different (p = 0.01). Calibration was less robust for 90-day predictions with both scores, with majority of the discrepancy being survival between 30 and 90 days for the highest risk patients (p < 0.01 for both MELD 3.0 and MELD-Na).

<table>
<thead>
<tr>
<th>I (days)</th>
<th>15</th>
<th>30</th>
<th>45</th>
<th>60</th>
<th>75</th>
<th>90</th>
</tr>
</thead>
<tbody>
<tr>
<td>So (t)</td>
<td>0.991</td>
<td>0.981</td>
<td>0.971</td>
<td>0.963</td>
<td>0.955</td>
<td>0.946</td>
</tr>
</tbody>
</table>

**Conclusion:** While MELD 3.0 is being considered to replace MELD-Na for organ allocation priorities in the US, it provides better calibration of short-term survival than MELD-Na as well, which would be useful for patient management plan and counseling.

SAT526

**CyberLiver Animal Recognition Test (CL-ART): a novel remote monitoring tool to assess minimal hepatic encephalopathy**

Kohilan Gananandan1, María Pilar Ballester2, Ahmed El Shabrawi1,3, Konstantin Kazankov4, Rajiv Jalan1, Ravan Boddu5, Ravi Kumar5, Maruthi Raja5, Anu Balaji5, Karen Louise Thomsen4, Raj Mookerjee4.

1The Liver Failure Group, UCL Institute for Liver and Digestive Health, United Kingdom; 2Hospital Clinic Universitari, Digestive Disease Department, Valencia, Spain; 3Endemic Hepatology and Gastroenterology, Egypt; 4Aarhus University Hospital, Department of Hepatology and Gastroenterology, Aarhus, Denmark; 5CyberLiver Limited, United Kingdom

Email: mapibafe@gmail.com

**Background and aims:** The CyberLiver Animal Recognition Test (CL-ART) is a novel smartphone application (app) that was developed as part of a program for remote monitoring of cirrhosis, and specifically, to diagnose non-overt hepatic encephalopathy and to guide need for intervention. The aim of this study was to compare CL-ART with established tests for minimal hepatic encephalopathy (MHE), as well as to assess its diagnostic performance, and establish an optimal cut-off for MHE.

**Method:** A prospective study of cirrhosis patients and healthy controls, applying clinical assessment and three different cognitive tests at a tertiary hepatology centre. The CL-ART test involved a timed recognition and appropriate naming of animals using a smartphone app; with time to perform test and failed attempts logged. EncephalApp Stroop Test and Psychometric Hepatic Encephalopathy Score (PHES) (used as the reference to diagnose MHE) were chosen as test comparisons. Pearson rank correlation and
Background and aims: Acute kidney injury during hospitalization in patients with liver cirrhosis is associated with increased mortality and chronic kidney disease on follow-up

Anna Cederborg1,2, Björn Lindkvist1,2, Evangelos Kalaitzakis3, Éinar S. Björnsson4,5, Hanns-Ulrich Marschall1,2.

1Institute of Medicine, Sahlgrenska Academy, University of Gothenburg, Gothenburg, Sweden; 2Department of Medicine, Sahlgrenska University Hospital, Gothenburg, Sweden; 3University of Crete, Department of Gastroenterology, University Hospital of Heraklion, Heraklion, Greece; 4Department of Internal Medicine, Landspitali University Hospital, Reykjavik, Iceland; 5Faculty of Medicine, University of Iceland, Reykjavik, Iceland

Email: anna.cederborg@vgregion.se

Background and aims: Acute kidney failure (AKI) in patients with advanced liver cirrhosis is associated with a poor prognosis. The aim of the study was to evaluate the impact of AKI, AKI progression, infections and acute on chronic liver failure (ACLF) grade 1 and 2 on the development of chronic kidney disease (CKD) and survival.

Method: A total of 313 patients admitted for complications as positive cultures or radiological findings, and CKD according to an estimated glomerular filtration rate (eGFR) < 60 ml/min/1.73 m². Results: AKI was present at admission in 27% of patients of whom 72% progressed in AKI stage during hospitalization, with a 3-month survival of 39% versus 78% (p < 0.001) in the patients without AKI. ACLF grade 1 or 2 was present in 24% of patients with a 3-month survival of 31% versus 78% among patients without ACLF (p < 0.001). Infections developed in 30% of patients during admission. Patients with prior decompensation (45%) had a lower 3-month survival if infected (50%) than compensated patients with infection (73%) and decompensated patients without infection (69%) (p < 0.001). Progression of AKI during admission was associated with a hazard ratio for mortality of 2.3 (1.6–3.2), even when adjusting for the presence of ACLF grad 1 or 2 and presence of infection, with a 3-month survival of 32%. Most patients with AKI who survived the first hospitalization presented with CKD at the following admission (82%) with a median follow-up of 2.2 (range 0.3–55.8) months.

Conclusion: Chronic kidney disease was common in patients with liver cirrhosis who survived AKI during the first hospitalization. Even though the presence of infection and ACLF grade 1 or 2 during admission were associated with a worse prognosis, the progression of AKI additionally increased the risk of mortality in patients with liver cirrhosis.

SAT527

Acute kidney injury during hospitalization in patients with liver cirrhosis is associated with increased mortality and chronic kidney disease on follow-up

Anna Cederborg1,2, Björn Lindkvist1,2, Evangelos Kalaitzakis3, Éinar S. Björnsson4,5, Hanns-Ulrich Marschall1,2.

1Institute of Medicine, Sahlgrenska Academy, University of Gothenburg, Gothenburg, Sweden; 2Department of Medicine, Sahlgrenska University Hospital, Gothenburg, Sweden; 3University of Crete, Department of Gastroenterology, University Hospital of Heraklion, Heraklion, Greece; 4Department of Internal Medicine, Landspitali University Hospital, Reykjavik, Iceland; 5Faculty of Medicine, University of Iceland, Reykjavik, Iceland

Email: anna.cederborg@vgregion.se

Background and aims: Acute kidney failure (AKI) in patients with advanced liver cirrhosis is associated with a poor prognosis. The aim of the study was to evaluate the impact of AKI, AKI progression, infections and acute on chronic liver failure (ACLF) grade 1 and 2 on the development of chronic kidney disease (CKD) and survival.

Method: A total of 313 patients admitted for complications as positive cultures or radiological findings, and CKD according to an estimated glomerular filtration rate (eGFR) < 60 ml/min/1.73 m². Results: AKI was present at admission in 27% of patients of whom 72% progressed in AKI stage during hospitalization, with a 3-month survival of 39% versus 78% (p < 0.001) in the patients without AKI. ACLF grade 1 or 2 was present in 24% of patients with a 3-month survival of 31% versus 78% among patients without ACLF (p < 0.001). Infections developed in 30% of patients during admission. Patients with prior decompensation (45%) had a lower 3-month survival if infected (50%) than compensated patients with infection (73%) and decompensated patients without infection (69%) (p < 0.001). Progression of AKI during admission was associated with a hazard ratio for mortality of 2.3 (1.6–3.2), even when adjusting for the presence of ACLF grad 1 or 2 and presence of infection, with a 3-month survival of 32%. Most patients with AKI who survived the first hospitalization presented with CKD at the following admission (82%) with a median follow-up of 2.2 (range 0.3–55.8) months.

Conclusion: Chronic kidney disease was common in patients with liver cirrhosis who survived AKI during the first hospitalization. Even though the presence of infection and ACLF grade 1 or 2 during admission were associated with a worse prognosis, the progression of AKI additionally increased the risk of mortality in patients with liver cirrhosis.

SAT528

Ascites bacterial DNA and IL-6 are promising tools in the diagnosis of spontaneous bacterial peritonitis

Arno Hagueneneger1, Niklas F Aehling2, Adam Herber1, Rhea Veelken1, Sandra Krohn1, Katharina Zeller1, Kathrin Jaeger1, Daniel Seehofer3, Sebastian Rademacher4, Robert Sucher1, Cornelius Engelmann1,5, Thomas Berg1,1 Leipzig University Medical Center, Division of Hepatology Department of Medicine II, Leipzig, Germany; 2Leipzig University Medical Center, IZKF FACS Core Unit, Leipzig, Germany; 3Department of Visceral, Vascular, Thoracic and Transplant Surgery, Leipzig, Germany; 4Campus Virchow-Klinikum, Charité-Universitätsmedizin Berlin, Department of Hepatology and Gastroenterology, Berlin, Germany

Email: niklas.aehling@medizin.uni-leipzig.de

Background and aims: Spontaneous bacterial peritonitis (SBP) is a common complication in patients with decompensated cirrhosis or acute on chronic liver failure. Diagnosis is based on an ascitic neutrophil count (PMN) of ≥250/µl. Its sensitivity is limited. We investigated, whether determination of bacterial DNA (bactDNA) or...
The diagnosis of SBP. BactDNA and ascitic IL-6 showed a positive correlation with a high likelihood ratio (Bayes factor [BFM], 2505), while procalcitonin showed poor discrimination with a low likelihood ratio (BFLO, 0.45). In ROC analysis, ascitic MR-pro-ADM had an optimal cut-off of ≥2.50 nmol/L to diagnose SBP (AUCROC, 0.746; 95% CI, 0.685–0.801; p <0.0001) (A). Multivariable logistic regression analysis identified three independent predictors of SBP that were included in the "SBP score": MR-pro-ADM ≥2.50 nmol/L (odds ratio [OR], 7.25; 95% CI, 2.04–25.79; p = 0.002), absolute polymorphonuclear leucocyte (PMN) count ≥250 cells/mm3 (OR, 14.38; 95% CI, 3.17–62.80; p = 0.002), and Child-Pugh score (OR, 1.91 nmol/L [IQR, 1.33–1.91]; p = 0.002). In Bayesian ANOVA, MR-pro-ADM was highly discriminant for SBP diagnosis with a high likelihood ratio (Bayes factor [BFM], 2505), while procalcitonin showed poor discrimination with a low likelihood ratio (BFLO, 0.45). In ROC analysis, ascitic MR-pro-ADM had an optimal cut-off of ≥2.50 nmol/L to diagnose SBP (AUCROC, 0.746; 95% CI, 0.685–0.801; p <0.0001) (A). Multivariable logistic regression analysis identified three independent predictors of SBP that were included in the "SBP score": MR-pro-ADM ≥2.50 nmol/L (odds ratio [OR], 7.25; 95% CI, 2.04–25.79; p = 0.002), absolute polymorphonuclear leucocyte (PMN) count ≥250 cells/mm3 (OR, 14.38; 95% CI, 3.17–62.80; p = 0.002), and Child-Pugh score (OR, 1.91 nmol/L [IQR, 1.33–1.91]; p = 0.002). In Bayesian ANOVA, MR-pro-ADM was highly discriminant for SBP diagnosis with a high likelihood ratio (Bayes factor [BFM], 2505), while procalcitonin showed poor discrimination with a low likelihood ratio (BFLO, 0.45). In ROC analysis, ascitic MR-pro-ADM had an optimal cut-off of ≥2.50 nmol/L to diagnose SBP (AUCROC, 0.746; 95% CI, 0.685–0.801; p <0.0001) (A). Multivariable logistic regression analysis identified three independent predictors of SBP that were included in the "SBP score": MR-pro-ADM ≥2.50 nmol/L (odds ratio [OR], 7.25; 95% CI, 2.04–25.79; p = 0.002), absolute polymorphonuclear leucocyte (PMN) count ≥250 cells/mm3 (OR, 14.38; 95% CI, 3.17–62.80; p = 0.002), and Child-Pugh score (OR, 1.91 nmol/L [IQR, 1.33–1.91]; p = 0.002). In Bayesian ANOVA, MR-pro-ADM was highly discriminant for SBP diagnosis with a high likelihood ratio (Bayes factor [BFM], 2505), while procalcitonin showed poor discrimination with a low likelihood ratio (BFLO, 0.45). In ROC analysis, ascitic MR-pro-ADM had an optimal cut-off of ≥2.50 nmol/L to diagnose SBP (AUCROC, 0.746; 95% CI, 0.685–0.801; p <0.0001) (A). Multivariable logistic regression analysis identified three independent predictors of SBP that were included in the "SBP score": MR-pro-ADM ≥2.50 nmol/L (odds ratio [OR], 7.25; 95% CI, 2.04–25.79; p = 0.002), absolute polymorphonuclear leucocyte (PMN) count ≥250 cells/mm3 (OR, 14.38; 95% CI, 3.17–62.80; p = 0.002), and Child-Pugh score (OR, 1.91 nmol/L [IQR, 1.33–1.91]; p = 0.002). In Bayesian ANOVA, MR-pro-ADM was highly discriminant for SBP diagnosis with a high likelihood ratio (Bayes factor [BFM], 2505), while procalcitonin showed poor discrimination with a low likelihood ratio (BFLO, 0.45). In ROC analysis, ascitic MR-pro-ADM had an optimal cut-off of ≥2.50 nmol/L to diagnose SBP (AUCROC, 0.746; 95% CI, 0.685–0.801; p <0.0001) (A). Multivariable logistic regression analysis identified three independent predictors of SBP that were included in the "SBP score": MR-pro-ADM ≥2.50 nmol/L (odds ratio [OR], 7.25; 95% CI, 2.04–25.79; p = 0.002), absolute polymorphonuclear leucocyte (PMN) count ≥250 cells/mm3 (OR, 14.38; 95% CI, 3.17–62.80; p = 0.002), and Child-Pugh score (OR, 1.91 nmol/L [IQR, 1.33–1.91]; p = 0.002). In Bayesian ANOVA, MR-pro-ADM was highly discriminant for SBP diagnosis with a high likelihood ratio (Bayes factor [BFM], 2505), while procalcitonin showed poor discrimination with a low likelihood ratio (BFLO, 0.45). In ROC analysis, ascitic MR-pro-ADM had an optimal cut-off of ≥2.50 nmol/L to diagnose SBP (AUCROC, 0.746; 95% CI, 0.685–0.801; p <0.0001) (A). Multivariable logistic regression analysis identified three independent predictors of SBP that were included in the "SBP score": MR-pro-ADM ≥2.50 nmol/L (odds ratio [OR], 7.25; 95% CI, 2.04–25.79; p = 0.002), absolute polymorphonuclear leucocyte (PMN) count ≥250 cells/mm3 (OR, 14.38; 95% CI, 3.17–62.80; p = 0.002), and Child-Pugh score (OR, 1.91 nmol/L [IQR, 1.33–1.91]; p = 0.002). In Bayesian ANOVA, MR-pro-ADM was highly discriminant for SBP diagnosis with a high likelihood ratio (Bayes factor [BFM], 2505), while procalcitonin showed poor discrimination with a low likelihood ratio (BFLO, 0.45). In ROC analysis, ascitic MR-pro-ADM had an optimal cut-off of ≥2.50 nmol/L to diagnose SBP (AUCROC, 0.746; 95% CI, 0.685–0.801; p <0.0001) (A). Multivariable logistic regression analysis identified three independent predictors of SBP that were included in the "SBP score": MR-pro-ADM ≥2.50 nmol/L (odds ratio [OR], 7.25; 95% CI, 2.04–25.79; p = 0.002), absolute polymorphonuclear leucocyte (PMN) count ≥250 cells/mm3 (OR, 14.38; 95% CI, 3.17–62.80; p = 0.002), and Child-Pugh score (OR, 1.91 nmol/L [IQR, 1.33–1.91]; p = 0.002). In Bayesian ANOVA, MR-pro-ADM was highly discriminant for SBP diagnosis with a high likelihood ratio (Bayes factor [BFM], 2505), while procalcitonin showed poor discrimination with a low likelihood ratio (BFLO, 0.45). In ROC analysis, ascitic MR-pro-ADM had an optimal cut-off of ≥2.50 nmol/L to diagnose SBP (AUCROC, 0.746; 95% CI, 0.685–0.801; p <0.0001) (A). Multivariable logistic regression analysis identified three independent predictors of SBP that were included in the "SBP score": MR-pro-ADM ≥2.50 nmol/L (odds ratio [OR], 7.25; 95% CI, 2.04–25.79; p = 0.002), absolute polymorphonuclear leucocyte (PMN) count ≥250 cells/mm3 (OR, 14.38; 95% CI, 3.17–62.80; p = 0.002), and Child-Pugh score (OR, 1.91 nmol/L [IQR, 1.33–1.91]; p = 0.002). The "SBP score" had an AUROC of 0.993 (95% CI, 0.929–1.000; p <0.0001) for diagnosing SBP (B, C). The SBP score was significantly higher among patients with SBP (23; IQR, 22.5–24.5) when compared to those with SBP after antibiotic initiation (15.5; IQR, 13.5–16.0), multifocal hepatocellular carcinoma and/or portal vein thrombosis (13.5; IQR, 13.25–14.75), or those without SBP (8 [IQR, 8–10]) (p <0.0001) (D).
Conclusion: We derived and validated the "SBP score" based on a rapid-assay sepsis-related biomarker (MR-pro-ADM) that significantly improved the diagnostic accuracy of SBP in cirrhotic patients. The usefulness of the "SBP score" deserves formal validation in large prospective studies.

SAT530
Non-invasive prediction of risk of liver-related events in non-alcoholic fatty liver disease patients
Monica Pons1, Jesús Rivera1, Grace Lai-Hung Wong2, Terry Cheuk-Fung Yip3, Adele Delamarre3, Tracy Davyduke4, M Mang4, Salvador Augustin1, Juan Manuel Pericàs1, 5, Victor de Lédinghen3, Vincent Wai-Sun Wong2, Juan G Abraldes4, Joan Genesca1, 5, 1Hospital Universitari Vall d’Hebron, Vall d’Hebron Institut de Recerca (VHIR), Vall d’Hebron Barcelona Hospital Campus, Universitat Autònoma de Barcelona, Liver Unit. Department of Internal Medicine, Barcelona, Spain; 2The Chinese University of Hong Kong, Department of Medicine and Therapeutics, Hong Kong; 3Hôpital Haut-Lévêque, Bordeaux University Hospital, Centre d’Investigation de la Fibrose Hépatique, INSERM U1312, Pessac, France; 4University of Alberta, Division of Gastroenterology (Liver Unit), Edmonton, Canada; 5Centro de Investigación Biomédica en Red de Enfermedades Hepáticas y Digestivas (CIBERehd), Instituto de Salud Carlos III, Madrid, Spain
Email: monica_xina@hotmail.com

Background and aims: Simple non-invasive tools for predicting liver-related events (LRE) in non-alcoholic fatty liver disease (NAFLD) are needed for prognostic stratification and clinical trial patient selection. We aimed at developing a risk prediction model based on non-invasive tests (NITs), including liver stiffness measurement (LSM), to determine the risk of developing LRE in NAFLD patients at point-of-care. In addition, we studied LRE incidence in compensated chronic liver disease (cACLD) LSM thresholds.

Method: This is a multicenter retrospective cohort study with NAFLD patients from 4 centers in Canada (n = 72), Hong Kong (n = 1537), France (n = 681) and Spain (n = 348). Patients included had available NITs (LSM by transient elastography and serological tests), had no prior decompensation and a minimum follow-up of 12 months. Patients with concomitant etiologies were excluded. LRE were defined as hepatocellular carcinoma, clinical decompensation, liver transplantation or liver-related death. Risk of LRE was modeled with a Cox regression model using well established predictors and selected by backwards elimination method combined with bootstrapping. The relationship between hazard ratio and NITs was assessed using a cubic spline function. A nomogram was derived from the model.

Results: 2638 patients were included (53% male, mean age 58.4 years (SD 12.4), mean BMI 30.0 kg/m2 (SD 5.7), and 60.8% with diabetes mellitus). Among them, 1820 (69%) had LSM <10 kPa, 479 (18%) LSM between 10 – 15 kPa and 339 (13%) LSM >15 kPa. Forty-five (1.7%) patients developed LRE during a median follow-up of 27 months (IQR 22 – 35 months). The incidence rate of LRE in patients with LSM <10 kPa was 0.04/100 patient-years, in LSM 10 – 15 kPa was 0.3/100 patient-years, in LSM 15 – 25 kPa was 2.1/100 patient-years, in LSM ≥25 kPa was 8.0/100 patient-years. Predictors evaluated in multivariate analysis were diabetes, BMI, platelet count, albumin and LSM. Only platelet count, albumin and LSM were retained in the final model. The performance for predicting LRE based on the area under the receiver operating curve (discrimination) was 0.92, also the calibration of the model was excellent. A nomogram was constructed to assess the individual risk of presenting events at 1, 2 and 3 years of follow-up (figure). The model is currently being validated in 3 external cohorts.

Conclusion: NAFLD patients with LSM <10 kPa (no-cACLD) have a very low incidence of LRE and could be followed in primary care, and the risk increases significantly in patients with LSM >15 kPa. This simple easy-to-use prediction tool for LRE could be very useful for prognostic stratification and selecting NAFLD patients for clinical studies.
SAT531
In-hospital falls and impaired nutritional status are independently associated with in-hospital mortality in patients with liver cirrhosis
Nada Abedin1, Moritz Hein1, Christoph Welsch1, Jörg Bojunga1, Stefan Zeuzem1, Georg Dultz1,2,1 Department of Internal Medicine I, University Hospital Frankfurt, Goethe University, Frankfurt am Main, Germany
Email: nada.abedin@kgu.de

Background and aims: Chronic liver disease is associated with severe complications leading to recurrent hospitalization and a high mortality in general. Complications associated with liver cirrhosis are one of the most frequent causes of death in hospitalized patients. This study aimed at detecting risk factors that can be addressed to increase patient safety and outcome.

Method: Hospitalized patients with liver cirrhosis between 2017 and 2019 in the department for gastroenterology at the University Hospital Frankfurt were included in a retrospective analysis. Clinical data, laboratory work and follow-up data from patients’ electronic files were gathered and assessed. Statistical analysis was performed using SPSS.

Results: In a total of 1985 hospitalizations our study revealed an in-hospital mortality of 9.6%. Median age was 61 years and 70.5% were male patients. Overall, patients who died during their stay had a significantly longer period of hospitalization (19.1 days vs. 7.7 days, p < 0.0001). 1016 cases were from patients with alcoholic liver disease, 15.2% were associated with Hepatitis C, 14.8% were patients with NASH. While there were significant clinical predictors (p < 0.0001) for in-hospital mortality in the univariate analysis, such as lower blood pressure, an ongoing infection and different lab values (higher CRP, hyponatremia, leukocytosis, elevation in creatinine), in the uni- and multivariate analysis two factors were independently associated with in-hospital mortality. These include a nutritional risk score >1 (p < 0.0001) for in-hospital mortality in the univariate analysis, such as lower blood pressure, an ongoing infection and different lab values (higher CRP, hyponatremia, leukocytosis, elevation in creatinine), in the uni- and multivariate analysis two factors were independently associated with in-hospital mortality. These include a nutritional risk score >1 (p = 0.006, OR 2.029, 95%CI) and a falling incident during hospitalization (p = 0.002, OR 3.495, 95%CI). As a general marker for severity of liver disease, the MELD Score was also independently associated with higher in-hospital mortality (p < 0.001, OR 4.404, 95%CI).

Conclusion: Patients with liver cirrhosis are at high risk for developing severe complications that can be fatal. Our study reveals two independently associated factors with in-hospital mortality in patients with liver cirrhosis, i.e. nutritional risk and in-hospital falls that can and must be addressed and screened for on admission to alleviate patients’ risk and allow for a better outcome.

SAT532
PD-1/PD-L1 pathway is related to infection development and early mortality in patients with cirrhosis
Adria Juanola1,2,3, Elisa Pose1,2,3, Delia Blaya4, Cristina Solé1,2,3,4, Gabriel Mezzano1, Natalia Jimenez-Esquível4, Joaquin Andrés Castillo1, Jordi Riberà3,4, Irene Portoles2,3,4, Martina Perez1,2,3,4, Laura Napoleone1,2,3, Ana Belén Rubio2,3, Marta Cervera2,3, Marta Carol2,3, Octavi Bassegoda1,2,3,4, Marta Coll2,3, Isabel Graupera1,2,3, Manuel Morales-Ruiz2,3,4, Mar Coll2,3, Isabel Graupera1,2,3,4, Gonzalo Crespo1,2,3, Else Solà1,2,3,4, Pere Gine1,2,3,4, 1Liver Unit, Hospital Clinic de Barcelona, Barcelona, Spain; 2Institut d’Investigacions Biomèdiques August Pi i Sunyer (IDIBAPS), Barcelona, Spain; 3Centre de Investigació Biomèdica en Red. Enfermedades Hepàtiques y Digestivas (CIBEREHD), Madrid, Spain; 4Biochemistry and Molecular Genetics Department, Hospital Clinic de Barcelona, Barcelona, Spain; 5Faculty of Medicine and Health Sciences, University of Barcelona, Barcelona, Spain; 6Institute for Immunity, Transplantation and Infection, Stanford University, Stanford, CA, USA
Email: juanola@clinic.cat

Background and aims: Infections, often recurrent, are a very important complication of advanced liver cirrhosis and represent a very common cause of hospitalization, acute kidney injury, ACLF and death. The high risk of infections in cirrhosis is associated, among others, with alterations of the intestinal microbiome as well as defective function in some immune cells. Recent studies in experimental animals suggest the existence of an activation of the PD1-PD-L1 pathway (Programmed cell death 1) that would produce an immuneparalysis and predispose to infections. It is unknown whether this pathway participates in the pathogenesis of infections in human cirrhosis. The aim of the present study was to evaluate the activity of the PD-L1 pathway in patients with cirrhosis and its relationship with the development of infections and mortality.

Method: Prospective study of 310 patients with cirrhosis in different disease stages (13% outpatients, 87% hospitalized). PD-1/PD-L1 pathway activity was estimated by measuring serum levels of PD1 and PD1L (ELISA), which assess the soluble isoform of PD1 (sPD1) and PD1L (sPD1L) expressed in lymphocytes and monocytes. Main outcomes of the study were infections and ACLF development and death during a 3-month follow-up period.

Results: During follow-up, 99 patients (32%) developed at least one new episode of infection. Baseline serum levels of sPD1 and sPD1L were higher in patients who developed a new infection compared to those patients who did not develop new infection (sPD1: 2.7 (2.3–3.3) vs 2.5 (2.1–3.0) pg/ml, p = 0.038; sPD1L: 160 (115–221) vs 129 (95–172) pg/ml, p = 0.002). On multivariate analysis, sPD1L together with liver function assessed by MELD Sodium, were the only two independent predictive factors of development of new infections during 3-month follow-up. One-hundred forty-eight patients had an active infection at inclusion. Patients with infection at baseline had higher levels of sPD1L compared to those patients who did not have infection [164 (115–224) vs 124 (94–161) pg/ml, respectively, p < 0.001]. During hospitalization, 30 patients (20%) with infection at baseline died. sPD1L, MELD Sodium and leukocyte count were independently associated with in-hospital mortality among this population. Finally, 16 patients without ACLF at inclusion, developed it during follow-up, sPD1L was higher among those who developed ACLF [182 (106/242) vs 121 (93–166) pg/ml, p = 0.001], irrespective of the presence of infection. Furthermore, sPD1L was the only independent predictor factor of ACLF at 3 months.

Conclusion: In patients with cirrhosis, serum levels of PD1L correlate with the development of infections, ACLF and short-term mortality. These results suggest the existence of an activation of the PD1-PD-L1 pathway in human cirrhosis that could be an important pathogenic factor for the development of infections and early mortality.

SAT533
Short term intravenous albumin effects in decompensated cirrhosis: about single hospitalization event
Han Seul Kj1, Moon Young Kim1, Yeonsi University Wonju College of Medicine, Department of Internal Medicine, Division of Gastroenterology and Hepatology, Wonju-si, Korea, Rep. Of South Email: drkimmy@yonsei.ac.kr

Background and aims: For intravenous administration of albumin, it is known that long-term administration has a positive effect on the survival rate of cirrhosis. We aimed to investigate the effects of short-term albumin administration on days of hospitalization and change of MELD score, creatinine level, complication during the hospitalization and short-term prognosis.

Method: We investigated patients who were admitted to a single-center hospital, due to acute decompensated events from January 2018 to December 2020. Causes of hospitalization include gastrointestinal bleeding, jaundice, hepatic encephalopathy, newly developed ascites requiring paracentesis and IV antibiotics administration, infection, hepatorenal syndrome, Acute on chronic liver failure. We excluded data about mortality during hospitalization due to aggressive management beyond the standard management. After investigating the total albumin dose administered to patients during hospitalization, patients who received 40 g or more per week and those who did not were compared and analyzed. The patients
Patients with myosteatosis vs those without, were more often female alcoholic, viral and other causes of liver disease respectively] were 65.3% with decompensated cirrhosis, 43.1%, 23.4% and 33.5% with 167 consecutive patients [67.6% male, MELD 12 (IQR 7–14.25 days, p = 0.008) and total complications event during hospitalization also tended to decrease (7 vs 10 cases, p = 0.4).

There was no difference between the two groups in the 3 months survival rate (10vs 10 case p = 0.88). And the decrease of creatinine level was not different between two groups (0.53 vs 0.51 p = 0.86), and that was same in decrease of MELD score (4.35 vs 3.53 p = 0.37). But in subgroup in CTP class C, the decrease of creatinine level was more prominent in high dose albumin group (0.60 vs 0.48 p = 0.4).

Conclusion: In the group of patients hospitalized for acute decompensation events, excluding mortality due to disease, albumin administration of 40 g or more per week was reducing the length of hospitalization of patients. In subgroup analysis, in the non-bleeding cases, and the higher CTP patients, the more effective it is. And it is expected that there will also be a creatinine reduction effect, and there seems to be a tendency to reduce the incidence of complications. It is recommended to consider active albumin administration when patients were hospitalized cause of acute decompensation.

SAT534 Myosteatosis is associated with sarcopenia, frailty and fat body composition abnormalities in liver cirrhosis

Eleni Geladari1, Theodoros Alexopoulos1, Meropi Kontogianni2, Ilianna Mani1, Larisa Vasileva1, Alexandros-Pantelis Tsigas2, Roxani Tenta2, Evangelia Stroumpoulou2, Alexandra Alexopoulou1. 1Medical School, National and Kapodistrian University of Athens, 2nd Department of Internal Medicine and Research Laboratory, Athens, Greece; 2School of Health Sciences and Education, Harokopio University, Department of Nutrition and Dietetics, Athens, Greece; 3Hippokration General Hospital, Department of Radiology, Athens, Greece Email: alexopou@ath.forthnet.gr

Background and aims: Myosteatosis is defined as increased fat infiltration in skeletal muscle and implies impaired muscle quality. Although it has been included in the recent sarcopenia criteria as suggested by the European Working Group on Sarcopenia in Older People (EWGSOP-2), further research is required exploring myosteatosis’ associations with clinical characteristics of patients with liver cirrhosis (LC). The aim was to investigate the prevalence of myosteatosis and potential associations with other body composition parameters and clinical characteristics in patients with LC.

Method: Computed tomography (SliceOmaticV4.3 software, Tomovision, Montreal, PQ) was used to assess muscle mass [skeletal muscle index (SMI, cm²/m²)] at the third lumbar vertebrae (L3). The same software was utilized to calculate visceral adipose tissue index (VAI, cm²/m²), subcutaneous adipose tissue index (SATI, cm²/m²) and VATI/SATI (VSR) ratio. Myosteatosis was defined as muscle radiodensity <33 Hounsfield Units (HU) at L3. Sarcopenia was diagnosed according to EWGSOP-2 criteria, muscle performance and frailty using the liver frailty index (LFI).

Results: 167 consecutive patients [67.6% male, MELD 12 (IQR 7–17), 65.3% with decompensated cirrhosis, 43.1%, 23.4% and 33.5% with alcoholic, viral and other causes of liver disease respectively] were included. Myosteatosis was identified in 59.3%, sarcopenia in 43.1% and frailty in 29.3% of the population. Patients with myosteatosis vs those without, were more often female (42.4% vs 17.6%, p = 0.001), older than 60 years of age (58.6% vs 39.7%, p = 0.012), sarcopenic (61.6% vs 16.2%, p < 0.001), frail (40.4% vs 13.2%, p < 0.001) and had more often compensated cirrhosis (71.7% vs 55.9%, p = 0.026). Moreover, patients with myosteatosis displayed higher VATI [55.4 (36.6–75.7)] vs 32.8 (20.7–56.6), p = 0.001], SATI [63.3 (37.0–95.1)] vs 46.8 (28.7–66.8), p = 0.005], VSR [0.99 (0.54–1.4)] vs 0.69 (0.43–1.18), p = 0.024] and decreased SPPB [10 (5.5–11) vs 11 (10–12), p < 0.001]. Liver disease etiology and body mass index did not differ between the groups.

Conclusion: High myosteatosis prevalence was demonstrated in this sample of patients with cirrhosis. Myosteatosis was associated with older age, presence of sarcopenia, frailty, decreased performance status, high visceral, and subcutaneous adiposity and more severe liver disease.

SAT535 Correction and prevention of hyponatremia in patients with cirrhosis and ascites: post hoc analysis of the ANSWER study database

Giacomo Zaccherini1, Maurizio Baldassarre1,2, Manuel Tufoni3, Oliviero Riggio4, Paolo Angelii6, Carlo Alessandri6, Sergio Neri7, Francesco Giuseppe Foschi8, Fabio Levantesi9, Aldo Airolì10, Loredana Simone11, Gianluca Sveggiati-Baroni12, Stefano Faggiuoli13, Giacomo Lafti14, Raffaele Cozzolongo15, Vito Di Marco16, Vincenzo Sangiovanni17, Filomena Morisco18, Pierluigi Toniutti19, Annalisa TORTORA20, Rosanna De Marco21, Silvia Nardelli22, Salvatore Piano2, Chiara Elia2, Mauro Bernardi1, Paolo Caraceni12,3. 1University of Bologna, Department of Medical and Surgical Sciences, Bologna, Italy; 2University of Bologna, Center for Applied Biomedical Research, Bologna, Italy; 3IRCCS Azienda Ospedaliero-Universitaria di Bologna, Bologna, Italy; 4Sapienza University of Rome, Department of Translational and Precision Medicine, Rome, Italy; 5University of Padua, Department of Medicine, Padua, Italy; 6Città della Salute e della Scienza Hospital, Division of Gastroenterology and Hepatology, Turin, Italy; 7Humanitas Medical Care Catania, Internal Medicine, Catania, Italy; 8AUSL of Romagna, Internal Medicine, Hospital of Faenza, Faenza, Italy; 9AUSL of Bologna, Internal Medicine, Hospital of Bentivoglio, Bentivoglio, Italy; 10Niguarda Hospital, Department of Hepatology and Gastroenterology, Milan, Italy; 11University Hospital of Ferrara, Gastroenterology Unit, Ferrara, Italy; 12Polytechnic University of Marche, Department of Gastroenterology, Ancona, Italy; 13Papa Giovanni XXIII Hospital, Gastroenterology and Transplant Hepatology, Bergamo, Italy; 14University of Florence, Department of Experimental and Clinical Medicine, Florence, Italy; 15National Institute of Gastroenterology S. De Bellis, Division of Gastroenterology, Castellana Grotte, Italy; 16University of Palermo, Biomedical Department of Internal and Specialist Medicine, Palermo, Italy; 17Azienda Ospedaliero di Rilevamento Nazionale dei Colli, Cotugno Hospital of Naples, Naples, Italy; 18Federico II University of Naples, Department of Clinical Medicine and Surgery, Naples, Italy; 19University of Udine, Department of Medical Area, Udine, Italy; 20Gemelli Foundation Catholic University, Unit of Gastroenterology, Rome, Italy; 21Hospital of Cosenza, Unit of Gastroenterology, Cosenza, Italy Email: giacomo.zaccherini@unibo.it

Background and aims: Hyponatremia is a frequent and ominous complication in patients with decompensated cirrhosis. Human albumin (HA) administration improves hyponatremia in patients with cirrhosis hospitalized because of acute decompensation, but no data are available on the effects of long-term HA administration. We aimed at determining whether long-term HA administration could help in treating and preventing hyponatremia in outpatients with decompensated cirrhosis and ascites.

Method: We performed a post-hoc analysis on the intention-to-treat population (431 patients) enrolled in the ANSWER trial, grouping patients according to their baseline serum sodium levels. Resolution rates of hyponatremia in hyponatremic patients and incidence rates (IRs) and IR ratios (IRR) of at least moderate hyponatremia (<130 mmol/l) during a follow-up of 18 months were calculated.
Results: 149 (35%) patients presented hyponatremia (<135 mmol/l) at baseline (74 vs 75 in the standard medical treatment [SMT]) and in the SMT+HA arms, respectively. 116 of them (78%) had mild hyponatremia (≥130 and <135 mmol/l), while 33 (22%) had at least moderate hyponatremia (<130 mmol/l). Patients with hyponatremia had higher Child-Pugh and MELD scores as compared to normonatremic patients. At baseline, hyponatremic patients randomized to receive long-term HA did not differ from those randomized to SMT. Normalization of hyponatremia (≥135 mmol/l) was reached more frequently and faster in SMT+HA than SMT group: 45% vs 28% (p = 0.042) after 1 month, and 71% vs 44% (p = 0.006) after 3 months. Long-term HA was also effective in preventing episodes of hyponatremia, as the incidence rate of at least moderate hyponatremia was significantly lower in the SMT+HA than in SMT arm, both in hyponatremic and non-hyponatremic patients (incidence rate ratios: 0.245 [CI 0.167–0.359, p < 0.001] and 0.539 [CI 0.338–0.859, p = 0.008], respectively.

Conclusion: Long-term HA administration appears an effective intervention in managing hyponatremia in outpatients with decomp ensated cirrhosis and ascites.

SAT536
Low incidence of adverse liver events in a real-world cohort of patients diagnosed with liver disease via a community diagnostic pathway
Alexander Smith1,2, Florina Borca2, Julie Parkes1, Janisha Patel2, Hang Phan1, Gallum Robins2, Ryan Buchanan1, 1University of Southampton, Faculty of Medicine, Southampton, United Kingdom; 2University Hospital Southampton NHS Foundation Trust, Southampton, United Kingdom
Email: asmith49@nhs.net

Background and aims: Community liver diagnostic pathways use non-invasive liver fibrosis tests to identify patients with compensated alcohol-related liver disease (ArLD) and non-alcohol related fatty liver disease (NAFLD). However, the longitudinal association between test scores and adverse liver events is uncertain.

Method: The Southampton Liver Pathway (SLP) involves fibrosis assessment with an enhanced liver fibrosis (ELF) score in primary care and transient elastography (TE). We retrospectively examined the occurrence of adverse liver events in patients with ArLD or NAFLD identified in the SLP. Patients with an ELF test taken between 1st January 2017 and 31st August 2019, TE conducted within 6 months of the ELF test and a negative non-invasive liver screen (e.g. chronic viral hepatitis, autoimmune profile, serum ferritin and transferrin saturation) were included in the analysis. Data were collected at baseline from hospital records including age, sex, BMI, history of alcohol excess, and known type 2 diabetes mellitus (T2DM).

Adverse liver events were defined a priori as development of ascites, spontaneous bacterial peritonitis, overt hepatic encephalopathy, variceal bleeding, and hepatocellular carcinoma. We performed a search of hospital electronic records for adverse liver events occurring from the date of ELF test up to 30th April 2021. Kaplan-Meier (KM) curves and hazard ratios (HR) with 95% confidence interval (CI) were produced from univariable cox regression for risk of adverse liver events, stratified by recognised cut-offs for advanced fibrosis for ELF score (>10.5 or ≤10.5) and TE (>15 or ≤15kPa).

Results: A total of 324 patients were identified with 57% NAFLD, 37% ArLD, 6% unclassified. Median follow-up was 29 months (IQR 23–40). 213 patients (66%) were male and median age was 61 years (IQR 50–69). Median BMI was 30 kg/m² (IQR 27–35) and 113 patients had T2DM (35%). Median ELF score was 10.5 (IQR 9.8–10.9) and median TE 7.2kPa (IQR 5.5–11.4). 152 (47%) patients had ELF >10.5 and 54 (17%) had TE >15kPa. Only 5 (1.5%) patients experienced an adverse liver event. KM curves are shown in Figure 1. The HR for prediction of adverse liver events according to ELF score was 4.10 (95% CI 0.46–36.68, p = 0.208) and for TE result 2.84 (95% CI 0.47–17.01, p = 0.254).

Conclusion: Patients from primary care populations with compensated liver disease diagnosed using non-invasive tests have a good medium-term prognosis. High ELF and TE results were not significantly associated with adverse liver events but this was affected by the low incidence of events in the follow-up period.

SAT537
The use of decompensated cirrhosis admission care bundles improves the standard of inpatient care but utilisation is poor across the UK
The Trainee Collaborative for Research and Audit in Hepatology UK1.
Email: oliver.tavabie@doctors.net.uk

Background and aims: The standard of inpatient care for patients with cirrhosis in the United Kingdom (UK) is variable. Previous reports have demonstrated that less than 50% of inpatients admitted with alcohol-related liver disease (ARLD) receive good care. UK hepatology and gastroenterology societies have developed standards to improve care of patients with decompensated cirrhosis in the first 24 hours of admission. These have been integrated into a number of care bundles. We aimed to audit the uptake of these bundles and assess the impact on patient outcomes across the UK.

Method: Trainees from across UK hospitals were invited to participate in this audit through the ToRcH-UK network. Patients admitted to hospital between 1/11/2019–30/11/2019 with decompensated cirrhosis were identified by coding used for the NHS Cirrhosis Quality Dashboard. Admission clinical, demographic and laboratory data were collected with outcome and trust-specific data. Sites were grouped by NHS region, specialist/non-specialist hepatology centre designation and outcome groups. Univariable and multi-variable analyses (MVA) were performed.

Results: 1224 admissions (1168 patients) from 104 hospitals (36 specialist hepatology centres) were included. Median age was 58 (IQR 48–68) and 61.6% were male. 62.3% of admissions were out of hours, 74.8% were for patients with ARLD, 85.1% had an established diagnosis of chronic liver disease with 67.2% having previously decompensated. Median model for end-stage liver disease (MELD) score was 17 (IQR 12–21) and admission inpatient mortality was 15.6%. Admission care bundles were used in 11.4% of admissions and there was significant regional variation in use (see Figure). Care bundle use was higher in patients with; ARLD (p < 0.0001), jaundice (p = 0.005) and those with higher MELD scores (19 [IQR 14–23] vs 16 [IQR 12–21], p = 0.001), and reduced in patients with gastrointestinal bleeding (p = 0.005). The use of a care bundle was associated with increases in the following: appropriate blood tests requests (p < 0.0001), septic screens (p = 0.0001), diagnostic paracentesis (p = 0.005), appropriate alcohol care (p = 0.0006) and acute kidney injury management (p = 0.0007). Mortality was higher in patients where a care bundle was used (p = 0.01). However, when adjusted for MELD score, age and critical care admission, care bundle use was not associated with mortality (adjusted odds ratio 0.97–2.65, p = 0.06).
Background and aims: The hepatitis B virus (HBV) is a significant burden of liver disease in Canada. We evaluated the effect of HBV treatment on all-cause mortality and liver-related mortality among individuals with HBV and cirrhosis in British Columbia (BC), Canada.

Method: This analysis used the BC Hepatitis Testers Cohort, which includes all individuals diagnosed with HBV since 1990 in BC, integrated with data on medical visits, hospitalizations, prescription drugs, and mortality. The study population included individuals who tested positive for HBV and were diagnosed with cirrhosis, followed from their HBV first testing date until death or December 31, 2020. We computed all-cause and liver-related mortality rates by HBV treatment status. We used inverse probability of treatment weighting (IPTW) to balance the baseline characteristics with the standardized mean difference (SMD) cut-off of 0.2 for treated and untreated individuals. We performed multivariable cox proportional hazard modeling to assess the effect of HBV treatment and coinfection with Hepatitis C virus (HCV) on all-cause and liver-related mortality in the overall sample and in the IPTW dataset.

Results: The analysis included 654 HBV-positive individuals with cirrhosis; 100 (15.3%) received HBV treatment. The mean follow-up for treated individuals was 10.29 (SD: 7.61) years and 5.84 (SD: 6.71) years for untreated individuals. A higher proportion of those treated compared to untreated were males [67 (67%) vs 370 (66.8%)], born between 1945 and 1964 [66 (75.9%) vs 330 (65.9%)], those of East and South Asian ethnicity [40 (40.0%) vs 108 (19.5%)], and those with liver cancer [20 (20.0%) vs 68 (12.3%)]. The highest all-cause (124.28; 95%CI: 112.70, 137.04 vs 44.71; 95%CI: 33.49, 59.69 per 1,000 person-years [PYs]); and liver-related mortality (75.74; 95% CI: 66.83, 85.85 vs 29.16; 95% CI: 20.39, 41.70 per 1,000 PYs) rates were higher among individuals who were not treated for HBV compared to those who were treated the liver-related. The multivariable models revealed that HBV-positive cirrhotic individuals who were not treated had a greater risk of dying from all causes (adjusted hazard ratio [aHR] 1.75; 95% CI: 1.25, 2.45) and liver-related mortality (adjusted sub-distribution HR [aSIR] 1.78; 95% CI: 1.19, 2.67) compared to treated individuals. Compared to individuals without co-infection HBV/HCV, those co-infected HBV/HCV, not treated for HBV infection had a higher hazard for both all causes and liver-related mortality (aHR 2.60; 95% CI 1.63, 4.14, and 2.93; 95% CI 1.68, 5.14 respectively). Other risk factors for all-cause and liver-related mortality included male sex and HCV infection.

SAT538
Effect of hepatitis B virus treatment on all causes and liver-related death among patients living with HBV with cirrhosis in British Columbia in a population-based cohort study
Makuza Jean Damascene1,2,3, Dahn Jeong2,4, Mawuena Binka2, Prince Adu2,4, Georgine Cuas, Hector Velasquez2,4, Amanda Yu2, Stanley Wong2, Maria Alvarez2, Sofia Bartlett2, Alnoor Ramji5, Email: makorofr@gmail.com

Background and aims: The hepatitis B virus (HBV) is a significant cause and liver-related mortality included male sex and HCV infection.

Conclusion: The use of admission care bundles improves the standard of care of patients with decompensated cirrhosis within the first 24 hours of admission. However, uptake is poor and variable across the UK. Work is required to understand the barriers to use to improve inpatient care for patients with decompensated cirrhosis.

SAT539
Secondary infections in hospitalizes patients with cirrhosis: epidemiology, clinical characteristics and prognostic relevance
Gustavo Pereira1, Caroline Baldin1, Juliana Piedade1, Nathalia Galfarid1, Barbara Rodrigues1, Raquel Godoy1, Camila Marques de Alcanatar Barreto1, Flavia Fernandes1, 1Bonsucesso General Hospital, Gastroenterology and Hepatology Unit, Rio de Janeiro, Brazil Email: ghspereira@gmail.com

Background and aims: Bacterial infections are frequent in cirrhotic patients and may induce a state of immune paralysis and, consequently, greater susceptibility to secondary infections. There is a paucity of data respect the frequency and clinical characteristics of secondary infections in this population. Our aim was to describe incidence and predictive factors of secondary infections and their correlation with prognosis.

Method: retrospective analysis of patients diagnosed with bacterial infections at admission, originally included in a prospective study of 318 cirrhotic patients. The incidence of secondary infections was assessed in 174 patients admitted to hospital. The clinical characteristics of patients with and without secondary infections were compared using the statistical software R.

Results: The incidence of secondary infections was 49% (85/174). The most frequent were respiratory infections (34%), urinary tract infections (20%), and wound infections (19%). The presence of secondary infections was independently associated with lower platelet count, higher albumin levels, and higher bilirubin levels. Patients with secondary infections had a higher risk of mortality (adjusted odds ratio 2.4 vs 1.2 for those without secondary infections).

Conclusion: HBV treatment was associated with a significant reduction in all-cause and liver-related mortality among individuals with cirrhosis.
Results: Plasma levels of total cfDNA and its mitochondrial and genomic components were significantly elevated in CLD patients when compared to healthy controls (p < 0.001). There was no significant difference across the cohorts in plasma coagulation markers, but serum platelet activation markers decreased significantly as liver disease progressed (p < 0.001) (Figure 1a). Interestingly, both mt- and gDNA correlated with serum platelet activation markers, CXCL4 (mtDNA r(s) = 0.34, 95% CI 0.19–0.47, gDNA r (s) = −0.45, 95% CI 0.57–0.32), CXCL7 (mtDNA r (s) = 0.32, 95% CI 0.17–0.46, gDNA r (s) = −0.58, 95% CI 0.68–0.46) and thrombospondin (mtDNA r (s) = 0.27, 95% CI 0.11–0.41, gDNA r (s) = −0.49, 95% CI 0.60–0.36) (Figure 1b). Host gDNA and platelet granule proteins were significantly associated with patient mortality (30- and 90-day), cirrhosis scores (Child-Pugh, MELD, CLIF-C) and routine haemostasis laboratory tests (platelets, INR, fibrinogen).

SAT540
Circulating cell-free DNA levels increment with worsening cirrhosis severity and associate with platelet exhaustion and mortality

Marilena Stamouli1, Jelle Adelmeijer2, Dana Huskins3, Savannah Rivera2, Kevin O’Reilly2, Elena Palma3, Neil Youngson4, William Berna4, Shilpa Chokshi1, Mark Roest3, Ton Lisman2, Vishal Patel1,4,6.

Background and aims: Chronic liver disease (CLD) is accompanied by changes in pro- and anti-haemostatic pathways, resulting in a fragile restored haemostatic balance. Thrombocytopenia is a common complication in decompensated cirrhosis (DC) and acute-on-chronic liver disease (ACLF), and granule storage pool deficiency has been shown to impair platelet function and favour bleeding. Circulating cell-free DNA (cfDNA) has been proposed to drive organ failure and interact with critical coagulation pathways and platelet function. The aim of this work was to characterise cfDNA in the evolution of CLD, coagulation dysfunction and associated organ failure.

Method: Plasma and serum haemostatic profiles were studied extensively in the full spectrum of CLD of increasing severity: stable cirrhosis (SC, n = 40), DC (n = 63), ACLF (n = 50), and were compared to healthy individuals (n = 40). Plasma-extracted cfDNA was also characterised by way of its host components (genomic (g) and mitochondrial (mt)). cfDNA content, coagulation and platelet activation markers were compared between groups and correlated with clinical characteristics.
Liver tumours: Clinical aspects except therapy

SAT554
Sugar sweetened beverage consumption and liver cancer risk
Xuehong Zhang1,2,3, Longgang Zhao4, Mace Coday5, David O. Garcia6, Xinyi Li6, JoAnn Manson1,2,3, Katherine McGlynn7, Yasmin Mosaic-Rahman8, Michelle Naughton9, Melissa Lopez-Pentecost10, Nazmus Saquib8, Howard Sesso2,3, Aladdin Shadyab1, Michael Simon12, Linda Snetselaar11, Fred Tabung11, Lesley Tinker11, Deirdre Tobias2,3, Trang VoPham14, 1Harvard Medical School, Boston, United States; 2Harvard T.H. Chan School of Public Health, Boston, United States; 3Brigham and Women's Hospital, Boston, United States; 4University of South Carolina, Columbia, United States; 5University of Tennessee, Memphis, United States; 6The University of Arizona, Tucson, United States; 7National Cancer Institute-Shady Grove, Rockville, United States; 8Albert Einstein College of Medicine, United States; 9The Ohio State University, Columbus, United States; 10Sulaiman Al Rajhi University, Al Bukayriyah, Saudi Arabia; 11University of California San Diego, La Jolla, United States; 12Wayne State University, Detroit, United States; 13The University of Iowa, Iowa City, United States; 14Fred Hutchinson Cancer Research Center, Seattle, United States

Background and aims: Intake of sugar-sweetened beverage (SSB), a postulated risk factor for obesity, diabetes, and cardiovascular disease, may drive insulin resistance and inflammation which are strongly implicated in liver carcinogenesis. However, evidence on the association between SSB intake and liver cancer is scarce. We hypothesized that higher SSB intake would be associated with a greater risk of liver cancer.

Method: We included 97,601 women aged 50–79 years from the Women’s Health Initiative Observational Study and Dietary Modification Trial comparison arm. SSB intake was defined as the sum of soft drinks and fruit drinks (1 serving = one 12 fl. oz can or 355 ml), which was assessed by a validated food frequency questionnaire administered at baseline between 1993 and 1998. Incident liver cancers were reported by self-administered questionnaires and further confirmed by medical record review. Cox proportional hazards regression models were used to estimate multivariable hazard ratios (HRs) and 95% confidence intervals (CIs) with adjustment for age, race and ethnicity, education, alcohol intake, smoking status, body mass index, non-steroidal anti-inflammatory drug use, physical activity, total caloric intake, and history of diabetes.

Results: After a median of 19.5 years follow-up, 206 women had confirmed liver cancer. Approximately 6.8% of women consumed ≥1 serving/day of SSB at baseline. Higher SSB intake was associated with a 99% greater risk of liver cancer (HR ≥1/day vs never to <3/month = 1.99, 95%CI = 1.25–3.18, P linear trend = 0.004) as compared to intake of <3 servings/month. Non-statistically significant positive associations with liver cancer were observed for fruit drinks (HR ≥1/day vs never to <3/month = 1.83, 95%CI = 0.80–4.17) and soft drinks (HR ≥1/day vs never to <3/month = 1.79, 95%CI = 1.05–3.07). Results were similar after further adjustment for coffee/tea intake, or history of liver diseases, or when liver cancer cases diagnosed within the first 2 years of follow-up or those with history of diabetes were excluded. Substitution analyses indicated replacing SSB with water and/or coffee or tea could significantly lower liver cancer risk.

Conclusion: Our findings suggest SSB as a potential modifiable risk factor for liver cancer in postmenopausal women. Studies in men and diverse populations are needed to examine these associations more comprehensively. If our findings confirmed, reducing SSB consumption might serve as a public health strategy to reduce liver cancer burden.

SAT555
Safety and effectiveness of vaccines against SARS-COV-2 in patients with liver cancer. VaeHep registry: response analysis 4 weeks after the second dose.
Elena Diago Sempere1, Ana Matilla2, Carlos Rodríguez3, Christie Perelló4, Beatriz Minguez5, María Varela5, Juan José Urquijo6, Javier Amperou6, Janie Prieto7, Laura Márquez Pérez7, Javier Crespo8, María Bermúdez8, Ana María Piedra Cerezo9, Moises Diago10, Belén Ruiz Antoran11, José Luis Calleja Panero11, 1Hospital Universitario La Paz, IDIAPAZ, Central Unit for Clinical Research and Clinical Trials, Madrid, Spain; 2H.G.U. Gregorio Marañon, Gastroenterology and Hepatology Department, Madrid, Spain; 3Hospital Universitario Marqués de Valdecilla, IDIVAL, Gastroenterology and Hepatology Department, Santander, Spain; 4Hospital Universitario Puerta de Hierro., Liver Unit. Gastroenterology and Hepatology Department, Majadahonda, Madrid, Spain; 5Hospital Universitario Vall d’Hebron, Liver Unit, Barcelona, Spain; 6Hospital Universitario Central de Asturias, Liver Unit. Gastroenterology and Hepatology Department, Oviedo, Spain; 7Hospital Universitario General de Valencia, Liver Unit. Gastroenterology and Hepatology Department, Valencia, Spain; 8Hospital Universitario Virgen del Rocio, Institute of Biomedicine of Seville (IBIS). Unit for the Clinical Management of Digestive Diseases, Sevilla, Spain; 9Hospital Urduliz-Alfredo Espinosa, Gastroenterology and Hepatology Department, Urduliz, Spain; 10Hospital Universitario Puerta de Hierro Majadahonda, IDIIPHIM, Clinical Pharmacology Department, Majadahonda, Madrid, Spain; 11Hospital Universitario Puerta de Hierro, IDIIPHIM and CIBEREHD, Department of Gastroenterology and Hepatology, Majadahonda, Madrid, Spain
Email: edialogosempere@gmail.com

Background and aims: Vaccines against SARS-CoV2 have been authorized with an efficacy of 95%. However registration studies have not included cancer patients at risk of lower immunogenicity. The aim of this study is to evaluate the immune response and safety after vaccination in patients with liver cancer.

Method: Case-control study, patients with primary liver cancer who received any of the COVID-19 vaccines were included. The immune response was evaluated by detecting tests against Spike protein by electrochemiluminescence. Study titers were defined as undetectable (<0.4 U/ml), suboptimal (0.4–250), and adequate (>250 U/ml). 1 Cancer-free individuals were selected as controls and matched for age and sex. A second control cohort of cirrhotic patients is ongoing. The results of the interim analysis corresponding to 4 weeks after the second dose are presented.

Results: 244 liver cancer patients and 340 controls were prospectively included. Liver cancer patients had a significant lower serologic response (<250 U/ml) 4 weeks after the second dose than the control group (18.9% vs 7.1%; p < 0.001) (Table 1).

<table>
<thead>
<tr>
<th>RESPONSE</th>
<th>ADEQUATE IG ≥ 250 U/ml</th>
<th>SUBOPTIMAL IG 0–250 U/ml</th>
<th>UNDETECTABLE IG &lt; 40 U/ml</th>
</tr>
</thead>
<tbody>
<tr>
<td>HCC PATIENTS</td>
<td>73, 4%</td>
<td>15, 6%</td>
<td>3, 3%</td>
</tr>
<tr>
<td>HEALTHY CONTROLS</td>
<td>92, 9%</td>
<td>6, 7%</td>
<td>0, 4%</td>
</tr>
</tbody>
</table>

In patients with liver cancer, age >60 years, recurrence at the time of vaccination, treatment with sorafenib, nolivumab, cabozantinib, Child-Pugh B, and BCLC D stage were significantly associated with an inadequate immune response. The adequate response after vaccination with Pfizer-BioNTech was significantly lower than with Moderna (74% vs 92%, p < 0.001). 36% of patients presented adverse effect 28 days after the second dose.

Conclusion: Liver cancer patients develop a significantly lower immune response to SARS-CoV-2 after two doses in comparison with general population. Factors influencing poorer response include age,
Background and aims: Cirrhosis is the main risk factor for the development of hepatocellular carcinoma (HCC). Six-monthly screening with ultrasound is advocated for the surveillance of cirrhotic patients. We recently showed that a glycomics-based test (GlycoCirrhoTest [GCT]) can provide additional information regarding the risk of HCC development in cirrhotic patients. The aim of this study is to provide an independent clinical validation of the GCT for the assessment of the risk of HCC development in cirrhosis.

Method: Validation study on serum samples of patients with established compensated cirrhosis (CHILD Pugh AandB) in a tertiary liver center. Serum N-glycan profiling was performed and GCT was calculated at baseline using DNA sequencer assisted fluorophore assisted capillary electrophoresis. During the follow-up period, patients were screened for the presence of HCC every 6 months with ultrasound and alpha foeto protein (AFP) measurements.

Results: A total of 198 cirrhotic patients were followed during a median follow-up time of 7 years. Twenty-nine patients developed HCC and one died during follow-up. At baseline, the mean GCT value was significantly higher in patients who developed HCC within 3 and 5 years compared to patients who did not develop HCC (Welch t-test, p value 3 years: 0.034, 5 years: 0.022). Hazard ratio for HCC development at 5 years based on GCT was 2.9 (95% CI, 1.2–7.0). Applying the same cut-off as from the proof-of-concept study (0.2), the negative predictive value of GCT for HCC development was 98.9%. Figure 1 illustrates the discriminative power of this biomarker in patients with cirrhosis. GCT is based on changes in serum protein glycosylation related to cirrhosis nodularity and malignant transformation.

Conclusion: This independent validation study confirms that GCT is a glycomics-based test that provides additional information for risk assessment of HCC development in cirrhosis. This information could be used to develop personalized HCC screening programs in cirrhotic patients according to the value of GCT. Moreover, refocusing of the screening resources to the reduced number of cirrhosis patients who truly are at elevated risk for developing HCC may result in earlier detection of more HCC cases, for instance by making contrast-enhanced MRI screening cost-effective.

SAT557
Benefits of tailored HCC surveillance programs on case-fatality rate and cancer-specific mortality using a modelling approach
Massih Ningarhari1, Abbas Mourad2, Claire Delacôte2, Line Carolle Ntandja Wandji1, Guillaume Lassailly1, Alexandre Louvet1, Sebastien Dharancy1, Philippe Mathurin1, Sylvie Deuffic-Burban3, 1CHU Lille, Maladies de l’Appareil Digestif, France; 2Université de Lille, INSERM, CHU Lille, UI286-INFINITE, France; 3Université de Paris, INSERM, IAME, France
Email: massih.ningarhari@chu-lille.fr

Background and aims: To validate screening programs of solid tumors, expert guidelines now recommend obtaining data supporting reduction of case-fatality rate and cancer-specific mortality. The present study evaluates the benefit of hepatocellular carcinoma (HCC) screening on those outcomes using a modelling approach.

Method: We designed a Markov model to assess 10-year outcomes of HCC surveillance in terms of case-fatality rate (CFR), disease-specific mortality and overall mortality per 100, 000 screened patients with compensated cirrhosis. The model simulates the occurrence of HCC, diagnosis through surveillance or symptoms according to tumor growth, treatment, and follow-up. The model evaluates screening in different scenarios varying annual HCC incidence (0.2%, 0.4% or 1.5%), surveillance interval (none, annual (12M), semestrial (6M) or trimestrial (3M)) and imaging modality (US, ultrasound, or MRI, magnetic resonance imaging).

Results: 6M-US screening in comparison to no surveillance reduced 10-year HCC-CFR from 76 to 45%. According to the size of the main tumor, CFRs decreased from 42 to 36% for main nodule size between 1–3 cm, 68 to 61% for main nodule size between 3–5 cm, and 83% to 82% for main nodule size larger than 5 cm. When annual incidences varied from 0.2%, 0.4% to 1.5%, the model predicts reductions of 289, 580 to 2, 110 HCC-related deaths, and of 209, 419 to 1, 521 total deaths, per 100, 000 screened patients, respectively. In terms of surveillance modalities, 6M-MRI and 3M-US, in comparison to the
recommended 6M-US, yielded reductions of CFRs and cancer-related mortality (−18% and −16%), that were as expected not affected by the variation of incidence. Conversely, effects on overall mortality varied according to annual HCC incidence. In comparison to 6M-US, for incidences varying from 0.2%, 0.4% to 1.5%, 6M-MRI reduced overall mortality from 0.3%, 0.5% to 1.7%, and 3M-US from 0.2%, 0.5% to 1.5%, respectively. Even with extended surveillance interval, 12M-MRI compared to 6M-US leads to a 6% reduction of cancer-related mortality.

Conclusion: Shortening US surveillance or using MRI would reduce HCC case-fatality rate and HCC-related mortality. Conversely, the effect on overall mortality appeared modest. The evaluation of case-fatality rates, absolute numbers of cancer-related and overall deaths, provides additional insights on HCC surveillance.

SAT538
T cell receptor sequencing reveals HCC diversity according to BCLC stages within liver tissue and peripheral blood
Yuwei Zhang1, Junxiao Wang2, Xiubin Li3, Hui Xie2, Yijin Wang1.
1Southern University of Science and Technology, School of Medicine, Shenzhen, China; 2The Fifth Medical Center of Chinese PLA General Hospital, Department of Invasive Technology, Beijing, China; 3The Third Medical Centre of Chinese PLA General Hospital, Department of Urology, Beijing, China
Email: yijinwang927015@163.com

Background and aims: T lymphocytes play important roles in human adaptive immune responses and antigen peptides recognition via specific T cell receptors (TCRs). Here we determined the TCR repertoires of tumor, adjacent tissue and PBMC in hepatocellular carcinoma (HCC) patients at different stages, aiming to give a new insight into disease pathogenesis and guiding immune therapy.

Method: We prospectively enrolled 30 patients who were initially diagnosed of HCC at BCLC-A (n = 10), BCLC-B (n = 10), BCLC-C (n = 10), from January 2017 to March 2019 at the 5th Medical Center, Chinese PLA General Hospital. Multi-Immunofluorescence by Tyrosine signal amplification assay was performed in each tumor biopsy to characterize suppressor T lymphocytes with Anti-CD3, Anti-PD1, Anti-CTLA4, and Anti-LAG3 antibodies. Tissue and PBMC samples were then analyzed by high-throughput deep sequencing of TCR using the ImmuHub TCR profiling system. Ethical approval was obtained from the Institutional Ethics Committee.

Results: The number of CD3+ cells was increased in BCLC_B and BCLC_C stages compared to BCLC_A stages, with the BCLC_B stage being the highest. The ratio of PD1+/CD3+ was significantly higher in BCLC_C than that in BCLC_A and BCLC_B. The number of LAG-3+ cells, as well as the ratio of LAG-3+/CD3+ were gradually increased from BCLC_A to BCLC_C stages (Fig 1).

Figure 1:

TCR were successfully sequenced in 78 samples from 28 patients. TRBV5-1, TRBV20-1, TRBJ2-1 and TRBJ2-7 were frequently used in all samples, but seemed no difference between HCC stages. TCR repertoires in tumor tissues are completely different to those in the PBMC, only 4.3% overlaps between tumors and adjacent tissues, and1.5% overlaps between tumors and PBMCs. Furthermore, a significant expansion of TCR clonality in PBMC, but not in tissues, were observed in BCLC_C patients, compared to BCLC_A and BCLC_B patients (Fig 2A–F). The results were further confirmed by analysis of D75 values (Fig 2G–I) and Shannon index (Fig 2J–L). There was no significant difference in CDR3 length between different stages, neither in PBMC, nor in tissues. Hydrophobic amino acids in both positions 6 and 7 amino acids were less used in BCLC_C than BCLC_A and BCLC_B, either in tumor, adjacent tissues or PBMC (Fig 3).
Despite the number of tumor infiltrating T cells was increased in the BCLC_C stage, most of which were inhibitory T cells, indicating unavailing anti-tumor effect. Through a deep, comprehensive and multidimensional analysis of TCR repertoires, our study found a significant increase in TCR clonality of PBMC in BCLC_C stage, but not in tumors and adjacent. In addition, we found that the use of hydrophobic amino acids at positions 6 and 7 of CDR3 decreased at BCLC_C stage. In conclusion, our findings provide new evidence for future clinical monitoring and immunotherapy of HCC patients.

Background and aims: In spite of recent developments it is still very challenging to differentiate hepatocellular carcinoma (HCC) from intrahepatic cholangiocarcinoma (iCCA). Clinical available methods as CT, MRI and contrast-enhanced ultrasonography demand highest operator skills to achieve a robust differentiation between HCC and iCCA. Here, we utilized NanoView’s ExoView® Reader to capture small EVs (sEVs) for further analysis and compared them to large EVs (lEVs) and assessed their clinical performances to differentiate HCC from iCCA. lEVs and sEVs differ in size and biogenesis.

Method: CD44v6+, CD133+ and double positive cells were confirmed on human CCA and HCC cell lines. sEVs and lEVs from patients’ sera were isolated by SEC columns or 10,000 g centrifugation. To quantify lEVs FACS was applied with AnnexinV (AnnV) serving as lEV marker. sEVs were captures with CD9, CD63 and CD81 on ExoView® Tetraspanin Chips according to manufacture’s instruction and analyzed for CD44v6 and CD133. Surface analysis of sEVs was performed with ExoView® R100 (NanoView Biosciences, Boston, USA) using their ExoView® Tetraspanin Kit. Data analysis was performed using ExoView® Analyzer 3.0.

Results: 1) CD133 and CD44v6 were differentially expressed in CCA and HCC cell lines, indicating their potential for differential diagnosis. 2) AnnV+CD44v6+ lEVs were 2.7-fold increased ($p \leq 0.001$) in iCCA patients (AUROC 0.83, 93.3% sensitivity, 71.0% specificity). AnnV+CD44v6+CD133+ lEVs and AnnV+CD133+ lEVs were not conclusive. 3) Individual sEV subpopulations as characterized by tetraspanins (CD9, CD63 and CD81) plus CD44v6 or CD133 were slightly non-significantly elevated without diagnostic relevancy in iCCA as CD63+CD144v6+ sEVs (1.36-fold) and CD9+CD44v6+CD133+ (1.43-fold), or reduced as CD9+CD44v6+ sEVs (0.63-fold). Except and contrary to our lEV data, CD63+CD133+ sEVs and CD9+CD133+ sEVs and CD81+CD133+ sEVs were increased by 6.5-fold ($p = 0.007$) and 3.6-fold ($p = 0.028$) and 9.7-fold ($p = 0.050$). Actually, best clinical performance was observed with CD63+CD133+ with calculated AUROC of 0.89 ($p = 0.009$) and 87.5% sensitivity and 100% specificity. As expected, no meaningful correlations ($r > 0.5$) were observed with AFP and CA19-9.

Conclusion: Our aim was to differentiate a confirmed liver cancer according to its cancer entity, i.e., if HCC or iCCA and to compare clinical performances of lEVs vs. sEVs. Interestingly, sEVs and lEVs performed contrary. AnnV+CD133+ lEVs performed weaker compared to CD63+CD133+ lEVs. Additionally, CD81+CD133+ sEVs were inferior to CD63+CD133+ lEVs, indicating that sEVs can be further divided into clinical relevant subpopulations by CD9, CD63 and CD81 sEVs plus a biomarker of interest, here CD133, to separate HCC from iCCA via an sEV-based liquid biopsy.

Studies were supported by the German Research Foundation to M.K. (Project# 410853455) and V.L.-K. (Project# 411345524).
SARCOPEANIA: An Important Prognostic Factor among Patients with Hepatocellular Carcinoma Treated with Sorafenib

Sang Hyun Choi1, Byoung Je Kim1, So Yeon Kim1, So Jung Lee1, Jae Ho Byun1. ‘Asan Medical Center, Radiology, Seoul, Korea, Rep. of South
Email: edwardchoi83@gmail.com

Background and aims: An understanding of the natural history of Liver Imaging Reporting and Data System (LI-RADS) is important. We assessed the imaging outcomes of LI-RADS v2018 categories in prospective hepatocellular carcinoma (HCC) surveillance cohort and determined imaging features significantly predictive of progression to a malignant LI-RADS category.

Method: The imaging outcomes of 183 patients (273 observations) prospectively enrolled between November 2011 and August 2012 were analyzed according to LI-RADS v2018. Cumulative incidences for progression to a malignant category (LR-3 or LR-M) and LR-4 or higher were calculated for each baseline category and compared using log-rank tests. Imaging features significantly predictive of progression to a malignant category were evaluated using Cox proportional hazards modeling.

Results: The 273 observations were initially categorized into 111 LR-1, 60 LR-2, 25 LR-3, and 27 LR-4. For LR-4 observations, the 1-year, 3-year, and 5-year cumulative incidences of progression to a malignant category were 18.5% (95% confidence interval [CI], 6.6–35.2%), 43.0% (95% CI, 23.1–61.5%), and 52.5% (95% CI, 25.9–73.5%), which were significantly higher than those of LR-1, LR-2, and LR-3 (p < 0.009) (Figure). For LR-3, the 1-year, 3-year, and 5-year cumulative incidences of progression to LR-4 or higher were 4.1% (95% CI, 1.1–10.4%), 13.9% (95% CI, 6.7–23.6%), and 23.1% (95% CI, 12.7–35.4%), which were significantly higher than those of LR-1 and LR-2 (p < 0.001). In multivariable analysis, size ≥1 cm (hazard ratio [HR] = 2.51, 95% CI, 1.08–5.84) and arterial-phase hyperenhancement (HR = 2.91, 95% CI, 1.28–6.62) were significantly independently associated with progression to a malignant category.

Conclusion: Long-term imaging outcomes differed significantly according to LI-RADS category. Size ≥1.0 cm and arterial-phase hyperenhancement were imaging features significantly predictive of progression to a malignant category.
SAT562
Diagnostic accuracy of protein-induced by vitamin K absence (PIVKA-II) for hepatocellular carcinoma (HCC) among caucasian cirrhotic patients with or without diagnostic serum a-fetoprotein (AFP) levels
Antonia Syriha1,2, Dionysia Mandilara2, Spyridon Pantzios2, Ioanna Statopoulou2, Georgia Barla2, Petros Galanis1,2, Ioannis Elefthinios1,2,1,2 General and Oncology Hospital of Kifisia “Agioi Anargyroi,” National and Kapodistrian University of Athens, Greece, Academic Department of Internal Medicine-Hepatogastroenterology Unit, Greece
Email: ielefs@nurs.uoa.gr

Background and aims: To evaluate the accuracy of serum biomarkers (AFP, PIVKA-II) for HCC diagnosis among patients with liver cirrhosis.
Method: 168 consecutive patients with liver cirrhosis (128 males, 91 with CTP score A, 89 with varices, 30 with portal vein thrombosis and 53 with diabetes) with (n = 68, HCC group) or without (n = 100, control group) concomitant histologically confirmed HCC were evaluated for serum levels of the two biomarkers, during a programmed outpatient visit. The mean age of the patients was 65 (± 10.8) years and they more often presented with alcoholic or non-alcoholic fatty liver disease (69/168, 41.1%), with the second and third causes of cirrhosis being chronic hepatitis C (44/168, 26.2%) or B (28/168, 16.7%) respectively. Patients with HCC were categorized to stage
0/A (n = 11), stage B (n = 16), stage C (n = 32) and stage D (n = 9), according to BCLC staging system.

Results: Mean/median levels of AFP (10835/155 vs 129/4.3, p < 0.001) and PIVKA-II (11095/2660 vs 864/46, p < 0.001) were significantly higher in HCC group compared to control group. The AUROC curve and the best proposed cut-off value for HCC diagnosis were 82.9% and 88.1%, respectively. The diagnostic accuracy of PIVKA-II among BCLC-C stage HCC patients was the best observed (AUROC = 88.1%, best proposed cut-off value = 655 mAU/ml). Excluding HCC patients with AFP levels above 400 ng/ml, the diagnostic accuracy of PIVKA-II in HCC continued to be significant (best proposed cut-off value 1089.53 mAU/ml) but the AUROC curve (72.1%) for HCC diagnosis was further reduced. It is worth mentioning that extremely high values of PIVKA-II (like those that are noticed in advanced HCC) were observed in 3 cirrhotic patients without HCC following treatment with acenocoumarol (the 2 of them) or having very low levels of vitamin K because of prolonged cholestasis due to sclerosing cholangitis (the third one). In these cases the diagnostic accuracy of the biomarker may be significantly affected.

Conclusion: Both biomarkers showed moderate accuracy for detecting HCC in patients with liver cirrhosis, when they were used separately. The diagnostic accuracy of PIVKA-II in patients with relatively low AFP levels (<400 ng/ml) remained at the same level.

SAT563
An easy to use score to predict survival in patients with hepatocellular carcinoma before the first transarterial chemoembolization session: AFP-DIAM score
Estelle Rebillard1, Benjamin Buchard2, Nicolas De Abreu3, Mathieu Boulin4, Anne Minello Franza5, Benoît Magnin6, Maud Reymond7, Leon Mut1, Bruno Pereira8, Armand Aberge1
1Centre hospitalier Universitaire Estang de Clermont-Ferrand, Department of Hepatology and Gastroenterology, Clermont-Ferrand, France; 2CHU Estaing, Medecine Digestive et Hepato-Bilaire, Clermont-Ferrand, France; 3CHU Estaing, Radiologie, Clermont-Ferrand, France; 4CHU Dijon, Pharmacie, Dijon, France; 5CHU Dijon, Hepatogastroenterologie, Dijon, France; 6CHU Gabriel-Montpied, Direction de la Recherche Clinique et Innovation, Clermont-Ferrand, France
Email: erebillard@chu-clermontferrand.fr

Background and aims: Transarterial chemoembolization (TACE) is widely used for the treatment of the hepatocellular carcinoma (HCC). TACE is recommended as a palliative treatment for patients with preserved hepatocellular function (either CHILD A or B7 without ascites), with a multinodular HCC without vascular invasion or associated metastasis, with a general preserved state. This profile corresponds to the B stage of the Barcelona Clinic Liver Cancer (BCLC) reference classification. This stage is very heterogeneous with a very different tumor profiles for a single therapeutic option available: TACE. Our aims were to develop a pre-therapeutic easy to use score, to assess the prognosis value of existing scores and to evaluate the prognosis value of the radiological response after two TACE sessions.

Method: 191 adult cirrhotic patients treated for HCC with TACE in our hospital from 2007 to 2017 were retrospectively included. We investigated the impact of liver function, patient characteristics and tumor burden on overall survival and developed a prognosis score using a regressing model to identify different prognostic groups in patients. Due to the low number of women, the score was only studied in male patients.

Results: Patients had a median age of 66 years and 126 patients were Child A. Two factors were associated with overall survival in the multivariate analysis: AFP > 500 ng/ml and the sum of the diameter of the nodules>130 mm (AFP-DIAM score). The score distinguishes two groups with significant difference survival time (median OS 28.3 months for a score = 0 versus 17.7 months for a score > 0). The score developed in this work was validated on an external cohort of 89 patients from Dijon University. Its discrimination capacity (c-index 0.58) is better than the existing scores (c-index STATE 0.55; c-index NIACE 0.54).

After two TACE, the radiological response with a threshold of –65% evaluated by mRECIST, identifies two groups with overall survival significantly different (30.1 versus 25.9 months; Se = 52%, Sp = 70%).

Conclusion: The AFP-DIAM score is a reliable and easy to use score which allows to distinguish two groups with different prognosis before first TACE session. An AFP-DIAM score > 0 identifies patients with dismal prognosis for which the question of a first-line treatment with an immunotherapy-tyrosine kinase inhibitor combination can be raised. Its use could provide further support to BCLC system to guide the therapeutic strategy of patients with HCC.

SAT564
Measurement of protease activity using novel plasma biosensors can accurately detect hepatocellular carcinoma
Tram Tran1, 2, Ben Holmes1, Chris Gulkia3, Anatoly Myaskovsky1, Andrea Shepard1, Mackenzie Rowe1, Sophie Cazanave1, Fayçal Touti1, Alejandro Balbin1, Wendy Winckler1, 2Glympse Bio; 2UCLA Division of Digestive Diseases
Email: tttdm@yahoo.com

Background and aims: Hepatocellular carcinoma (HCC) is the 5th leading cancer globally. Suboptimal adherence to routine surveillance and late diagnosis limit treatment options, thus new diagnostic options are needed for at-risk patients. Dysregulated protease activity may occur in HCC in biological pathways including tumor invasion of extracellular matrix, matrix remodeling, inflammation and fibrinolysis. Glympse’s novel liquid biopsy (LBx) technology using fluorogenic biosensors and machine learning can sensitively measure protease activity in plasma samples.

Aims: Assess protease activity changes in plasma of diagnosed HCC patients compared to healthy controls.

Method: We screened >600 peptide substrates to identify a panel of 21 biosensors that interrogate multiple biological pathways implicated in HCC pathogenesis (LBx-HCC). Retrospective plasma samples were obtained from two independent cohorts of patients (pts) diagnosed with HCC (cohorts A and B). Protease biosensor cleavage was assayed from plasma by fluorimetry, and the relative signal was used for classification by regularized logistic regression using 100 cross-validation (80% train, 20% validation splits). Independent classifier models were developed for each cohort and cross-tested without retraining in the second cohort to assess robustness.

Results: In cohort A, 30 pts diagnosed with HCC (M 77%, age 55.8 ± 9.9, BMI 22.3 ± 2.3, Asian 96% and 80% HBV/HCV etiology) were compared to 17 healthy controls (M 59%, age 35.8 ± 12.6, BMI 28.2 ± 4.5, Caucasian 59%/Asian 24%/Caucasian 17%). In cohort B, 10 pts diagnosed with HCC (M 50%, age 59.0 ± 15.4, BMI 23.6 ± 4.7, Caucasian 90% and no underlying viral disease) were compared to 37 healthy controls (M 65%, age 59.2 ± 9.4, BMI 25.8 ± 2.9, Caucasian 100%).

We performed LBx-HCC in all 94 subjects from both cohorts of pts and controls. Protease biosensors were highly effective at differentiating between pts with HCC and healthy controls in both cohorts (cohort A AUC = 0.94 [CI 0.87-1.1] and cohort B AUC = 0.96 [CI 0.89-1.1] (Figure). Importantly, the AUC remains above 0.94 even when naively applying a pre-trained classifier in one cohort to the other despite the differences in the disease etiology of each cohort. The most significant biosensors in HCC were cleaved by DPP4, Cathepsin C, MMP2 and KLK1.
Conclusion: In this study of two independently tested, diverse cohorts of patients with known HCC vs. healthy controls, Glympse’s plasma liquid biopsy platform using protease biosensors was highly effective at detecting HCC, with AUCs above 0.94. In the future, this technology could be used in surveillance strategies for earlier, easier, and more accurate diagnosis of HCC.

SAT565
On treatment alpha-fetoprotein reductions predict immunotherapy efficiency in patients with hepatocellular carcinoma
Bernhard Scheiner1,2, Katharina Pomej1,2, Lorenz Balcar1,2, Tobias Meischl1,2, Christian Müller1,2, Michael Trauner1, Matthias Pinter1,2. Medical University of Vienna, Division of Gastroenterology and Hepatology, Department of Internal Medicine III, Vienna, Austria;2Medical University of Vienna, Liver Cancer (HCC) Study Group Vienna, Division of Gastroenterology and Hepatology, Department of Internal Medicine III, Vienna, Austria
Email: bernhard.scheiner@meduniwien.ac.at

Background and aims: Immunotherapy with atezolizumab plus bevacizumab represents the new standard of care in systemic frontline treatment of hepatocellular carcinoma (HCC). Biomarkers to predict treatment success are an unmet need. An alpha-fetoprotein (AFP) decrease on treatment might identify patients with a favourable response to immunotherapy.

Method: Patients with HCC treated with PD-(L)1-based immunotherapy between June 2016 and October 2021 at the Medical University of Vienna were included. We investigated the impact of AFP response on radiological response (mRECIST 1.1) as well as time-to-progression (TTP), progression-free survival (PFS) and overall survival (OS). AFP response was defined as AFP decrease by ≥25% from baseline at week 6 or AFP within normal range at week 6 after immunotherapy initiation identifies patients with favourable radiological response and survival.

SAT566
Gender differences in hepatocellular carcinoma: is it all due to adherence to surveillance? A study of 1,716 patients over 3 decades
Wei-Lun Liou1, Terence Tan1, Kaina Chen1, Boon Bee George Goh1, Pik Eu Jason Chang1, Chee-Kiat Tan1. Singapore General Hospital, Department of Gastroenterology and Hepatology, Singapore
Email: liouweilun@gmail.com

Background and aims: Hepatocellular carcinoma (HCC) is one of the commonest causes of cancer-related death worldwide. There is well-established gender disparity in the incidence of HCC, with men 4 times more common than women. Whether gender is an independent factor for HCC survival is debatable. We study the influence of gender on clinical characteristics of HCC and on survival.

Method: We have an ongoing HCC database since 1988 enrolling patients with HCC seen in our department. Clinical data were prospectively captured. We studied and compared demography, HCC characteristics and survival between men and women. Survival analysis was censored on 31 October 2015 with input from our National Registry of Deaths.

Results: There were 1,716 HCC patients as of August 2021. 343 (20.0%) were women. Women were significantly older at HCC diagnosis (median 69 vs 62 years, p < 0.001). Women had a significantly higher incidence of non-viral liver disease (33.8% vs 24%, p < 0.001). In terms of specific aetiology, autoimmune liver disease was more common (2% vs 0.2%), and alcohol was less common (0.9% vs 5.8%) in women (both p < 0.001). More women were diagnosed via regular HCC surveillance (37.9% vs 29.6%, p = 0.003). Hence, women had less-advanced HCC at diagnosis as seen by higher frequency of single lesion (60.8% vs 52.7%, p < 0.001), smaller median tumour diameter (30 mm vs 39.5 mm, p = 0.038), lower frequency of portal vein tumour thrombus (19.4% vs 33.4%, p < 0.001) and less distant metastases (7.7% vs 11%, p = 0.043). Similarly,
significantly more women were in BCLC stages 0/A (39.7% vs 28.4%, p < 0.001). The overall median survival was significant better in women (10.1 vs 6.1 months, p = 0.003). When stratified by surveillance status, there was no significant gender difference in survival.

Conclusion: In this large cohort of Asian patients, women diagnosed with HCC were significantly more adherent to HCC surveillance and hence presented with less advanced HCC and had better overall survival than men. The gender difference in survival is likely due to women having better adherence with HCC surveillance.

SAT567 Non-alcoholic fatty liver disease and increased risk of incident primary liver tumours: a meta-analysis of observational cohort studies
Andrea Dalbeni1, Alessandro Mantovani2, Simone Conci2, Tommaso Valigi2, Alfredo Guglielmi2, David Sacerdotti2.
University of Verona, Medicine, Verona, Italy; 2University of Verona, Verona, Italy
Email: andrea.dalbeni@aovr.veneto.it

Background and aims: We performed a meta-analysis of cohort studies to quantify the magnitude of the association between non-alcoholic fatty liver disease (NAFLD) and risk of incident primary liver tumors, including hepatocellular carcinoma (HCC), cholangiocarcinoma (CC) and hepatoc-choanoicarcinoma (HCC-CC).

Method: We systematically searched PubMed, Scopus and Web of Science databases from the inception date to 30 June 2021, using predefined keywords, to identify observational cohort studies conducted in individuals in whom NAFLD was diagnosed by imaging techniques, International Classification of Diseases codes or biopsy. Meta-analysis was performed using random-effects modelling.

Results: We included 9 cohort studies for a total of 9, 134, 982 middle-aged individuals (10.6% with NAFLD) and 7, 026 incident cases of primary liver tumors, over a median follow-up of 10 years. NAFLD was significantly associated with a nearly 2-fold increased risk of developing primary liver tumors (random-effects hazard ratio [HR] 2.07, 95% confidence interval [CI] 1.62–2.65; I² = 97.2%). After stratifying the eligible cohort studies by country, we observed that among non-Asian individuals the presence of NAFLD was associated with an approximately 3-fold increased risk of developing primary liver tumors (random-effects HR 2.88, 95% CI 1.78–4.66; I² = 97.2%), whereas such association was less strength amongst Asian individuals (random-effects HR 1.55, 95% CI 1.33–1.80; I² = 79.6%).

Regarding different types of primary liver tumors, NAFLD was associated with a 3.2-fold increased risk of developing HCC (random-effects HR 3.21, 95% CI 1.93–5.33; I² = 96.7%), as well as with a 46% increased risk of developing CC or HCC-CC (random-effects HR 1.46, 95% CI 1.27–1.69; I² = 80.7%). Sensitivity analyses did not substantially alter these findings. Funnel plot did not reveal any significant publication bias.

Conclusion: This meta-analysis confirms that NAFLD is associated with an increased risk of developing primary liver tumors (especially HCC) over a median follow-up of 10 years. Further research is required to elucidate the complex link between NAFLD and different types of primary liver tumors.

SAT568 Characterization of gut microbiota and exploration of potential predictive model for hepatocellular carcinoma microvascular invasion
Ningning Zhang1, Zeyu Wang1, Jiayu Lv2, Yang Liu1, Tian Liu1, Shuwen Zhang2, Wang Li1, Lan Gong1,4, Xiaodong Zhang3, Emin El-Omar1,4, Wei Lu1. 1Department of Hepatobiliary Oncology, Liver Cancer Center, Tianjin Medical University Cancer Institute and Hospital, National Clinical Research Center for Cancer, Key Laboratory of Cancer Prevention and Therapy, Tianjin Medical University, Tianjin, China; 2Department of Hepatology, Tianjin Third Central Hospital, Tianjin, China; 3Department of Medicine, University of New South Wales, Sydney, Australia; 4Microbiome Research Centre, St George and Sutherland Clinical School, University of New South Wales, Sydney, Australia; 5Department of Gastrointestinal Cancer Biology, Liver Cancer Center, Tianjin Medical University Cancer Institute and Hospital, National Clinical Research Center for Cancer, Key Laboratory of Cancer Prevention and Therapy, Tianjin Medical University, Tianjin, China
Email: mail44luwei163.com

Background and aims: The correlation between gut microbiota and microvascular invasion (MVI) in hepatocellular carcinoma (HCC) patients remains unclarified. Prediction of MVI through gut microbiota analysis of HCC patients would be of accurate, non-invasive and very convenient assessment. The aim of the present study was to investigate the characteristics of gut microbiota in HCC-MVI patients and establish a microbial prediction model of HCC-MVI based on microbiome study.

Method: Fecal samples were collected from 59 HCC patients (24 of the total with MVI disease) and 16 healthy controls, and further analyzed by 16S rRNA amplicon sequencing. Bioinformatics methods were used to analyze the obtained sequence data. The diagnostic performance of microbiome characteristics in predicting MVI was assessed by receiver operating characteristic (ROC) curves. The correlation between gut microbiota and tumor microenvironment (TME) in HCC-MVI group were further analyzed with Immunohistochemistry and immunofluorescence assay.

Results: A significant differentiation trend of microbiota composition and structure was observed between the HCC-MVI group and those without vascular invasion (HCC-NVI). Compared with HCC-NVI group and healthy controls, Klebsiella, Proteobacteria, Prevotellaceae and Enterobacteriaceae were significantly enriched, whereas Firmicutes, Ruminococcus and Monoglobaceae were significantly decreased in HCC-MVI fecal samples. Klebsiella was considered to be the key microbiome signature for HCC-MVI patients. The area under the curve of the established HCC-MVI microbial prediction model was 94.81% (95% confidence interval: 87.63%–100%). The percentage of M2 type tumor-associated macrophage (TAMs) was increased in HCC-MVI group compared with HCC-NVI group (p < 0.001). M2-type TAMs in TME was negatively correlated with Shannon and Simpson index of HCC-MVI gut microbiota (all p < 0.01). In addition, predicted KEGG pathways showed that the functional differences in metabolic pathways of microbiome varied with groups.
CFDHCC scoring system for hepatocellular carcinoma using circulating cell-free DNA and machine learning algorithm based on dual screening for SAT569

**Conclusion:** The results indicated that differences existed in the fecal microbiome of HCC-MVI patients and healthy controls, the prediction model of HCC-MVI established with certain gut bacteria signature may have potential to predict HCC-MVI and the characteristics of fecal microbiome in HCC patients may associate with TME, though future larger-sample studies are required to validate this supposition.

**SAT569**

Machine learning algorithm based on dual screening for hepatocellular carcinoma using circulating cell-free DNA and CFDHCC scoring system


**Background and aims:** Hepatocellular carcinoma is diagnosed clinically by computed tomography or magnetic resonance imaging with or without level of serum AFP. However, there is a problem of high cost and radiation hazard to perform the above tests every time for diagnosis. While the current gold standard for diagnosing HCC is tumor biopsies, it only provides a limited snapshot of tumors and vary in sensitivity due to difficulties in identifying lesions. Therefore, we designed a non-invasive, low cost liquid biopsy platform based on circulating cell-free DNA (cfDNA) for the early diagnosis and evaluation of prognosis for HCC.

**Method:** Our platform was consisting of the polydopamine-silica hybrids alginate beads, in order to enhance the cfDNA adsorption. Overall, 249 individuals were enrolled in this study, including 152 patients with HCC, 43 patients with liver cirrhosis (LC), 24 patients with alcoholic liver disease (LA), and 30 healthy individuals (HD). We integrated the expression profiles of plasma cfDNA and cfDNA-AFP to establish a cfDNA score (cfDHCC) specific to HCC patients using a series of machine learning techniques, including the k-means cluster analysis, elbow method, and principal component analysis.

**Results:** Plasma cfDNA levels were the highest among patients with HCC (median: 0.25 ng/µL), followed by LC (0.18 ng/µL), LA (0.11 ng/µL), and HD (0.06 ng/µL), p value <0.001. The AUROC of plasma cfDNA levels was 0.713 (p = 0.001), 0.592 (p = 0.066), and 0.805 (p < 0.001) for detecting HCC from LC, LA, and HD groups, respectively. The AUROC of cfDNA-AFP to differentiate HCC from LC, LA, and HD were 0.861 (p < 0.001), 0.744 (p < 0.001), and 0.971 (p < 0.001), respectively. In TACE-treated HCC patients, in the evaluation of overall survival using the cfDHCC score, the group with the high cfDHCC score showed a trend of poorer prognosis than the group with the low cfDHCC score (47.7 ± 5.6 vs. 65.7 ± 4.4 months, p = 0.077). Moreover, the group with the high cfDHCC score showed a poorer prognosis than the group with the low cfDHCC score, when the cfDHCC score was used in the evaluation of recurrence-free survival for recurrence with tumor multilocality (23.2 ± 5.5 vs. 54.0 ± 4.6 months, p = 0.001) or marginal recurrence (27.4 ± 6.3 vs. 41.1 ± 6.3 months, p = 0.061) in TACE-treated HCC patients.

**Conclusion:** Our novel platform showed high diagnostic and prognostic capabilities. Our results presented herein indicate that cfDNA using polydopamine-silica hybrids alginate beads could be a promising tools for HCC diagnosis and evaluation of prognosis. It could be potentially utilized in the clinic as a reliable system for identifying HCC in early stages, guiding therapeutic decisions, and improving overall survival of HCC patients.

**SAT570**

Sarcopenia impairs survival and treatment efficacy in patients with hepatocellular carcinoma undergoing immunotherapy

Bernhard Scheiner, Katharina Lampichler, Katharina Pome, Lucian Beer, Lorenz Balcar, Tobias Meischl, Christian Müller, Michael Trauner, Martina Scharitzer, Dietmar Tamandl, Matthias Pinter, Bernhard Scheiner, Medical University of Vienna, Division of Gastroenterology and Hepatology, Department of Internal Medicine III, Vienna, Austria; Medical University of Vienna, Liver Cancer (HCC) Study Group Vienna, Division of Gastroenterology and Hepatology, Department of Internal Medicine III, Vienna, Austria; Medical University of Vienna, Department of Biomedical Imaging and Image-Guided Therapy, Vienna, Austria.

**Background and aims:** Sarcopenia is a common problem in patients with cirrhosis and hepatocellular carcinoma (HCC) and frequently...
impairs the clinical course of these patients. The impact of baseline sarcopenia on survival and treatment efficacy in HCC patients undergoing immunotherapy has yet to be evaluated.

**Method:** Patients with HCC treated with PD- (L)1-based immunotherapy between June 2016 and October 2021 at the Medical University of Vienna were included. Sarcopenia was defined by transversal psoas muscle thickness (TPMT) at <12 mm/m in men and <8 mm/m in women at the level of the third lumbar vertebrae using cross-sectional imaging (CT/MRI) at baseline. We investigated the impact of sarcopenia on radiological response (mRECIST 1.1) as well as time-to-progression (TTP), progression-free survival (PFS) and overall survival (OS).

**Results:** TPMT was evaluated at a median of 20 (IQR 0–38) days prior to first immunotherapy infusion and sarcopenia was present in 37/83 (45%) patients. Sarcopenia at baseline was much more prevalent in men (53%) compared to women (19%, p = 0.006) and the presence of sarcopenia was associated with a worse radiological response (which was evaluable in 68 patients): complete/partial response (CR/PR): 11.5% vs. 35.7%, stable disease (SD): 30.8% vs. 40.5, progressive disease (PD): 57.7% vs. 23.8% (p = 0.011). Patients with sarcopenia also had a significantly worse outcome (evaluable in 81 patients due to early loss-of-follow-up in 2 patients): time-to-progression (TTP): 2.5 (95%CI: 1.9–3.1) vs. 10.4 (95%CI: 8.7–12.1) months (p = 0.010); progression-free survival (PFS): 2.3 (95%CI: 1.8–2.7) vs. 9.2 (95%CI: 2.5–15.9) months (p = 0.002); overall survival (OS): 5.3 (95%CI: 2.5–8.0) vs. 22.6 (95%CI: 8.6–36.6) months (p = 0.012). Even after multivariable adjustment for baseline Child-Pugh stage, ECOG PS >1, presence of macrovascular invasion or extrahepatic metastasis and baseline AFP levels (IU/ml), sarcopenia (aHR: 2.24, 95%CI: 1.17–4.31, p = 0.016) remained an independent predictor of survival.

**Conclusion:** The presence of sarcopenia as determined by TPMT measurement at the level of the third lumbar vertebrae prior to treatment initiation significantly impairs survival and treatment efficacy in HCC patients undergoing immunotherapy.

**SAT571**

**Comparable efficacy between on-going vs. initiation of antiviral therapy at the time of curative treatment for hepatitis B virus-related hepatocellular carcinoma**

Mi Na Kim¹, Beom Kyung Kim², Su Jong Yu³, Seung Up Kim². ¹CHA Bundang Medical Center, CHA University School of Medicine, Department of Internal Medicine, Seongnam, Korea, Rep. of South; ²Yonsei University College of Medicine, Department of Internal Medicine, Seoul, Korea, Rep. of South; ³Seoul National University College of Medicine, Department of Internal Medicine, Seoul, Korea, Rep. of South 

**Background and aims:** Antiviral therapy (AVT) should be applied for patients with newly-diagnosed hepatocellular carcinoma (HCC), if HBV DNA is detectable. We compared the long-term prognosis between patients with on-going AVT and those who initiated AVT at the time of curative treatments for HBV-related HCC.

**Method:** Between 2013 and 2018, patients with HBV-related HCC who received curative treatments were considered eligible. Primary outcomes were HCC recurrence and overall mortality.

**Results:** In the study population (n = 545), the cumulative probabilities of HCC recurrence at 1, 3, and 5 years was statistically similar between patients in on-going AVT group (oAVT group, 9.9%, 29.4%, and 39.5%, respectively) and those in the initiation AVT group (iAVT group, 13.1%, 27.8%, and 40.2%, respectively) (p = 0.670 by log-rank test). The cumulative probabilities of overall mortality was also comparable between the 2 groups (4.2%, 10.8%, and 10.8%, respectively, in oAVT group vs. 1.5%, 7.1%, and 10.8%, respectively, in iAVT group) (p = 0.670 by log-rank test). The cumulative probabilities of overall mortality was also comparable between the 2 groups (4.2%, 10.8%, and 10.8%, respectively, in oAVT group vs. 1.5%, 7.1%, and 10.8%, respectively, in iAVT group) (p = 0.381 by log-rank test). The risk of the early (<2 years) and late (≥2 years) recurrence was statistically similar between the 2 groups (all p > 0.05 by log-rank tests). Propensity score matching and inverse probability of treatment weighting analysis also yielded a similar risk of HCC recurrence and overall mortality between the 2 groups (all p > 0.05 by log-rank tests).

**Conclusion:** The long-term prognosis of patients who received curative treatments for newly diagnosed HBV-related HCC was comparable regardless of the timing of AVT initiation.
SAT572

Immune-related adverse events and clinical outcomes in unresectable hepatocellular carcinoma: a single-institute retrospective analysis

Antonela Cammarota1,2, Nicola Personeni1,2, Tiziana Pressiani1, Antonio D’Alessio2,2, Valentina Zanuso1,2, Silvia Bozzarelli1, Laura Giordano1, Lorenza Rimassa1,2, Armando Santoro1,2.

1Humanitas Research Hospital, Oncology and Hematology Unit, Cascina Perseghetto, Italy; 2Department of Biomedical Sciences, Pieve Emanuele, Italy; 3Imperial College London, Department of Surgery and Cancer, London, United Kingdom

Email: antonella.cammarota@humanitas.it

Background and aims: Immune checkpoint inhibitors (ICIs), as monotherapy or in combinations, have broadened the treatment landscape of unresectable hepatocellular carcinoma (HCC), either in first-line or in further lines. The prognostic role of multitarget inhibitors–induced adverse events has been proven in HCC patients (pts) and the development of immune-related adverse events (irAEs) has been associated with improved outcomes in other cancer types, such as melanoma and non-small cell lung cancer. Despite initial evidence of correlation, whether or not irAEs can predict outcomes in unresectable HCC still needs to be confirmed. In this retrospective analysis we aimed to assess the association between grade (G) ≥ 3 irAEs and the efficacy outcomes, namely overall response rate (ORR), OS, progression-free survival (PFS) among pts with unresectable HCC treated with ICIs.

Method: ORRs were calculated as the sum of complete and partial responses per RECIST 1.1 and compared using chi-squared test. OS and PFS were estimated using the Kaplan-Meier method and survival curves were compared using log-rank test. Statistical significance was set at p = 0.05 and all reported p values are two-sided.

Results: From August 2015 to March 2021, 110 pts with unresectable HCC received ICIs within clinical trials available at our Institution. A total of 58 pts (52.7%) received ICIs as first-line systemic treatment and 36 pts (32.7%) received single-agent ICI. Overall, 38 pts (group A) developed G ≥ 3 toxicities whereas 72 pts (group B) experienced no or G < 3 toxicities. The most common G ≥ 3 AEs were hepatic (29.8%), dermatological (13.2%) and gastrointestinal (7.9%) toxicities. ORR was 18.4% in group A and 11.1% in group B (p = 0.96). Median PFS was 6.9 and 3.9 months (HR 0.66, 95% CI 0.43–0.99, p = 0.04) and median OS was 17.6 and 9.1 months (HR 0.52, 95% CI 0.32–0.84, p = 0.04) in group A and B, respectively (Figure 1).

Conclusion: Despite the small sample size and the retrospective nature, our analysis suggests that the development of G ≥ 3 irAEs might correlate with survival outcomes in unresectable HCC. Prospective analyses are needed to confirm these results, hopefully providing further insights on possible predictive biomarkers.

SAT573

Multistage epigenome-wide association study identifies highly accurate epigenomic signatures in association with hepatocellular carcinoma: The HCC epigenome score

Abderrahim Oussalah1, Ryan Hlady2, Sébastien Hergalant1, Jean-Pierre Bronowicki1, Jean-Louis Guéant1, Chen Liu3, Keith Robertson2. 1University of Lorraine, INSERM UMR_S 1256, Nutrition, Genetics, and Environmental Risk Exposure (NGERE), Faculty of Medicine of Nancy, F-54000 Nancy, France; 2Department of Molecular Pharmacology and Experimental Therapeutics, Mayo Clinic, Rochester, MN, 55905, USA; 3Department of Pathology, Yale School of Medicine, New Haven, CT, 06510, USA

Email: abderrahim.oussalah@univ-lorraine.fr

Background and aims: Hepatocellular carcinoma (HCC) represents the most common primary malignant tumor of the liver. Epigenetic alterations are a common hallmark of human cancer. We recently developed the smoothing method for calculating and visualizing data from epigenome-wide association studies (EWASs) and demonstrated its utility for identifying highly accurate epigenomic signatures in DNA methylation analyses (patent pending, EP21306458). The primary aim was to look for significant epigenomic signatures associated with HCC through a multistage EWAS approach.

Method: We conducted four-step epigenome association studies of HCC in 357 cases and 239 controls originating from four independent cohorts. In stage #1 (derivation study), we analyzed the epigenome-wide DNA methyleme profiles generated from 21 HCC and 100 non-HCC liver tissue samples using the Infinium Human Methylation 450 K BeadChip. We derived an epigenomic score based on the top significant CpG signatures, the “HCC Epigenome Score.” We assessed the diagnostic accuracy of the “HCC Epigenome Score” in two replication cohorts using HCC and non-HCC tissue samples (stage #2: 26 vs. 83; stage #3: 306 vs. 50, respectively). In stage #4, we performed six independent epigenome association study using epigenome-wide DNA methyleme profiles generated from 10 plasma samples of patients with (n = 4) or without HCC (n = 6).

Results: The epigenome-wide association study highlighted 105 CpG probes in 13 top loci (CpG islands) associated with the HCC phenotype (RUNX3, KCNA3, DNM3, FOXL2/FOXL2NB, SHISA3, HCC7, BVES, EYA4, CELF2, MIR129-2, PRKCB, SEPT9, and LPAR2) (Figure, panel A) (patent pending, EP21306459). In hierarchical clustering analysis, the 105 CpG probes were highly discriminant between HCC and non-HCC samples (Figure, panel B). In ROC analysis, the HCC Epigenome Score had an AUROC of 0.960 (95% CI, 0.788–100; p < 0.0001) for detecting HCC samples. In replication studies on tissue samples (stages #2 and #3), all the 13 loci were significantly associated with the HCC phenotype. Random effect meta-analysis confirmed the significance of the 13 top loci. In ROC analysis that used individual-level data, the HCC Epigenome score had an AUROC of 0.955 (95% CI, 0.935–0.969; p < 0.0001) for detecting HCC. According to the underlying chronic liver disease, the HCC Epigenome score had AUROCs of 0.992 (95% CI, 0.968–0.998; p < 0.0001); 0.982 (95% CI, 0.935–0.995; p < 0.0001); 0.950 (95% CI, 0.671–1.000; p < 0.0001); 0.908 (95% CI, 0.845–0.952; p < 0.0001), and 0.952 (95% CI, 0.902–1.000; p < 0.0001) for HCV, HBV, NASH, alcohol, and other etiologies, respectively. Using plasma circulating cell-free DNA (stage #4), the HCC epigenome score discriminated between HCC and non-HCC patients.

Conclusion: Using four independent cohorts, we derived and validated the HCC epigenome score that showed high diagnostic accuracy for diagnosing HCC.
Figure: (abstract: SAT573)
BACKGROUND AND AIM: Hepatocellular carcinoma (HCC) is a major cause of liver cancer-related death worldwide. It usually occurs in cirrhosis with different aetio-pathogenesis. Serum IL-6 is a pro-inflammatory cytokine that increases considerably in pathological settings such as trauma, inflammation and neoplasia. Based on pre-clinical data in HCC, IL-6 signalling leads to tumour progression or local recurrence. Aim of our study is to clarify if the levels of IL-6 are associated with HCC progression and its different aetio-pathogenesis in cirrhotic patients.

METHOD: 111 consecutive HCC cirrhotic patients (with different stages and aetio-pathogenesis) were enrolled and compared with 36 cirrhotic patients without HCC. Patients were divided according to Child Pugh (CP) class and severity of HCC disease (BCLC). The major anthropometric and biochemical parameters, particularly serum IL-6, were collected. The degree of sarcopenia was also considered using TC count.

RESULTS: IL-6 levels were different between advanced and not advanced HCC (p = 0.01), while no difference in IL-6 levels was documented in CP-C with and without HCC; however, IL-6 levels were higher in advanced HCC (OR 4.58 CI: 1.19–17.55; p = 0.001). IL-6 levels were different also between different ethiologies of cirrhosis; in particular, no differences in viral and metabolic cirrhosis, low levels (p < 0.001) in alcoholic and higher in autoimmune HCC or in combination of different aetiologies. IL-6 correlated also with sarcopenia severity (p < 0.001) especially in advanced HCC patients (p < 0.001). In no HCC CP-C patients, IL-6 was not correlated with sarcopenia. In linear regression IL-6 was correlated with AFP (p < 0.001, r = 0.57). In multivariate analysis IL-6 was linked with aetio-pathogenesis, cancer progression, sarcopenia, CP and lymphocytes count.

CONCLUSION: These data suggest that IL-6 is higher in inflammatory states (like cirrhosis with CP-C) but it has a closer relation with advanced HCC and could be a marker for the disease itself. IL-6 seems to be also a predictor of sarcopenia especially in advanced HCC patients. Also, cirrhosis aetio-pathogenesis has shown different IL-6 levels, documenting a different inflammatory setting. IL-6 could be a new marker to classify advanced HCC and a possible future drug target considering the different cirrhotic aetio-pathogenesis.

SAT574
Interleukin-6 as a new marker for advanced sarcopenic HCC patients with different cirrhotic aetiology
Andrea Dalbeni1, Filippo Cattazzo1, Antonio Vella1, Giovanna Zanoni1, Michele Revillaqua1, Jasmin Kassem1, Anna Mantovani1, Simone Conci1, Tommaso Campagnaro1, Alfredo Guglielmi1, Michele Bevilacqua1, Jasmin Kassem1, Anna Mantovani1, Michele Milella1, David Sacerdoti1, 1University of Verona, Medicine, Verona, Italy

Email: moje@clin.au.dk

Background and aims: Interleukin-6 (IL-6) is a pro-inflammatory cytokine that increases considerably in pathological settings such as trauma, inflammation and neoplasia. Based on pre-clinical data in HCC, IL-6 signalling leads to tumour progression or local recurrence. Aim of our study is to clarify if the levels of IL-6 are associated with HCC progression and its different aetio-pathogenesis in cirrhotic patients.

Method: 111 consecutive HCC cirrhotic patients (with different stages and aetio-pathogenesis) were enrolled and compared with 36 cirrhotic patients without HCC. Patients were divided according to Child Pugh (CP) class and severity of HCC disease (BCLC). The major anthropometric and biochemical parameters, particularly serum IL-6, were collected. The degree of sarcopenia was also considered using TC count.

Results: IL-6 levels were different between advanced and not advanced HCC (p = 0.01), while no difference in IL-6 levels was documented in CP-C with and without HCC; however, IL-6 levels were higher in advanced HCC (OR 4.58 CI: 1.19–17.55; p = 0.001). IL-6 levels were different also between different ethiologies of cirrhosis; in particular, no differences in viral and metabolic cirrhosis, low levels (p < 0.001) in alcoholic and higher in autoimmune HCC or in combination of different aetiologies. IL-6 correlated also with sarcopenia severity (p < 0.001) especially in advanced HCC patients (p < 0.001). In no HCC CP-C patients, IL-6 was not correlated with sarcopenia. In linear regression IL-6 was correlated with AFP (p < 0.001, r = 0.57). In multivariate analysis IL-6 was linked with aetio-pathogenesis, cancer progression, sarcopenia, CP and lymphocytes count.

Conclusion: These data suggest that IL-6 is higher in inflammatory states (like cirrhosis with CP-C) but it has a closer relation with advanced HCC and could be a marker for the disease itself. IL-6 seems to be also a predictor of sarcopenia especially in advanced HCC patients. Also, cirrhosis aetio-pathogenesis has shown different IL-6 levels, documenting a different inflammatory setting. IL-6 could be a new marker to classify advanced HCC and a possible future drug target considering the different cirrhotic aetio-pathogenesis.

SAT576
Time-trends in cholangiocarcinoma incidence-a danish nationwide cohort study
Morten Daniel Jensen1, Joe West2,3, Frank Viborg Mortensen4, Peter Jepsen1. 1Aarhus University Hospital, Department of Hepatology and Gastroenterology, Aarhus N, Denmark; 2University of Nottingham, Lifespan and Population Health, School of Medicine, NG5 1Pb, United Kingdom; 3Nottingham University Hospitals NHS Trust and the University of Nottingham, NIHR Nottingham Biomedical Research Centre (BRC), Nottingham, United Kingdom; 4Aarhus University Hospital, Department of Surgical Gastroenterology, Aarhus N, Denmark

Email: moje@clin.au.dk

Background and aims: Cholangiocarcinoma (CCA) is a usually fatal primary liver cancer originating from the biliary epithelium. Extensive surgery is the only curative treatment, and adjuvant chemo- and/or radiotherapy is standard. Up-to-date data on incidence are crucial for our understanding of the disease and for designing trials of interventions. Therefore, we set out to examine incidence of CCA in a nationwide Danish cohort.

Method: We included all Danish patients, N = 2600, with an ICD-10 diagnosis code of CCA (intrahepatic [iCCA]: C221; extrahepatic [eCCA]: C240) in the Danish Cancer Registry, between 1999-2019. We computed the standardized annual incidence rates of CCA in the Danish population using publicly available data on population demographics and standardized to the Danish population in 1999. We estimated the annual change in CCA incidence using a Poisson regression model.

Results: The standardized incidence rate (SIR) for iCCA increased from 0.41 (95% confidence interval [CI] 0.26–0.63) in 1999 to 1.90 (95% CI 1.55–2.31) in 2019 (Incidence rate ratio [IRR]: 4.59 [95% CI 2.89–7.28]), while the SIR for eCCA decreased from 1.75 (95% CI 1.41–2.14) in 1999 to 0.85 (95% CI 0.62–1.13) in 2019 (IRR: 0.48 [95% CI 0.34–0.69]). The overall SIR of total CCA (iCCA and eCCA) was 1.89 (95% CI 1.78–2.01) for men and 2.13 (95% CI 2.02–2.26) for women, and the trend of increasing IR for iCCA and decreasing IR for eCCA was observed in both sexes. The SIR of total CCA increased from 2.16 (95% CI 1.79–2.60) in 1999 to 2.79 (95% CI 2.35–3.27) in 2019, yielding an IRR of 1.29 (95% CI 1.01–1.64) and an annual increase of 2.51% (95% CI 1.81–3.22).

Conclusion: The incidence of CCA has increased since 1999, driven by a 4-fold increase in incidence of intrahepatic CCA while incidence of extrahepatic CCA has decreased by half. The reasons for this pattern are unclear but are likely due to changing environmental exposures over time.
Hierarchical fusion strategy of deep learning networks (HFS-Net) consists of three stages based on U-Net and DenseU-Net. The first stage segments tumors in a slice and estimates the tumor size. The second stage uses customized networks for segmenting small and large tumors adaptively. The third stage integrates the outcomes of the first two stages and uses a 3D U-Net to segment 3D liver tumors. Global dice, sensitivity, precision and F1 score were used to measure the performance of HFS-Net model.

**Results:** The 2D DenseU-Net using triple phase images was more effective for segmenting small tumors, whereas the 2D U-Net using portal venous phase images was more effective for segmenting large tumors. The HFS-Net performed better, compared with the single-strategy deep learning model in segmenting small and large tumors. In the test set, the HFS-Net model achieved good performance in identifying HCC on dynamic CT images, with global dice of 82.8%. The overall sensitivity, precision and F1 score were 84.3%, 75.7% and 0.796 per slice, respectively, and 92.2%, 93.2% and 0.927 per patient, respectively. The sensitivity in tumors <2 cm, 2–5 cm and >5 cm were 57%, 79.2% and 89.5% per slice, respectively, and 72.7%, 93.8% and 100% per patient, respectively.

**Conclusion:** The HFS-Net model achieved good performance in the detection and segmentation of HCC from dynamic CT images. Automatic 3D tumor segmentation from dynamic CT scans using HFS-Net can support radiologic diagnosis and facilitate automatic radiomics analysis.

**SAT577**

*Changing global epidemiology of liver cancer from 1990 to 2019: NASH is the fastest growing cause of liver cancer*

Daniel Huang1,2, Amit Singal3, Yuko Kono1, Hashem El-Serag4, Rohit Loomba1. 1University of California San Diego, La Jolla, United States; 2Yong Loo Lin School of Medicine, Singapore, Singapore; 3UT Southwestern Medical Center, Dallas, United States; 4Baylor College of Medicine, Houston, United States

**Email:** roloomba@ucsd.edu

**Background and aims:** The major etiologies for liver cancer are hepatitis B virus (HBV), hepatitis C virus (HCV), alcohol, and non-alcoholic steatohepatitis (NASH). Over the last three decades, there have been changes in the etiology and burden of liver cancer due to increasing alcohol consumption, rising obesity rates and advances in prevention and treatment of HBV and HCV. We assessed the temporal trends in the incidence, mortality rates, disability-adjusted life-years (DALYs) secondary to liver cancer, and the contributions of various liver disease etiologies.

**Method:** We estimated the annual frequencies and age-standardized rates (ASRs) of liver cancer incidence, death and DALYs, from 1990 to 2019 by country, region and etiology using data obtained from the 2019 Global Burden of Disease study.

**Results:** In 2019 globally, there were 534,000 incident cases, 485,000 deaths, and 12.5 million DALYs due to liver cancer. Between 1990 and 2019, there was a 43% increase in the frequency of incident cases of liver cancer and a 33% increase in liver cancer deaths. However, the incidence ASR fell from 7.0 per 100,000 in 1990 to 6.9 per 100,000 in 2019, and the death ASR fell from 6.8 per 100,000 to 6.3 per 100,000. In 2019, the highest frequency of deaths occurred in the Western Pacific (52%), followed by South-East Asia (15%), Europe (13%), the Americas (10%), the Eastern Mediterranean region (6%) and Africa (4%). The annual percentage change of the death ASRs by country between 1990 and 2019 is shown in Figure 1. The greatest rise in death ASRs occurred in the Americas (annual percentage change [APC] 1.15%), followed by Europe (APC 0.71%) and South-East Asia (APC 0.64%). DALYs increased by 175% in the Americas, 131% in the Western Pacific and 125% in Europe between 1990 and 2019.
Liver resection is the only curative therapeutic option for large hepatocellular carcinoma (>5 cm), but survival is less good than in smaller tumors mostly because of the high recurrence rate. There is currently no proper tool for relapse risk stratification. We investigated for prognostic factors before and after hepatectomy for a single large HCC.

**Method:** We retrospectively identified 119 patients who underwent liver resection for a single large HCC in 2 tertiary care French centers, and collected pre and post-operative clinical, biological and radiological features. The primary outcome was overall survival at 5 years. Secondary outcomes were recurrence-free survival at 5 years, and prognostic factors for recurrence.

**Results:** 84% of the patients were male, and the mean age was 66 years old (58–74). 39 (33%) had Child-Pugh A cirrhosis, and mean Model for End-Stage Liver disease score was 6 (6–8). Etiology of liver disease was predominantly alcohol-related (48%), followed by non-alcoholic steatohepatitis (22%), hepatitis B (18%) and C (10%). Mean tumor size was 70 mm (55–110). Median overall survival was 72.5 months (IC 95%: 56.2–88.7), and five-year overall survival was 55.1 ± 7.4%. The median recurrence-free survival was 26.6 months (IC95%: 16.0–37.1), and five-year recurrence-free survival was 37.8 ± 5.5%. In multivariable analysis, pre-operative prognostic factors of recurrence were baseline AfP > 7 ng/ml (p < 0.001), portal invasion on imagery (p = 0.003) and cirrhosis (p = 0.020). With these factors, we obtained a simple recurrence-risk scoring system that classified 3 groups with different disease-free survival medians (p < 0.001): no risk factor (65 months), 1 risk factor (36 months), ≥2 risk factors (8.9 months). After liver resection, the presence of satellite nodules was the only significant predictive factor on a multivariate analysis. Adding this value to our pre-operative score, we obtained a pre- and post-operative score that was able to differentiate 4 groups with significantly different disease-free survival medians.

**Conclusion:** Liver resection is the only curative option for large HCC and we confirmed that survival can be satisfying in experienced centers. Recurrence is the main issue of surgery, and we proposed a simple pre-operative score that could help identifying patients with the most worrying prognosis, possible candidates for combining therapy.
SAT580
Deep view on HCC gene signatures and their comparison with other cancers
Yuquan Qian1, Timo Itzel1,2, Matthias Ebert1,3, Andreas Teufel1,2,3.
1Medical Faculty Mannheim, University of Heidelberg, Department of Medicine II, Mannheim, Germany; 2Medical Faculty Mannheim, University of Heidelberg, Division of Hepatology, Division of Bioinformatics, Department of Medicine II, Mannheim, Germany; 3Medical Faculty Mannheim, University of Heidelberg, Clinical Cooperation Unit Healthy Metabolism, Center for Preventive Medicine and Digital Health Baden-Württemberg, Mannheim, Germany Email: andreas.teufel@medma.uni-heidelberg.de

Background and aims: Throughout the past two decades, numerous HCC-dependent gene expression signatures have been published, but none of them made it into clinical practice. Setting up a comparative transcriptomics profiling approach, we therefore explored the specificity of these signatures to HCC as this may be a critical with respect to clinical usage.

Method: From the existing publications, we collected HCC gene signatures and evaluate them in independent genome wide gene expression profiles of patients suffering from HCC. Evaluations were performed using four different (commercial and non-commercial) gene expression profiles, particularly a modified version of the ProfileChaser, Oncomine Premium, GENEVA, and SigCom LINCS for assigning similar pre-analyzed profiles to our signatures of interests. These results were screened for different cancer entities. We furthermore evaluated common core genes, overlapping pathways, and generation approaches among these HCC gene signatures.

Results: Although the specificity of the investigated HCC signatures varied significantly, none of the signatures exhibited strict specificity to HCC. Many signatures expressed similar profiles in other tumors, especially to renal, breast, and colorectal cancers and particularly those signatures designed to distinguish between good and poor survival of patients. Specificity of HCC gene signatures proved difficult, we furthermore found that no common core genes, few overlapping pathways, and a significant heterogeneity in signature generation approaches among HCC gene signatures may account for this phenomenon.

Conclusion: Our study shows the poor specificity of current HCC gene signatures, and demonstrates that the clinical use and independent validation of HCC genetic signatures remains challenging. Overall, our data suggest the necessity of standards in tissue preparation and store, as well as signature generation, statistical methods and independent validation.

Figure: Gene signature query results of four bio-tools. LC: Liver Cancer, OC: Other Cancers. The color represents the number of datasets matched in each tool; grey means no datasets matched.

SAT581
Causes of death after Intrahepatic cholangiocarcinoma diagnosis: a population-based study
Anas Elgenidy1, Ahmed Abdelwahab2, Prasun Jalal2. 1Faculty of medicine, Cairo University, Cairo, Egypt, Cairo, Egypt; 2Baylor College of Medicine, Department of Medicine, Gastroenterology and Hepatology Division, Houston, United States Email: Ahmed.Abdelwahab@bcm.edu

Background and aims: Intrahepatic cholangiocarcinoma (ICCA) has shown a substantial increase in mortality globally. On the contrary, perihilar cholangiocarcinoma (pCCA) and distal cholangiocarcinoma (dCCA) have been decreasing; however, studies on causes of death in ICCA patients remain limited. We aim to focus on and evaluate the causes of death after ICCA diagnosis.

Method: In this retrospective cohort, we studied 276, 712 ICCA patients diagnosed between 2004 and 2016 in the United States. The standardized mortality ratio (SMRs) with 95% confidence intervals (CIs) for each cause of death using the SEER*Stat software version 8.3.9.2.

Results: Out of the 276, 712 patients diagnosed with ICCA, 203, 914 (73.7%) were between 50 and 79 years (The mean age at diagnosis was 63.51 years); 220, 648 (79.7%) were white, and 144, 942 (52.4%) were females. 35, 814 patients (12.9%) died during the follow-up period with a mean age of 70.83 years. The highest number of deaths (34, 444; 96.2%) occurred within the first year following the diagnosis. During all latency periods, 3, 339 (9.3%) deaths were from ICCA, and 27, 790 (77.6%) were from other cancers. The most common cancer causes were lung and bronchus cancer (9862; 27.5%) followed by pancreatic cancer (3475; 9.7%), and 4, 685 (13.1%) from non-cancer causes. Cardiovascular diseases were the leading non-cancer causes (SMR 1.95; 95% CI (1.85–2.06)), followed by Chronic Obstructive Pulmonary Disease and related Conditions (SMR 2.52; 95% CI (2.29–2.78)).

Conclusion: Following ICCA diagnosis, the most common cause of death was lung and bronchus cancer followed by pancreatic cancer and ICCA, and cardiovascular disease represents a substantial percentage of non-cancer deaths (4.97%). Our findings provide
SAT582
Genes modulating liver fat accumulation and lipogenesis predict development of hepatocellular carcinoma among direct antiviral agents treated cirrhotics C with and without viral clearance
Ginevra Mocchetti¹, Antonio Acquaviva¹,², Giulia Francesca Manfredi¹,², Michela Emma Burlone², Francesca Baorda¹,², Davide Di Benedetto¹,², Ramana Mallela Venkata¹, Rosalba Minisini¹, Cristina Rigamonti¹,², Giulia Francesca Manfredi¹,², Davide Di Benedetto¹,², Università del Piemonte Orientale, Department of Translational Medicine, Novara, Italy; ²AOU Maggiore della Carità, Division of Internal Medicine, Novara, Italy. Email: michela.burlone@uniupo.it

Background and aims: Genetic risk score (GRS) is a polygenic scoring system that estimates the predisposition to accumulate liver fat combining PNPLA3 (rs738409), TM6SF2 (rs58542926), MBOAT7 (rs641738) and GCKR (rs1260326) polymorphisms. GRS score was related to the probability to de novo hepatocellular carcinoma (HCC) development in HCV cirrhotic patients, treated with direct antiviral agents (DAA). In this setting, it is suggested that HSD17B13: TA variant; in particular, male gender (HR 6.75, CI 1.62–28.2, p = 0.009), GRS ≥0.457 (75th percentile) predicted the onset of HCC regardless of gender, diabetes, albumin, INR and FIB4 (HR 2.89, CI 1.19–7.07, p = 0.02). The goodness of the model was improved by adding SVR achievement and presence of HSD17B13 variant; in particular, male gender (HR 6.75, CI 1.62–28.2, p = 0.009), GRS ≥0.457 (HR 4.24, CI 1.59–11.33, p = 0.004), carriage of the splice variant HSD17B13: TA (HR 0.24, CI 0.07–0.75, p = 0.015) and failure to achieve SVR (HR 7.7, CI 2.38–25, p = 0.001), were independent predictors of de novo HCC.

Conclusion: The study results confirmed that genes modulating lipogenesis and liver fat are important risk factors for the development of HCC in HCV cirrhotic patients treated with DAA.
Conclusion: The present study demonstrated the potential negative prognostic role of sTREM-2 on overall HCC survival. However, future prospective studies are necessary to elucidate whether the systematic assessment of sTREM-2 concentrations could be useful to predict the survival in HCC patients.

SAT584
Bone mineral density is a predictor of mortality in female patients with cholangiocarcinoma undergoing palliative treatment
Markus Jördens1, Linda Wittig1, Georg Flüggen1, Sven H Loosen1, Christoph Roderburg1, Tom Lüdde1. 1Düsseldorf
Email: christoph.roderburg@med.uni-duesseldorf.de

Background and aims: Cholangiocellular adenocarcinoma (CCA) is a rare and aggressive malignancy originating from the bile ducts. Its general prognosis is poor as therapeutic options are limited. Often, patients present at advanced stages of disease and palliative chemotherapy remains the only treatment option. So far prognostic markers to assess the outcome of chemotherapeutic treatment in CCA are limited. We evaluated bone mineral density (BMD), a marker for the body composition as prognostic tool in patients with advanced CCA.

Method: 75 patients with advanced CCA that were treated at the department of Gastroenterology, Hepatology and Infectious Diseases or department of General, Visceral and Pediatric Surgery of the University Hospital Düsseldorf were included into this analysis. 64 patients received chemotherapy, 11 best supportive care. Bone mineral density was analyzed at the first lumbar vertebra, using CT scans in venous phase and the local PACS (IntelliSpace PACS, Philips, Amsterdam, The Netherlands).

Results: We identified an optimal cut-off of 167 HU for BMD, with patients above that value having a significantly improved overall survival (474 (95%CI: 297–651) days vs. 254 (95%CI: 211–297) days; log rank X² (1) = 6.090; p = 0.014; Figure 3C). The prognostic value for BMD was confirmed using univariate (HR 2.313 (95%CI: 1.170–4.575); p = 0.016) and multivariate (HR 4.143 (95%CI: 1.974–14.343); p = 0.025) Cox regression analysis. Subgroup analysis revealed, that the prognostic value of BMD was only present in women and not in men, suggesting sex specific differences.

Conclusion: Our data suggest, that BMD might represent a valuable and easy accessible independent prognostic marker in patients with advanced CCA for overall survival. Interestingly, subgroup analysis showed sex specificity of this marker only relevant in women.

SAT585
Multiparametric ultrasound approach using a tree based decision classifier for the inconclusive focal liver lesions evaluated by contrast enhanced ultrasound
Tudor-Voicu Moga1,2, Ciprian David1, Alina Popescu1, Kaluca Lupusoru1, Darius Herdeea1, Ana–Maria Ghiciuchi1, Camelia Foncea1, Adrian Burdan1, Roxana Sirili1, Mirela Danila1, Ioan Sporea1. 1Victor Babes University of Medicine and Pharmacy, Division of Gastroenterology and Hepatology, Department of Internal Medicine II, Center for Advanced Research in Gastroenterology and Hepatology, Timisoara, Romania; 2Victor Babes University of Medicine and Pharmacy, Division of Gastroenterology and Hepatology, Department of Internal Medicine II, Center for Advanced Research in Gastroenterology and Hepatology, Timisoara, Romania; 3Faculty, “Politehnica” University of Timisoara, Electronics and Telecommunications, Timisoara, Romania
Email: moga.tudor@gmail.com

Background and aims: Multi-parametric ultrasound (MPUS) is a concept by which the examiner is encouraged to use the latest features of the ultrasound machine. The aim of this study was to reanalyze the inconclusive focal liver lesion (FL) at CEUS using the MPUS approach with the help of a tree based decision classifier.

Method: We retrospectively analyzed FL’s that were inconclusive at CEUS examination in our Department over a period of two years (2017–2018). All the reexamined lesions had a second line imaging modality performed: (CE-CT), (CE-MRI) or biopsy considered as the reference method. CEUS inconclusive FLs had been previously evaluated by ultrasound (US) experts with more than 10 years of experience in CEUS, using a single US machine. MPUS reanalysis followed a three steps algorithm: liver stiffness measurement (LSM), time-intensity curve analysis (TIC) and parametric imaging feature (PI). After processing all steps of the algorithm a binary decision tree classifier (BDTC) was used towards a software assisted decision.

Results: From the 91 inconclusive FLs evaluated, 34 were HCC, 13 metastasis, 7 haemangioma, 7 regenerative nodules, 5 focal fatty alteration, 3 fatty free areas, 4 cholangiocarcinoma’s, 2 abscesses, 5 adenomas and 11 were other benign lesions. AREA was the only TIC-CEUS parameter that showed significant difference between malignant and benign lesion with a cut-off of > -19.3 dB for wash out phenomena, (AUROC = 0.58, Se = 74.0%, Sp = 45.7%). By adding the value of elastography we increased the performance to an AUROC of 0.72 and sensitivity of 90.2% for detecting malignant lesions with wash-out. MPUS correctly classified 66/91 lesions with an accuracy of 72.3%. Using the binary decision tree classifier (BDTC) algorithm we correctly classified 71/91 lesions according to their malignant or benign status, with an accuracy of 78.0%, Sensitivity = 62%, Specificity = 45% and Precision = 80%.
Conclusion: By reevaluating the inconclusive FLLs at CEUS using MPUS, we managed to determine that 78% of the lesions were malignant and in 26% of them we establish the lesion type.

SAT586
Adherence to hepatocellular carcinoma screening in patients with hepatitis C cirrhosis treated with direct-acting antivirals against hepatitis C
Elisa Saul Suarez Zambrano1, Silvia Acosta-Lopez1, Dacil Diaz Bethencourt2, Maria Soledad Garrido1, Ruth Suarez Darias1, Francisco Andres Perez Hernandez1.1 Our Lady of Candelaria University Hospital, Santa Cruz de Tenerife, Spain
Email: suarezelisa@gmail.com

Background and aims: Hepatocellular carcinoma (HCC) screening is indicated for patients with hepatitis C cirrhosis (HCV-C) via biannual ultrasound scan. The risk of HCC and its mortality rate persist after sustained virologic response (SVR), so screening must be maintained. This study aims to analyse HCC screening adherence in patients with HCV-C after SVR and risk factors involved in low adherence. As a secondary aim, we analyse the incidence of HCC and BCLC stage at diagnosis.

Method: A descriptive, trans-sectional, and observational study in which we included patients that have been diagnosed VHC and treated with direct antiviral agents (DAA) between September 2014 and July 2019 with a minimum follow-up period of one year. Demographic and clinical variables were recorded at first specialised consultation. The level of adherence to screening was categorised as ‘adequate’ if it was conducted within a range of six months. A comparative analysis was carried out, employing nonparametric statistic tests in order to compare the two groups of study (either adequate or inadequate screening processes). Also, a binary logistic regression analysis was carried out in order to determine variables associated to an inadequate screening. For all the analysis, statistical significance was set p < 0.05.

Results: 385 patients (114 female) were included. Average age was 57.4 (10.3 SD). The average follow-up was 35.8 months (25 SD); 41.5% had an adequate screening (36.5% for men and 53.5% for women). Screening was adequate only in 20.6% (27/131) for intravenous drug users (IVDU) and 26.4% (24/91) for patients with mental health disorders. The binary multivariate logistic regression analysis showed IVDU history (OR 2.23) as the only independent risk factors for an inadequate HCC screening process. Nevertheless, the use of AFP for the detection of HCCR is not established. We have assessed longitudinal AFP levels in patients who underwent OLT for HCC.

Method: In this retrospective monocentric study all patients who underwent OLT due to HCC between 2010 and 2020 in one University Hospital were included. Inclusion criteria were diagnosis of HCC, HCC recurrence (HCCR), and a follow-up period of one year. AFP values were measured before OLT, monthly thereafter, and written informed consent. AFP was measured by COBAS assay (Roche, Switzerland, upper limit of normal (ULN) = 7 ng/ml). AFP levels were reported as data from patient records.

Results: A total of 80 patients were included and followed for a mean time of 58 ± 40 (range 1–132) months (end of observation = EOBS) after OLT. HCC recurred in 20 patients (25%) after a mean of 33 ± 30 months. In the group without HCCR median serum AFP levels dropped from 5.7 (range 1.7–871) before to 2.7 (1.2–7.7) ng/ml at month 3 after OLT (p < 0.001), and remained similar until EOBS (4.1 (1.5–62.8), p = 0.915). In contrast, in the HCCR group median AFP level decreased from 76.7 (1.7–762) at before OLT to 6.1 (1.1–6, 393) ng/ml (p = 0.010) at month 3 after OLT, but increased to 751.3 (1.38–628, 400) ng/ml at EOBS (p = 0.002) (Figure). In 15 patients (75%) with elevated AFP at HCCR, including two with AFP below ULN until OLT, after OLT AFP increased above ULN by a mean of 3.3 ± 6 (0–9) months before radiologic confirmation of HCCR. Patients with HCCR within the first 12 months after OLT (n = 7) had significantly higher median AFP levels at OLT, months 3, 6 and 12 after OLT as compared to patients with HCCR after 12 months or no HCCR (OLT: 165.2 (31.3–2, 762) ng/ml vs. 5.9 (1.7–871), p < 0.001; 3 months: 11 (4.9–6, 393) vs. 2.7 (1.1–7.7), p < 0.001; 6 months: 134 (4.6–1, 307) vs. 2.31 (0.82–83), p < 0.001; 12 months: 16, 398.7 (7.3–60, 500) vs. 2.8 (0.9–9.7), p < 0.001).

SAT587
Closely monitored alpha-fetoprotein allows early detection of hepatocellular carcinoma recurrence after orthotopic liver transplantation
Magdalena Hahn1, Adam Herber1, Rami Al-Sayegh1, Janett Fischer1, Anne Ollrich1, Sebastian Rademacher2, Daniel Seehofer2, Sebastian Ebel3, Timm Denecke3, Thomas Berg3, Florian van Bömmel1, 1 Leipzig University Medical Center, Division of Hepatology, Department of Medicine II, Leipzig, Germany; 2 Leipzig University Medical Center, Department of Visceral, Transplant, Thoracic and Vascular Surgery, Leipzig, Germany; 3 Leipzig University Medical Center, Department of Diagnostic and Interventional Radiology, Leipzig, Germany
Email: florian.vanboemmel@medizin.uni-leipzig.de

Background and aims: After orthotopic liver transplantation (OLT) for patients with hepatocellular carcinoma (HCC), HCC recurrence (HCCR) is frequent and has a poor prognosis. An alpha-fetoprotein (AFP) value >1, 000 ng/ml before OLT is used to identify patients at high risk for HCCR. However, the use of AFP for the detection of HCCR is not established. We have assessed longitudinal AFP levels in patients who underwent OLT for HCC.

Method: In this retrospective monocentric study all patients who underwent OLT due to HCC between 2010 and 2020 in one University Hospital were included. Inclusion criteria were diagnosis of HCC, HCC recurrence (HCCR), and a follow-up period of one year. AFP values were measured before OLT, monthly thereafter, and written informed consent. AFP was measured by COBAS assay (Roche, Switzerland, upper limit of normal (ULN) = 7 ng/ml). AFP levels were correlated as data from patient records.

Results: A total of 80 patients were included and followed for a mean time of 58 ± 40 (range 1–132) months (end of observation = EOBS) after OLT. HCC recurred in 20 patients (25%) after a mean of 33 ± 30 months. In the group without HCCR median serum AFP levels dropped from 5.7 (range 1.7–871) before to 2.7 (1.2–7.7) ng/ml at month 3 after OLT (p < 0.001), and remained similar until EOBS (4.1 (1.5–62.8), p = 0.915). In contrast, in the HCCR group median AFP level decreased from 76.7 (1.7–762) at before OLT to 6.1 (1.1–6, 393) ng/ml (p = 0.010) at month 3 after OLT, but increased to 751.3 (1.38–628, 400) ng/ml at EOBS (p = 0.002) (Figure). In 15 patients (75%) with elevated AFP at HCCR, including two with AFP below ULN until OLT, after OLT AFP increased above ULN by a mean of 3.3 ± 6 (0–9) months before radiologic confirmation of HCCR. Patients with HCCR within the first 12 months after OLT (n = 7) had significantly higher median AFP levels at OLT, months 3, 6 and 12 after OLT as compared to patients with HCCR after 12 months or no HCCR (OLT: 165.2 (31.3–2, 762) ng/ml vs. 5.9 (1.7–871), p < 0.001; 3 months: 11 (4.9–6, 393) vs. 2.7 (1.1–7.7), p < 0.001; 6 months: 134 (4.6–1, 307) vs. 2.31 (0.82–83), p < 0.001; 12 months: 16, 398.7 (7.3–60, 500) vs. 2.8 (0.9–9.7), p < 0.001).
SAT588
Predictors of survival of patients with hepatocellular carcinoma in best supportive care
Claudia Campani1, Laura Bucci2, Valentina Adotti1, Martina Rosi1, Umberto Arena2, Stefano Gatto1, Franco Trevisani2, Fabio Marra1, Ita.Li.Ca. Study Group2. 1University of Florence, Firenze, Italy; 2Alma Mater Studiorum-Università di Bologna, Bologna, Italy
Email: fabio.marra@unifi.it

Background and aims: The prognosis of patients with hepatocellular carcinoma (HCC) is very variable. Patients unfit to receive any type of treatment are managed with best supportive care (BSC), and their median overall survival (OS) is around 3–6 months, although longer values may be observed in clinical practice. Aim of this study was to identify prognostic factors associated with longer survival in patients with HCC treated with BSC.

Method: We retrospectively evaluated the clinical characteristics of 916 patients, recorded in the Ita.Li.Ca. database, who had an indication for BSC. We analyzed both patient and tumor characteristics to identify predictors of better OS.

Results: Median age was 71y and 75% of patients were male. Etiology included chronic viral infection (48.7%), alcohol use disorder (20.7%) and non-alcoholic steatohepatitis (4.1%). Approximately 50% of patients had a performance status 0–1 and were in Child-Pugh B class. Median MELD was 13. 60% of patients had a multifocal HCC with a median number of 2 lesions and a median size of 35 mm. 369 patients had vascular invasion. Median alpha-fetoprotein was 63.2 ng/ml. The median OS was 9 months (CI 7.7;10.2). No differences in terms of OS were observed considering the etiology of liver disease. Among comorbidities, heart disease was associated with lower OS (p = 0.015), Abdominal pain (p < 0.001), vomiting (p = 0.014), fatigue (p = 0.01), and a worse liver function (p < 0.001) were associated with shorter OS. Patients with multifocal HCC had a better OS (12 mo; CI 10–13.9) compared to those with monofocal HCC (8 months; CI 6.5–9.5) (p < 0.001). Lack of vascular invasion was also associated with a better OS (14 months, CI 12.2–15.7, p < 0.001). No significant differences were observed comparing patients with or without metastasis (p = 0.310). Patients who had an active treatment before BSC had significantly longer OS than those for whom BSC was the only treatment (561 patients, p < 0.001). Survival in BCLC-A patients was longer than in other stages. No differences in OS were found comparing BCLC-B and -C groups. Patients in BSC with a median OS longer than 6 months had more lesions (p = 0.005), higher levels of albumin (p = 0.003), lower bilirubin (p < 0.001) and alpha-fetoprotein (0, 001), and a lower median MELD (p < 0.001). A weak association was found between survival shorter than 6 months and the presence of cirrhosis (p = 0.012), alcohol consumption (p = 0.046), and obesity (p = 0.007), hypercholesterolemia (p = 0.002), hypertriglyceridemia (p = 0.006) symptoms (p = 0.02), vascular invasion (p < 0.001), and non-multifocal HCC (p < 0.001). Similar results were found comparing patients with a mOS longer or shorter than 12 months.

Conclusion: In a large series of patients with HCC in BSC we identified several clinical and tumor characteristics associated with the length of survival.

SAT589
Serum exosomal miRNA-720 as a diagnostic marker for hepatocellular carcinoma
Jin Min Kim1, Hye Seon Kim1, Jin Seoub Kim1, Ji Won Han2, Soon Kyu Lee1, Heechul Nam1, Pil Soo Sung3, Si Hyun Bae4, Jong Young Choi1, Seung Kew Yoon1, Jeong Won Jang1. 1The Catholic University of Korea, Seoul St. Mary’s Hospital, Seoul, Korea, Rep. of South Email: garden@catholic.ac.kr

Background and aims: Hepatocellular carcinoma (HCC) remains with a poor prognosis, largely due to late detection. Highly accurate biomarkers are urgently needed to detect early-stage HCC. Exosomal microRNAs (miRs) recently emerged as a biomarker for various cancers. Our study aims to explore the diagnostic performance of serum exosomal miR-720 for HCC.

Method: Exosomal miRNA was measured by quantitative real-time PCR. A correlation analysis was done between exosomal miR-720 and tumor or clinico-demographic data of patients with HCC. The receiver operating characteristic (ROC) curve was applied to assess the diagnostic capacity of serum exosomal miR-720 for HCC, in comparison with AFP (α-fetoprotein) and prothrombin-induced by vitamin K absence or antagonist-II (PIVKA-II).

Results: miR-720 was chosen as a potential HCC marker through microarray, due to significantly differential expression between tumor and non-tumor samples. Serum exosomal miR-720 was significantly upregulated in patients with HCC (n = 114) and other liver disease (control, n = 30), with the higher area under the ROC curve (AUC = 0.931) than the other markers. Particularly, serum exosomal miR-720 showed superior performance in diagnosing small HCC (<5 cm; AUC = 0.930) to AFP (AUC = 0.802) or PIVKA-II (AUC = 0.718). Exosomal miR-720 levels marginally correlated with tumor size and number. The proportion of high-level miR-720 increased with intrahepatic tumor stage progression. Unlike AFP or PIVKA-II showing significant correlation with aminotransferase levels, exosomal miR-720 exhibited no correlation with aminotransferase levels.

Conclusion: Serum miR-720 is an excellent biomarker for diagnosis of HCC, with better performance than AFP or PIVKA-II. Its diagnostic utility is maintained even for small HCC and not affected by aminotransferase levels.

Key words: Hepatocellular carcinoma; Exosome; MicroRNA; Biomarkers; Diagnosis.

SAT590
Prospective evaluation of combining three biomarkers and image tools for early detection of hepatocellular carcinoma: an interim analysis
Hyung Joon Yim1, Tae Hyung Kim2, Soon Ho Um3, Yeon Seok Seo2, Young Kull Jung1, Ji Hoon Kim1, Young-Sun Lee1, Sun Young Yim4, Won Hyeok Choe5, Jae Young Jang6, Byoung Kuk Jang6, Dae Won Jun7, Eileen Yoon8,9, Yoon Jun Kim10, Hyung Joon Kim11, Chang Wook Kim12, Si Hyun Bae13, Jeong Won Jang12, Han Ah Lee14, Do Young Kim15, 1Korea University Ansan Hospital, Internal Medicine, Ansan, Korea, Rep. of South; 2Korea University Anam Hospital, Internal Medicine, Korea, Rep. of South; 3Korea University Guro Hospital, Internal Medicine, Korea, Rep. of South; 4Konkuk University School of Medicine, Internal Medicine, Korea, Rep. of South; 5Soonchunhyang University College of Medicine, Internal Medicine, Korea, Rep. of South; 6Keimyung University School of Medicine, Internal Medicine, Korea, Rep. of South; 7Hanyang University College of Medicine, Internal Medicine, Korea, Rep. of South; 8Yonsei University College of Medicine, Internal Medicine, Korea, Rep. of South; 9Seoul National University College of Medicine, Internal Medicine, Korea, Rep. of South; 10Chung-Ang University College of Medicine, Internal Medicine, Korea, Rep. of South; 11The Catholic University of Korea, Internal Medicine; 12Inje University College of Medicine, Internal Medicine; 13Ewha Womans University College of Medicine, Internal Medicine; 14Yonsei University College of Medicine, Internal Medicine
Email: gudwns21@korea.ac.kr

Background and aims: Early detection of hepatocellular carcinoma (HCC) is critically important for the improvement of prognosis.
Although combining AFP and ultrasonography (US) are the standard modalities for surveillance of HCC, combining other tumor biomarkers such as PIVKA-II or AFP L3 with AFP is currently suggested to improve the detection rates of HCC. However, prospective evaluation of combinations of such biomarkers has been rarely performed. The present study aimed to confirm the utility of combination of biomarkers and imaging modalities for early detection of HCC patients with liver cirrhosis.

**Method:** Patients with histologically or clinically confirmed liver cirrhosis were enrolled at 14 tertiary hospitals in Korea. Patients with elevated AFP (>20 ng/ml), hepatic nodule ≥1 cm by US or liver CT, or Child-Pugh score ≥11 points were excluded. HCC surveillance using AFP, AFP L3, PIVKA-II, and US were performed every 6 months. In addition, liver CT was scanned every 12 months.

**Results:** A total of 2810 patients/year were followed-up prospectively. Among them, HCC developed in 56 patients. Under this intensive surveillance program, most of HCCs detected were at early stage (50/56 were BCLC stage 0 or A, 48/56 were TNM stage 1, 54/56 were modified UICC stage 1 or 2) and the mean size of HCCs was 1.8 cm (1.3–2.6). The sensitivity of the biomarkers was 42.9% for AFP, 48.2% for AFP L3, 39.3% for PIVKA-II, 59.0% for combination of the three markers when the sensitivity was set to be ≥90%; Three-combination was the highest and the AFP L3 was the next. We assessed the area under the receiver operating curves (AUROC) for one, two, and three combination of the biomarkers such as AFP (0.598), AFP+AFP L3 (0.646), AFP+PIVKA-II (0.664), and AFP+AFP L3+PIVKA-II (0.688), and found that the three combination was the best. In addition, when incorporated the three biomarkers into GALAD (Gender, Age, L3, AFP, and DCP [= PIVKA-II]) score, the AUROC was 0.778, which is the better. The AUROC improved by adding US (0.820) or liver CT (0.864) on combination of three biomarkers.

**Conclusion:** For early detection of HCCs, a combination of three biomarkers (AFP, AFP L3, PIVKA-II) or GALAD score was shown to be useful in this prospective evaluation. Adding imaging modalities improved the performance further.

**SAT591**

A natural experiment investigating the impact of waiting time on post-transplant survival for patients with hepatocellular carcinoma: randomization by blood group

Berend Beumer1, Wojciech Polak1, Robert De Man2, Herold J. Metselaar2, Jan Ijzermans1. 1Erasmus MC Transplant Institute, Department of Surgery, Division of HPB and Transplant Surgery, Rotterdam, Netherlands; 2Erasmus MC Transplant Institute, Department of Gastroenterology and Hepatology, Rotterdam

Email: b.beumer@erasmusmc.nl

**Background and aims:** When listing for liver transplantation we can transplant as soon as possible or introduce a test of time to better select patients as the tumor’s biological behavior is observed. Knowing the degree of harm caused by time itself is essential to advise patients and decide on the maximum duration of the test-of-time. Therefore, we investigated the causal effect of waiting time on post-transplant survival for patients with HCC.

**Method:** We analyzed the UNOS-OPTN dataset and exploited the natural experiment created by blood groups. Relations between variables were described in a causal graph. Inverse probability weighting was used to address selection bias. Confounding biases were avoided using instrumental variable analysis, with an additive hazards model in the second stage. The causal effect was evaluated as a contrast between a scenario in which all patients waited 2 months and one in which all patients waited 12 months. Upper bounds of the test-of-time were evaluated for probable scenarios by means of simulation.

**Results:** The F-statistic of the first stage was 86.3. The effect of waiting 12 months versus 2 months corresponded with a significant drop in overall survival of 5.07%/95%CI [0.277; 9.69] and 8.33%/95% CI [0.47; 15.60] at 5- and 10-years post-transplant, respectively. The median survival significantly dropped by 3.41 years from 16.21 years 95%CI [15.98; 16.60] to those waiting 2 months to 12.80 years 95%CI [10.72; 15.90] for those waiting 12 months. No significant effect modification by tumor size or number was found.

**SAT592**

Baveno VII criteria identify varices needing treatment in patients with hepatocellular carcinoma of different BCLC stages undergoing curative hepatectomy

Grace Lai-Hung Wong1, Terry Cheuk-Fung Yip1, Angus Wong1, Brian Chan1, Matthew Fong1, Vincent Wai-Sun Wong1, Stephen L. Chan2, Kelvin Ng3. 1The Chinese University of Hong Kong, Medical Data Analytic Centre (MDAC) and Department of Medicine and Therapeutics, Hong Kong; 2The Chinese University of Hong Kong, State Key Laboratory of Translational Oncology, Department of Clinical Oncology, Hong Kong; 3The Chinese University of Hong Kong, Department of Surgery, Hong Kong

Email: wonglaihung@cuhk.edu.hk

**Background and aims:** The latest Baveno VII consensus, which was published in late 2021 discussed the use of non-invasive tools for the diagnosis of compensated advanced chronic liver disease (cACLD)
and clinically significant portal hypertension (CSPH). We aimed to investigate the predictive value of Baveno VII consensus, as well as other LSM and platelet cutoffs, to predict the presence of varices needing treatment (VNT) in patients with HCC of different stages Barcelona Clinic Liver Cancer staging system (BCLC) undergoing curative hepatectomy.

**Method:** This was a prospective cohort of patients with confirmed diagnosis of HCC. Patients underwent transient elastography examination before HCC treatment. Patients were prospectively followed for VNT, defined as all grade II to III varices (≥5 mm), and small varices found in patients with Child-Pugh C cirrhosis, and any varices presenting red-wale signs, fibrin clot or active bleeding.

**Results:** 712 patients (83.3% male, median age 62 years old) were recruited from March 2013 to April 2019. Most patients (76%) suffered from chronic hepatitis B infection, 405 (57%) and 595 (84%) patients had platelet count ≥150 × 10^9/L and <150 × 10^9/L respectively. Majority of the patients (n = 389, 55%) had HCC of BCLC stage A, whereas 69 (10%) patients had stage B, and 121 (17%) patients had stage C tumour. The median follow-up duration of patients was 45.8 months. The median liver stiffness measurement (LSM) was 10.5 kPa (Range: 7.0 – 20.6 kPa); 461 (65%) patients had LSM ≤ 15 kPa, 516 (72.5%) patients had LSM ≤ 20 kPa and 554 (77.8%) patients had LSM ≤ 20 kPa. Patients of BCLC stage 0 and stage A HCC had lower LSM (9.6 kPa and 9.5 kPa respectively), compared to those of BCLC stage B and C HCC (13.2 kPa and 20.6 kPa respectively). VNT occurred in 57 (8.0%) patients, which occurred a bit more commonly in BCLC stage C (12 patients, 10.0%) than earlier stages of HCC (stage 0, 8.7%; stage A, 7.5%; stage B, 7.6%; Table 2). In patients who fulfilled Baveno VII criteria, i.e. LSM ≤ 20 kPa together with a platelet count above 150 × 10^9/L, only fourteen (2.0%) patients had VNT. In all BCLC stages of HCC, the proportion of patients with VNT was below 5% (1.5% in stage 0, 1.3% in stage A, 3.1% in stage B, and 3.3% in stage C), which support the validity and applicability of Baveno VII criteria in all BCLC stages of HCC.

**Background and aims:** Risk factors for hepatocellular carcinoma (HCC) include cirrhosis and diabetes, but patient- and disease-related factors in prognosis have not been widely explored. Evidence highlights ethnic disparity in HCC stage at presentation and survival in the USA; White patients present earlier and survive longer, but there is little evidence evaluating any disparity in the UK. We sought to evaluate the factors associated with HCC stage at presentation and survival in a UK population.

**Method:** We retrospectively analysed data from referrals to HCC multidisciplinary teams in 4 regional centres: East London and Essex, Nottingham, Coventry, and Bristol, between 2007 and 2021, where data available. We included all patients with confirmed diagnosis of HCC. Early stage at presentation was defined as Barcelona Clinic Liver Centre (BCLC) Stages 0 and A, late stage was defined as BCLC Stages C and D. Analyses were conducted using Cox regression models for survival and logistic regression models for stage at presentation, all adjusted for age, sex, aetiology of liver disease, HCC surveillance and centre.

**Results:** We included 1357 patients with a median follow-up of 12 months. 31% of patients had Non-Alcoholic Fatty Liver Disease (NAFLD), 33% had Viral hepatitis, and 18% had Alcoholic Liver Disease (ALD) (Figure 1).

**Conclusion:** This was the first long-term follow-up study of HCC patients undergoing curative hepatectomy supporting the validity and applicability of the new Baveno VII criteria for selecting patients to undergoing screening endoscopy for VNT. The validity was consistent across different BCLC stages of HCC.

**Grant support:** This work was supported by the Health and Medical Research Fund (HMRF)-Food and Health Bureau (Reference no.: 07180216) awarded to Grace Wong.
In patients with diabetes, metformin use was independently associated with early-stage presentation (OR 1.932, \( p = 0.008 \)) and survival (HR 0.912, \( p = 0.304 \)).

**Conclusion:** In this multi-centre study, White patients were less likely to die following a diagnosis of HCC compared to other ethnicities.

Diabetes status was not an independent predictor of survival but, among patients with diabetes, those on metformin were almost twice as likely to present with early-stage disease, and were less likely to die, consistent with existing evidence for a protective role of metformin in HCC.

HCC surveillance was a predictor of overall survival but not in patients with NAFLD who are at greater risk of developing non-cirrhotic HCC and for whom the current outpatient surveillance programme may require modification.

**SAT594**

**Use of machine learning to predict the histopathological ImmunoScore in hepatocellular carcinoma on multiparametric MRI**

Junlin Yang¹, Annabella Shewarega¹, Jessica Santana¹, Vasily Pekurovsky², Xuchen Zhang², MingDe Lin², David Madoff², Lawrence Staib³, Julius Chapiro¹, James Duncan¹.¹ Yale University, Radiology and Biomedical Engineering, New Haven, United States; ²Yale University, Pathology, New Haven, United States

**Background and aims:** Immunotherapy is the new first-line treatment for advanced-stage hepatocellular carcinoma (HCC) and combinations with locoregional therapies are currently under investigation for intermediate disease stages. However, tumor response to immunotherapy is highly variable and depends on immunological features of the tumor microenvironment at baseline. Histopathologic biomarkers such as the ImmunoScore are potent predictors of response to immunotherapy, however, they are not readily available given the need for tissue sampling. Accordingly, there is an unmet need for non-invasive surrogate markers for the immunological state of HCC prior to allocation of therapy. The purpose of this study is to establish ground proof for the ability of machine learning to extract radiomic features from multi-parametric MRI to predict ImmunoScores in HCC.

**Method:** This study included 17 individual HCC lesions with whole-tumor gross and histopathology obtained via hepatectomy or orthotopic liver transplantation within 30 days of preoperative abdominal contrast-enhanced MRI. The ImmunoScore, an index indicating the density of CD3+, CD4+, and CD8+ tumor-infiltrating T-lymphocytes both in the tumor center and tumor margin, was assessed by a board-certified pathologist. ImmunoScores of 0–2 signified immunologically “cold” tumors while scores of 3–4 signified immunologically “hot” tumors. Arterial and delayed venous phases of the contrast-enhanced T1-weighted MRI were used to segment both tumors and the whole liver volume. The segmentation masks were used to train an autoencoder with binary cross-entropy and mean squared error (MSE) loss. The latent codes consist of 128 features of the contrast-enhanced T1-weighted IT, delayed IT, and T2-weighted IT. The latent codes were used to evaluate the histopathologic state of the tumor and were used to predict the likelihood of tumor response as the next study end point.

**Results:** Leave-one-out cross-validation was used to evaluate the model performance. The linear regression model showed good performance in predicting the ImmunoScore, with a F1 score 58.42, an AUC of 86.67, and an accuracy of 70.59. The random forest model showed a greater degree of predictiveness with a F1 score 88.24, an AUC of 85.83, and an accuracy of 88.24.

**Conclusion:** Machine learning-based extraction of radiomic features from multi-phasic MRI may serve as a non-invasive surrogate for ImmunoScore prediction of HCC, potentially facilitating immunophenotyping of tumors prior to allocation to immunotherapy. These results demonstrate a proof of principle and require external validation and prospective evaluation in larger clinical cohorts with tumor response as the next study end point.
median follow-up after LT was 30.6 months. The mean survival post HCC recurrence after LT was 17 months (range: 1–50.9). Among the 71 patients with available 18F-FDG PET imaging data, 53 (74.6%) were negative and 18 (25.3%) were positive. Among the 47 patients with available choline-PET imaging data, 25 (53.1%) were negative and 22 (46.8%) were positive. In univariate and multivariate analysis, HCC recurrence after LT is correlated with 18F-FDG PET positivity before LT (p = 0.03, r = 0.262), but not with choline PET positivity (p = 0.98) and histological findings on liver explant: active HCC nodules (p = 0.002), microvascular invasion (p < 0.001) and macrovascular invasion (p < 0.001).

**Conclusion:** In our cohort, HCC recurrence after LT is a serious adverse event, as it occurs early, is often already metastatic at diagnosis and impacts drastically the survival after LT. HCC recurrence risk after LT could be predicted by the 18F-FDG PET positivity before LT. Further validation is needed but this could be a signal of a potential role of PET imaging for better selecting HCC candidates for LT.

**SAT596**

Germline genetic risk factors for the development of hepatocellular carcinoma among patients with cirrhosis: a genome-wide association study of U.S. veterans

David Kaplan1,2, Marijana Vujkovic1,2, Daniel D ochterman3, Kirk Wangensteen1, Poornima Devineni4, Tae-Hwi Linus Schwantes-An5, Anoop Sendamarai4, Purushtotham Karnam1, Emily Sileo4, Tori Anglin3, Trina Norden-Krichmar6, Philip Tsao7, Timothy Morgan8, Saiju Pyarajan4, Julie Lynch1,2, Benjamin Voight1, Kyong-Mi Chang1,2.

1University of Pennsylvania, Philadelphia, United States; 2Corporal Michael J. Crescenz VA Medical Center, Philadelphia, United States; 3VA Salt Lake City Health Care System, United States; 4Center for Data and Computational Sciences, United States; 5Indiana University School of Medicine, Indianapolis, United States; 6University of California Irvine, Irvine, United States; 7VA Palo Alto Healthcare System, Palo Alto, United States; 8VA Long Beach Healthcare System, Long Beach, United States; 9University of Massachusetts College of Nursing, United States

Email: dkaplan@pennmedicine.upenn.edu

**Background and aims:** Hepatocellular carcinoma (HCC) remains a highly mortal cancer with an approximate 20% 5-year survival rate. The primary risk factor for the development of HCC is the presence of cirrhosis, most commonly caused by chronic hepatitis B (HBV) infection, chronic hepatitis C (HCV) infection, alcohol-related liver disease (ALD) and increasingly non-alcoholic fatty liver disease/non-alcoholic steatohepatitis (NAFLD/NASH). Multiple somatic driver gene candidates in HCC including but not limited to TERT, CTNNB1, TP53, myc, ARID1A, ARID2, AXIN1 have been identified. However, few studies have evaluated germline genetic risk factors for HCC development and none have isolated genes specifically associated with HCC evolving from cirrhosis. The purpose of present study was to identify genetic risk factors for HCC in patients with cirrhosis associated with metabolic and non-metabolic causes of chronic liver disease.

**Method:** A clinical phenotype consistent with HCC and/or cirrhosis was generated for MVP participants based upon ICD9/10 codes, exclusion of metastatic cancers using VA clinical cancer registry data, FIB-4 scores, and identification of disease etiology using a validated algorithm. Cirrhosis controls were required to have ≥ 3 years follow-up without identification of HCC. Ancestry-specific and multi-ancestry genome-wide association analyses (customized Affymetrix Axiom Array with total 723,305 SNPs) were performed comparing HCC cases and cirrhosis controls, with the covariates of age, age squared, sex, etiology and first 10 principal components of genetically defined ancestry.

**Results:** From ~650,000 MVP participants, 3,445 HCC cases and 9,626 cirrhosis controls were identified with both metabolic and non-metabolic causes of chronic liver disease. Median time from cirrhosis to HCC diagnosis in cases was 1.9 years [IQR 0.0–5.5], and median cancer-free follow-up of controls was 5.8 years [IQR 4.4–8.1]. Multi-ancestry analysis identified 2 novel trans-ancestry loci associated with carcinogenesis that met genome wide significance (5 × 10⁻⁸, EPHA2/ARHGEF19, LINC00824 marking a cancer risk locus on 8q24.21 with multiple candidate genes including MYC) as well as one additional African-specific locus and one Hispanic-specific locus.

**Conclusion:** Our effort using population-based MVP biobank has identified novel germline genetic risk loci for HCC evolving out of cirrhosis. Efforts are ongoing to expand our sample size and identify external cohorts for further replication. Future work would include validation of these genetic markers as biomarkers for selection for intensified HCC surveillance.

**POSTER PRESENTATIONS**
A comparative analysis of Elecsys GALAD and Elecsys GAAD score to detect early-stage hepatocellular carcinoma in an international cohort

Henry Ly Chan1, Arndt Vogel2, Thomas Berg3, Enrico de Toni4, Masatoshi Kudo5, Jörg Trojan6, Katharina Malinowsky7, Wenzel Schöning8, Konstantin Kroeniger9, Kairat Madin10, Ashish Sharma11, Teerha Piratvisuth12.

Background and aims: The combination of gender (sex) and age plus serum biomarkers alpha-fetoprotein (AFP), Lens culinaris agglutinin-reactive fraction of AFP (AFP-L3) and protein-induced by vitamin K absence-II (PIVKA-II) forms the GALAD algorithm, a promising aid in the detection of early-stage hepatocellular carcinoma (HCC). Here, we present results from the first study comparing the clinical performance of the Elecsys® GALAD and Elecsys GAAD (gender [sex], age, AFP and PIVKA-II) algorithms for differentiating early-stage HCC and benign chronic liver disease (CLD).

Method: Adult patients were prospectively enrolled at 9 hospitals in Germany, Thailand, Hong Kong and Japan. Eligible HCC cases had first-time HCC diagnosis confirmed by ultrasound or liver biopsy. Eligible CLD controls had imaging-confirmed absence of HCC (within 12 months), and presence of cirrhosis or non-cirrhotic: chronic hepatitis B/C virus (HBV/HCV), alcoholic liver disease (ALD) or non-alcoholic steatohepatitis (NASH). Serum levels of PIVKA-II, AFP and AFP-L3 were measured using Elecsys assays on the cobas e 601 analyzer. The established cut-offs for HCC detection were 20 ng/ml for AFP 2.47 for Elecsys GALAD, and 2.57 for Elecsys GAAD scores (range 0–10 for both).

Results: A total of 465 patients (246 with HCC and 219 CLD controls) were included. Among the HCC/CLD cohorts, mean age was 63.5/52.5 years, 81.7%/59.8% were male and 71.1%/28.9% had cirrhosis. Among HCC patients, 43.5% had early-stage HCC (Barcelona Clinic Liver Cancer [BCLC] 0 and A). Of 219 CLD controls, one was excluded from final analysis due to incomplete biomarker data. Elecsys GAAD and GALAD algorithms showed similar performance for discriminating between HCC and CLD (Table): sensitivity for identification of early-stage (72.9% vs 73.8%) and all-stage (85% vs 85.8%) HCC was comparable, and specificity was >90% for both scores. AUCs were similar across cirrhotic (87.6% vs 87.5% for early-stage, 92.9% vs 92.8% for all-stage HCC) and non-cirrhotic (91.2% vs 91.1%; 93.6% both) etiologies. The performance of Elecsys GAAD and GALAD algorithms were superior to AFP alone (Table).

<table>
<thead>
<tr>
<th>Assay/algorithm (cut-off)</th>
<th>AUC Early-stage HCC</th>
<th>Sensitivity</th>
<th>Specificity</th>
<th>AUC All-stage HCC</th>
<th>Sensitivity</th>
<th>Specificity</th>
</tr>
</thead>
<tbody>
<tr>
<td>AFP (20 ng/ml)</td>
<td>82.4</td>
<td>36.4</td>
<td>98.2</td>
<td>87.1</td>
<td>50.4</td>
<td>98.2</td>
</tr>
<tr>
<td>(77.4–87.5)</td>
<td>(77.4–87.5)</td>
<td>(77.4–87.5)</td>
<td>(77.4–87.5)</td>
<td>(77.4–87.5)</td>
<td>(77.4–87.5)</td>
<td>(77.4–87.5)</td>
</tr>
<tr>
<td>GAAD (2.57)</td>
<td>91.3</td>
<td>72.9</td>
<td>92.2</td>
<td>94.8</td>
<td>85.0</td>
<td>92.2</td>
</tr>
<tr>
<td>(88.–94.6)</td>
<td>(88.–94.6)</td>
<td>(88.–94.6)</td>
<td>(88.–94.6)</td>
<td>(88.–94.6)</td>
<td>(88.–94.6)</td>
<td>(88.–94.6)</td>
</tr>
<tr>
<td>GALAD (2.47)</td>
<td>91.3</td>
<td>73.8</td>
<td>90.8</td>
<td>94.7</td>
<td>85.8</td>
<td>90.8</td>
</tr>
<tr>
<td>(87.9–94.6)</td>
<td>(87.9–94.6)</td>
<td>(87.9–94.6)</td>
<td>(87.9–94.6)</td>
<td>(87.9–94.6)</td>
<td>(87.9–94.6)</td>
<td>(87.9–94.6)</td>
</tr>
</tbody>
</table>

All results shown as % (95% CI)
drainage of liver abscesses (3 hepatologists/1 interventional radiologist, 12/2021 through 03/2022, single center; 400+ biopsies, 50+ ablations annually). To increase visibility of liver lesions (hepatocellular and cholangiocellular carcinoma, metastases) contrast-enhanced ultrasound imaging was used if needed. Use of this mixed reality technology in hepatological interventions was immediate and self-explanatory. Addition of a head-mounted display for the procedures allowed reduced movements of the operating physicians and led to increased focus on the intervention since the examiner stays in situ while having the patient, operating field and the needle in one visual field.

**Conclusion:** Use of this mixed reality technology in hepatological interventions such as biopsies of focal liver lesions, tumor ablations and liver abscess drainage proved to be useful. This proof of concept showed for the first time that using mixed-reality technology in ultrasound-guided liver interventions is feasible and associated with advantages such less movement during biopsy/ultrasound-guided intervention allowing a better focus on the intervention sight, lower risk of contamination of the sterile field. In addition, live recording by this device was useful for physicians in training in order to review their interventions later.

**SAT599**

**Type 2 diabetes combined with portal vein tumor thrombosis worsens prognosis in patients with hepatocellular carcinoma**

Debora Angrisani1, Marco Guarracino2, Nunzia Farella3, Filomena Morisco4, Carmine Coppola4, Francesco Izzo5, Angelo Salomone Megna6, Alessandro Federico8, Vincenzo Messina9, Gerardo Nardone10, Guido Piai11, Enrico Ragone12, Luigi Elio Adinolfi13, Giuseppe D’Adamo14, Maria Stanzione15, Giampiero Francica16, Marcello Persico17, Vincenzo De Girolamo18, Coppola Nicola19, Lucia Roco20, Gian Giuseppe Di Costanzo21, Raffaella Tortora22, 1AORN Cardarelli, Hepatology Unit, Naples, Italy; 2AORN Cardarelli, Hepatology Unit, Naples, Italy; 3AORN Ospedale dei colli, Malattie Infettive ad indirizzo eoinfettivocentrico, Naples, Italy; 4University Federico II, Dipartimento di Medicina Clinica e Chirurgia, Naples, Italy; 5O.O.RR Area Stabiese; 6U.O. di Epatologia ed Ecografia Interventistica, Gragnano, Italy; 7Azienda Ospedaliera San Pio, OC Malattie Infettive, Benevento, Italy; 8Università della Campania Vanvitelli, Department of Clinical and Experimental Medicine, Naples, Italy; 9AORN Sant’Anna e San Sebastiano, UOC Malattie infettive, Caserta, Italy; 10Federico II University, Dipartimento di Medicina Clinica e Chirurgia, Naples, Italy; 11AORN Sant’Anna e San Sebastiano; 12UOSS Fisiopatologia Epatica con Servizio di Assistenza ai Tumori, IRCCS Fondazione Pascale; 13Università della Campania Vanvitelli, UO Medicina Interna, Marcianise, Italy; 14PO Umerto I, UO Medicina Interna, Nocera Inferiore, Italy; 15Università della Campania Vanvitelli, Dipartimento di Salute Mentale e Fisica e Medicina Preventiva, Naples, Italy; 16PO Pineta Grande, UO Medicina Interna, Castel Volturro, Italy; 17Ospedale San Giovanni di Dio e Ruggi d’Aragona, Dipartimento di Medicina Clinica Medica, Epatologia e LungoDegenzae, AOU O. R. San Giovanni di Dio Ruggi e D’Aragona, Salerno, Italy; 18ALS Napoli 1 –, PSI Napoli EST, Unità complessa di Gastroenterologia, Napoli, Italy; 19Università della Campania Vanvitelli, Dipartimento di salute mentale e medicina Pubblica, Naples, Italy.

Email: deborangrisani@hotmail.it

**Background and aims:** Type 2 diabetes combined with portal vein tumor thrombosis worsens prognosis in patients with hepatocellular carcinoma.

**Method:** We analyzed data of 2243 patients from an online region-wide database (Progetto EpatoCarcinoma Campania) collected at 18 community and academic centers located in the Campania region, South of Italy. The database covered the period from January 2013 to April 2021. Kaplan-Meier curves were used to investigate survival in different groups.

**Results:** There were 398 thrombotic events, 81% of the thrombosis were neoplastic. In 32% of cases the thrombus involved the main trunk, while it involved the right 1st order branch and left 1st order branch in 27% and 11% of cases, respectively. Patients with thrombosis had a risk of death doubled compared to patients without thrombosis. There was no difference in OS in patients with PVTT at the main trunk, or in the left or right portal vein. One hundred and twenty patients with PVTT had type 2 diabetes as comorbidity; in 9% of cases the hepatic disease had a metabolic cause. Patients with diabetes and PVTT had the highest risk of death [HR = 1.02 (0.88–1.18); p = 0.756], although the presence of diabetes was not related to overall survival (Figure).
General sonographers and/or radiologists perform most surveillance and do not use structured reporting, felt desirable by most respondents. Poor views on US are approached heterogeneously with patients variably offered ongoing US, CT or different MRI protocols. Secondary surveillance is variable, typically using regular CT or MRI with contrast every 3–6 months for 2–5 years before 90% return to US surveillance.

**Conclusion:** Most responding UK NHS hospitals follow 6-monthly surveillance guidance for primary HCC surveillance. However, data recording of HCC screening practice is variable with limited data collection regarding compliance, yield and quality. HCC US screening is mostly performed by non-specialists without standardised reporting with inconsistent approaches to poor views. The quality of HCC screening may be improved by consistent resourcing, standardised pathways, data collection and quality assurance.

---

**Table 1: Summary of results.** Median (range). CLD chronic liver disease.

<table>
<thead>
<tr>
<th>Category</th>
<th>Median (range)</th>
<th>HPB centres (n = 15)</th>
<th>Non-HPB centres (n = 24)</th>
</tr>
</thead>
<tbody>
<tr>
<td>No. of consultants managing CLD</td>
<td>5 (2–19)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Lead HCC consultant?</td>
<td>90%</td>
<td></td>
<td></td>
</tr>
<tr>
<td>No. of CLD specialist nurses (SN)?</td>
<td>3 (0–13)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Lead Hepatology nurse?</td>
<td>67%</td>
<td></td>
<td></td>
</tr>
<tr>
<td>iQILS accreditation?</td>
<td>18%</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Database of CLD patients?</td>
<td>33%</td>
<td></td>
<td></td>
</tr>
<tr>
<td>SNs involved in HCC?</td>
<td>2 (0–10)</td>
<td>1.5 (0–5)</td>
<td></td>
</tr>
<tr>
<td>No. of patients under HCC surveillance</td>
<td>1250 (300–3000)</td>
<td>500 (100–1250)</td>
<td></td>
</tr>
<tr>
<td>Median no. of patients/consultant</td>
<td>156 (27–750)</td>
<td>145 (43–500)</td>
<td></td>
</tr>
<tr>
<td>Median no. of patients/SN HCC surveillance programme?</td>
<td>140 (60–1500)</td>
<td>233 (54–1250)</td>
<td></td>
</tr>
<tr>
<td>Administrative support?</td>
<td>10%</td>
<td>36%</td>
<td></td>
</tr>
<tr>
<td>Written protocol for HCC surveillance?</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Is HCC surveillance explained to the patient?</td>
<td>No 8%</td>
<td>Verbal 46%</td>
<td>Written and verbal 46%</td>
</tr>
<tr>
<td>Regular audit of HCC detection?</td>
<td>13%</td>
<td></td>
<td></td>
</tr>
<tr>
<td>US reported using a template?</td>
<td>20%</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Agreed pathway for poor views?</td>
<td>Yes 28%</td>
<td>No 72%</td>
<td></td>
</tr>
<tr>
<td>Offer CT or MRI for primary surveillance?</td>
<td>Yes 59%</td>
<td>No 41%</td>
<td></td>
</tr>
<tr>
<td>Secondary HCC surveillance database?</td>
<td>41%</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Written protocol for secondary surveillance?</td>
<td>33%</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Author</td>
<td>Affiliation</td>
<td>Abstract Numbers</td>
<td></td>
</tr>
<tr>
<td>--------</td>
<td>-------------</td>
<td>-----------------</td>
<td></td>
</tr>
<tr>
<td>Aagaard, Niels Kristian</td>
<td>S611 (FRI491)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Aardema, Charles</td>
<td>S719 (SAT115)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Aas, Christer E.</td>
<td>S221 (THU257)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Aass, Hans Christian Dalsbotten</td>
<td>S826 (SAT348)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Aas, Hans Christian Dalsbotten</td>
<td>S826 (SAT348)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Abadia, Marta</td>
<td>S90 (OS127)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Abazia, Cristiana</td>
<td>S626 (FRI522)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Abbas, Nadir</td>
<td>S96 (OS137), S526 (FRI269)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Abdelaal, Amr</td>
<td>S776 (SAT246)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Abdelanbi, Mohamed Noureldin Hassan Ali</td>
<td>S675 (SAT022)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Abdelhasseb, Dalia</td>
<td>S566 (FRI351)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Abdelmalek, Manal</td>
<td>S721 (SAT119), S722 (SAT120)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Abdelmalek, Manal F.</td>
<td>S10 (LB001), S495 (FRI210)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Abdelrhman, Abo Zed</td>
<td>S137 (THU035)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Abdelwahab, Ahmed</td>
<td>S928 (SAT581)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Abdo, Ayman</td>
<td>S479 (FRI178)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Abergel, Armand</td>
<td>S349 (THU511), S417 (FRI042), S549 (FRI317), S584 (FRI388), S640 (FRI550), S918 (SAT563)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Åberg, Fredrik</td>
<td>S80 (OS109), S413 (FRI036), S419 (FRI046)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Abecia, Leticia</td>
<td>S177 (THU155)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Abedin, Nada</td>
<td>S907 (SAT531)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Abedekina, Daniel</td>
<td>S645 (FRI559)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Abo, Kanon</td>
<td>S260 (THU335)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Abergel, Armand</td>
<td>S349 (THU511), S417 (FRI042), S549 (FRI317), S584 (FRI388), S640 (FRI550), S918 (SAT563)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Adanir, Haydar</td>
<td>S820 (SAT316), S858 (SAT410), S861 (SAT416), S864 (SAT421)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Adebayo, Danielle</td>
<td>S49 (OS063)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Adeva, Jorge</td>
<td>S107 (OS157)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ademir, Haydar</td>
<td>S820 (SAT316), S858 (SAT410), S861 (SAT416), S864 (SAT421)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Adegbeke, Kehinde</td>
<td>S899 (SAT518)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Adent, Jelle</td>
<td>S335 (THU484)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Addeh, Xavier</td>
<td>S547 (FRI314)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Adibekian, Alexander</td>
<td>S645 (FRI559)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Adinolfi, Luigi Elio</td>
<td>S938 (SAT599)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Adisa, Olayinka</td>
<td>S225 (THU266)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Adiguzel, Mehmet</td>
<td>S778 (SAT248)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Adinolfi, Luigi Elio</td>
<td>S938 (SAT599)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Adjakou, Kizito</td>
<td>S899 (SAT518)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Adkins, Jordan</td>
<td>S838 (SAT358)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Adomako, Samuel</td>
<td>S107 (OS156)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Adomako, Samuel</td>
<td>S107 (OS156)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Adolph, Timon</td>
<td>S126 (THU017)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Adon, MaryVic</td>
<td>S832 (SAT358)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Adonti, Valentina</td>
<td>S932 (SAT588)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Adora, Kizito</td>
<td>S838 (SAT358)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Adrah, Annie</td>
<td>S766 (SAT216)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Adraneda, Celina</td>
<td>S298 (THU406), S877 (SAT446)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Adrien, Lannes</td>
<td>S496 (FRI215), S497 (FRI216), S507 (FRI235)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Adu, Prince</td>
<td>S43 (OS051), S520 (THU223), S528 (THU378), S910 (SAT538)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Aehling, Phillip</td>
<td>S904 (SAT258)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Aerssens, Jeroen</td>
<td>S265 (THU343)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Aerts, Maridil</td>
<td>S107 (OS156)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Aeschbach, Thomas</td>
<td>S244 (THU302), S247 (THU309), S845 (SAT385)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Afek, Arnon</td>
<td>S784 (SAT258), S804 (SAT291)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Afgen, Silvia</td>
<td>S527 (FRI271)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Afonso, Catarina</td>
<td>S304 (THU420)</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

*Page numbers for abstracts are followed by the abstract number(s) in parentheses.*
Author Index

Alkhazashvili, Maia, S219 (THU253), S221 (THU258), S233 (THU283), S267 (THU347)
Alkhouri, Naim, S14 (LB005), S75 (OS101), S87 (OS121), S151 (THU064), S159 (THU077), S242 (FR1052), S427 (FR1060), S453 (FR1090), S495 (FR1220), S727 (SAT131), S730 (SAT139), S731 (SAT142), S732 (SAT143)
Alkim, Huseyn, S861 (SAT416)
Allah, Belimi Hibat, S19 (OS008), S942 (JOURNAL OF HEPATOLOGY)
Allam, Dalia, S19 (OS008), S49 (OS063)
Allard, Marc Antoine, S935 (SAT595)
Allam, Alina, S138 (THU037), S414 (FR1037), S438 (FR1084)
Allen, Samantha, S554 (FRI327)
Allen, Sophie, S364 (THU537)
Allen, Kathryn, S138 (THU036), S159 (THU077), S422 (FR1052), S570 (FR1360)
Alvarado-Tapiaus, Edilmar, S64 (OS1082), S90 (OS127), S91 (OS128), S137 (THU035), S370 (THU548), S625 (FR1520), S627 (FR1523), S886 (SAT494), S900 (SAT520)
Álvares-da-Silva, Maria Reis, S19 (OS008), S49 (OS063)
Alvarez-Alvarez, Ismael, S396 (FRI011)
Álvarez-Ossorio, Angela Rojas, S450 (FR1055), S708 (SAT087)
Alvarez-Navascués, Carmen, S324 (THU464), S328 (THU471)
Alvarez-Ossorio, Angelina Rojas, S450 (FR1055), S708 (SAT087)
Alvarez-Sola, Gloria, S643 (FR1554), S757 (SAT198)
Alvaro, Cristina, D268 (THU348), S587 (FR1394)
Alvaro, Domenico, S107 (OS157), S648 (FR1564)
Alvaro, Frank, S558 (FR1334)
Alves de Castro, Pedro, S55 (FR1323)
Alves, Rogério, S137 (THU034)
Alwayn, Ian, S798 (SAT280)
Amadeo, Gianluca, S372 (THU566), S375 (THU573), S530 (FR1276), S927 (SAT578)
Amado, Luis Enrique Morano, S581 (FR1384)
Amano, Yuichiro, S7 (GS009)
Amaral, Hussam, S230 (THU277)
Amirali, Khadija, S419 (FR1045), S455 (FR113), S671 (SAT014)
Amirali, Bruna, S120 (THU004), S480 (FR1179), S735 (SAT153)
Amirali, Marion, S154 (FR1248), S521 (FR1260)
Almoula, Carolina, S114 (OS168), S406 (FR1027), S792 (SAT270), S792 (SAT271)
Alonso, Cristina, S419 (FR1045), S455 (FR113), S671 (SAT014)
Amor, Alain, S59 (OS074)
Aldaftani, Saleh, S5 (GS008), S154 (THU065), S785 (SAT260), S810 (SAT300)
Alric, Laurens, S72 (OS093), S833 (SAT360)
Al-Rubai, Latif, S96 (OS137)
Al-Sayegh, Rami, S382 (THU586), S931 (SAT587)
Al-Sayegh, Rola, S65 (OS084)
Al Shabeeb, Reem, S445 (FR1097)
Alsoud, Deema, S230 (THU277)
Alsaw, Khalid, S154 (THU065), S479 (FR1178)
Altangere, Enkhjargal, S824 (SAT342)
Altenburg, Arwen, S198 (THU198)
Altenmüller, Johannes, S321 (THU458)
Alte, Adriana, S786 (SAT261)
Altmann, Heidi, S11 (LB002)
Alulak, Joseph, S48 (OS061)
Alvihare, Varuna, S120 (THU005), S371 (THU350), S403 (FR1022), S771 (SAT236), S812 (SAT304)
Alvain, Aofie, S569 (FR1336), S570 (FR1360)
Alvarado-Tapias, Edilmar, S64 (OS1082), S90 (OS127), S91 (OS128), S137 (THU035), S370 (THU548), S625 (FR1520), S627 (FR1523), S886 (SAT494), S900 (SAT520)
Álvares-da-Silva, Maria Reis, S19 (OS008), S49 (OS063)
Alvarez-Alvarez, Ismael, S396 (FR1011)
Alvarez, Irene Perez, S222 (THU261)
Alvarez, Laura, S46 (OS056)
Alvarez, Maria, S17 (OS005), S43 (OS051), S209 (THU233), S282 (THU378), S910 (SAT538)
Álvarez-Velázquez, Carmen, S324 (THU464), S328 (THU471)
Álvarez-Ossorio, Angelina Rojas, S450 (FR1055), S708 (SAT087)
Álvarez-Sola, Gloria, S643 (FR1554), S757 (SAT198)
Alvaro, Cristina, D268 (THU348), S587 (FR1394)
Alvaro, Domenico, S107 (OS157), S648 (FR1564)
Alvaro, Frank, S558 (FR1334)
Alves de Castro, Pedro, S55 (FR1323)
Alves, Rogério, S137 (THU034)
Alwayn, Ian, S798 (SAT280)
Amadeo, Gianluca, S372 (THU566), S375 (THU573), S530 (FR1276), S927 (SAT578)
Amado, Luis Enrique Morano, S581 (FR1384)
Amano, Yuichiro, S7 (GS009)
Amaral, Adam, S59 (OS074), S931 (SAT587)
Amor, Alain, S59 (OS074)
Aldaftani, Saleh, S5 (GS008), S154 (THU065), S785 (SAT260), S810 (SAT300)
Alric, Laurens, S72 (OS093), S833 (SAT360)
Al-Rubai, Latif, S96 (OS137)
Al-Sayegh, Rami, S382 (THU586), S931 (SAT587)
Al-Sayegh, Rola, S65 (OS084)
Al Shabeeb, Reem, S445 (FR1097)
Alsoud, Deema, S230 (THU277)
Alsaw, Khalid, S154 (THU065), S479 (FR1178)
Altangere, Enkhjargal, S824 (SAT342)
Altenburg, Arwen, S198 (THU198)
Altenmüller, Johannes, S321 (THU458)
Alte, Adriana, S786 (SAT261)
Author Index

Aslanikashvili, Ana, S214 (THU243), S216 (THU247), S216 (THU248)
Aslan, Rahmi, S19 (OS008), S49 (OS063)
Aspas, Jessica, S743 (SAT170)
Asphaug, Lars, S130 (THU022)
Aspichueta, Patricia, S46 (OS056), S175 (THU074), S175 (THU076), S69 (FRI064), S651 (FRI571), S665 (SAT001), S689 (SAT050)
Aspinall, Alexander, S143 (THU045)
Aspinall, Richard, S22 (OS013), S96 (OS137)
Aspite, Silvia, S627 (FRI524)
Asraf, Keren, S804 (SAT291)
Asrani, Sumeet, S19 (OS008), S49 (OS063), S805 (SAT292)
Assawasuwannakit, Suraphon, S722 (SAT121)
Asselah, Tarik, S13 (LB0048), S245 (THU034), S249 (THU039), S288 (THU389), S288 (THU390), S291 (THU393), S300 (THU411), S349 (FRI317), S354 (FRI388), S829 (SAT352), S840 (SAT373), S864 (SAT422), S881 (SAT453)
Assenat, Eric, S392 (FRI006)
Assinger, Alice, S788 (SAT264), S799 (SAT283)
Atallah, Edmond, S22 (OS013), S16 (OS172)
Atay, Ali, S782 (SAT255)
Athanasiadis, Emmanuel, S742 (SAT167)
Athwal, Varinder, S104 (OS152)
Atienza, Francisco, S555 (FRI329)
Atif, Mo, S189 (THU181)
Atik, Cecilia, S374 (THU570), S380 (THU582)
Atkinson, Stephen, S11 (LB002), S34 (OS034), S122 (THU008), S124 (THU013), S132 (THU026), S135 (THU031), S140 (THU040), S352 (THU516)
Atsukawa, Masanori, S12 (LB0048)
Babudieri, Sergio, S596 (FRI414)
Babalis, Daphne, S34 (OS034)
Babas, An, S627 (THU347)
Aba, Masaya, S295 (THU041)
Bach, Charlotte, S738 (SAT160)
Bacheller, Philippe, S20 (OS010), S780 (SAT252)
Bach, David, S580 (FRI383)
Back, Sudhir, S9 (OS011), S94 (OS133)
Backhouse, Dianne, S63 (OS079), S885 (FRI492)
Bak, Koen, S30 (OS026)
Badalamenti, Giuseppe, S387 (THU599)
Badal, Bryan, S126 (THU016)
Badia-Aranda, Esther, S127 (THU018)
Badyak, Stephen, S465 (FRI149)
Bae, Ho S, S836 (SAT366)
Baek, Yanghyon, S572 (FRI365)
Baena, Sheila, S743 (SAT170)
Bae, Si Hyun, S146 (THU053), S490 (FRI202), S820 (SAT317), S932 (SAT589), S932 (SAT590)
Bae, Sung Min, S468 (FRI156), S469 (FRI157)
Baez-Ortega, Adrian, S741 (SAT165)
Bahn, Jonas, S604 (FRI462)
Baiano, Cassandra, S415 (FRI038)
Bai, Chosha, S264 (THU341)
Baiyes, Anna, S90 (OS127), S367 (THU542), S524 (FRI265)
Baiyes, Gerard, S685 (SAT041)
Bail, Brigitte Le, S372 (THU566)
Bailey, Adam, S320 (THU456), S320 (THU457), S321 (THU459), S322 (THU460)
Bailey, Michael, S3 (GS005)
Bair, Ming-Jong, S595 (FRI410)
Bai, Ru, S669 (SAT009)
Bai, Wei, S92 (OS130), S619 (FRI508), S621 (FRI512), S628 (FRI526)
Bajaj, Jasmohan S, S126 (THU016)
Bak, Minick, S100 (OS036), S67 (OS087)
Bakardjiev, Anna, S871 (SAT434)
Baker, Fadi Abu, S292 (THU395), S845 (SAT384)
Bakiev, Shokhista, S235 (THU288)
Bakker, Barbara, S539 (FRI298)
Balaban, Hatice Yasemin, S820 (SAT316), S861 (SAT416)
Balabanska, Rozalina, S299 (THU408), S867 (SAT427)
Balaban, Yasemin, S858 (SAT410)
Balaji, Anu, S903 (SAT526)
Balakrishnan, Anand, S745 (SAT177)
Balakrishnan, Narmada, S247 (THU308)
Balasubramanian, Srijit, S770 (SAT234)
Balbin, Alejandro, S508 (FRI236), S918 (SAT564)
Balcar, Lorenz, S18 (OS007), S24 (OS017), S92 (OS131), S354 (THU519), S372 (THU567), S374 (THU571), S376 (THU574), S383 (THU588), S428 (FRI062), S532 (FRI280), S535 (FRI287), S617 (FRI505), S618 (FRI506), S629 (FRI257)
Author Index

Bechmann, Lars, S378 (THU579), S682 (SAT035)
Beck, Andrew, S700 (SAT071), S708 (SAT088)
Becker, Britta, S250 (THU315)
Becker, Hans, S83 (OS113)
Becker, Mark, S455 (FRI112)
Becker, Swa, S385 (THU594)
Beckford, Racquel, S812 (SAT130)
Beckmann, Sonja, S509 (FRI238)
Beck-Nielsen, Henning, S9 (CS012)
Bédard, Nathalie, S675 (SAT022)
Bedard, Philippe, S395 (FRI010)
Bed, Cheikh Mohemed, S245 (THU304)
Bélaïdi, Souad, S547 (FRI314)
Bel, Maria Del, S161 (THU081)
Belanger, Agné
Bello, Arnaud Del, S122 (THU009)
Bell, Andrew, S700 (SAT071), S708 (SAT088)
Belanger, Agné
Bello, Arnaud Del, S122 (THU009)
Bellet, Jonathan, S17 (OS006)
Bellant, Lucio, S578 (FRI376), S807 (SAT296)
Bell, Elaine, S412 (FRI040)
Bell, Andrew, S700 (SAT071), S708 (SAT088)
Belanger, Agné
Bello, Arnaud Del, S122 (THU009)
Bellet, Jonathan, S17 (OS006)
Bellant, Lucio, S578 (FRI376), S807 (SAT296)
Bell, Elaine, S412 (FRI040)
Bell, Andrew, S700 (SAT071), S708 (SAT088)
Belanger, Agné
Bello, Arnaud Del, S122 (THU009)
Bellet, Jonathan, S17 (OS006)
Bellant, Lucio, S578 (FRI376), S807 (SAT296)
Bel, Bedir, Cihan, S513 (FRI245)
Belasri, Ines, S547 (FRI314)
Belkhejil, Elke, S853 (SAT401)
Behrends, Christian,
Benedetto, Davide Di, S929 (SAT582)
Benedetto, Fabrizio Di, S789 (SAT266)
Benenati, Francesco, S862 (THU579), S324 (THU501)
Bell, Andrew, S700 (SAT071), S708 (SAT088)
Belanger, Agné
Bello, Arnaud Del, S122 (THU009)
Bellet, Jonathan, S17 (OS006)
Bellant, Lucio, S578 (FRI376), S807 (SAT296)
Bell, Elaine, S412 (FRI040)
Bell, Andrew, S700 (SAT071), S708 (SAT088)
Belanger, Agné
Bello, Arnaud Del, S122 (THU009)
Bellet, Jonathan, S17 (OS006)
Bellant, Lucio, S578 (FRI376), S807 (SAT296)
Bel, Bedir, Cihan, S513 (FRI245)
Belasri, Ines, S547 (FRI314)
Belkhejil, Elke, S853 (SAT401)
Behrends, Christian,
Benedetto, Davide Di, S929 (SAT582)
Benedetto, Fabrizio Di, S789 (SAT266)
Benenati, Francesco, S862 (THU579), S324 (THU501)
Bell, Andrew, S700 (SAT071), S708 (SAT088)
Belanger, Agné
Bello, Arnaud Del, S122 (THU009)
Bellet, Jonathan, S17 (OS006)
Bellant, Lucio, S578 (FRI376), S807 (SAT296)
Bel, Bedir, Cihan, S513 (FRI245)
Belasri, Ines, S547 (FRI314)
Belkhejil, Elke, S853 (SAT401)
Behrends, Christian,
Author Index

Bogdanowicz, Karolina, S34 (OS034)
Boghici, Dan, S259 (THU334)
Boglione, Lucio, S825 (SAT346)
Bogomolov, Pavel, S4 (GS006), S828 (SAT351), S829 (SAT352)
Bohan-Keane, Mary, S569 (FRI358), S570 (FRI360)
Boilet, Gautier, S250 (THU314)
Boillot, Olivier, S772 (SAT239)
Boiselle, Carri, S58 (OS073)
Boix, Loreto, S381 (THU453), S500 (FRI222), S562 (FRI573)
Bojunga, Jörg, S253 (THU317), S254 (THU351), S907 (SAT351)
Bökererink, Roos-Anne, S525 (FRI266)
Bokun, Tomislav, S612 (FRI494)
Bolca, Selin, S180 (THU161)
Bolch, Maximilian, S381 (THU584), S828 (SAT351), S829 (SAT352)
Bolch, István, S24 (OS016)
Bolch, Stephen, S354 (THU495), S570 (FRI360)
Bolchev, Stéphane, S228 (THU273)
Bolch, Maximilian, S354 (THU584), S828 (SAT351), S829 (SAT352)
Bolcho, Long, S228 (THU273)
Bolchak, Maksim, S354 (THU584)
Bolchov, Anna, S228 (THU273)
Bolch, Maximilian, S354 (THU584), S828 (SAT351), S829 (SAT352)
Bolch, István, S24 (OS016)
Bolch, Stephen, S354 (THU495), S570 (FRI360)
Bolchev, Stéphane, S228 (THU273)
Bolch, Maximilian, S354 (THU584), S828 (SAT351), S829 (SAT352)
Bolch, István, S24 (OS016)
Bolch, Stephen, S354 (THU495), S570 (FRI360)
Bolchev, Stéphane, S228 (THU273)
Bolch, Maximilian, S354 (THU584), S828 (SAT351), S829 (SAT352)
Bolch, István, S24 (OS016)
Bolch, Stephen, S354 (THU495), S570 (FRI360)
Bolchev, Stéphane, S228 (THU273)
Bolch, Maximilian, S354 (THU584), S828 (SAT351), S829 (SAT352)
Bolch, István, S24 (OS016)
Bolch, Stephen, S354 (THU495), S570 (FRI360)
Bolchev, Stéphane, S228 (THU273)
Bolch, Maximilian, S354 (THU584), S828 (SAT351), S829 (SAT352)
Bolch, István, S24 (OS016)
Bolch, Stephen, S354 (THU495), S570 (FRI360)
Bolchev, Stéphane, S228 (THU273)
Bolch, Maximilian, S354 (THU584), S828 (SAT351), S829 (SAT352)
Bolch, István, S24 (OS016)
Bolch, Stephen, S354 (THU495), S570 (FRI360)
Bolchev, Stéphane, S228 (THU273)
Bolch, Maximilian, S354 (THU584), S828 (SAT351), S829 (SAT352)
Bolch, István, S24 (OS016)
Bolch, Stephen, S354 (THU495), S570 (FRI360)
Bolchev, Stéphane, S228 (THU273)
Broqua, Pierre, S715 (SAT105),
Bronstein, Jeff, S1 (GS001)
Bronsert, Peter, S2 (GS003)
Bronte, Fabrizio, S624 (FRI517)
Broseus, Julien, S905 (SAT529)
Brosch, Mario, S11 (LB002)
Brosov, Julian, S905 (SAT529)
Brosgart, Carol, S274 (THU361)
Brosnan, M. Julia, S7 (GS009), S425 (FRI058)
Brouwer, Sarah, S93 (OS132)
Brown, A, S868 (SAT428)
Brown, Elizabeth, S446 (FRI029)
Brown, Sarah, S88 (OS124)
Brown, Joanne, S484 (SAT392)
Brown, Kenneth, S277 (THU368)
Brownlee, Lorna, S733 (SAT146)
Brown, Marius, S64 (OS081)
Brown, Maxine, S551 (FRI321)
Brown, Robert, S899 (SAT517)
Brozat, Jonathan Frederik, S193 (THU187),
S339 (THU493)
Brudanet, Amelie, S205 (THU227)
Bueggermann, Yannick, S250 (THU315)
Bruggmann, Philip, S238 (THU291)
Brusa, Radan, S671 (SAT104)
Bruijs, Jordi, S381 (THU584)
Brujats, Ana, S370 (THU548)
Brujats, Anna, S91 (OS128), S502 (FRI226),
S625 (FRI520), S627 (FRI523),
S900 (SAT520)
Brammer, Daniel, S738 (SAT160)
Brunar, Helmut, S854 (SAT403)
Bruneau, Julie, S206 (THU230)
Brunelli, Laura, S758 (SAT201)
Brunetto, Maurizia, S4 (GS006),
S292 (THU394), S564 (FRI347),
S578 (FRI746), S828 (SAT351),
S829 (SAT352), S864 (SAT422)
Brunnauer, Philipp, S497 (FRI217),
S663 (FRI957), S739 (SAT162)
Bruns, Tony, S100 (OS143), S335 (THU484),
S339 (THU493), S342 (THU500)
Brusilovskaya, Ksenia, S360 (THU529),
S362 (THU534), S466 (FRI152),
S472 (FRI164), S753 (SAT191)
Brustia, Raffaele, S375 (THU573),
S927 (SAT578)
Bruzzone, Chiara, S671 (SAT014)
Bryce, Kathleen, S277 (THU368)
Brizca, Hrvoje, S702 (SAT075)
Bucciona, Daniela, S87 (OS122),
S600 (FRI453)
Bucci, Laura, S382 (THU587),
S932 (SAT588)
Buchanan, Ryan, S42 (FRI048),
S200 (THU218), S909 (SAT356)
Buchard, Benjamin, S349 (THU511),
S417 (FRI042), S640 (FRI550),
S918 (SAT563)
Buch, Stephan, S11 (LB002)
Bucker, Arno, S460 (FRI122)
Bucic, Teras, S630 (FRI399)
Budau, Grant, S483 (FRI187), S762 (SAT208)
Budeebaraz, Myagmarjav, S235 (THU287)
Budzynski, Andrzej, S746 (SAT179),
S759 (SAT203)
Buechter, Matthias, S378 (THU579)
Buettner, Stefan, S107 (OS157)
Bugge, Anne, S670 (SAT013)
Buggisch, Peter, S16 (OS003),
S662 (FRI445), S585 (FRI391)
Bughanesi, Elisaabeta, S154 (THU609),
S425 (FRI058), S436 (FRI078),
S437 (FRI081), S448 (FRI102),
S452 (FRI108), S671 (SAT014),
S675 (SAT021)
Bujanda, Luis, S46 (OS056), S59 (OS074),
S77 (OS103), S107 (OS157),
S648 (FRI564), S665 (SAT001)
Bu, Jiyoung, S921 (SAT569)
Bukulatjip, Sarah, S239 (THU294),
S305 (THU442)
Bulato, Cristina, S358 (THU526)
Bulbul, Rakibul Hassan, S244 (THU301)
Bulkey, Alison, S516 (FRI251)
Bullens, Sherry, S534 (FRI285)
Buller-Taylor, Terri, S209 (THU233)
Bungay, Helen, S330 (THU475)
Bungard, Andra, S235 (THU287)
Bunting, Stuart, S404 (FRI203),
S534 (FRI285)
Bu, Qingfa, S695 (SAT062)
Buque, Xabier, S648 (FRI564),
S651 (FRI571), S665 (SAT001),
S689 (SAT500)
Burred, Vinod, S710 (SAT091)
Burak, Kelly, S143 (THU045)
Burbasa, Barbara, S520 (THU257)
Burden, Adrian, S930 (SAT855)
Burden-teh, Esther, S22 (OS013)
Burdette, Dana, S251 (THU317)
Bureau, Christophe, S61 (OS076),
S524 (FRI265), S630 (FRI529)
Burger, David, S580 (FRI383)
Burger, Katharina, S692 (SAT056)
Burgermeister, Elke, S408 (FRI029)
Burghart, Lukas, S315 (THU449),
S545 (FRI309)
Burgio, Valentina, S748 (SAT180)
Burlone, Michela Emma, S929 (SAT582)
Burman, Julio, S312 (THU442)
Burmc, Rani, S860 (SAT413)
Burns, Gareth, S842 (SAT377)
Burns, Keith, S137 (THU035)
Burr, Patrick, S949 (SAT062), S54 (OS069),
S154 (THU069), S306 (THU423),
S338 (THU526), S569 (FRI399),
S627 (FRI524), S821 (SAT138)
Burrell, Sue, S516 (FRI251)
Burt, Alastair, S137 (OS001)
Burden, Julius, S312 (THU449)
Bury, Brian, S19 (OS008), S49 (OS063),
S229 (THU384), S297 (THU405),
S285 (THU383), S218 (THU252),
S255 (THU325), S218 (THU240),
S207 (THU231), S212 (THU240),
S218 (THU252), S255 (THU325),
S257 (THU330), S269 (THU350),
S277 (THU367), S285 (THU383),
S286 (THU384), S297 (THU405),
S300 (THU411), S316 (THU450),
S581 (FRI384), S824 (SAT344), S832 (SAT358),
S869 (SAT430), S872 (SAT437)
Burton, Maxine, S510 (FRI010)
Butler, Marcus, S395 (FRI010)
Butrymowicz, Isabel, S549 (FRI137),
S584 (FRI388)
Bussay, Mihaela, S216 (THU247),
S229 (THU275), S587 (FRI395),
S595 (FRI397), S590 (FRI400),
S590 (FRI401)
Author Index

Chen, Tsung Po, S162 (THU084)
Chen, Wanqing, S82 (OS011)
Chen, Wei, S494 (FRI209)
Chen, Wen-Chi, S625 (FRI520)
Chen, Xiaojiao, S182 (THU165)
Chen, Xin, S744 (SAT172)
Chen, Xin-Yue, S70 (OS091), S844 (SAT382), S870 (SAT432)
Chen, XinYu, S838 (SAT369)
Chen, Xuanmeng, S767 (SAT218)
Chen, Yan, S377 (THU577)
Chen, Yaw-Sen, S119 (THU001)
Chen, Yi, S1 (GS001)
Chen, Yi-Cheng, S102 (OS148), S575 (FRI371), S576 (FRI372)
Cheng, Yongping, S70 (OS091)
Chen, Yu, S74 (OS097), S803 (SAT289)
Chen, Yu-Ju, S514 (FRI247)
Chen, Yunfu, S254 (SAT233), S854 (SAT404)
Chen, Yunru, S879 (SAT449)
Chen, Yutong, S215 (THU245)
Chen, Zhaobin, S669 (SAT009)
Chen, Zhiping, S22 (OS014), S421 (FRI050)
Chen, Xin, S852 (SAT399)
Chen, Yi-Cheng, S102 (OS148), S575 (FRI371), S576 (FRI372)
Cheng, Yongping, S70 (OS091)
Chen, Yu, S74 (OS097), S803 (SAT289)
Chen, Yu-Ju, S514 (FRI247)
Chen, Yunfu, S254 (SAT233), S854 (SAT404)
Chen, Yunru, S879 (SAT449)
Chen, Yutong, S215 (THU245)
Chen, Zhaobin, S669 (SAT009)
Chen, Zhiping, S22 (OS014), S421 (FRI050)
Chen, Xin, S852 (SAT399)
Ch, Chien, Michael, S848 (SAT392)
Childs, Kate, S253 (THU321)
Chimakurthi, Ramu, S332 (THU749)
China, Louise, S104 (OS151), S342 (THU499), S524 (FRI265)
Chines, Valeria, S259 (THU333)
Chinnaratha, Asif, S898 (SAT516)
Chiong, Justin, S580 (FRI383)
Chiriac, Stefan, S573 (FRI368)
Chiritza, Dragos, S795 (SAT276)
Chitadze, Nazibrola, S233 (THU283), S267 (THU347)
Chitnis, Amit, S831 (SAT356)
Chiu, Keith Wan Hang, S78 (OS105)
Chiu, SM, S824 (SAT344)
Chiu, Yencheng, S683 (SAT420)
Chi, Xiaolong, S22 (OS014), S421 (FRI050)
Chi, Xin, S852 (SAT399)
Chkhartishvili, Nikoloz, S587 (FRI395), S590 (FRI400), S590 (FRI401)
Chlipicki, Stefan, S759 (SAT203)
Chng, Chinhly, S548 (FR1316)
Chng, Elaine, S32 (OS030), S431 (FRI068), S481 (FRI181), S486 (FRI194), S493 (FR1207), S619 (FR1509), S623 (FR1516)
Chotik, Gabriel, S399 (FRI017), S584 (FRI388)
Choe, Byung-Ho, S666 (SAT425)
Choe, Hun Jee, S163 (THU087)
Cho, Eun Ju, S303 (THU417)
Cho, Won Hyouk, S932 (SAT590)
Cho, Heejin, S303 (THU417), S862 (SAT418)
Choi, Gwang Hyeon, S275 (THU633)
Choi, Han Hoon, S852 (SAT400), S861 (SAT415)
Choi, Ho Jong, S820 (SAT317)
Choi, In-cheol, S473 (FRI166)
Choi, In Young, S468 (FRI155), S469 (FRI157)
Choi, Jaehyuck, S468 (FRI156), S469 (FRI157)
Choi, Jin Yong, S767 (SAT229)
Choi, Jongggi, S275 (THU363), S454 (FRI310), S833 (SAT361), S842 (SAT378), S891 (SAT503)
Choi, Jong Young, S820 (SAT317), S932 (SAT589)
Choi, Moon Seok, S273 (THU359)
Choi, Sang Huy, S916 (SAT361)
Choi, Won-Mook, S610 (FRI488), S833 (SAT361), S842 (SAT378), S870 (SAT433)
Choi, Young Hyeok, S798 (SAT281), S799 (SAT282)
Choi, Yun-Jung, S322 (THU461), S477 (FRI174)
Cho, Jai Young, S798 (SAT281)
Cho, Ju-Yeon, S275 (THU363)
Chokkalingam, Anand, S560 (FRI340)
Chokshi, Shilpa, S68 (OS089), S120 (THU004), S188 (THU178), S480 (FRI179), S639 (FRI547), S647 (FRI562), S911 (SAT540)
Cho, Kyung Joo, S653 (FRI575), S735 (SAT194)
Cholongitas, Evangelos, S429 (FRI063)
Cho, Mi-La, S820 (SAT317)
Chong, Jia Ling, S431 (FRI068), S493 (FRI207)
Chong, Lee-Wen, S595 (FR1410)
Chong, Young Eun, S862 (SAT418)
Chong, Ingrid, S269 (THU350), S300 (THU411), S589 (SAT412)
Chopra, Aditya, S309 (THU437)
Chorostowska-Wynimko, Joanna, S515 (FRI250)
Choteschovskiy, Niklas, S464 (FRI147)
Choudhry, Anam, S548 (FRI316)
Choudhury, Ashok, S19 (OS008), S53 (OS066), S530 (THU512), S539 (FRI014)
Choudhury, Gourab, S14 (LB006)
Chou, Yukimasa, S56 (THU522)
Chou, Roger, S557 (FR1332), S557 (FR1333), S591 (FR404)
Chow, Benjamin, S164 (THU089)
Chow, Matthew, S134 (THU029)
Chow, Yong Kuo, S485 (FR191)
Cho, Young Youn, S484 (FRI189)
Christensen, Diana Hedevang, S172 (THU104)
Christensen, Hannah, S256 (THU328)
Christensen, Lee, S554 (FRI327)
Christensen, Morten, S475 (FRI169)
Christensen, Peer, S550 (FR1319)
Christiansen, Michael Michael, S450 (FRI104)
Christianet, Montserrat Fraga, S253 (THU322)
Christmas, Michael, S300 (FRI294), S338 (FRI295)
Chris, Z., S447 (FRI100)
Chromy, David, S555 (FRI328)
Chuang, Jay, S427 (FRI060)
Chuang, Wan-Long, S458 (FRI118), S595 (FR1410), S849 (SAT393)
Chuang, WL, S588 (SAT428)
Chulanov, Vladimir, S4 (OS006), S103 (OS149), S828 (SAT351)
Chu, Lily, S343 (THU502)
Chung, Brian K., S27 (OS021), S604 (FRI463)
Chung, Chuhuan, S318 (THU453), S319 (THU455), S427 (FRI060), S700 (SAT071)
Chung, Diana, S88 (OS123), S715 (SAT106), S716 (SAT107), S716 (SAT108), S731 (SAT142)
Chung, Enoch, S592 (FR1405)
Chung, Han Yang, S42 (OS049)
Chung, Raymond, S36 (OS037), S264 (THU341), S592 (FR1405)
Chung, Wooh Jin, S572 (FRI365), S916 (SAT560)
Churkin, Alex, S448 (FR1396)
Churuangsuk, Chaoyong, S722 (SAT121)
Chu, Yu-De, S638 (FRI546)
Chu, Yu-Ju, S294 (THU398)
Author Index

Dickey, Amy, S516 (FRI251)
Dieguez, Maria Luisa Gonzalez,
Didier, Michel, S872 (SAT436)
Di Caterino, Tina, S423 (FRI054),
Diaz-Quintana, Antonio, S132 (THU027)
Diaz-Moreno, Irene, S132 (THU027)
Diaz-Mitoma, Francisco, S100 (OS145)
Diaz, Sebastian, S137 (THU034)
Díaz-Mejía, Nely, S316 (THU450)
Díaz, María Paz, S218 (THU252)
Diaz, Luis Antonio, S137 (THU034)
Díaz-González, Álvaro, S59 (OS074),
Diatta, Omar, S207 (THU231), S208 (THU232)
Di Maira, Giovanni, S747 (FRI173)
Di Girolamo, Julia, S558 (FRI334)
Di Giorgio, Angelo, S518 (FRI255),
S519 (FRI256)
Di Girolamo, Julia, S558 (FRI334)
Dicken, Christopher, S764 (SAT212)
Dickson, Rolland, S15 (OS002)
Didier, Michel, S872 (SAT436)
Dieguez, Maria Luisa Gonzalez,
S114 (OS169), S406 (FRI027)
Diehl, Lauri, S194 (THU189),
S684 (SAT040), S832 (SAT358),
S835 (SAT364)
Dieterich, Douglas T, S298 (THU407),
S590 (FRI402), S836 (SAT366),
S848 (SAT390)
Dieterich, Douglas T., S432 (FRI070),
S436 (FRI078)
Dietrich, Peter, S163 (THU085)
Dietz, Christopher, S823 (SAT341)
Dietz, Julia, S15 (OS001), S16 (OS003),
S855 (FRI391)
Diz, Cristina, S90 (OS127)
Di Fabio, Romano, S97 (OS139)
Di Gialleonardo, Luca, S436 (FRI079)
Di Giorgio, Angelo, S518 (FRI255),
S519 (FRI256)
Di Girolamo, Julia, S558 (FRI334)
Diken, Mustafa, S464 (FRI147)
Dikopoulos, Nektarios, S823 (SAT341)
Dill, Michael, S262 (THU338)
Dillon, John, S17 (OS005), S411 (FRI033),
S415 (FRI038), S473 (FRI165),
S495 (FRI214), S564 (FRI348)
Di Maria, Giovanni, S477 (FRI173)
Di Maria, Tommaso, S114 (OS168),
S406 (FRI027), S811 (SAT301),
S811 (SAT303)
Di Marco, Vito, S448 (FRI011)
Dimitriadi, Stavros, S57 (OS072A),
S58 (OS072B)
Dimitrova, Dessislava, S72 (OS094)
Dinani, Amreen, S168 (THU097),
S169 (THU098), S170 (THU099),
S291 (THU392), S301 (THU413)
Dincic, Dinc, S820 (SAT316), S858 (SAT410),
S861 (SAT416), S864 (SAT421)
Ding, Dora, S427 (FRI060)
Ding, Huiguosu, S408 (FRI029)
Ding, Wei, S183 (THU168)
Ding, Weinao, S287 (THU388),
S296 (THU403), S326 (THU468),
S504 (FRI292)
Ding, Yanhua, S89 (OS125), S837 (SAT367),
S865 (SAT423), S894 (SAT509)
Ding, Yuming, S338 (FRI294),
S538 (FRI295)
Dini, Luciana, S763 (SAT211)
Diniz, Mariana, S55 (OS072B)
Dinkelborg, Katja, S263 (THU339)
Dion, Sophie, S527 (FRI270)
Dion, Jessica, S675 (SAT022)
Dion, Sarah, S639 (FRI548)
Diotallevi, Marina, S665 (SAT002)
Diofr, Assane, S202 (THU221)
Diofr, Boubacar, S304 (THU419)
Diofr, Daouda, S304 (THU419)
Di Pasqua, Laura Giuseppina,
S702 (SAT074)
Diichwolf, Melissa, S137 (THU034),
S780 (SAT251)
Dirks, Meike, S624 (FRI191)
Di Rocco, Maja, S515 (FRI249)
Dirsch, Verena, S711 (SAT093)
Di Sandro, Stefano, S795 (SAT275)
Discher, Thomas, S16 (OS003),
S585 (FRI391)
Di Somma, Sarah, S769 (SAT233)
Distrificio, Alfio, S703 (SAT077)
Di Tocco, Francesca Casusculli,
S259 (THU333)
Di Tommaso, Luca, S528 (FRI272)
Ditt, Vanessa, S197 (THU197)
Divani-Patel, Sapna, S805 (SAT292)
Dixit, Bharat, S834 (SAT362)
Dixon, Dan A., S84 (OS116)
Dixon, Emmanuel Dauda, S469 (FRI158),
S688 (SAT049), S760 (SAT204)
Dijazoul, Sonia, S542 (FRI033)
Do, Ai-Thien, S875 (SAT442)
Dobracka, Beat, S585 (FRI390)
Dobracka, Witold, S592 (FRI046)
Dobrowolska, Krystyna, S585 (FRI390)
Dobson, Susan L., S804 (SAT291)
Do, Son, S875 (SAT442)
Do, Son, S875 (SAT442)
Doolman, Ram, S804 (SAT291)
Dorner, Marcus, S55 (OS070)
Douiri, Abdel, S809 (SAT298)
Doukas, Michael, S194 (THU189),
S644 (FRI556)
Douglas, John, S167 (OS005),
S297 (THU404), S567 (FRI353)
Dorn, Karen, S55 (OS070)
Dorn, Livia, S545 (FRI039)
Dorrell, Lucy, S872 (SAT437)
Douglas, John, S167 (OS005),
S297 (THU404), S567 (FRI353)
Dorrell, Lucy, S872 (SAT437)
Dorner, Marcus, S55 (OS070)
Downie, Bryan, S318 (THU453)
Author Index

El-Moustaid, Fadoua, S597 (FRI416)
Elortza, Felix, S37 (OS039), S46 (OS056),
El-Omar, Emad, S920 (SAT568)
Ellis, Jim, S666 (SAT004)
Ellis, Ewa, S665 (SAT002), S756 (SAT197)
Ellik, Zeynep Melekoglu, S858 (SAT410)
Ellenrieder, Volker, S85 (OS118)
Ellik, Carla, S758 (SAT199)
Eraki, Tamer Al, S566 (FRI351)
Elston, Robert, S12 (LB004A), S13 (LB004B),
Eltepu, Laxman, S853 (SAT402)
Embade, Nieves, S671 (SAT014)
Elwood, Chelsea, S43 (OS051)
El, Kariem, Lima Awad, S3 (GS004)
Elizalde, Montserrat, S757 (SAT198)
Elia, Chiara, S908 (SAT535)
Elizalde, Maria, S500 (FRI222),
Elkrief, Laure, S127 (THU019),
El-Karim, Lima Awad, S3 (GS004)
Elzafar, Esra, S240 (THU326)
Elia, Chiara, S908 (SAT535)
Elizalde, Maria, S500 (FRI222),
Elkhashab, Magdy, S427 (FRI060),
Ellenrieder, Volker, S85 (OS118)
Ellik, Carla, S758 (SAT199)
El, Kariem, Lima Awad, S3 (GS004)
Elzafar, Esra, S240 (THU326)
Elia, Chiara, S908 (SAT535)
Elizalde, Maria, S500 (FRI222),
Elkhashab, Magdy, S427 (FRI060),
Author Index

Fink, Jodok Matthias, S710 (SAT090)
Finnegan, Sarah, S95 (OS135)
Finnemore, Alexander, S687 (SAT064)
Fiorentino, Francesca, S34 (OS034)
Fischer, Elke, S224 (THU265)
Fischer, Janett, S11 (LB002), S184 (THU169), S379 (THU581), S382 (THU586), S860 (SAT414), S931 (SAT587)
Fischer, Lutz, S983 (SAT507)
Fischer, Petra, S193 (THU187)
Fischer, Susan, S306 (THU431)
Fisseha, Henok, S19 (OS008), S49 (OS063)
Fits, Daniel, S313 (THU444)
Fitzgerald, Megan, S824 (SAT343), S846 (SAT386)
Flack, Steve, S96 (OS137)
Flaherty, John F., S4 (GS006), S103 (OS149), S244 (THU302), S828 (SAT351), S829 (SAT352), S837 (SAT368), S845 (SAT385), S846 (SAT417), S866 (SAT425)
Flaßhove, Alexander, S193 (THU187)
Fleckman, M. Wayne, S142 (THU043)
Fleischman, M. Wayne, S142 (THU043)
Fleming, John, S7 (OS007)
Fleming, John, S17 (OS016)
Fleming, John, S193 (THU187)
Fleischer-Stepniwskas, Katarzyna, S565 (FRI350)
Flensted-Jensen, Mathias, S724 (SAT124)
Fletcher, Simon, S53 (OS067), S251 (THU177), S276 (THU365), S835 (SAT364), S841 (SAT376)
Fleury, Hervé, S249 (THU313)
Flisak, Robert, S565 (FRI350), S585 (FRI390), S592 (FRI406)
Fliss-Isakov, Naomi, S148 (THU056)
Flocco, Anna, S831 (SAT356)
Floreni, Annarosa, S317 (THU452), S335 (THU484)
Flores-Costa, Roger, S361 (THU530), S362 (THU533), S370 (THU549), S674 (SAT019)
Florecu, Madalina, S795 (SAT276)
Flores, Joan Ericka, S498 (FRI218)
Fornaro, Lorenzo, S748 (SAT180)
Fornaro, Lorenzo, S748 (SAT180)
Forsberg, Cecilia, S333 (THU480)
Fortén, Eva, S19 (OS008), S34 (OS034), S49 (OS063), S122 (THU008), S124 (THU013), S141 (THU041), S266 (THU345), S352 (THU516)
Forssman, Cecilia, S333 (THU480)
Forsmeyer, Dirk, S383 (THU590)
Forstén, Aino, S100 (OS145)
Forstnäs, Per, S383 (THU590)
Fortea, Jose Ignacio, S90 (OS127), S624 (FRI181), S774 (SAT242)
Fortuna, Brett, S770 (SAT235)
Fortune, Brett, S779 (SAT250)
Fortún, Jesús, S14 (OS169)
Fortuny, Marta, S724 (SAT125)
Forzenigo, Laura Virginia, S578 (FRI376)
Forzani, Francesco Giuseppe, S908 (SAT353)
Foster, Erin, S726 (SAT130)
Foster, Graham, S44 (OS053), S238 (THU291), S551 (FRI321)
Foster, John, S530 (FRI327)
Foster, Neil, S34 (OS034)
Foster, Robert, S650 (FRI568), S660 (FRI590), S660 (FRI591), S726 (SAT130)
Foti, Michelangelo, S645 (FRI559), S652 (FRI572)
Fournier, Claire, S193 (THU187)
Fournier, Claire, S193 (THU187)
Fournié, Fayssoil, S579 (FRI381)
Fournier, Céline, S425 (FRI058), S448 (FRI102), S452 (FRI108), S722 (SAT120)
Fournier, Claire, S593 (FRI047)
Fournier, Margot, S645 (FRI559), S652 (FRI572)
Fowler, Kathry, S451 (FRI107), S454 (FRI110), S701 (SAT073)
Fourcans, Anna Ludovica, S159 (THU078), S167 (THU095), S578 (FRI366), S682 (SAT036), S682 (SAT037), S698 (SAT068), S703 (SAT077), S706 (SAT084)
Franca, Maria Manuela, S442 (FRI091)
Francesca Manfredi, Giulia, S929 (SAT583)
Franceschini, Barbara, S758 (SAT201)
Francica, Giampiero, S938 (SAT599)
Francione, Paolo, S159 (THU078), S167 (THU095)
Francisco, Simon, S249 (THU313)
Franco, Andrea Jimenez, S685 (SAT041)
Franco, Andrea Jiménez, S677 (SAT027), S678 (SAT028), S681 (SAT034)
Franco, Brunella, S84 (OS115)
Francoz, Claire, S772 (SAT239), S817 (SAT310)
Franque, Sven, S9 (GS011), S90 (OS127), S459 (FRI120), S502 (FRI226), S516 (FRI252), S692 (SAT055), S709 (SAT089), S721 (SAT119), S722 (SAT120)
Franke, Andra, S325 (THU466), S604 (FRI462)
Frank, Leonie, S599 (FRI451)
Franklin, James, S938 (SAT600)
Frankova, Son, S36 (FRI290), S593 (FRI408)
Franks, Hester, S116 (OS172)
Franza, Anne Minello, S72 (OS093), S833 (SAT360), S840 (SAT373), S918 (SAT563)
Fratielli, Remo, S503 (FRI227), S868 (SAT429), S880 (SAT450)
Fraser, Andrew, S17 (OS005)
Fraser, Chris, S240 (THU297), S581 (FRI384)
Fraser, Hannah, S256 (THU328)
Fraser, Melissa, S558 (FRI334)
Fraser, Simon, S42 (OS048)
Frassineti, Giovanni Luca, S748 (SAT180)
Fraughen, Daniel, S531 (FRI279)
Frederick, R. Todd, S61 (OS060)
Frederiksen, Peder, S415 (FRI039)
Freed, Robert, S770 (SAT234)
Freedman, James, S16 (OS007)
Freer, Alice, S334 (THU483)
Freilich, Bradley, S719 (SAT114)
Fertla, Marta, S149 (THU060)
Frijdl, Frederik, S471 (FRI162)
Frelin, Lars, S860 (SAT413)
Frenquell, Luca, S737 (SAT157)
Frentsmiedl, Verena, S711 (SAT093)
Frey, Olivier, S703 (SAT078)
Frias, Juan R., S732 (SAT143)
Frias, Maria Carnevali, S577 (FRI373)
Author Index

Fricke, Gert, S712 (SAT095)
Fridriksson, Ragnheidur H., S573 (FRI366)
Friederich, Philip W., S306 (THU431)
Friedman, Scott, S160 (THU080), S343 (THU502), S455 (FRI113), S474 (FRI168), S688 (SAT046), S714 (SAT003)
Fried, Michael, S449 (FRI103)
Friedrichsen, Martin, S720 (SAT116)
Friedmann, Tomer, S387 (THU097)
Friesland, Martin, S250 (THU315)
Fries, Helmut, S463 (FRI146), S471 (FRI161), S690 (SAT051)
Fritsch, Thea-Charlotte, S380 (THU360), S385 (THU364)
Frohlich, Stefan, S655 (FRI581)
Fritzsche, Sarah, S655 (FRI581)
Frost, Gary, S179 (THU158)
Fu, Rebecca, S265 (THU344)
Furlan, Alessandro, S442 (FRI091)
Furrie, Elizabeth, S495 (FRI214)
Furusyo, Norihiro, S875 (SAT442)
Gaal, Luc Van, S692 (SAT055)
Gabbaia, Daniela, S378 (THU578), S478 (FRI176), S479 (FRI177)
Gabernet, Gisela, S38 (OS042)
Gabiati, Claudia, S210 (THU126)
Gabriel, Maria Magdalena, S624 (FRI519)
Gabunia, Tamar, S587 (FRI395), S590 (FRI400), S590 (FRI401)
Galano, Adrian, S13 (LB004A), S288 (THU389), S291 (THU393), S880 (SAT452), S881 (SAT453)
Gadenne, Cloé, S758 (SAT199)
Gagger, Anuj, S251 (THU318), S832 (SAT358)
Gagliardi, Constance, S417 (FRI042)
Gallard, Constance, S376 (THU574)
Gajownik, Urszula Ewa, S291 (THU393), S880 (SAT452), S881 (SAT453)
Gal, Frédéric Le, S271 (THU355)
Galhardo, Patricia, S137 (THU034)
Galhardo, Ruth, S590 (FRI400), S590 (FRI401)
Gabunia, Tamar, S587 (FRI395), S590 (FRI400), S590 (FRI401)
Gambardella, Gennaro, S84 (SAT115)
Gamboso, Martina, S306 (THU423), S578 (FRI370), S815 (SAT311)
Gambino, Carmine Gabriele, S18 (OS007), S49 (OS006), S92 (OS131), S989 (SAT308), S989 (SAT511)
Gane, Edward J., S16 (OS004), S58 (OS073), S69 (OS090)
Ganesh, Nivrith, S98 (OS140)
Ganger, Daniel, S394 (FRI008)
Gang, Sujin, S798 (SAT282), S799 (SAT282)
Ganizate, Salome, S764 (SAT213)
Ganne-Carrié, Nathalie, S572 (SAT093), S127 (THU019), S372 (THU566), S504 (FRI228), S833 (SAT360), S840 (SAT373)
Gannon, Catherine, S552 (FRI322), S572 (FRI364)
Gannoun, Lila, S736 (SAT155)
Ganova-Raeva, Lilia, S221 (THU258)
Ganzzel, Rasmus Hvidbjerg, S418 (FRI044), S611 (FRI491)
Gao, Bo, S636 (FRI540)
Gao, Jin-Neng, S595 (FRI410)
Gao, Min, S215 (THU245)
Gao, Jing, S492 (FRI206), S786 (SAT262), S788 (SAT265)
Gao, Ning, S723 (SAT122)
Gao, Rong, S694 (SAT059), S723 (SAT123), S730 (SAT140), S735 (SAT154)
Gao, Xiaochun, S182 (THU165)
Gao, Xu, S883 (SAT488)
Author Index

He, Handan, S70 (OS091)
Heikenwälder, Mathias, S11 (LB003), S38 (OS042), S47 (OS09), S83 (OS114), S649 (FRi65), S655 (FRi581)
Hei, Franz Josef, S80 (OS108)
Heilig, Christoph, S599 (FRi407)
Heil, Martintha, S246 (THU306), S247 (THU307)
Heim, Katriin, S54 (OS068), S196 (THU194)
Heimann, Melina, S325 (THU466)
Hein, Moritz, S907 (SAT351)
Heinrich, Sophie, S783 (SAT257)
Heinze, Markus, S192, S193 (THU187)
Heinzel, Femke, S368 (THU543), S645 (FRi558)
Hei, Lulu, S402 (FRI021), S803 (SAT289)
Heinze, Annelies Van, S913 (SAT556)
Heckelhiller, Lukas, S937 (SAT598)
Heek, Annelies Van, S913 (SAT556)
Heck, Jennis, S334 (THU483)
He, Jingchun, S559 (FRI337)
Hermann, Pernille, S9 (GS012)
Hermans-Borgmeyer, Irm, S83 (OS114)
Hermies, Xander, S107 (OS156)
Hernandez, Candido, S268 (THU348), S581 (FRI384), S586 (FRI393), S587 (FRI394)
Hernandez, Christinie, S547 (FRi314)
Hernandez, Francisco Andris Pérez, S581 (FRI384), S931 (SAT586)
Hernandez-Gea, Virginia, S54 (OS069), S57 (OS072A), S136 (THU033), S367 (THU542), S502 (FRi226), S524 (FRi265), S630 (FRi259)
Hernandez, Jose Luis Perez, S19 (OS008), S49 (OS063)
Hernandez, Larissa, S487 (FRi195)
Hernandez, Nélia, S308 (THU435)
Hernandez, Rocio Munoz, S450 (FRI105), S708 (SAT087)
Hernandez, Rosario, S63 (OS060)
Hernandez, Ubaldo Benitez, S573 (FRi366)
Hernandez, Ana, S199 (THU199)
Hernández, Candido, S268 (THU348), S581 (FRI384), S586 (FRI393), S587 (FRI394)
Hernandez, Jose Luis Perez, S19 (OS008), S49 (OS063)
Herranz, José María, S112 (OS165), S643 (FRI554), S218 (THU252)
Herranz, Andrea, S218 (THU252)
Herranz, Jose Maria, S643 (FRi554), S697 (SAT064)
Herranz, José María, S112 (OS165), S500 (FRi222), S644 (FRi557)
Herrera, Hilde, S9 (GS011)
Herrero, Francisco Sanz, S222 (THU261)
Herrero, Jose Ignacio, S114 (OS168), S150 (THU061), S406 (FRi227), S792 (SAT271), S802 (SAT288)
Herrero, Laura, S749 (SAT193)
Herrmann, Eva, S15 (OS001)
Hershkovich, Leeor, S851 (SAT398)
Hertz, Toni, S148 (THU057), S623 (SAT341), S860 (SAT041)
Herve, Hugo, S715 (SAT105)
Hervet, Jeremy, S542 (FRi303)
Hervieu, Maëva, S766 (SAT216)
Haskim, Jeong, S13 (LB004B), S288 (THU389), S288 (THU390), S291 (THU393), S569 (FRi357), S572 (FRi365), S586 (FRi392), S872 (SAT437), S881 (SAT453)
Heglar, Brian, S534 (FRI285)
Hegmar, Hannes, S30 (OS026)
Hettich, Joanne, S312 (THU442)
Henshaw, Henry, Linda, S5 (GS008), S144 (THU048)
Henry, Eugenia, S443 (FRi093), S486 (FRi195)
Henry, Aus, S144 (THU048)
Henry, Austin, S144 (THU048)
Henflin, Barbvard, S545 (FRI309)
Henne, Nathalie, S692 (SAT055)
Hennan, Jim, S75 (OS101), S71 (SAT094)
Hennigh, Daniel, S10 (OS020)
Hennings, Samuel, S683 (SAT038)
Hennor, Roland, S611 (FRi492), S615 (FRi500)
Hernández, Candido, S268 (THU348), S586 (FRI393), S587 (FRI394)
Hernandez, Jose Luis Perez, S19 (OS008), S49 (OS063)
Hernandez, Larissa, S487 (FRi195)
Hernandez, Nélia, S308 (THU435)
Hernandez, Rocío Munoz, S450 (FRi105), S708 (SAT087)
Hernández, Rosario, S63 (OS060)
Hernandez, Uladlo Benitez, S573 (FRi366)
Hernández, Candido, S268 (THU348), S581 (FRI384), S586 (FRI393), S587 (FRI394)
Hernandez, Jose Luis Perez, S19 (OS008), S49 (OS063)
Hernandez, Larissa, S487 (FRi195)
Hernandez, Nélia, S308 (THU435)
Hernandez, Rocío Munoz, S450 (FRi105), S708 (SAT087)
Hernández, Rosario, S63 (OS060)
Hernandez, Uladlo Benitez, S573 (FRi366)
Herola, Antonio García, S268 (THU348), S586 (FRI393), S587 (FRi394)
Herrera, Jon, S416 (FRi041)
Herranz, Andrea, S218 (THU252)
Herranz, Jose Maria, S643 (FRi554), S697 (SAT064)
Herranz, José María, S112 (OS165), S500 (FRi222), S644 (FRi557)
Herrera, Hilde, S9 (GS011)
Herrero, Francisco Sanz, S222 (THU261)
Herrero, Jose Ignacio, S114 (OS168), S150 (THU061), S406 (FRi227), S792 (SAT271), S802 (SAT288)
Herrero, Laura, S749 (SAT193)
Herrmann, Eva, S15 (OS001)
Hershkovich, Leeor, S851 (SAT398)
Herta, Toni, S148 (THU057), S623 (SAT341), S860 (SAT041)
Herve, Hugo, S715 (SAT105)
Hervet, Jeremy, S542 (FRi303)
Hervieu, Maëva, S766 (SAT216)
Author Index

Idilman, Ramazan, S19 (OS008), S259 (THU334)
Idalsoaga, Francisco, S81 (OS139), S259 (THU334)
Ichai, Philippe, S349 (THU511)
Ibrahim, P., S464 (FRI148)
Icaza, Maru, S487 (FRI195)
Iannone, Andrea, S564 (FRI347)
Ibdah, Jamal, S92 (OS139), S259 (THU334)
Iborra, Ignacio, S724 (SAT125)
Iannacone, Matteo, S97 (OS139), S259 (THU334)
Iavarone, Massimo, S54 (OS069), S57 (OS072A), S223 (THU263), S578 (FRI376)
Ibañez, Luis, S90 (OS127), S157 (THU074), S158 (THU076)
Ibarra, Cesar, S77 (OS103)
Ibdah, Jamal, S692 (SAT057)
Iborra, Ignacio, S724 (SAT125)
Ibrahim, P., S464 (FRI148)
Icza, Maru, S487 (FRI195)
Ichaï, Philippe, S349 (THU511), S935 (SAT595)
Idalsoaga, Francisco, S81 (OS110), S137 (THU034)
Idliman, Ramazan, S19 (OS008)
Iqbal, Shahed, S276 (THU365)
Iqbal, Afshan, S759 (SAT202)
Ilgoo, Akin, S338 (THU491)
Ildinbaum, Victoria, S784 (SAT258), S804 (SAT291)
Inder, Akin, S338 (THU491)
Indolfi, Giuseppe, S203 (THU222), S591 (FRI404)
Indritz, Nevin, S13 (LB004A), S88 (SAT453)
Infantino, Giuseppe, S448 (FRI101), S725 (SAT127)
Ingliz, Patrick, S582 (FRI385)
Inglo, Sarah, S564 (FRI348)
Ingvast, Sofie, S471 (FRI162)
Inias, Jose A., S681 (SAT033)
Innes, Hamish, S11 (LB002), S170 (OS005), S560 (FRI339)
Innocenti, Tommaso, S770 (SAT235)
Inoue, Jun, S12 (LB004A), S880 (SAT452)
Inoue, Koai, S857 (SAT442)
Inoue, Takako, S272 (THU358)
Invernesi, Pietro, S94 (OS134), S96 (OS136), S335 (THU484), S404 (FRI024)
Iozzo, Robert, S672 (SAT016)
Ippolito, Davide, S96 (OS136)
Irbes-Depe, Marie, S73 (OS096), S74 (OS099), S441 (FRI089)
Irizarriaga-Lejarreta, Marta, S671 (SAT104)
Ishida, Yuji, S252 (THU319)
Ishino, Takamasa, S615 (FRI501), S897 (SAT514)
Ishizaki, Kenta, S430 (FRI067), S444 (FRI095)
Ismail, Marwa, S62 (OS078), S313 (THU443)
Ismail, Mohamed, S875 (SAT441)
Isoneni, Helena, S312 (THU441)
Isla, Ariel, S845 (SAT384)
Israelsen, Mads, S2 (OS002), S9 (OS102), S129 (THU021), S299 (THU392), S475 (FRI171), S500 (FRI223)
Issachar, Assaf, S64 (OS081), S774 (SAT241), S793 (SAT272), S855 (SAT406)
Issa, Fadi, S809 (SAT298)
Ito, Yosihito, S563 (FRI346)
Ittz, Emmanuel, S375 (THU573)
Itzel, Timo, S928 (SAT580)
Iwatsuka, Kentaro, S673 (SAT017)
Iwasaki, Hirohiko, S172 (THU103)
Iwashita, Kento, S430 (FRI067), S444 (FRI095)
Ivancics, Tommy, S109 (OS159), S778 (SAT249), S800 (SAT286), S801 (SAT287)
Ivanova, Elena, S42 (OS049), S557 (FRI332), S558 (FRI335)
Iwaisako, Keiko, S183 (THU167)
Iwaki, Michihiro, S430 (FRI067)
Iwana, Terunao, S615 (FRI501), S897 (SAT514)
Iwasaki, Hiroki, S172 (THU103)
Iwasawa, Kentaro, S673 (SAT017)
Iyengar, Sowmya, S191 (THU184), S329 (THU474), S358 (THU525)
Iyer, Janani, S700 (SAT071), S708 (SAT088), S711 (SAT094)
Iyer, Rajalakshmi, S427 (FRI060)
Izquierdo-Alarte, Paula, S103 (OS150)
Izquierdo-Sánchez, Laura, S77 (OS103), S192 (THU185), S671 (SAT014)
Izumi, Namiki, S379 (THU580)
Izzo, Francesco, S938 (SAT399)
Izy, Manhal, S807 (SAT296)
Jahn, Alan, S434 (FRI075)
Jaber, Samir, S349 (THU511)
Jachs, Mathias, S18 (OS007), S92 (OS131), S359 (THU527), S390 (FRI003), S532 (FRI280), S535 (FRI287), S545 (FRI309), S555 (FRI328), S617 (FRI505), S629 (FRI527), S629 (FRI528), S631 (FRI531), S632 (FRI533), S829 (SAT353), S830 (SAT354), S843 (SAT379)
Jack, Kathryn, S277 (THU368)
Jackson, Akil, S672 (SAT166)
Author Index

Jing, He, S56 (OS071)
Jing, Zhang, S165 (THU091), S870 (SAT432)
Jin, He, S89 (OS125)
Jin, Rui, S26 (OS020), S685 (SAT042)
Jin, Young-Joo, S870 (SAT433)
Jirsa, Milan, S536 (FRI290)
Jin Bauer, David, S355 (FRI287), S545 (FRI309), S555 (FRI238)
Johannes, Chang, S895 (SAT510)
Johannessen, Asgeir, S2 (GS002), S9 (GS012), S49 (OS063)
Johansson, Edvin, S420 (FRI047)
Johansen, Stine, S2 (GS002), S9 (GS012), S49 (OS063)
Johnstone-hume, Claire, S337 (THU489)
Johnson, Saraha, S692 (SAT057)
Jing, Zhang, S165 (THU091), S870 (SAT432)
Jin, He, S89 (OS125)
Jin, Rui, S26 (OS020), S685 (SAT042)
Jin, Young-Joo, S870 (SAT433)
Jirsa, Milan, S536 (FRI290)
Jin Bauer, David, S355 (FRI287), S545 (FRI309), S555 (FRI238)
Johannes, Chang, S895 (SAT510)
Johannessen, Asgeir, S2 (GS002), S9 (GS012), S49 (OS063)
Johansson, Edvin, S420 (FRI047)
Johansen, Stine, S2 (GS002), S9 (GS012), S49 (OS063)
Johnstone-hume, Claire, S337 (THU489)
Johnson, Saraha, S692 (SAT057)
Jing, Zhang, S165 (THU091), S870 (SAT432)
Jin, He, S89 (OS125)
Jin, Rui, S26 (OS020), S685 (SAT042)
Jin, Young-Joo, S870 (SAT433)
Jirsa, Milan, S536 (FRI290)
Jin Bauer, David, S355 (FRI287), S545 (FRI309), S555 (FRI238)
Johannes, Chang, S895 (SAT510)
Johannessen, Asgeir, S2 (GS002), S9 (GS012), S49 (OS063)
Johansson, Edvin, S420 (FRI047)
Johansen, Stine, S2 (GS002), S9 (GS012), S49 (OS063)
Johnstone-hume, Claire, S337 (THU489)
Johnson, Saraha, S692 (SAT057)
Author Index
Author Index

Lee, Chul-min, S160 (THU079), S224 (THU264), S435 (FRI077), S438 (FRI082), S438 (FRI083), S439 (FRI086), S589 (FRI098), S728 (SAT135), S729 (SAT136)
Lee, Dae Ho, S444 (FRI095), S701 (SAT072)
Lee, Danbi, S545 (FRI101), S842 (SAT378)
Lee, David Uihwan, S203 (THU224), S204 (THU225)
Lee, Dong Ho, S78 (OS30), S303 (THU417)
Lee, DongHo, S163 (THU087)
Lee, Gil Won, S489 (FRI199)
Lee, Hae Won, S798 (SAT281)
Lee, Han Ah, S283 (THU379), S875 (SAT442), S932 (SAT509)
Lee, Han Ch, S545 (FRI310), S842 (SAT378)
Lee, Hee Seung, S653 (FRI157), S755 (SAT194)
Lee, Hye Eun, S701 (SAT072)
Lee, Hye Won, S653 (FRI75), S755 (SAT194)
Lee, Hyo Young, S160 (THU079), S224 (THU264), S435 (FRI077), S589 (FRI098), S728 (SAT135), S729 (SAT136)
Lee, Hyunsuk, S163 (THU087)
Lee, Hyun Woong, S872 (SAT437)
Lee, I-Cheng, S109 (OS160), S375 (THU572), S925 (SAT576)
Lee, Jack, S569 (FRI358)
Lee, Jae Geun, S799 (SAT282)
Lee, Jaejun, S146 (THU053)
Lee, Jeffrey, S440 (FRI087)
Lee, Jenny, S74 (OS097), S448 (FRI102), S452 (FRI108)
Lee, Jeong-Hoon, S78 (OS104), S275 (THU363)
Lee, Jeremy, S473 (FRI165)
Lee, Jina, S508 (FRI236)
Lee, Jyeon, S35 (OS035)
Lee, John, S569 (FRI358), S570 (FRI360)
Lee, Jonghyun, S435 (FRI077)
Lee, Jong Suk, S468 (FRI156), S469 (FRI157)
Lee, Jun Kyu, S820 (SAT317), S932 (SAT589)
Lee, Sunjae, S568 (OS089)
Lee, Su-Youen, S473 (FRI166)
Lee, Taihee, S921 (SAT609)
Lee, Tai Ping, S548 (FRI131)
Lee, Tzong-Hsi, S595 (FRI410)
Lee, William M., S394 (FRI068)
Lee, Won Kee, S377 (THU367)
Lee, Yeonju, S483 (FRI187)
Lee, Yi-Ts, S377 (THU575)
Lee, Yong-An, S694 (SAT059)
Lee, Young-Sun, S932 (SAT590)
Lee, Yun Bin, S78 (OS104), S667 (SAT005), S862 (SAT418)
Lee, Yu Rim, S377 (THU576), S572 (FRI365), S916 (SAT560)
Lefebvre, Eric, S308 (THU343), S466 (FRI152)
Lefebvre, Rémy, S181 (THU163)
Lefere, Sander, S106 (OS155), S562 (FRI344)
Leff, Phillip, S511 (THU064)
Legros, Nathalie, S584 (FRI389)
Legry, Vanessa, S359 (THU258)
Lehtimäki, Terho, S413 (FRI036)
Lehtimäki, Tiina, S690 (SAT052)
Lehtimäki, Tiina E., S458 (FRI117)
Leibowitz, Randy, S301 (THU413)
Leicht, Hans Benno, S166 (THU092)
Lei, Jin, S388 (THU600)
Leisegang, Rory, S862 (SAT417), S866 (SAT425)
Leith, Damien, S19 (OS008), S49 (OS063), S290 (THU891)
Leithead, Joanna, S96 (OS137)
Leitmann, Bobby, S562 (SAT208)
Leivers, Martin, S880 (FRI451)
Lekbab, Bouchra, s207 (THU044)
Lek, Chee Chong, S694 (SAT059)
Le, Kha, S733 (SAT145), S824 (SAT343), S835 (SAT365), S846 (SAT386), S871 (SAT435)
Le, Khanh, S203 (THU224), S204 (THU225)
Lemagoaraou, Tristan, S270 (THU352)
Lemaigre, Frédéric, S736 (SAT155)
Lemaitre, Elise, S349 (THU511)
Lemoine, Maud, S23 (OS015), S233 (THU282), S238 (THU332), S290 (THU391), S295 (THU401), S345 (THU505)
Lemoinne, Sara, S319 (THU454)
Lemos, Jozelda, S137 (THU034)
Lemp, Florian, S265 (THU344), S871 (SAT434)
Lenci, Ilaria, S249 (THU313), S569 (FRI359)
Lennergren, Hans, S368 (THU543), S645 (FRI558)
Lenne, Xavier, S205 (THU227)
Len, Oscar, S114 (OS169)
Lens, Sabela, S53 (OS067), S55 (OS070), S90 (OS127), S99 (OS141), S207 (THU231), S208 (THU232), S263 (THU340), S286 (THU385), S570 (FRI361), S582 (SAT400), S857 (SAT409), S861 (SAT415)
Lenzi, Marco, S326 (THU467)
Lenz, Oliver, S8 (OS10), S838 (SAT370), S864 (SAT422)
Leo, Carlin, S385 (THU595)
Leonardi, Claudio, S559 (FRI336)
Leonard, Mark, S565 (FRI330)
Leonel, Thais, S99 (OS141), S263 (THU340), S286 (THU385), S607 (FRI468)
Leong, Alvin, S679 (SAT030)
Leonhardt, Silke, S309 (THU436)
Leoni, Gianluca, S249 (THU133)
Leoni, Laura, S153 (THU067)
Leoni, Simona, S166 (THU093)
Leow, Wei Qiang, S431 (FRI068)
Le Pabic, Estelle, S72 (OS093)
Le, Phuc, S151 (THU064)
Leoparttari, Stefano, S763 (SAT211)
Leps, Christian, S464 (FRI147)
Le, Quang, S700 (SAT071), S711 (SAT094)
Lequoy, Marie, S372 (THU566)
Leroy, Vincent, S72 (OS093), S375 (THU573), S530 (FRI276), S532 (FRI281), S582 (FRI386), S780 (SAT252), S791 (SAT269), S927 (SAT578)
Lesage, Candice, S392 (FRI006)
Le-Seyec, Jacques, S639 (FRI548)
Leshno, Moshe, S279 (THU371)
Leslie, Jack, S385 (THU595), S640 (FRI551), S646 (FRI561), S660 (FRI590)
Lesiak, Andrew, S809 (SAT298)
Lesnik, Gerald, S21 (OS012), S891 (SAT052)
Lessenich, Paul, S460 (FRI122)
Lester, Will, S404 (FRI023)
Lei, Suoing, S342 (THU010)
Leszczynska, Aleksandra, S471 (FRI161), S690 (SAT051)
Leung, Howard Ho-Wai, S431 (FRI069)
Levernesi, Fabio, S908 (SAT335)
Levesque, Eric, S791 (SAT269)
Levi, Ana, S668 (SAT008)
Levi, Laura, S665 (SAT002), S756 (SAT197)
Levine, Fred, S742 (SAT166)
Levi, Shira, S387 (THU597)
Levitsky, Josh, S779 (SAT250)
<table>
<thead>
<tr>
<th>Name</th>
<th>ID</th>
<th>Journal</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>Li, Guojun, Li, Guanlin, Li, Guangming, Li, Hang Lam, Li, Hongming, Li, Hu</td>
<td>S838 (SAT369), S827 (THU369), S823 (FRI351), S761 (SAT207), S685 (SAT423), S240 (THU296)</td>
<td>Journal of Hepatology</td>
<td>2022 vol. 77(S1)</td>
</tr>
</tbody>
</table>
Author Index
Li, Peng, S357 (THU524), S402 (FRI021),
S803 (SAT289)
Li, Pengfei, S86 (OS120)
Lipnevich, Igor, S269 (THU351)
Li, Qian, S454 (FRI110)
Li, Rui, S867 (SAT427)
Li, Ruidong, S276 (THU365)
Li, Shen, S36 (OS037)
Li, Shuang, S22 (OS014)
Lisman, Ton, S367 (THU542), S617 (FRI505),
S911 (SAT540)
Lissing, Mattias, S530 (FRI275)
Li, Tan, S803 (SAT289)
Li, Tinghong, S182 (THU165)
Littlejohn, Margaret, S251 (THU318),
S305 (THU422)
Liu, Beibei, S224 (THU265)
Liu, Boqiang, S56 (OS071)
Liu, Boya, S848 (SAT391)
Liu, Changchun, S501 (FRI224)
Liu, Chao, S182 (THU165)
Liu, Chen, S923 (SAT573)
Liu, Cheng, S853 (SAT401),
S853 (SAT402)
Liu, Chuan, S501 (FRI224), S616 (FRI502),
S623 (FRI515), S636 (FRI540)
Liu, Chun-Jen, S595 (FRI410), S863 (SAT420)
Liu, Dengxiang, S182 (THU165)
Liu, Diana, S811 (SAT302), S813 (SAT307)
Liu, Feng, S344 (THU504), S431 (FRI068),
S481 (FRI181), S685 (SAT042)
Liu, Fuquan, S501 (FRI224)
Liu, Gang, S837 (SAT367)
Liu, Hanyang, S684 (SAT040)
Liu, Huan, S22 (OS014)
Liu, Hui, S408 (FRI029)
Liu, Jiacheng, S287 (THU388),
S296 (THU403), S326 (THU468),
S504 (FRI229)
Liu, Jiaye, S637 (FRI543)
Liu, Jieming, S836 (SAT366)
Liu, Jing, S215 (THU245)
Liu, Jingrui, S89 (OS125), S894 (SAT509)
Liu, Kara Marie, S37 (OS041)
Liu, Kuan, S86 (OS120)
Liu, LiLi, S870 (SAT432)
Liu, Na, S883 (SAT488)
Liu, Ning, S636 (FRI540)
Liu, Peidi, S94 (OS133)
Liu, Shangbin, S60 (OS075)
Liu, Shi, S642 (FRI552)
Liu, Shirong, S636 (FRI540)
Liu, Shunai, S852 (SAT399)
Liu, Su, S404 (FRI023)
Liu, Tian, S920 (SAT568)
Liu, Tong, S122 (THU008), S132 (THU026),
S185 (THU173), S674 (SAT020)
Liu, Weijian, S669 (SAT009)
Liu, Wenhui, S443 (FRI093), S486 (FRI193)
Liu, Xiao, S86 (OS119)
Liu, Xiaohui, S165 (THU091)
Liu, Xiaojing, S879 (SAT449)
Liu, Xinchang, S854 (SAT404)
Liu, YaLi, S870 (SAT432)
S982

Liu, Yan, S185 (THU173), S280 (THU372),
S281 (THU376), S846 (SAT387)
Liu, Yang, S244 (THU302), S247 (THU309),
S845 (SAT385), S866 (SAT425),
S920 (SAT568)
Liu, Yanna, S501 (FRI224), S616 (FRI502)
Liu, Yao, S477 (FRI175)
Liu, Yen-Chun, S102 (OS148), S575 (FRI371),
S576 (FRI372), S873 (SAT438)
Liu, Yi, S879 (SAT449), S883 (SAT488)
Liu, Yilin, S326 (THU468)
Liu, Ying, S686 (SAT045)
Liu, Yixin, S883 (SAT488)
Liu, Yun Peng, S384 (THU591)
Liu, Yu-Pei, S182 (THU165)
Liu, Zhaoli, S566 (FRI352), S608 (FRI485)
Liu, Zhicheng, S26 (OS020)
Liu, Zongyi, S181 (THU164)
Livingstone, Callum, S415 (FRI038)
Livingston, Sherry, S394 (FRI008)
Li, Wai Keung, S78 (OS105)
Li, Wang, S920 (SAT568)
Li, Wei, S384 (THU591)
Li, Wei-Zhe, S827 (SAT349)
Li, Wenhao, S698 (SAT066), S934 (SAT593)
Liwinski, Timur, S325 (THU466)
Li, Xiaoguo, S616 (FRI502)
Li, Xiaojiao, S89 (OS125)
Li, Xiaomei, S92 (OS130), S619 (FRI508),
S621 (FRI512), S628 (FRI526)
Li, Xin, S616 (FRI502)
Li, Xinyi, S912 (SAT554)
Li, Xiubin, S914 (SAT558)
Li, Yan, S726 (SAT128)
Li, Yiguang, S287 (THU388),
S296 (THU403), S326 (THU468),
S504 (FRI229)
Li, Ying, S477 (FRI175)
Li, Yinyin, S388 (THU600)
Li, Yizhao, S88 (OS123)
Li, Yueni, S489 (FRI200)
Li, Yujia, S408 (FRI029)
Li, Yujin, S492 (FRI206)
Li, Yun, S402 (FRI021), S744 (SAT171)
Lizardi, Javier, S487 (FRI195)
Li, Zewen, S182 (THU165)
Li, Zongfang, S883 (SAT488)
Lkhagva-Ochir, Oyungerel, S235 (THU287)
Llaneras, Jordi, S44 (OS052), S277 (THU367)
Llarch, Neus, S381 (THU584)
Lledó, Jose Luis, S381 (THU584)
Lleo, Ana, S47 (OS058), S93 (OS132),
S107 (OS157), S308 (THU435),
S326 (THU467), S335 (THU484),
S528 (FRI272), S758 (SAT201),
S761 (SAT206)
Llewellyn, Jessica, S740 (SAT163)
Llinares, María Esther, S527 (FRI271)
Llop, Elba, S90 (OS127)
Llovet, Josep M., S45 (OS055),
S385 (THU595)
Llovet, Laura Patricia, S607 (FRI468)
Lloyd, Andrew, S103 (OS149),
S305 (THU421), S565 (FRI349)
Journal of Hepatology 2022 vol. 77(S1) | S940–S1020

Lloyd, Carla, S551 (FRI321)
Lloyd, Emily, S855 (SAT405)
Lloyd, Jonathan, S745 (SAT177)
Lloyd, Josephine, S34 (OS034)
Loarca, Lorena, S759 (SAT202)
Lobato, Cirley, S137 (THU034)
Locarnini, Stephen, S251 (THU318),
S305 (THU422), S834 (SAT362)
Lo, Ching-Chu, S595 (FRI410)
Lockart, Ian, S561 (FRI343), S568 (FRI356)
Lockman, Khalida Ann, S434 (FRI075)
Lockwood, Mark, S97 (OS139)
Lodge, John, S493 (FRI208)
Loeffler, Juergen, S486 (FRI194),
S493 (FRI207)
Lo, Gin-Ho, S625 (FRI520)
Logiodice, Federica, S477 (FRI173)
Loglio, Alessandro, S196 (THU194),
S223 (THU263), S843 (SAT379),
S843 (SAT381), S868 (SAT429),
S880 (SAT450)
Lohoues, Marie Jeanne, S19 (OS008),
S49 (OS063)
Lohse, Ansgar, S224 (THU265),
S257 (THU329), S317 (THU452),
S321 (THU458), S333 (THU481),
S893 (SAT507)
Lohse, Ansgar W., S54 (OS069),
S206 (THU229), S315 (THU447),
S325 (THU466), S604 (FRI462),
S823 (SAT341)
Lok, Anna, S180 (THU162)
Lok, James, S276 (THU366),
S281 (THU375), S571 (FRI363),
S812 (SAT304)
Lomas, David, S534 (FRI285)
Lombardelli, Letizia, S477 (FRI173)
Lombardelli, Stephen, S516 (FRI251)
Lombardi, Andrea, S223 (THU263)
Lombardi, Martina, S425 (FRI057)
Lombardi, Rosa, S159 (THU078),
S167 (THU095), S682 (SAT036)
Lombardo, Daniele, S259 (THU333)
Lonardi, Sara, S748 (SAT180)
Londoño, Maria Carlota, S54 (OS069),
S324 (THU464), S325 (THU465),
S334 (THU482), S607 (FRI468),
S809 (SAT298)
Long, Brian, S540 (FRI299)
Long, Edward, S880 (SAT451)
Longerich, Thomas, S11 (LB003),
S655 (FRI581), S710 (SAT090),
S927 (SAT579)
Longet, Stephanie, S57 (OS072A)
Long, Jiang, S745 (SAT177)
Longo, Miriam, S682 (SAT036),
S682 (SAT037), S698 (SAT068),
S703 (SAT077), S706 (SAT084)
Longo, Salvatore, S404 (FRI024)
Longworth, Louise, S39 (OS044)
Lonjon-Domanec, Isabelle, S8 (GS010),
S72 (OS094)
Lønsmann, Ida Lønsmann, S435 (FRI076)
Loo, Jing Hong, S567 (FRI354)


Author Index

Mereu, Tiziana, S806 (SAT294)
Merino, Victor, S442 (FRI091)
Merino, Xavier, S658 (FRI587)
Meritet, Jean François, S393 (FRI007)
Merie, Jean Claude, S791 (SAT269)
Merie, Philippe, S5 (OS007)
Mere, Uta, S562 (FRI345), S823 (SAT341)
Meral, Manuela, S815 (SAT311)
Meroni, Marica, S167 (THU095), S675 (SAT021), S682 (SAT036), S682 (SAT037), S698 (SAT068), S706 (SAT084)
Meroueh, Chady, S138 (THU320)
Mertens, Peter Rene, S659 (FRI589)
Mian, Saad, S189 (THU181)
Michtov, Ralitsa, S37 (OS041)
Michalak, Sophie, S73 (OS096), S496 (FRI215), S497 (FRI216)
Michałowski, Łukasz, S156 (THU072)
Michaud, Baptiste, S20 (OS029)
Michaud, Donald, S298 (THU170)
Michaud, Sébastien, S156 (THU072)
Michaud, Francis, S156 (THU072)
Michaud, François, S156 (THU072)
Michaël, Marthe, S561 (FRI346)
Michal, Miroslav, S138 (THU320)
Michalakis, Kostas, S156 (THU072)
Michaels, Christopher, S156 (THU072)
Michaels, Katerina, S156 (THU072)
Michaels, Kristina, S156 (THU072)
Michaels, Laura, S156 (THU072)
Michaels, Martin, S156 (THU072)
Michaels, Michael, S156 (THU072)
Michaels, Sara, S156 (THU072)
Michaels, Stefan, S156 (THU072)
Michaels, Thomas, S156 (THU072)
Michaels, Ursula, S156 (THU072)
Michaels, Volker, S156 (THU072)
Michailidou, Elisavet, S429 (FRI063)
Michalk, Sophie, S73 (OS096), S496 (FRI215), S497 (FRI216)
Michalowski, Lukasz, S156 (THU072)
Michaud, Baptiste, S20 (OS029)
Michaud, Donald, S298 (THU170)
Michalakis, Kostas, S156 (THU072)
Michaels, Christopher, S156 (THU072)
Michaels, Katerina, S156 (THU072)
Michaels, Kristina, S156 (THU072)
Michaels, Laura, S156 (THU072)
Michaels, Martin, S156 (THU072)
Michaels, Sara, S156 (THU072)
Michaels, Stefan, S156 (THU072)
Michaels, Thomas, S156 (THU072)
Michaels, Ursula, S156 (THU072)
Michaels, Volker, S156 (THU072)
Michaels, Werner, S156 (THU072)
Michalova, Janina, S156 (THU072)
Michalova, Jana, S156 (THU072)
Michalova, Jindrich, S156 (THU072)
Michalova, Jitka, S156 (THU072)
Michalova, Jitka, S156 (THU072)
Michalova, Jitka, S156 (THU072)
Michalova, Jitka, S156 (THU072)
Michalova, Jitka, S156 (THU072)
Michalova, Jitka, S156 (THU072)
Michalova, Jitka, S156 (THU072)
Michalova, Jitka, S156 (THU072)
Michalova, Jitka, S156 (THU072)
Michalova, Jitka, S156 (THU072)
Michalova, Jitka, S156 (THU072)
Michalova, Jitka, S156 (THU072)
Michalova, Jitka, S156 (THU072)
Michalova, Jitka, S156 (THU072)
Michalova, Jitka, S156 (THU072)
Michalova, Jitka, S156 (THU072)
Michalova, Jitka, S156 (THU072)
Michalova, Jitka, S156 (THU072)
Michalova, Jitka, S156 (THU072)
Michalova, Jitka, S156 (THU072)
Michalova, Jitka, S156 (THU072)
Michalova, Jitka, S156 (THU072)
Michalova, Jitka, S156 (THU072)
Michalova, Jitka, S156 (THU072)
Michalova, Jitka, S156 (THU072)
Michalova, Jitka, S156 (THU072)
Michalova, Jitka, S156 (THU072)
Michalova, Jitka, S156 (THU072)
Michalova, Jitka, S156 (THU072)
Michalova, Jitka, S156 (THU072)
Michalova, Jitka, S156 (THU072)

Author Index

Mohn, Raphael, S381 (THU585)
Mohs, Antje, S654 (FRI578)
Moa, Riccardo, S503 (FRI227)
Moigboi, Christiana, S279 (THU370), S281 (THU375), S287 (THU387)
Moiseev, Sergey, S574 (FRI70)
Mol, Bregje, S330 (THU491)
Moles, Anna, S465 (FRI150)
Molina-Aguilar, Christian, S476 (FRI172)
Molina, Esther, S792 (SAT271)
Molina, Manuel Flores, S675 (SAT022)
Molinari, Nicolas, S122 (THU009)
Molin, Alba Pueyo, S65 (OS085)
Molli, Anna, S763 (SAT211)
Mollenkopf, Sarah, S552 (FRI327)
Mongale, Emily, S554 (FRI327)
Monguzzi, Erika, S325

Montag, Mark, S17 (OS005)
Montalvao, Rebeca, S226 (THU273)
Montana, Noé Axel, S194 (THU189), S251 (THU317)
Montañés, Rosa, S91 (OS128)
Montano-Loza, Aldo J, S313 (THU443), S317 (THU452), S318 (THU453), S326 (THU467), S631 (FRI530), S775 (SAT244), S815 (SAT311), S892 (SAT504)
Monteiro, Jaume, S93 (OS132)
Montegut, Julie, S872 (SAT436)
Monte, Maria, S59 (OS074)
Monteiro-Vallejo, Rocío, S459 (FRI119), S708 (SAT087)
Montes, Pedro, S137 (THU034)
Montet, Xavier, S645 (FRI559)
Monti, Monica, S564 (FRI347)
Montironi, Carla, S136 (THU033), S139 (THU039)
Montoliu, Carmina, S51 (OS065)
Mookerjee, Raj, S344 (THU503), S889 (SAT495), S903 (SAT526)
Moon, Andrew, S201 (THU219), S223 (THU262)
Moon, Christina, S194 (THU189), S832 (SAT358)
Mooney, Anne, S169 (THU098)
Mooneyhyan, Ellen, S43 (OS050), S230 (THU278), S231 (THU279), S238 (THU292), S240 (THU295)
Moonka, Dilip, S612 (FRI493), S778 (SAT249)
Moore, Celia, S188 (THU178)
Moore, David, S696 (SAT063)
Moore-Gillon, Claudia, S345 (THU505)
Moore, J. Bernadette, S104 (OS151)
Moore, Karen, S814 (SAT308)
Moore, Kevin, S460 (FRI121)
Moore, Yvette, S116 (OS172)
Mora, Alfonso, S689 (SAT050)
Mora, Andrés Martínez, S40 (OS045)
Mor, Adi, S27 (OS022)
Moradpour, Darius, S97 (OS138), S253 (THU322), S355 (THU520)
Morales, Albert, S652 (FRI573), S672 (SAT016)
Morales-Ruiz, Manuel, S896 (SAT512), S901 (SAT522), S902 (SAT524), S907 (SAT532)
Morandini, Francesca, S872 (SAT436)
Moro, Albert, S652 (FRI573), S672 (SAT016)
Mor, Inbal, S765 (SAT214)
Morrison, Martine C., S671 (SAT014), S676 (SAT024), S677 (SAT025), S681 (SAT033), S698 (SAT067)
Morow, Linda, S730 (SAT139), S732 (SAT143)
Mortensen, Christian, S154 (THU068), S331 (THU477)
Mortensen, Frank Viborg, S925 (SAT575)
Mosca, Antonella, S706 (SAT084)
Moseley, Scott, S526 (FRI268)
Moskon, Miha, S607 (FRI469), S766 (SAT217)
Moslem, Ali, S228 (THU273)
Mospan, Andrea, S449 (FRI103)
Moss, Adyr, S15 (OS002)
Moss, Alastair, S409 (FRI031)
Mosavar-Rahmani, Yasmin, S912 (SAT554)
Mossialos, Elias, S444 (FRI094)
Mossavijarijali, Alireza, S228 (THU273)
Motamed, Maryam, S775 (SAT244), S892 (SAT504)
Motta, Benedetta Maria, S425 (FRI057)
Mottler, Karsten, S606 (FRI467), S703 (SAT079)
Mouch, Saif Mahmud Abu, S292 (THU108)
Mouhot, Nicolas, S313 (THU443), S317 (THU452), S318 (THU453), S326 (THU467), S631 (FRI530), S775 (SAT244), S815 (SAT311), S892 (SAT504)
Mourad, Abbas, S426 (FRI059), S913 (SAT557)
Moura, Luís Manuel, S597 (FRI415)
Moura, Miguel, S192 (THU185)
Moussa, Sam, S14 (LB005)
Moutoukos, Ilias, S742 (SAT167)

Journal of Hepatology 2022 vol. 77(S1) | S940–S1020

S989
Piedade, Juliana, S910 (SAT539)
Pierce, Glenn, S404 (FRI023)
Pierce, Theodore, S454 (FRI110)
Pieri, Giulia, S578 (FRI376)
Piermatteo, Lorenzo, S249 (THU313), S284 (THU380), S284 (THU381), S389 (SAT371)
Pieterman, Elizabeth, S681 (SAT033)
Pietrangelo, Antonello, S389 (SAT371)
Pietri, Olivia, S547 (FRI314)
Pietschmann, Thomas, S263 (THU339)
Pignata, Luca, S769 (SAT233)
Pinalt, Matteo, S751 (SAT186)
Pielebro, Björn, S58 (OS073)
Pillai, Anjana, S372 (THU567), S383 (THU588)
Pimenta, Dominic, S460 (FRI121)
Pinato, David J., S180 (THU161)
Piñero, Iris, S873 (SAT257)
Pinpathomrat, Nawamin, S188 (THU177)
Pinquier, Jean-Louis, S733 (SAT145)
Pintelon, Isabel, S709 (SAT089)
Pinter, Matthias, S315 (THU449), S354 (THU519), S372 (THU567), S374 (THU571), S376 (THU574), S383 (THU588), S352 (FRI280), S355 (FRI287), S617 (FRI505), S618 (FRI506), S631 (FRI531), S632 (FRI533), S753 (SAT189), S919 (SAT565), S921 (SAT570)
Pintore, Lorenzo, S815 (SAT311)
Pinyol, Roser, S45 (OS055)
Pinzani, Massimo, S666 (SAT004), S668 (SAT008), S737 (SAT157)
Piombanti, Benedetta, S477 (FRI173), S649 (FRI567)
Piombino, Diego, S137 (THU034)
Pipeck, Joseph, S558 (FRI334)
Pipestone, Rosaria Maria, S703 (SAT077)
Pique-Gili, Marta, S45 (OS055)
Piquet-Pellorce, Claire, S639 (FRI145)
Pirade, Anita, S788 (SAT264)
Pirani, Tasneem, S403 (FRI022)
Pirari, Ron, S742 (SAT166)
Piravitrasuth, T, S824 (SAT344)
Piravitrasuth, Teerha, S12 (LB004A), S186 (THU175), S187 (THU176), S188 (THU177), S880 (SAT452), S937 (SAT597)
Pirenne, Jacques, S781 (SAT253), S783 (SAT256)
Pirisi, Mario, S483 (FRI185), S929 (SAT582), S929 (SAT583)
Piriot, Boris, S135 (THU032)
Pirone, Loris, S153 (THU067)
Pirosu, Andrea, S256 (THU327)
Pisapio, Giuseppe, S187 (THU095)
Pisapia, Pasquale, S84 (OS115)
Pisaturo, Marientonietta, S217 (THU250)
Piscaglia, Fabio, S79 (OS107), S166 (THU093)
Pischke, Sven, S206 (THU229), S257 (THU239)
Piscopo, Fabiola, S84 (OS115)
Piscociglio, Salvatore, S660 (FRI592)
Pistelli, Pierluca, S821 (SAT318)
Pistello, Mauro, S282 (THU394)
Pistorio, Valeria, S465 (FRI150)
PinKänen, Kari, S111 (OS162)
Pitrova, Veronika, S593 (FRI408)
Pittau, Gabriella, S800 (SAT285), S935 (SAT595)
Plagianakos, Christina, S62 (OS078), S313 (THU443)
Planas, Alejandra, S149 (THU059), S440 (FRI088)
Plank, Lindsay, S890 (SAT500)
Plant, James, S548 (FRI316)
Plebani, Mario, S49 (OS062)
Plesniak, Robert, S12 (LB004A), S13 (LB004B), S288 (THU389), S288 (THU390), S291 (THU393), S880 (SAT452), S881 (SAT453)
Plessier, Aurélie, S61 (OS076), S524 (FR1265)
Plevris, John, S397 (FRI013), S434 (FRI075), S712 (SAT096)
Plissonnier, Marie-Laure, S246 (THU306), S247 (THU307), S356 (THU522), S766 (SAT216)
Plotnikov, Alexander, S387 (THU597)
Poca, Maria, S64 (OS082), S91 (OS128), S370 (THU548), S627 (FR1253), S886 (SAT494), S900 (SAT520)
Poch, Esteban, S902 (SAT524)
Pochet, Nathalie, S649 (FRI565)
Poch, Tobias, S604 (FRI462)
Pocurull, Anna, S587 (SAT409)
Podlaha, Ondrej, S383 (SAT364)
Podrug, Kristian, S612 (FRI494)
Poent, Alexander, S338 (THU491)
Poetter-Lang, Sarah, S24 (OS017), S320 (THU457)
Poggiel, Carsten, S748 (SAT181)
Pohl, Junika, S185 (THU171), S189 (THU180)
Poirier, Charles, S805 (SAT293)
Poission, Johanne, S508 (FRI237)
Poljoca, Kristina, S12 (LB004A), S13 (LB004B), S288 (THU389), S288 (THU390), S291 (THU393), S880 (SAT452), S881 (SAT453)
Polak, Wojciech, S109 (OS159), S807 (SAT296), S815 (SAT311), S933 (SAT591)
Polanco, Prido, S151 (THU064)
Polat, Kamil Yalcin, S820 (SAT316)
Polat, Kamil Yalcin, S820 (SAT316)
Polci, Barbara, S820 (SAT316)
Polci, Barbara, S820 (SAT316)
Polci, Barbara, S820 (SAT316)
Polci, Barbara, S820 (SAT316)
Polci, Barbara, S820 (SAT316)
Polci, Barbara, S820 (SAT316)
Polci, Barbara, S820 (SAT316)
Polci, Barbara, S820 (SAT316)
Polci, Barbara, S820 (SAT316)
Polci, Barbara, S820 (SAT316)
Polci, Barbara, S820 (SAT316)
Polci, Barbara, S820 (SAT316)
Polci, Barbara, S820 (SAT316)
Polci, Barbara, S820 (SAT316)
Polci, Barbara, S820 (SAT316)
Author Index

Rafei-Shamsabadi, David, S2 (GS003)
Raffaele, Brustia, S107 (OS157)
Raffa, Giuseppina, S259 (THU333)
Ragab, Shaimaa, S586 (FRI351)
Raggi, Chiara, S47 (OS058), S477 (FRI173), S649 (FRI367), S651 (FRI370)
Ragone, Enrico, S938 (SAT599)
Raguene-Nicol, Celine, S639 (FRI548)
Rahav, Galia, S784 (SAT258)
Rahbari, Mohammad, S655 (FRI581)
Rahbari, Nuh N., S661 (FRI954)
Rahematpura, Suditi, S19 (OS008), S49 (OS063)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahman, F., S99 (OS142)
Rahman, F. D., S226 (THU269), S230 (THU278), S231 (THU279), S235 (THU288), S238 (THU292), S240 (THU295)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Rahimi, Robert, S779 (SAT250), S868 (SAT493)
Yoneda, Masato, S425 (FRI058), S430 (FRI067), S448 (FRI102), S452 (FRI108)
Yongliang, Zhao, S717 (SAT111)
You, Joon, S303 (THU417)
You, Jeong-Ju, S589 (FRI398)
You, Juwhan, S100 (OS144)
You, Shao-li, S803 (SAT289)
You, Shih-yun, S873 (SAT439), S880 (SAT451)
Yousif, Jenna, S612 (FRI493)
Youssef, Amir, S875 (SAT441)
Yousuf, Hassan, S531 (FRI279)
You, Young Kyoung, S820 (SAT317)
Yutina, Henriette, S33 (THU477), S887 (SAT495)
Yu, Amanda, S17 (OS005), S43 (SAT051), S209 (THU233), S282 (THU378), S910 (SAT538)
Yuan, Jie, S92 (OS130), S619 (FRI508), S621 (FRI512), S628 (FRI526)
Yuan, Luning, S744 (SAT172)
Yuan, Xiaojian, S559 (FRI337)
Yuan, Yuan, S872 (SAT437)
Yuan, Yulin, S182 (THU165)
Yubao, Zheng, S344 (THU504)
Yun, Lilly, S251 (THU318)
Yuan, Mun-Fang, S13 (LB004B), S69 (OS059), S78 (OS105), S177 (THU154), S266 (THU346), S272 (THU358), S273 (THU360), S275 (THU364), S288 (THU389), S288 (THU390), S291 (THU393), S299 (THU408), S284 (SAT343), S824 (SAT344), S831 (SAT357), S835 (SAT365), S836 (SAT366), S848 (SAT392), S849 (SAT393), S850 (SAT396), S851 (SAT397), S852 (SAT400), S841 (SAT415), S864 (SAT422), S867 (SAT427), S871 (SAT435), S872 (SAT437), S876 (SAT443), S878 (SAT448), S881 (SAT453)
Yu, Hua, S540 (FRI299)
Yu, Meng, S669 (SAT009)
Yu, Ming-Lung, S119 (THU001), S154 (THU069), S458 (FRI118), S595 (FRI410), S683 (SAT420), S875 (SAT442)
Yumita, Se, S615 (FRI501), S897 (SAT514)
Yun, Jeong-Hwan, S78 (OS105), S154 (THU069), S155 (THU071), S209 (THU234), S240 (FRI048), S249 (FRI048), S429 (FRI064), S447 (FRI100)
Younossi, Elena, S209 (THU234), S420 (FRI048), S429 (FRI064), S447 (FRI100)
Younossi, Issah, S154 (THU069), S155 (THU071), S209 (THU234), S445 (FRI097)
Younossi, Youssef, S5 (OS008), S156 (THU073)
Younossi, Zobair, S5 (OS008), S31 (OS028), S144 (THU048), S148 (THU058), S150 (THU062), S154 (THU069), S155 (THU071), S156 (THU073), S209 (THU234), S409 (FRI030), S416 (FRI040), S420 (FRI048), S429 (FRI064), S445 (FRI097), S447 (FRI100), S762 (SAT208), S785 (SAT260), S810 (SAT300)
You, Shaoli, S803 (SAT289)
Author Index

Zocco, Maria Assunta, S507 (FRI234)
Zoldan, Katharina, S100 (OS143),
S710 (SAT090)
Zoller, Heinz, S470 (FRI159), S537 (FRI292),
S829 (SAT353), S830 (SAT354)
Zöllner, Caroline, S823 (SAT341)
Zöllner, Dominik, S915 (SAT559)
Zomorodi, Katie, S834 (SAT363),
S846 (SAT388), S847 (SAT389)
Zong, Zhixin, S847 (SAT389)
Zorde-Khavlevsky, Elina, S764 (SAT213)
Zorzano, Antonio, S674 (SAT019)
Zougmore, Honore, S270 (THU352)
Zou, Guangyong, S416 (FRI040)
Zou, Guizhou, S70 (OS091)
Zou, Haixia, S726 (SAT128), S726 (SAT129)
Zoulmin, Fabien, S72 (OS093),
S245 (THU303), S246 (THU306),
S247 (THU307), S356 (THU522),
S766 (SAT216), S824 (SAT344),
S833 (SAT360), S868 (SAT429),
S880 (SAT450)
Zou, Xiantong, S463 (FRI126)
Zubiaga, Ana, S651 (FRI571),
S665 (SAT001)
Zucman-Rossi, Jessica, S639 (FRI548)
Zuin, Massimo Giovanni, S61 (OS077),
S539 (FRI297)
Zule, Maria A., S500 (FRI222)
Zulkhuu, Delgersaikhan, S235 (THU287)
Zuluaga, Paola, S199 (THU199)
Zulueta, Javier, S802 (SAT288)
Zurawek, Dariusz, S759 (SAT203)
Zurera, Coral, S199 (THU199)
zu Siederdissen, Christoph Hoener,
S248 (THU311)
Zwaenepoel, Karen, S637 (FRI544)
Zwanziger, Denise, S341 (THU498)
Zwinderman, Aeilko, S74 (OS097)
Disclosures: no commercial relationships

The following abstract submitters have indicated that they have no relationships with commercial entities that might be perceived as having a connection with their presentation:

Niels Kristian Aagaard
Christer F. Aas
cristiana abazia
Nadir Abbas
Fariba Abdassi
Gian Luca Abbati
Jane Abbott
Amr Abdelaal
Manal Abdelmalek
Abd Zed Abdelraheem
Ahmed Abdelwahab
Mostafa Abdo
Aymen Abdo
Kabbani Abdul-Rahman
Kanun Abe
Leticia Abecia
Nada Abedin
Stephan Aberle
Hanna Aberra
Itziar Abete
Natali Abeywickrama Samarakoon
George Abouda
Marwan Abouljoud
Michal Abrahám
George Abraham
Arun Abraham
Juan Abraldes
Joanna Abramczyk
Ifat Abramovich
Rinat Abramovitch
Luis Abreu de Carvalho
Fadi Abu Baker
Muhammad Radzi Abu Hassan
Samira Abu Jhaisha
Saif Mahmud Abu Mouch
Naim Abu-Freia
Yehia Abugabal
Jeries Abu-Hanna
Mohamed Abu-Nada
Abdelrahman Aburaia
Ameer Abutaleb
Akaki Abutidze
Antonio Accetta
Laia Aceituno
Maria Achalandabaso
Weber Achim
Silvia Acosta-López
Antonio Acquaviva
Gupse Adali
René Adam
Svetlana Adamcova Selcanova
Ekaterine Adamia
Monika Adamowicz
David Adams
Huyen Adams
Leon Adams
Haydar Adanir
Pietro Addeo
Marylyn Addo
Adeyinka Adejumo
Hammoutene Adel
Jelle Adelmeijer
Jorge Adeva
Mopelela Adeyemo
Oyedele Adeyi
Xavier Adhoute
Mehmet Adigüzelt
Luciano Adorini
Valentina Adotti
Annie Adrait
Celina Adrianeda
Prince Adu
Niklas F. Aehling
Maridi Aerts
Nezam Afshar
Luciano Afkesh
Silvia Affo
João Afonso
Marta B. Afonso
Catarina Afonso
Samagra Agarwal
Pankaj Aggarwal
Sandeep Aggarwal
Nancy Agmon-Levin
Polyxeni Agorastou
Bella Agranovich
Chiara Agrati
Adile Agresta
Ferran Aguilar
Laia Aguilar
Juan Ramón Aguilar
Beatriz Aguilar-Brao
A. Aguílera
Ricardo Aguilera Rosales
Victoria Aguilera Sancho
George Agyapong
Lee Han Ah
Noora Ahlholm
Shafqat Ahmad
Nabil Ahmed
Kinza Ahmed
Charisse Ahmed
Mohamed Ahmed
Syed Ahmed
Muneeb Ahmed
Sang Bong Ahn
Sang Hoon Ahn
Joseph Ahn
Lisa Ahne
Adriana Ahumada
Riccardo Aiese Cigliano
Hiroshi Akata
Maria Elena Ainora
Rhona E Aird
Aldo Airoldi
Shinichi Aishima
Lola Ajayi
Saima Ajaz
Veeral Ajmera
Ulas Akarca
Mesut Akarsu
Meral Akdogan Kayhan
Mohammad Khalil Akhter
Tomoyuki Akita
Murat Akylidiz
Al Shaima Al Hinai
Rola Al-Sayeghi
Reem Al Shabeeb
Amr Al Shebel
Aftab Ala
Balqis Al Abdul Karim
Walid Al-Akkad
Seema Alam
Ali Al-Anbaki
Atef Alattar
Marko Alavanja
Maryam Alavi
William Alazawi
Romain Albenois
Hannes Alber
Cathy Alberda
Angel Alberich-Bayarri
Matthew Albert
Cecilia Albert-Antequera
Somaya Albaihisi
Agustín Albillos
Jan Albin
Thomas Albrecht
Nicola J Wekwer Albrechtsen
Joseph Alcorn
Rafael Aldabe
Mark Aldersley
Luca Aldighetti
Disclosures

Rafael Alejandre
Soo Aleman
Vanessa Alemanni
Daniel Alemu
Yusef Alenezi
Carlo Alessandria
Maria Grazia Alessio
Loredana Alessio
Sophie Alex
Leigh Alexander
Adibekian Alexander
Ian Alexander
Fuchs Alexandra
Gonçalo Alexandrino
Theodoros alexopoulos
Alexandra Alexopoulou
Ana Alfaro
Clara Alfaro-Cervello
Ludovico Alfarone
Bazga Ali
Ahmad Ali
Fatima Ali
Angela Alibrandi
Eleonora Alimenti
Anna Alisi
Benard Aliwa
Tom Alix
Saad AlKaabi
Mohammad Alkhatib
Maia Alkhazashvili
Huseyn Alkim
Dalia Almassri
Marc Antoine Allard
Sophie Allen
Kathryn Allen
Rocio Aller
Rocio Aller de la Fuente
Francesca Alletto
Michael Allison
Chakib Alloui
Caroline Allsop
Lena Allweiss
Hussam Almasri
Bruna Almeida
Alessandro Almeida
Marion Almes
Carolina Almohalla
Carmen Alonso Martin
Saleh Alqahtani
Laurent Alric
Laith Al-Rubaify
Rami Al-Sayegh
Deema AlSoub
Khalid Alswat
Enkhjargal Altangerel
Arwen Altenburg
Johannes Altenmüller
Adriana Alter
Heidi Altmann
Joseph Alukal
Varuna Aluvihare
Aoiif Alvais
Edilmar Alvarado-Tapias
Mario Reis Álvares-da-Silva
Laura Alvarez
Maria Álvarez
Ismael Alvarez-Alvarez
Carmen Álvarez-Navascués
Gloria Álvarez-Sola
del Rio Alvaro
Frank Alvaro
Rogério Alves
Claudia Alves Couto
Pedro Alves de Castro
Diego Alves Vieira
Ian Alwayn
Guliana Amaddeo
Pedro Amado Villanueva
Suneetha Amara
Benon Amare
Raphael Ambros
Josep Amengual
Johnny Amer
Clara Amiama Roig
Lidia Amigo
Oliver E Amin
Janaki Amin
Mohammad Amin Fallahzadeh
Daphni Ammon
Simona Amodeo
Angela Maria Amorini
Javier Ampuero
Rachida Amzal
Samira Amzou
Qi An
Weimin An
Qian An
Despina Anagnostou
Abhinav Anand
Hanish Anand
Utpal Anand
Dimitrios Anastasiou
Julian Anders
Maria Margarita Anders
Peter Andersen
Jesper Andersen
Patricia Anderson
R. Rox Anderson
Jenine Anderson
Monique Andersson
Emma Andersson
Raul J. Andrade
Antonio Andrade
Eleonora Andreassi
Ana Andreaesoon
Ana Andreazza
Pietro Andreone
Thibault Andrieu
Le Shaun Ang
Peter Angel
Francesco Angelico
Federica Angelone
Martin Angerer
Tori Anglin
Debora Angrisani
Juan Anguita
Peter Angus
Geerts Anja
Johan Ankarklev
Maliki Ankvay
Piekariska Anna
Ay Anne-Sophie
Monica Annunziata
Francesco Annunziata
Maria Paola Anolli
Azim Ansari
Corinne Antoine
Benedicte Antoine
Laura Antolini
María Dolores Antón Conejero
Christoph Antoni
Teresa Antonini
Luiz Antônio Rodrigues de Freitas
Steen Antonsen
Michela Antonucci
Amir Anushiravani
Ling Ao
Oluwemii Aoko
Myriam Aouadi
Lynda Aoudjehane
Maider Apodaka-Biguri
Giuseppe Aprile
Bashar Asel
Marco Aquino
Juan Pablo Arab
Mohammad Arbabpour
Carlos Aracil
Kumiko Arai
Juan Pablo Arancibia
Ana María Aransay
Carlos Araújo
Aloysious Aravinthan
Ander Arbelaitz
Jose M Arbones Mainar
Marcello Arca
Ricardo M Arcay
Sara Arcelus
Sara Archer
Alba Ardevol
Maria Archederra
Bethlehem Arefaine
Umberto Arena
Víctor Arendt
Nicoline Stender Arentoft
Josep Maria Argemi
Josep Maria Argemi
Pamela Argiriadi
Derya Ari
Pascu Ariana
Ana Arias
María Teresa Arias Lose
Sena Arici
Silvia Ariño Mons
Makoto Arita
Pertrru Arkkila
Juan Armendariz-Borunda
Carolina Armengol
Susana Armesto
Xiimen Armijos
Paige A Armstrong
Matthew Armstrong
Katherine Arndtz
Jorge Arnold
Alexander Arnold
Joud Arnok
Samantha Arokiasamy
Johanna Arola
Anil Arora
Sanjeev Arora
Vinod Arora
Maria Arranz
Isabel Arranz-Salas
Marco Arrese
Fernanda Arriaga-González
Disclosures

Margaret Bassendine  
Christine Basis  
Dustin Bastaich  
Gorka Bastarrrika Alemañ  
Nina Bastati  
Ramon Bataller  
Suvd Batbaatar  
Enkhtuul Batbold  
Andrew Bathgate  
Ayse Batirel  
Rui Batista  
Clara Batista  
Uyanga Bat-Osor  
Martine Baudin  
Ulrike Bauer  
Jens Bauer  
Anja Baumann  
Cédric Baumann  
Alina Bauschen  
Joseph A Baur  
Nurcan Baykam  
David Bayne  
Fabio Becce  
Chiara Becchetti  
Morten Beck Trelle  
Britta Becker  
Hans Becker  
Racquel Beckford  
Henning Beck-Nielsen  
Cheikh Mohamed Bed  
Nathalie Béard  
Erin Bedford  
Pierre Bedossa  
Lewis Beer  
Lucian Beer  
Niko Beerenwinkel  
Neelu Begum  
Jaideep Behari  
Cynthia Behling  
Christian Behrends  
Patrick Behrendt  
Lawrence J. Beilin  
Hicran Bektaş  
Ines Belasri  
Assia Belblidia  
Elaine Bell  
John Bell  
Sally Bell  
Dawn Belland  
Agnes Bellanger  
Jonathan Bellet  
Luca Saverio Belli  
Ernest Belmonte  
Luciano Beltrão Pereira  
Chantal Bemeur  
Ziv Ben Ari  
Yasmina Ben Merabet  
Amel Ben Saad  
Gil Ben Yaacov  
Souad Benali  
Felix Bende  
Sofie Bendixen  
Shifra Ben-Dor  
Flemming Bendtsen  
Livja Benedetti  
Paula Benencio  
Bertram Bengsch  
Johan Bengtsson  
Federica Benini  
Laura Benitez  
Carlos Benitez  
Alberto Benito  
Asier Benito-Vicente  
Jaya Benjamin  
Salvador Benlloch  
Amine Bennmassauoud  
William Bennet  
Andrew Bennett  
Michael Bennett  
Kris Bennett  
Jennifer Benselin  
Gilbert Bensimon  
Hadar Benyamini  
Christian Benzing  
Chinmay Bera  
Hanna Berak  
Clarissa Berardo  
Carmen Berasain  
Françoise Berby  
Michael D. Bereket  
Marina Berenguer  
Laura Beretta  
Thomas Berg  
Christoph Berg  
Estefanía Berge Garrido  
Hilmar Berger  
Michael Berger  
Hilmar Berger  
Ina Bergherm  
Anthony Bergin  
Andreas Bergmann  
Ottar M. Bergmann  
Raoul Bergner  
Riika Mari Berg-Pedersen  
Annika Bergquist  
Nega Berhe  
Elina Berliha  
Claudia Berlin  
Maria Bermúdez  
Carmen Bernal  
William Bernal  
Vanessa Bernal Monterde  
Daniel Bernal Serrano  
Irantzu Bernales  
Lucie Bernard  
Pierre-Henri Bernard  
Christina Bernardes  
Dave Bernasconi  
Thierry Berney  
Christine Bernsmeier  
David Bernstein  
Natalie Lie Bernsten  
Marie-Luise Berres  
Frederik Berrevoet  
Matthias Berse  
Cristina Bertelli  
Ada Bertoli  
Esther Bertran  
Annalisa Berzigotti  
Camille Besch  
Alain Besch  
Ali Bessisow  
Florent Besson  
Fernando Bessone  
Jan Best  
Dominik Bettinger  
Briana Betz  
Boris Beudeker  
Ulrich Beuers  
Berend Beumer  
Michele Bevilacqua  
Lisa Bewersdorf  
Pooja Bhadoria  
Ajeet Singh Bhadoria  
Khushpreet Bhandal  
Bal Raj Bhandari  
Rajan Bhandari  
Rahima A. Bhanji  
Sanjay Bhanot  
Adil Bhat  
Puja Bhatia  
Sangeeta Bhatia  
Megha Bhatnagar  
Dipankar Bhattacharya  
Ruveena Bhavani  
Gautam Bhave  
Sheng Bi  
Jolanta Białkowska  
Francesca Biancianiello  
Marcello Bianchini  
Cristiana Bianco  
Yesim Bican  
Markus Bickel  
Charles Biddle-Snead  
Laure Bidou  
Laurent Biertho  
Pablo Bifani  
Scott Biggins  
Mirna Biglione  
Daniela Bignamini  
Chhagan Bihari  
Bikrant Bihari Lal  
Marcel Bijvelds  
Itdoa Bilbao  
Itxarone Bilbao  
Angela Bilbao  
Ines Bicic-Curcic  
Elisa Biliotti  
Griffiths Bill  
Antoon Billet  
Kharmen Billimoria  
Andrew Billin  
Marc Bilodeau  
Laurent Bilodeau  
Vasundhra Bindal  
Laure Bindels  
Patrick Bindels  
Harald Binder  
Chabi Bindia  
Mawuena Binka  
Paula Binks  
Teresa Binter  
Nazrila Hairizan Binti Nasir  
Marco Biolato  
Roberta Biondi  
Mia Biondi

S1024 Journal of Hepatology 2022 vol. 77(S1) | S1021–S1064
Disclosures

Christian Casar
Stefano Cascinu
Antonio Cascio
Johnny Cash
Rosario Casillas
Elia Casirati
Markus Casper
Martien P. M. Caspers
Cristopfe Cassinotto
Helena Castañé
Felipe Cantañedo
Luis A Cantaño González
Andrés Castano-García
Vincent Castelain
Javier Castell
Paul Castellani
Marien Castellanos-Fernandez
Inmaculada Castello
Inmaculada Castelló Miralles
Lluís Castells
Corinne Castelnau
Agustin Castiella
Federico Castillo
Mauricio Castillo
Joaquín Andrés Castillo
Maria Castillo-Catoni
Rui Castro
Stefania Casu
Mireia Casulleras
Francesca Casusceli di Tocco
Filippo Cattazzo
Xavier Causse
Lourianne Cavalcante
Luisa Cavalietto
Daniela Cavallone
Giuliana Cavalloni
Anna Cavazza
Madeleine Caven
Nora Cazzagon
Marina Elena Cazzaniga
M. Cea
Francesca Ceccherini Silberstein
Stefano Cecchi
Amie Ceesay
Sahabat Ceken
Yesim Cekin
Ayhan CEKIN
Guven Celebi
Ferya Celik
Ferit Cepek
Dorival Celine
Ciro Celsa
Jaroslav Cendrowski
Elisabetta Ceni
Michele Cennamo
Delphine Centeno
Federica-Grazia Centonze
Théo Cerceau
Eira Cerda Reyes
Roberto Ceriani
Ferruccio Ceriotti
Andreas Cerny
Orlando Cerocchi
Federico Cerutti
Marta Cervera
Matteo Cescon
Annalisa Cespiati
Yagmur Cetin Tas
Cendrine Chaffaut
Sarinder Chahal
Julien Chaigneau
Sanjay Chainani
Giorgi Chakhunashvili
Avisek Chakravortyi
Julia Chalaye
Suryanarayana Challa
Benjamin Challis
Mathieu Chalouni
Marck Chamley
Po-Lin Chan
Huan-Reat Chan
Wah-Kheong Chan
Winston Chan
Stephen Chan
Edwin, Shih-Yen Chan
Brian Chan
Lap Kwan Chan
Connie Chan
Vidya Leha Chandran
Karthik Chandrasekharan
Mei-Hwei Chang
Jiabao Chang
Tsung-Yen Chang
Pik Eu Jason Chang
Ting-Tsung Chang
Jung-Chin Chang
Chun-Chao Chang
Te-Sheng Chang
Kyong-Mi Chang
Mei-Hwes Chang
Kuo-Kuan Chang
Kyong-Mi Chang
Keith M. Channon
Dessy Chantal
Veena Chantarangkul
Yee Chao
Hann-Hsiang Chao
Daniel Chao
Matthew Chapman
Roger W.G. Chapman
Fleur CHAPUS
Hakim Charfi
Margaux Charles
Sarah Charman
Vivek Charu
Praneet Chaturvedi
Hau-Tak Chau
Rahul Chaudhari
Binita Chaudhary
Ayushi Chauhan
Roberta Chaves
Frederico Chaves Salomão
Kazuaki Chatayama
Sukhdeep Steven Cheema
Isabelle Chemin
Yaw-Sen Chen
Huey-Ling Chen
Yu-Ju Chen
Ping Chen
Wangjing Chen
Chien-Hung Chen
Yu Chen
Dongbo Chen
Hongsong Chen
Pu Chen
Huanming Chen
Hong Chen
Youngping Chen
Xinyue Chen
Lingzi Chen
Jinjun Chen
Sui-Dan Chen
Kaina Chen
Lynna Chen
Tianyan Chen
Ming-Huang Chen
Jinjun Chen
Hong Chen
Guofeng Chen
Zhennhua Chen
Jilin Chen
Jing Chen
Xin-Yue Chen
Shuai Chen
Jenny Chen
Hui Chen
Qiuying Chen
Hui Chen
Yutong Chen
Sui-Dan Chen
Chien-Hung Chen
Yunfu Chen
Ping Chen
Lin Chen
Yunfu Chen
Wen-Chi Chen
Hanying Chen
Chien-Hung Chen
Owen Chen
Yi-Cheng Chen
Jyh-Jou Chen
Pei-jer Chen
Tsung Po Chen
Jennifer Chen
Jiaxian Chen
Hsiu-Hsi Chen
Sam Li-Sheng Chen
Bowen Chen
Qi Chen
Chiyi Chen
Chun-Ting Chen
Guei-Ying Chen
Xin-Yue Chen
Chien-Hung Chen
Min Chen
Long Chen
Yunru Chen
Jun Chen
David, Hsing Yu Chen
Jiaxian Chen
Hong Chen
Zhi-Wei Chen
Min Chen
Jiaxian Chen
Zhi Chen
Xuanmeng Chen
Beishan Chen
Shuai Chen
Zhennhua Chen
Xiaoqiao Chen
Mingkai Chen
Swee Lin Chen Yi Mei
Benny Cheng
Ho Ming Cheng
Disclosures

Rosanna De Marco
Nicola De Maria
Eleonora De Martín
Vincent de Meijer
Kevin De Muynck
Stefania de Pascalis
Aurora De Ponti
Anita De Rossi
Peta E. de Ruiter
Victoire De Salins
Teresa De Santis
Evelien de Schepper
Martina De Siena
Annalisa De Silvestri
Paolo De Simone
Andrea De Sinno
Rozanne de Veer
Clara De Venuto
Andrea De Vito
Winnok De Vos
Elsemiek De Vries
Rudi de Waart
Floor de Weijer
Benedicte De Winter
Koos de Wit
James Dear
Jose Debes
marylione debette-gratien
Antoine Deboutreau
Thomas Decaens
Jochen Decaecker
Alexander Dechene
Charlotte Decker
Sofie Decock
Jean-Luc Decout
Marie Decraecker
George Dedoussis
Alexandra S Deeks
Vashist Deelchand
Luc Defreyn
Elisabetta Degasperi
Bruno Degeest
Erik Degerman
Helena Degrutoe
Jeroen Dekervel
Maria Del Barrio
Maria Del Barrio Azaceta
Maria Del Ben
Paola Del Bianco
Maria Estela del Castillo
Pilar del Hoyo Gordillo
Carmen Del Pozo-Calzada
Claire Delacôte
Heloise Delagreverie
Adèle Delamarre
Elizabeth Delarocque-Astagneau
Vahire Delaune
Yael Delayahu
Ellen Deleus
Igotz Delgado
Alberto delgado
Igotz Delgado
Evangelina Delgado
Andrea Delgado Nieves
Sophia Delicou
bénédicte delire
Thomas Delmi
Degré Delphine
Pierre Deltenre
Jean Delwaele
Klaus Dembowsky
Barbara Demediuk
Anna Demetriou
Jake Demetris
Aicha Demidem
Mehmet Demir
Coskun Ozer Demirtas
Elif Demirtas
Vanessa Den Heyer
Calli Deng
Timm Denecke
Huan Deng
Aiyun Deng
Jiang Deng
Yangyang Deng
Mei Deng
Gerald Denk
Alban Denys
Meghan Derenoncourt
Mathilde Deridder
Rita Derua
Haiilemichael Desalegn
Khalil Desboeufs
Marc Deschene
Sebastian Deschler
Chantal Desdouets
Romain Desert
Paul Desmond
Trinidad Desonges Corrales
Lise Desquilles
Sönke Detlefsen
Sylvie Deuffic-Burban
Melanie Deutsch
anouk dev
Nidhini Devadas
Kalpana Devalia
Neslihan Deveci
Poornima Devi
Lindsey Devischer
Dhruti Devshi
Deepika Devuni
Maria Dezan
Thangjam Dhabali
Amanda Dhagapan
Amitpal Dhillon
Abhishek Dhanda
Ashwin Dhandh
Ameet Dhar
Sebastien Dhary
Sébastien Dhary
Neerav Dharia
Srisir Dharmapuri
Anil Dhawan
Koenraad D'Hollander
Elisabeth Dhondt
Roslyn Dhurkay
Fabrizio Di Benedetto
David Di Benedetto
Fabrizio Di Benedetto
Chiarl Di Bonaventura
Tina Di Catenino
Alessia Di Costanzo
Giovanni Giuseppe Di Costanzo
Luca Di Galleone
Angelo Di Giorgio
Julia Di Girolamo
Tommaso Di Maira
Giovanni Di Maira
Tommaso Di Maira
Vito Di Marco
Sabina Di Matteo
Laura Giuseppe Di Pasqua
Giovanni Di Perri
Maja Di Rocco
Stefano Di Sandro
Sarah di Somma
Gian Luca Di Tanna
Luca Di Tommaso
Daniel E. Di Zeo-Sánchez
Gheorghe Diaconescu
Moises Diago
Moisés Diago
Elena Diago Sempre
Aldiouma Diallo
Kalilou Diallo
Alpha Diallo
Michail Diamantidis
Omar Diatta
Fernando Diaz
Luis Antonio Diaz
Sebastian Diaz
Luis Antonio Diaz
Alba Diaz
María Paz Díaz
Alba Díaz
Dáciel Díaz Bethencourt
Fernando Diaz Fontela
Alvaro Diaz Gonzalez
Juan Carlos Diaz Martin
Álvaro Diaz-González
Nely Díaz-Mejía
Irene Díaz-Moreno
Mauricio Díaz-Muñoz
Antonio Diaz-Quintana
Rolland Dickson
Lütjohann Dieter
Peter Dietrich
Julia Dietz
Christopher Dietz
Cristina Díez
Mustafa Diken
Nektarios Dikopoulos
Michael Dill
Stavros Dimitriadis
Amreen Dinani
Dinc Dincer
Wei Ding
Yanhua Ding
Weimao Ding
Huiguo Ding
Yuming Ding
Mariana Diniz
Petra Dinjar Kujundžić
Katja Dinkelborg
Sarah Dion
Jessica Dion
Sophie Diong
Marina Diotallevi
Assane Diouf
Daouda Diouf
Boubacar Diouf
Melisa Dirchwolf
Meike Dirks
Verena Dirsch
Disclosures

Joris Erdmann  Jonathan Fallowfield  Guillermo Fernández Varo
Fatih Eren  Sarah Faloong  Inmaculada Fernández Vázquez
Merve Eren Durmuş  Gregory Fan  María Victoria Fernández-Baca
Arthur Erhoeven  Jian-Gao Fan  Maite G Fernández-Barrena
Graf Erika  Xiude Fan  José Fernández-Checa
Jonas Eriksson  Chiara Fanelli  Felipe Fernández-Cuenca
Mert Erkan  Chengwen Fang  María Fernández-Fernandez
Nicole Erler  May Faraj  Isabel Fernández-Lizaranzu
Iris Erlund  Achilles Fardellas  Paula Fernández-Palanca
Tatiana Ermolova  Rasm Farejov  Mirian Fernández-Vaquero
Gaizka Errazti Olartekoetxea  Nunzia Farella  Ainhoa Fernández-Yunquera
Marco Erreni  Silvia Fargion  Janina Ferrand
Stephanie Erschfeld  Hesso Farhan  Luigi Ferrante
Graf Erika  Fabio Farinati  Alberto Ferrarese
Jonas Eriksson  Erik Farin-Blattacker  Erika Ferrari
Mert Erkan  Naba Farooqui  Maria Lucia Ferraz
Nicole Erler  Anna Farriols  Carlos Ferre Arcil
Iris Erlund  Matteo Fassan  Caterina Ferrerccio
Tatiana Ermolova  Ifrah Fatima  Marcelo Simão Ferreira
Arthur Erhoeven  Erika Fatta  Ignacio Ferreira
Graf Erika  Günter Fauler  Livia Garcia Ferreira
Stephanie Erschfeld  Rosemary Faulkes  Ignacio Ferreira
Mert Erkan  Stéphanie Faure  Raphaella Ferreira
Nicole Erler  Muhammad Fayaz  Jose Manuel Ferreira
Iris Erlund  Alessandro Federico  Silvia Ferri
Tatiana Ermolova  Carlo Federico Perno  Luigina Ferrigno
Arthur Erhoeven  Uli Fehrenbach  Andrea Ferrigno
Graf Erika  Michael Feigh  Helen Ferrry
Jonas Eriksson  Jeanette Feizi  Philip Georg Ferstl
Mert Erkan  Nicole Feldbacher  Petros Fessas
Nicole Erler  Alexandre Feldman  Davide Festi
Iris Erlund  Ariel Feldstein  Raja Omar Fiaz
Arthur Erhoeven  Anna Feliu-Prius  Alexander Fich
Graf Erika  Sean Felix  Anja Figge
Jonas Eriksson  Catarina Félix  Anita Figredo
Mert Erkan  Emanuele Felli  Pierre Filhine-Tresarrieu
Nicole Erler  Paolo Feltracco  Gabriela Adriana Filip
Iris Erlund  Martijn Fenaux  Tajana Filipek Kanizaj
Tatiana Ermolova  Mary Fenech  Natalia Filipek
Arthur Erhoeven  Ying-Hua Feng  Celine Filippi
Graf Erika  Wenke Feng  Leonardo Filippo
Jonas Eriksson  Bo Feng  Natalie Filmann
Mert Erkan  Dandan Feng  Roberto Filomia
Nicole Erler  l-Cher Feng  Ane-Kristine Finbraten
Iris Erlund  Ruiu Feng  Jodok Matthias Fink
Tatiana Ermolova  Rebecca Fennell  Fabian Finkelmeier
Arthur Erhoeven  Cyrille Fess  Armin Finkenstedt
Graf Erika  Anna Ferenc  Alexander Finnemore
Jonas Eriksson  Catherine Ferguson  Francesca Fiorentino
Mert Erkan  Onur Ferhanoglu  Janett Fischer
Nicole Erler  Idoia Fernández-Puertas  Susan Fischer
Iris Erlund  Diogo A. E. Fernandes  Lutz Fischer
Tatiana Ermolova  Christopher C. Fernandes  Janett Fischer
Arthur Erhoeven  Sara Fernandes  Petra Fischer
Graf Erika  Flavia Fernandes  Elke Fischer
Jonas Eriksson  Roberto Fernandez  Henok Fisseha
Mert Erkan  Emma Fernandez  Daniel Fitting
Nicole Erler  Javier Fernandez  Steve Flack
Iris Erlund  Ainha Fernandez  Alexander Flahove
Tatiana Ermolova  Enrique Claudio Fernandez  Berthou Flavien
Arthur Erhoeven  Javier Fernandez  M. Wayne Fleischman
Graf Erika  Marcos Fernandez Fondevila  Katarzyna Fleischer-Stepnienksa
Jonatan Fernandez Garcia  Jonatan Fernandez Garcia  Mathias Flensted-Jensen
Samuel Juan Fernandez Prada  Hervé Fleury
David Fernandez Ramos  Alexander Flahove
Conrado Manuel Fernandez Rodriguez  Robert Flisiak
Conrado Fernandez-Rodriguez  Naomi Fliss-Isakov
Alejandro Fernandez Soro  Gianina Flocco
Ylva Flederus

S1032  Journal of Hepatology 2022 vol. 77(S1) | S1021–S1064
Disclosures
Disclosures

Miguel García-Deltoro
Eduardo García-Fuentes
Selene García-García
Francisco García-García
José Manuel García-Heredia
Mireia García-López
María del Rosario García-Lozano
Pedro Pablo García-Luna
María-Victoria García-Mediavilla
Carmelo García-Monzon
Carmelo García-Monzón
Enrique García-Nieto
Guillermo García-Porrero
Ester García-Pras
Montserrat García-Retortillo
Montserrat García-Retortillo
M. Carmen García-Ruiz
Francisco Javier García-Samaniego Rey
Guadalupe García-Tsao
Matteo Garovich
Garima Garg
Sumit Garg
Harshit Garg
Catherine Gargan
Pratibha Garh
Aleksander Garlicki
Moira Garraus
Grace Garrett
Isabel Garrido
Marta Garrido
Maria Soledad Garrido
Eveline Gart
Cynthia Garvey
Lærke Gasbjerg
Frida Gasca
Slavko Gasparov
Mikel Gastaca
Sheila Gato Zambrano
Nikolaos Gatselis
Sophie Gensluckner
Sokratia Georgaka
Jacob George
Nivya George
Alexandra Georgieva
Chrysanthos Georgiou
Cyrill Géraud
Athenais Gerber
Victor Gerdes
Florian Gerhardt
Martin Gercke
Alessio Gerussi
Anne Gervais
Vladimer Getia
Tom Gevers
Philipp Geyer
Joachim Geyer
Natalia Geyvandova
Aamir Ghafoor Khan
Ahmed Ghallab
Mohsen Ghanbari
Marc Ghany
Mahyar Chavemi
Cristian Gheorghie
Bart Ghesquière
Michaël Ghez
Michele Chieliemetti
Imerzoukene Ghiles
ana-maria ghiuchici
Indrajit Ghosh
Alip Ghosh
Indrajit Ghosh
Alia Ghraieb
Marco Giaccheto
Amato Giacca
Joyce Madison Giaocfi
Eleonora Giacopuzzi Grigoli
Vincenzo Giambra
Yi Lin Gian
Andrea Gianatti
Eдоardo Giovanni Giannini
Jeanne-Marie Giard
Karyna Gibbons
John Gibbons
Benjamin Gibert
Katja Giersch
Baptiste Giguet
Mar Gil
Hilla Giladi
Hêlène Gilgenkrantz
Antonio Gil-Gomez
Upkar Gill
Justine Gillard
Patrick Gillevet
Elizabeth Gilligan
Matthew Gillum
Mark Gillyon-Powell
Claudia Gil-Pitarch
Rubén Gil-Redondo
Derek Gilroy
Concepcion Gimeno Cardona
Concepcion Gimeno Cardona
Stefano Gimanni Corradini
Claudia Gior‘
Sabrina Giometto
Laura Giordano
Domenico Giosa
Alvaro Giráldez-Gallego
Enrico Girardi
Pablo J. Giraud
Dewan Girir
Morgane Girier-Dufournier
Irina Girlesanu
Yabete Girma
Stefano Gitto
Matthew Gittus
Mauro Giuffré
Paolo Giuffrida
Previtali Giulia
Felice Giulian
Nathalie Giuly
Michela Giurucin
Gianluca Giusti
Monika Gjorgieva
Megan Glancy
Susanne Glasgow
Dieter Glebe
Lise Lotte Glud
Simeï Go
Chun Goddard
Raquel Godoy
Henri Goedertz
Ashish Goel
Amit Goel
Benjamin Goeppert
Jens Peter Goetze
Ketevan Goginashvili
Maya Gogtay
Boon Bee George Goh
Narosa Goliketxea
Hale Gökcan
Pinar Goğçen
Pegah Golabi
Srinivasa Reddy Golamari
David Goldberg
Daniel Goldenberg
David GoldFarb
Robert D. Goldin
Robert Goldin
Nora Goldmann
Amanda Goldring
Chloe Goldsmith
Kerrie Goldsmith
Francois Goldwasser
Rita Golfini
Rithvik Golla
George Golovko
Nicolas Golse
Rachel Gomel
William Gomes
Alberto Gómez
Concepción Gómez
Silvia Gómez Araugo
Miguel Ángel Gómez Bravo
Judith Gómez-Camarero
Elena Gómez Domínguez
Pilar Gómez Rodríguez
Beatriz Gómez Santos
Neus Gomez-Muñoz
Antonio M. Gómez-Orellana
Daniela Gompelmann
João Gonçalves
Tal Gonen
Cynthia Gong
Xiyong Gong
Öykü Gönül Geyik
Disclosures
Disclosures
Disclosures

Chien-Wei Huang
Ching-I Huang
Yan Huang
Yun Huang
Pinzhu Huang
Isabel Huang-Doran
Gavin Huangfu
Sina Hübener
Samuel Huber
Markus Huber
Samuel Huber
Wolfgang Hübl
Evis Hudson
Peter Huebener
Lucas Hueffner
Anna Huerta
Norbert Hueser
Catherine Huet
Mie Balle Hugger
Timothy Hughes
Rex Wan-Hin Hui
Vicki Wing-Ki Hui
Samuel Hui
Laura Huiban
xiang huiling
Sam Hulme
Lauren Hulshof
Ya-Wen Hung
Yi-Ping Hung
Chao-Hung Hung
Chiu Hung-Chih
Sally Hunsberger
Mallory Hunt
Peter Hunyady
Anne Huppertsberg
Adoración Hurtado
Mehreen Husain
Ioana-Alexandra Husar-Sburlan
Norbert Hüser
Dana Huskens
Md Razeen Ashraf Hussain
Yaqza Hussain
Sadam Hussain Bhat
Arif Hussenbux
George Hussey
David Hutchinson
Tomasz Hutch
Lynn Huyc
Jae-Seok Hwang
Seong Gyu Hwang
Jae-Seok Hwang
Shin Hwang
Paul Wuh-Liang Hwu
Ashley Hyde
Theresa Hydes
Philip Hylemon
Tuulia Hyötyläinen
Arinda Hysenj
Sung Hee Hyun
Kang Hyunsoo
Antonino Iacarino
Speranta Iacob
Viktoria Iakovleva
Andrea Iannone
Giulia Iannone
Massimo Iavarone
Luis Ibañez
Cesar Ibarra
Carolina Ibarrola de Andrés
Jamal Ibdah
Ignacio Iborra
Manu Icaza
Philippe ICHAI
Francisco Idalgoaga
Ramazan Idilman
Akio Ido
Donatella Ieluzzi
Samuelle Iesari
Dolapo Igboin
Teresa Iglesias
Ainhoa Iglesias
Olivas Ignasi
Mina Ignat
Abdul Ilhayhid
Manami Iida
Hiroko Iijima
Jan IJzermans
Hitoshi Ikeda
Yujii Ikeda
Kenichi Ikejima
Gabriela Ilionsky
Megan Illingworth
Nicholas Ilott
sarah Iltache
Gene Im
Theresa Im
Gene Im
Yu Ri im
Kento Imao
Michio Imamura
Fumiaki Imamura
Franz Immer
Paata Imnadze
Dilara Inan
Mercedes Iñarrairaegui
Nevin Ince
Volkan Ince
Simone Incicco
Victoria Indenbaum
Akin Inderson
Vineeth Indira Chandran
Giuseppe Indolfi
Nevin Indriz
Mirtha Infante
Stefany Infante
Giuseppe Infantino
Sarah Inglis
Sofie Ingvar
José A. Iniá
Hamish innes
Tommaso Innocenti
Kaori Inoue
George Ioannou
David Ippolito
Afshan Iqbal
Maria Iraburu Elizalde
Marie Irles-Depe
Paula Iruzubieta
Katharine Irvine
James Irving
Sophie Irwin
Bordes Isabelle
Vasily Isakov
Nora Isbener
David Iser
Takamasa Ishino
Marwa Ismail
Helena Isoniemi
Ariel Israel
Eran Israel
Mads Israelen
Fadi Issa
Assaf Isschar
emmanuel itti
Antonella Iuliano
Pavlo Ivanchov
Dana Ivancovskyy Wajcman
Tommy Ivancs
Elena Ivanova
Keiko Iwasako
Michihiro Iwaki
Terunao Iwanaga
Hirohiko Iwasaki
Kentaro Iwasawa
Sowmya Iyengar
Rajalakshmi Iyer
Paula Izquierdo-Altarejos
Laura Izquierdo-Sánchez
Francesco Izzo
Manhal Izy
Samir Jabber
Kathryn Jack
Clive Jackson
Kathy Jackson
Janett Jacobo
Angus Jacobs
Hodje Jacqueline C.
Christian Jacqueline
Elmar Jaackel
Ravi Jagatia
Rukmini Jagdish
Bettina Jaggemann
Jennifer Jager
Johannes Jäger
Dirk Jäger
Shashidhar Jaggaiahgari
Vinay Jahagirdar
Andreas Jahnert
Kavita Jain
Carolin E. M. Jakob
Gustav Jakobsson
Prasun Jalal
Alpha Omar Jallow
Biyanka Jaltotage
Larry James
Carole Jamey
Nigel B Jamieson
Thomas Jamieson
Muhammad Jamil
Daniela Janeckeova
Sabina Jancauskienė
Byoung Kuk Jang
Jae Young Jang
Yeeun Jang
Jeong Won Jang
Maciej K. Janik
Naveed Janjua
Justyna Janocha-Litwin
Kamil Janowski
Christian Jansen
Sonja Jansen-Skoupy
Ralf Jansen-Langenstein
Veerle Janssens
Filip Janssens
Disclosures

Umesh KAPIL
Gilaad Kaplan
David E Kaplan
Leonard Kaps
Sarah Kaps
Andras Kapus
Ghania Kara-Ali
Oguz Karabay
Sedat Karademir
Dimitrios Karagiannakis
Raffi Karagozian
Sercin Karakulukçu
Theofanis Karapatanis
Zeki Karasu
Ani Kardashian
Mohammad Ehsanul Karim
Gres Karim
Revital Kariv
Thomas Karlas
Vanessa Karlen
Tom Hemming Karlsen
Purushotham Karnam
Wikrom Karnsakul
Ewa Karpińska
Palaniswamy Karthikeyan
Anu Karunanithy
Constantine Karvellas
Kornelia Karwowska
Joyce Kasavuli
Ahmed Kaseb
Lisa Kaser
Minal Kashyap
Zain Kasmani
Jasmin Kassem
Lorn Kategaya
Katharina Katharina Staufer
Jakob Kath
Jaeger Kathrin
Jun Kato
Matschenz Katrin
Panzitt Katrin
Petros Katsioulides
Antonios Katsoumas
Sarah Kattakuzhy
Antonis Kattamis
Benedikt Kaufmann
Paul Kaufmann
Benedikt Kaufmann
Savneet Kaur
Impreet Kaur
Navpreet Kaur
Amanpreet Kaur
Kanudeep Kaur
Kanav Kaushal
Vishal Kaushik
Hannu Kautiainen
Mary Kavanagh
Hidehiko Kawai
Nobuyoshi Kawamura
Keigo Kawashima
Richard Kay
Tahrima Kayes
Ajamete Kaykas
Konstantin Kazankov
Mingxia Ke
Jeremy Keane
Andrew Keaveny
Stergios Kechagias
Jaap Keijer
Nanda Keijzer
Verena Keitel-Anselmino
Graham Kemp
William Kemp
Agnieszka Kempinska-Podhorodecka
Jan Kemspsik
Patrick Kennedy
Oliver Kennedy
James Kennedy
Kevin Kennedy
Vakhtang Kerashvili
Annarein Kerbert
Jakob Kerbl-Knapp
Nanda Kerker
David Kershonobich
Remco Kersten
Emilie Kerstens
Satish Keshav
Rosemary Keshinro
Sahar Keshvari
Onur Keskin
Annika Kessler
Sonja Keßler
Takaomi Kessoku
Guo Sen Kew
Ilisiya Khaertynova
Myat Khaing
Salim Khakoo
Atfeh Khakpour
Jaafar Khaleed
Mandana Khalili
Korosh Khalili
Wafa Khamri
Khalid mahmud Khan
Uqba Khan
Muhammad Khan
Uzma Khan
Sabiha Khan
Shahid Khan
Juned Khan
Zahrat Khan
Arshi Khanam
Kamil Khanipov
Amardeep Khanna
Rajeev Khanna
Nadia Khatoon
Nora Khatib
Andre Khazak
Nino Khetsuriani
Vikas Khillan
Het Htet Toe Wai Khine
Davit Khilgheytan
Olga Khomich
Irma Khonelidze
Sharin Elizabeth Khorsandi
Mina Khoshdeli
Saita Khowaja
Yury Khudyakov
Gitten Khwairakpam
Rania Kibiche
Alexandra K. Kiemer
Amanda Kiliaan
Murat Kilç
Saskia Kilmer
Jong Man Kim
Beom Kyung Kim
Young Seok Kim
DongYun Kim
Gi-Ae Kim
Byung Seok Kim
So Yeon Kim
Byoung Je Kim
Gi-Ae Kim
Doohyun Kim
Jung Kuk Kim
Yohan Kim
Jung Kuk Kim
Dae Jin Kim
Kang Mo Kim
Seon-Ok Kim
Ye-Jee Kim
Sanghwa Kim
Namjeong Kim
Jason Kim
Kang Mo Kim
DaWon Kim
Tae Hyung Kim
Seung Up Kim
Beom Kyung Kim
Mi Na Kim
Adam Kim
Seung Up Kim
Irene Kim
Chul Hoon Kim
Sungmin Kim
Mi Mi Kim
Sarang Kim
Seok Hyeun Kim
Byung Seok Kim
Terri Kim
Jin Un Kim
Andre D. Kim
Chanyang Kim
Chul Hoon Kim
Albert Kim
Jong Man Kim
Bong Wan Kim
Dong-Sik Kim
Byung Ik Kim
Hye Seon Kim
Jin Seoub Kim
Ji Min Kim
Rattana Kim
Ji Hoon Kim
Tae Hyung Kim
Hyung Joon Kim
Chang Wook Kim
Do Young Kim
Yong Ook Kim
Jin-Wook Kim
Moon Young Kim
Beom Kyung Kim
Elena Kim
Hyeree Kim
Moon Young Kim
Ji Hyun Kim
Hyun Young Kim
Sang Kyum Kim
Oliver Kimberger
Nina Kimer
Renate Kimmeler
Leona Kim-Schluger
Yusuke Kimura
Masaki Kimura
Disclosures

Bettina Langhans
Simon Langkjær Sørensen
Lucas Langlois
Taro Langner
Lorenzo Lani
Sarah Lanigan
Gandi Lanke
Amalie Lang
Matthias Lannoo
Nicolas Lanthier
Michael Lanuti
Martine Lapalus
Ariane Laparra-Ramakichenin
Syria Laperche
Nathanael Lapidus
Ainhoa Lapitz
Mathieu Laplante
Carmen Lara Romero
Christopher Lark
Dominique Larrey
Juan Ramón Larrubia
Hélène Larrue
Steen Larsen
Frederik Larsen
Anne Larson
Alberto Lasagni
Melanie Laschinger
Caroline Lacoux-Combe
Guillaume Lassailly
Maja Laszczyńska
Maria U Latasa
Muhammad Umair latif
Mercedes Latorre Sánchez
Marianne Latournerie
Cathrine Lau
Jasmine Lau
David Lauber
Georg Lauer
Alexis Laurent
Astrid Laurent Bellue
Mette Lauridsen
Tea Lund Laursen
Mandy Lauw
Marie Lauzon
Gareth Lavery
Marla Lawriksen
Matthew Law
Daniel Lazar
Shanny Layani
Stefan Lazar
Raul Lazarre
Don Lazas
Mariana Lazaro
Giuseppe Lazzarino
Khanh Le
Phuc Le
Suong Le
Brigitte Le Bail
Frédéric Le Gal
Maude Le Gall
Adrien Le Guennec
Estelle Le Pabic
Benjamin Leaker
Carina Leal
Louise Lebedel
Elena Lebedeva
Jerome Lebigot
Fanny Lebossé
Salvatore Lecca
André Lechel
Christian Lechler
Isabelle Leclercq
Sophie Leclercq
Laurence Lecomte
Osial Ledesma Juárez
Ni-Chung Lee
Joon Hyeok Lee
Nerissa Lee
Brian Lee
Jaejun Lee
Jenny Lee
Brian Lee
Jyjeon Lee
Yu Rim Lee
Changheyeong Lee
So Jung Lee
David Uihwan Lee
Chee Leng Lee
Jong Suk Lee
Sang Hyun Lee
Seonmyeong Lee
Jong Suk Lee
Sang Hyun Lee
Seonmyeong Lee
Han Chu Lee
Danbi Lee
Chiehju Lee
Pei-Chang Lee
I-Cheng Lee
Dong Ho Lee
Jeremy Lee
Willaim M. Lee
Su-yeon Lee
Pei-Chang Lee
Han Chu Lee
Danbi Lee
Byung Seok Lee
Taehee Lee
Tai PIng Lee
Rheun-Chuan Lee
Han Ah Lee
Yi-te Lee
Hye Won Lee
Hee Seung Lee
Yu Rim Lee
Won Kee Lee
Hyo Young Lee
Chul-Min Lee
Jack Lee
John Lee
Jonghyun Lee
Hyo Young Lee
Byung Seok Lee
Yu Rim Lee
Changheyeong Lee
Richard Lee
Jeffrey Lee
Jun-Hyuk Lee
Joo Ho Lee
Hye Won Lee
Hee Seung Lee
Alicia Lee
Kwang-Woong Lee
Boram Lee
Hae Won Lee
Jae Geun Lee
Disclosures
Disclosures

S1046 Journal of Hepatology 2022 vol. 77(S1) | S1021–S1064
Disclosures

Sara Montagnese
Marzia Montalbano
Paolo Montalto
Iaarah Montalvo
Valle Montalvo-Romeral
Noé Axel Montanari
rosa montañés
Maria Monte
Rocío Montero-Vallejo
Pedro Montes
Xavier Montet
Monica Monti
Carla Montironi
Carmina Montoliu
Anne Mooney
Dilip Moonka
Karen Moore
Yvette Moore
J. Bernadette Moore
Celia Moore
David Moore
Kevin Moore
Joanna Moore
Claudia Moore-Gillon
Orna Mor
Inbal Mor
Orna Mor
Alfonso Mora
Darius Moradpour
Dalia Morales Arraez
Manuel Morales-Ruiz
Luis Enrique Morano Amado
Bárbara Morán
Richard Moreau
Sulleman Moreea
teresa moreira
Antoine Morel
Carola Maria Morell
Maria Cristina Morelli
Rémi Morello
Christophe Moreno
M. Jesús Moreno-Aliaga
Alazne Moreno-Lanceta
Victoria Moreno-Manzano
Marsha Morgan
Katie Morgan
Marsha Morgan
Timothy Morgan
Paul Morgan
Katie Morgan
Cecilia Morgantini
Mattia Mori
Yasuhiro Mori
Trevor Mori
Rosa M Morillas
Maki Morinaga
Martina Morini
Filomena Morisco
Naoki Morita
Steven Morley
Timothy Morley
Steven Morley
Joanne Morling
Francoise Mornex
Berna Morova
Martine C. Morrison
Linda Morrow
Christian Mortensen

Frank Viborg Mortensen
Christian Mortensen
Antonella Mosca
Miha Moskon
Alireza Moslem
Adyr Moss
Yasmin Mossavar-Rahmani
Elias Mossialos
Lorena Mosteiro González
Alireza Mosusavijarafai
Maryam Motamedrad
Benedetta Maria Motta
Karsten Motzler
Lien-Juei Mou
Miguel Moura
Luís Manuel Moura
Carla Maria Moura Marinho
Abbas Mourad
Ilias Moutsopoulos
Ferenc Mozes
Anna Mrzljak
Francy Mubenga
Giulio G. Muccioli
Marcus Mücke
Victoria Mücke
Alexandra Mueller
Sebastian Mueller
Martina Mueller-Schilling
Robert Muga
Abdullah Ghassan Farik Muhammad
Taj Muhammad
Saad Muhammad
Ambreen Muhammad
Andrew Muir
Salma Mujib
Sujit Mukherjee
Sarmistha Mukherjee
Atish Mukherji
Sramana Mukhopadhyay
Nizar Mukhtar
Avinash Mukkala
Sebastien Mulé
Thomas Mules
Ashwini Mulgaonkar
Giacomo Mulinacci
Kate Mullany
Kate Muller
Tobias Müller
Sophie Elisabeth Müller
Tobias Müller
Christian Müller
Tobias Müller
Christian Müller
Tobias Müller
Sascha Müller
Beat Mühlhaup
Daniela Mühle
Beat Mühlhaupt
Nawakodchamon Mungnamtrakul
Stefan Munker
Munkhjaya Munkhaabatar
Chris Munoz
Linda Muñoz
Rocio Muñoz Hernandez
Eva Muñoz-Couselo
Daneela Muntanau
sarwa Darwish Murad
Harumi Murakami

Ayato Murata
Paolo Muratori
Luca Muratori
Aleksandra Murawska-Ochab
Antonio Murgia
Donald Murphy
Sandra Murphy
Ruth Murphy
Sam Murray
Syed Murtaza-Baker
Marianette Murzi P
Erkin Musaev
Fabrice Muscari
Kamran Mushtaq
Cristina Musolino
Daniela Musi
Orlando Musso
Leon Muti
David Mutimer
Mahvish Muzaffar
Cristina-Maria Muzica
Robert Myers
Theodora Mylopoulou
Bich N Guyen
Mees N.S. de Graaf
Ekaterina Nabatchikova
Pamela Nabetu
Puria Nabilou
Nathalie Nachmannson
Fatema Nader
Luisa Nader
Fatema Nader
Devika Nadkarni
Mohammad Naffaa
Shunjii Nagai
Koki Nagai
Shintaro Nagashima
Michael Nagel
Judith Nagel
Anika Nagelkerke
Abha Nagral
Yang Won Nah
Sven Nahnsen
Pierre Nahon
Leandra Naira Zambelli Ramalho
Miyuki Nakagawa
Shinichi Nakagawa
Atsushi Nakajima
Yasunari Nakamoto
Shingo Nakamoto
Daichi Nakamura
Atsushi Nakamura
Masato Nakamura
Hiroyuki Nakanishi
Toshiaki Nakano
Kazuhiko Nakao
Raouf Nakhlieh
Karsten Nalbach
Rajkumar Nalinikanta
Heechul Nam
Olivier Morley
Yueming Nan
Prossie Lindah Nankya
Nikolai Naoumov
Cecilia Napodano
Laura Napoleone
Salvatore Napoli
Laura Napoli
Disclosures

Steven Olde Damink
Christopher Oldroyd
Jacqueline O'Leary
Sara Olesen
Tronina Olga
Peter Olinga
Pol Olivas
Filippo Oliveri
Ana Olivo
Alexander Olkus
Rupert Öllinger
Isabelle Olivier-Hourmand
Victor Olaszvsky
Inge Christoffer Olsen
Carlos Oltmanns
John Olynyk
Tea Omonovik Colaric
Morgan Ondeka
Agnes Bee Leng Ong
Janus Ong
Albert Ong
Stefano Ongarelo
Gabriel Oniscu
Kristina Önnerhag
Lorenzo Onorato
Ye Hutun Oo
Geraldine Ooi
Doreena Oosterhuis@rug.nl
Philip Oravetz
Marie-Amelie Ordan
Kevin O'Reilly
Matej Orešič
Marju Orho-Melander
Vichit Ork
Stian Magnus Staurung Orlien
Valeria Orlowa
necati ormeci
Denise Oró
Joanne Orouke
James Orr
Enrique Ortega G.
Aida Ortega-Alonso
Ana Ortiz-Velez
Julia Ortez
Gabriel Osborn
Ana Oshaughnessy
Valentino Osti
Sisse Rye Ostrowski
Tessa Ostyn
Alejandra Otero
Alejandra Otero Ferreiro
Elena Oton
Kari Otterdal
Tobias Otto
Jacobus Otto
Xiaxuan Ou
Nadia Ouayba
Linda Oude Griep
Ronald Oude-Elferink
Marine Oudot
Serge Ouoba
Abderrahim Oussalah
Denis Ouzan
Louise Owen
Collins Oduor Owino
Chung Owyang
Evelin Oxtrud
Julen Oyarzabal
Michitaka Ozaki
Umut Ozbek
Mustafa Özçürümez
Kamil Ozdil
Burcin Özdirik
Hasan Ozen
Digdem Ozer Etki
Ann-Kathrin Ozga
Elkin Ozgonul
Jonathan Ozik
Serdar Özsuzen
Omer Oztutemiz
Aditya Vikram Pachisia
Sabrina Paci
Beatriz Pacín Ruiz
Gemma Packer
Nagaraja Rao Padaki
Cynthia Padilla
Ana Padilla
Susana Padrones
Slobodan Paessler
Duilio Pagano
Sabrina Pagano
Georges-Philippe Pageaux
Katja Pahkala
Prabhjyoti Pahwa
Madhava Pai
Yong-Han Paik
Seung Woon Paik
Yong Han Paik
James Paik
Elena Paillaud
Anita Paisant
Nuno Paiva
Ravindra Pal
Naaventhian Palaniyappan
Yaseelan Palarasah
pascale palaspain
Asis Palazón
Ana Palazzo
Mor Palidor
Andrea Palermo
Giuseppina Palladini
Joan Pallares
Giada Pallini
Elena Palma
Carolina Santos Palma
Elena Palma
Nicki Palmer
Silvia Palmisano
Elena Palmisano
Adriana Palom
Giorgio Palu
Rafal Paluszkiewicz
Viníyendra pamecha
Claudia Pamo
Quwei Pan
Lianguy Pan
Dimitra Panagiotoglu
Sarjukumar Panchal
Alessandra Pandolfo
Nadia Panera
Antonio Panero
Elena Panettieri
Jing Pang
Marcus Panning
Spyridon Pantzios
Marlene Panzer
Simon Panzer
Marlene Panzer
Erika Paolini
Veronica Paon
Ioanna Papagjouvann
Chiara Papalin
Tim Papaluka
Zafiris Papanikolaou
Margarita Papathedoridi
Ana Papikiauri
Valérie Paradis
Anupama Parasar
Romain Parent
Elisabetta Parente
Albert Parés
Anna Parfieniuk-Kowerda
Stefanie Parisi
Jun Yong Park
Min Kyung Park
Soo Young Park
Jung Gil Park
Eun Jin Park
Jina Park
Min Kyung Park
Young Joo Park
Jun Yong Park
Hye Jung Park
Soo Young Park
Young Joo Park
Huiyul Park
Jung Gil Park
Huiyul Park
Jun Yong Park
Soo Been Park
Min-Jung Park
Neung Hwa Park
Jeongwoo Park
Julie Parkes
Emine Parlak
Yavuz Emre Parlar
Lucia Parlati
Marie Parnot
Cristina Parolin
Marina Parra-Robert
Craig Parzynski
Alina Pascale
Sonia Pascual
Tania Pastor
Helena Pastor
Mirella Pastore
Roberta Pastorelli
Daniele Pastore
Frane Pastrovic
Sama Siva Rao Pasulapeti
David Patch
Janisha Patel
Poulam Patel
Harshil Patel
Kajal Patel
Priti Patel
Niharika Patel
Nishi Patel
Janisha Patel
Sameer Patel
Vishal Patel
Disclosures
Disclosures

Carlos Rodríguez
Rubén Rodríguez Agudo
Elías Rodríguez Cuéllar
Juan Carlos Rodríguez Duque
Juan Carlos Rodríguez Duque
Maria Mercedes Rodríguez Gazari
Begoña Rodríguez Iruretagoyena
Sergio Rodriguez-Cuenca
María Rodríguez-Cundin
Juan Carlos Rodríguez-Duque
Francisco Rodríguez-Frias
Juan Carlos Rodríguez-San Juan
Elisabet Rodríguez-Tomàs
Elke Roeb
Natascha Roehlen
Stephanie Roessler
Henk P. Roest
Mark Roest
Shari Rogal
Magdalena Rogalska
Benjamin Rogers
Marché Roget
Sumati Rohilla
Natascha Röhlen
Nataliya Rohr-Udilova
Cristina Roig
Morganer Roinard
Angela Rojas Alvarez-Ossorio
Mayra Rojas Lara
Carla Rojo
Diego Rojo Lázaro
Johana Rokka
Zachary Rokop
Al Sayegh Rola
Oren Rom
Renato Romagnoli
Veronica Romagnoli
Eva Roman
Stefano Romeo
Orazio Romeo
Seam Romeo
Barbara Römer
Marta Romero
Sarah Romero
Gustavo Romero
Horacio Romero Castillo
Manuel Romero Gomez
Sarai Romero Moreno
Martin Rann Madsen
Luisa Ronzoni
Riccardo Ronzoni
Floris Roos
Maria C. Roque-Cuèllar
Bertrand Roqueyre
Fredrik Rorsman
Isabelle Rosa
Luis Alejandro Rosales Rentería
Michelle Rosario
Thomas Rösch
Ayub Rose
Stefan Rose-John
William Rosenberg
Nofar Rosenberg
Vered Rosenberg
Aaron Rosenberger
Emma Rosenbluth
Jonas Rosendahl
Maria Rosestedt
Martina Rosi
Rajkumari Rosie
Sebastian Rosigkeit
Arianna Rosina
Francesca Rosini
Tania Roskams
Elen Rosler
Oskar Rosmark
Olivier Rosmorduc
Fredrik Rosqvist
Gayle Ross
Kendra Ross
Tania Rosselli Del Turco
Noortje Rossen
Natalia Rosso
Rhonda J. Rosychuk
Nitzan Roth
Anjali A. Röth
Ori Rotstein
Woo Sun Rou
Francoise Roudot Thoraval
Francoise Roudot-Thoraval
Dominique Roulot
Martin Roumain
Sotiris Roussos
Marine Roux
Perrine Roux
Julien Roux
Elisabetta Rovida
Ian Rowe
Berengere Roy
Akash Roy
Laura Royo
Nir Rozenblum
Teona Rozina
Laura Rubbia-Brandt
Ángel Rubin
Ana Belén Rubio
Rafael Rubio Garcia
Marika Rudler
Javier Rueda-Gotor
Darius Ruether
Pierre Rufat
Elena Ruffoni
André Ruge
Hardik Rugwani
Patricia Ruiz
Lourdes Ruiz
Pablo Ruiz
Paula Ruiz
Belén Ruiz Antoran
Mikel Ruiz de Gauna
Paloma Ruiz-Blazquez
Francisco Ruiz-Cabello
Nathapat Rujeerapaiboon
Jody Rule
Patricia Rullier
Massimiliano Ruscica
Anthony Russell
Francesco Paolo Russo
Maria Madeleine Rüthrich
Kelsey Rutland
Stephanie Rutledge
Andrea Ruzzenente
Jennifer Ryan
Pablo Ryan
Marno Ryan
Jennifer Ryan
John Ryan
Mikael Ryden
Stephen Ryder
Je Ho Ryu
Antonio Sa Cunha
Kustaa Saarinen
Constantino Sábado
Gul Sabeen Azam Ghorezai
Guadalupe Sabio
Sergio Sabroso
Patrizia Saccomandi
David Sacerdoti
Federica Sacilotto
Sophie-Caroline Sacleux
Sophie Sacleux
FarsanehSadeghlar
Matthew Sadler
Anwaar Saed
Diego Saenz de Urturi
Maria Saez-Palma
Rifaat Safadi
Ricky Safer
Olga Sagalova
Sagar Sagar
Hacer Sahin
Roland Sahli
Amandeep Sahota
Iván Sahuco
Melissa Saichi
Yusuke Saigusa
Akhileshe Saini
donakonda saintin
Mauricio Sainz-Barriga
Tomoko Saito
Satoru Saito
Tomoko Saito
Carlo Saitta
Haresh Sajiir
Jenna Sajous
Mehdi Sakka
Takafumi Sakuma
Margarita Sala
Sultan Salahuddin
Grgrur Salii
Javier Salamanca Santamaría
ephrem salamé
Johannes Salomon
Massimiliano Salati
Maria Salatiello
María Magdalena Salcedo
Magdalena Salcedo
Maria Teresa Salcedo
Omar Saldarriaga
Natalia Saleev
Siamak Salehi
Ahmed Salhab
Faouzi Saliba
Kanita Salic
Henriët Salie
Daniel Salinas
José Antonio Salinas
Shadi Salloum
Sidra Salman
Veikko Salomaa
Federico Salomone
Angelo Salomone Megna
Romina Salpini

S1054 Journal of Hepatology 2022 vol. 77(S1) | S1021–S1064
Disclosures

Howard Sesso
Veronica Setiawan
Han Seul Ki
Vasillis Sevastianos
Joseph Sexton
Moussa Seydi
Orhan Seggin
Shaun Shadaker
Aladdin Shadyab
Eva Shagla
Mohammad Ali Shagran
Naina Shah
Vijay Shah
Hasnain A. Shah
Vijay Shah
Sital Shah
Syed Hassan Bin Usman Shah
Sabeen Shah
Dipam Shah
Wasuiddin Shah
Afshin Shahnazav
Sarah Shalaby
Shalimar
Amirhossein Shamsaddini
Dandan Shan
Ying Shang
Jia Shang
Dazhuang Shang
Eileen Shannon
Chen Shao
Shilpee Sharma
Nupur Sharma
Shvetank Sharma
Mithun Sharma
Sanctha Sharma
Eilon Sharon
Lali Sharvadze
Varsha Shasthry
S Muralikrishna Shasthry
Jawaid Shaw
David Shaw
Blake Shaw
Katy Shaw-Saliba
Shaoping She
Jessica Shearer
I-Shyan Sheen
Sabreena Sheikh
Louis Shekhtman
Yue Shen
Joanne X. Shen
Xinping Shen
Lu Shen
Joanne X. Shen
Liang Shen
Wei Shen
Jifang Sheng
Wu ShengDi
Liz Shepherd
David Sheridan
Morris Sherman
Somay Sheshadri
Abhishek Sheth
Kirti Shetty
Jun-Ping Shi
Liang Shi
Jianjuan Shi
Zhenzhen Shi
Shaojun Shi

Dongyan Shi
Xiaojun Shi
Lei Shi
Xiaojun Shi
Yu Shi
Oren Shibolet
Gamal Shiha
Sonjelle Shilton
Ju Hyun Shim
Wan Seob Shim
Toshihide Shimizu
Yuki Shimada
Masahito Shimizu
Norikazu Shimizu
Hyun Phil Shin
Jungwoo Shin
Rachel Shingaki-Wells
Harold Shlevin
Amir Shloimai
Saeed Shoaie
Pooya Shokoohi
Mohamed Shoreibah
michal Shoshkes-Carmel
Weinian Shou
Naglaa Shoukry
Shreesh Shrestha
Merica Shrestha
Eyal Shteayer
Po-Yeh Shu
Ruchi Shukla
Tengfei Si
Stefanie Sichelschmidt
Mohammad Siddiqui
hamda siddiqui
Cyril Sieberhan
Matthieu Siebert
Hartwig R. Sieber
Chloe Siegele-Brown
Martin Siegele-Brown
Armando Sierralta
Majken Siersbæk
William Sievert
Susan Siew
Alejandro Sifrim
Michael Sigal
Keith Sigel
Giordano Sigon
Rebeca Sigüenza
Bryndis Sigurdardottir
Masoumeh Sikaroodi
Emily Sileo
Marianna Siletta
Rachel Silk
Mario Jorge Silva
Rita de Cássia Martins Alves da Silva
Giovanni Silva
Hugo Silva
Eliane Silva
Fabio Silveira
Sharmaine Jia Ying Sim
Adelia Simao
André L. Simão
Alina Simonz
Francesca Simionato
Paolo Simioni
Rafael Simo Canonge
Guilherme Simões
Claudia Marquez Simões
Disclosures

Sara Stinson
Alexander Stockdale
Lena Stockhoff
Anna Stoelinga
Oana Stoica
Tatjana Stojakovic
Geurt Stokman
Janis M. Stoll
Andrew Stolz
Joanne Stone
Mark Stoooe
Gianfranca Stornaiuolo
Caterina Stornello
Alistair Story
Lisa Stothers
Alastair J Strain
Robin Strand
Christian Strassburg
Robert Strassl
Beate Straub
Maximilian Strauss
Richard Stravitz
David Streem
Adrian Streinu-Cercel
Lea Strelleer
Helena Stevens
Philipp Striedl
Philipp Ströbel
Karoline Strobl
Stefienn Strocka
Cezar Stroescu
Giacomo Stroffolini
Luisa J Ströh
Oskar Ström
Evangelia Stroumpouli
Benedikt Strunz
Eliana Stucchi
Ita.Li.Ca. Study Group
Ashley Stueck
Roberta Stupia
Nathalie Sturm
Lukas Sturm
Michael Stürzl
Ketevan Stvilia
Grace Su
Jie Su
Chuang-Mei Su
Wei-Wen Su
Ying-Hsiu Su
Emilio Suarez
Ruth Suarez Darias
Elisaau Suarez Zambrano
Mohsan Subhani
Miroslava Subic-Levero
Ram Subramanian
Robert Sucher
Andrea Sucks dorff
Abid Suddle
Aya Sugiyama
Masaya Sugiyama
Jeong II Sun
Kyung-Suk Sun
Sanggyun Sun
Wattana Sukeepaisarnjaroen
Jana Suklan
Sukriti Sukriti
Siriporn Sukswatamanuay
André Sulen
Stefan Sulk
Richard Sullivan
Laurent Sulpice
S Suman
Yoshiho Sumida
Donglin Sun
Haoyu Sun
Xiu Sun
Junfeng Sun
Huan Sun
Vinay Sundaram
Jeya Anice Sundararaj
Vijaya Sundararajan
Lidia Surace
Pallavi Surana
Julian Surey
Sophia Surguladze
Davies Susan
Norman Sussman
Nancy Sutter
Tania Suttichaimongkol
Gianluca Svegliati-Baroni
Jens Svenningsen
Leo Swadling
Kelly Swanson
Adam Syanda
Svenja Sydor
Wing-Kin Syn
Antonia Syriha
Silje S Syversen
Ferenc Szalay
Benedykt Szczepankiewicz
Thomas Szekeres
Jan-Willem Taanman
Daniela Tabacelva
Fehmi Tabak
David Tabernero
Ray Tabibiazar
Martina Taborelli
Fred Tabung
Stefano Tacconi
Vania Tacher
Stela Taci
Tamar Taddei
Tamar H Taddei
Linus Schwantes-An Tae-Hwi
Irgen Tafaj
Carmen G. Tag
Nikoletta Maria Tagkou
Yusri Taha
Yuki Tahata
Ehsaneh Taheri
Dean Tai
Chia-Hung Tai
Chi-Ming Tai
Chiara Taibi
Anne Tailleux
Falguni Tailor
Won Young Tak
Hyoseon Tak
Hitomi Takada
Hirokazu Takahashi
Kazuki Takahashi
Satoru Takahashi
Kenta Takaura
Yasuhiro Takikawa
Arslan Talat
Mats Talbäck
Thomas Talbot
Jantjie Taljaard
Anjan Jyoti Talukdar
Steve Yew-chong Tam
Joshua Tan
Nobuharu Tamaki
Dietmar Tamandl
Roberto Tambucci
Matthias Tammenga
Athena Tampaki
Jaclyn Yizhen Tan
Chee-Kiat Tan
Terence Tan
Huang Keat Tan
Hua Tan
Zhi Tan
Yong Chuan Tan
Ek Khoon Tan
Wei Lian Tan
Kenneth K. Tanabe
Atsushi Tanaka
Shohei Tanaka
Yasuhiro Tanaka
Junko Tanaka
Elena Tanashchuk
Francesco Tandoi
Puneeta Tandon
Manish Tandon
Puneeta Tandon
Sunil Taneja
Wei Tang
Liangjie Tang
Shanghong Tang
Xia-Han Tang
Liang-Jie Tang
Weiming Tang
An Tang
Jinglin Tang
Tianyu Tang
Pisit Tangkijvanich
Marion Tanguy
Kawin Tangvoraphonkhai
Xinxing Tantai
Lars Tanum
Yusha Tao
Graciela Tapia
Monica Tapias
Sambir Tarai
Giovanni Targher
Branden Tarlow
Sara Tarot
Yasmina Tashkent
Xhimi Tata
Kristi Tata
Ryosuke Tateishi
Tomohide Tatsumi
Jörg Täubel
Richard Taubert
Kojo Taura
Jan Tauwaldt
Ludgero Tavares
Alessandro Taovelli
Wei Xuan Tay
Yuh Ling Amy Tay
John Tayek
Ally Taylor
Guy Taylor
Simon Taylor-Robinson
Anna Thomas
Lutz Thomas
Sherin Sarah Thomas
Sherin Thomas
Rachel Thomas
Alexander Thompson
Laura Thompson
Clare Thompson
Hayley Thompson
Alexander Thompson
Helen Thompson-Jones
Karen Louise Thomsen
Douglas Thorburn
Marianna Thordardottir
Anders Thorell
Katrine Thorhauge
James Thorne
Claire Thorne
Karla Thornton
Zak Thornton
Karla Thornton
Georgia Threadgold
Paul J. Thuluvath
Christine Thumann
Prem Harichander Thuraisaj
Mark Thrusz
Anja Tiede
Matthieu Tihy
Patrick Tilleul
Dina Tiniakos
Lesley Tinker
Tom Tipton
Claudio Tiribelli
Kattleya Tirona
Esther Titos
Thais Tittanegro@gmail.com
Sarah Tizzard
Douglass Tjandra
E.T.L. Tjwa
Bryce Tkachuk
Deirdre Tobias
Tsuyoshi Todo
Daniel Todt
Manana Todua
Karin Toet
Flemming Tofteng
Yaman Tokat
Katsushi Tokunaga
Dagmar Tolenaars
Marieta Toma
Lidia Tomasello
Melissa Tomasi
Krzyztof Tomasiewicz
Giovanni Tomassoli
Santiago Tomé
Lukas Tometten
Sabine Tomez
Jeremy Tomlinson
James Tonascia
Steven YC Tong
Maria Manuela Tonini
Pierluigi Toniutto
Marta Tonon
Matilde Topa
Mark Topazian
Emilie Toresson Gripp
Andreas Törnell
Luis Toro
Nikolaj Torp
Miguel Torralba
Manuel Torralbo
Xavier Torras
Aldo Torre
Pietro Torre
Maria Torrens
Jason Torres
Ferran Torres
Joana Torres
Gloria Torres
Barbara Torres Guerola
Lilian Torres Made
Raffaella Tortora
Annalisa Tortora
Raffaella Tortora
Guido Torzilli
Giulia Tozetti
Christian Toso
Yann Touchefeu
Issam Tout
Dana Toy
Hidenori Toyoda
Nurdan Tozun
Giulia Tozzi
Despina Trafali
Samuel Trammell
David Trampert
Henri Tran
Sarah Tran
Steven Trasino
Julia Traub
Janina Trauth
Christian Trautwein
James traylor
Timothy Tree
Sombat Treeprasertsuk
Nirupma Trehanpati
Valentina Tremaroli
Giada Tria
Evangelos Triantafyllou
Adam Trickey
Anca Trifan
Pascale Trimoulet
Gaurav Tripathi
Dhiraj Tripathi
Gaurav Tripathi
Dinesh Mani Tripathi
Harshita Tripathi
Kartikaya Tripathi
Armando Tripodi
Martin Tripler
Parth Trivedi
Palak Trivedi
Roberto Ivan Troisi
Jacopo Troisi
Giancarlo Troncone
Matthias Trost
James F. Trotter
Francesca Maria Trovato
Francesca Trovato
Ming Chao Tsai
Yung-Ping Tsai
Yo-Yu Tsao
Philip Tsao
Keren Tsaraf
Yee-Kit Tse
Disclosures

Marc Zentar
Jasmin Zessner-Spitzenberg
Mujdat Zeybel
Murat Zeytunlu
Haoran Zhang
Luyong Zhang
Peng Zhang
Jiayuan Zhang
Xinlian Zhang
Yuwei Zhang
Guoqiang Zhang
Hongxu Zhang
Guofan Zhang
Ji-Yuan Zhang
Lihua Zhang
Saisai Zhang
Dengwei Zhang
Rui Zhang
Zhijun Zhang
Hong Zhang
Qin Zhang
Wen-hua Zhang
Bo Zhang
Hua Zhang
Shi-Jin Zhang
Shuwen Zhang
Xinrong Zhang
Hong Zhang
Lei Zhang
Ingrid Wei Zhang
Yong Zhang
Mingxin Zhang
Haoran Zhang
Luyong Zhang
RanRan Zhang
Ingrid Wei Zhang
Siyi Zhang
Wei Zhang
Yan Zhang
Wenjun Zhang
Wenhong Zhang
Jiming Zhang
Yangzi Zhang
Linzhi Zhang
Gaoli Zhang
Jiaxuan Zhang
Lukan Zhang
Xinrong Zhang
Xi Zhang
Lukan Zhang
Liting Zhang
Xian-Man Zhang
Dazhi Zhang
Shuang Zhang
Zhenfeng Zhang
Stephanie Zhang
Qingge Zhang
Liting Zhang
Guo Zhang
Shuangxia Zhang
Shuie Zhang
Xuehong Zhang
Bigeng Zhao
Wei-Guo Zhao
Xun Zhao
Lili Zhao
Qianwen Zhao
Derrick Zhao
Wenjuan Zhao
Xin Zhao
Jieling Zhao
Xiaoling Zhao
Longgang Zhao
Sergei Zhavoronok
Ming-Hua Zheng
Tian-lei Zheng
sujun Zheng
Huanwei Zheng
Tian-lei Zheng
sujun Zheng
Ming-Hua Zheng
Xin Zheng
Haoyang Zheng
Freeman Zheng
Quixian Zheng
Ming-Hua Zheng
Iris Zhorov
Jian Zhou
Yu-jie Zhou
Huiping Zhou
Taotao Zhou
Xue Zhou
Xingping Zhou
Dan Zhou
Xingping Zhou
Haoming Zhou
Shi-Yi Zhou
Xiqiao Zhou
Yi Zhou
Hongwei Zhou
Xin Zhou
Hongwei Zhou
Shijia Zhu
Xiaoxue Zhu
Yanfang Peipei Zhu
Yong-Fen Zhu
Shijia Zhu
Xiaoxue Zhu
Rui Zhu
Pei-Wu Zhu
Chuanwu Zhu
Li Zhu
Dedong Zhu
Chengqian Zhu
Dedong Zhu
Chengqian Zhu
Ping Zhu
Yunxia Zhu
Xiaodong Zhuang
Ekaterina Zhuravleva
Bogna Ziarikiewicz-Wróblewska
Mariana Ziatyee
Krzysztof Zieniewicz
Yuan Zihang
Michal Žiličan
Christine Zimmer
Sebastian Zimny
Gudula Zimper
Marianne Ziol
Alexander Zipprich
Hans Zischka
Konstantinos Zisimopoulos
Giovanni Zito
Milorad Zjalic
Maria Assunta Zocco
Katharina Zoldan
Caroline Zöllner
Dominik Züller
Elina Zorde-Khavlevsky
Antonio Zorzano
Guizhou Zou
Haixia Zou
Honore Zougmore
Ana Zubiaga
Jessica Zucman-Rossi
Maria A. Zulet
Delgersaikhan Zulkuhu
Paola Zuluaga
Javier Zulueta
Dariusz Zurawek
Coral Zurera
Karen Zwaenepoel
Denise Zwanziger
Aeillo Zwinderman
Isabelle Leclercq
Dessy Chantal
Sebastian Bott
Laurent Dumas
Evangelos-Panagiotis Daskalopoulos
Hrag Esfahani
The following abstract submitters have indicated that they have relationships with commercial entities that might be perceived as having a connection with their presentation:

Charles Aardema
Marta Abadia
Dalia Abdelhassab
Manal F. Abdelmalek
Dzhamal Abdurakhmanov
Fredrik Åberg
Armand Abergel
Kushala Abeysekera
Abhishek. Abhishek
Jean Louis Abitbol
Katie Abraham
Juan G Abraldes
Frida Abramov
Naim Abu-Freha
Oliver Ackaert
Christin Ackermann
Emily Acter
Vera Adamkova
Timo Adams
Nathalie Adda
Femi Adekunle
Olayinka Adisa
Timon Adolph
MaryVic Adona
Lannes Adrien
Jeroen Aerssens
Thomas Aeschbacher
Kosh Agarwal
Abhishek Aggarwal
Alessio Aghemo
Germaine D. Agollah
Vatche Agopian
Gifone Aguiar Rocha
Victoria Aguilera Sancho
Chukwuemeka Agwuocha
Arnon Aharon
Gustaf Ahlén
Håkan Ahlström
Alaa Ahmad
Mahmoud Ahmed
Nabeel Ahmed Maqbool
Sang Hoon Ahn
Sojin Ahn
Vijay Ahuja
Elmar Aigner
Melanie Aikebuse
Menachem Ailenberg
Guruprasad Aithal
Muhammad-Mujtaba Akanmu
Peter Akerblad
Fatih Akisik
Norio Akuta
Tamer Al Eraki
Afif Al Atra
David Al-Adra
Kishore Alagere Krishnamurthy
Antoine Alam
Matthew Albert
Dafne Alberti
Agustin Albitos
Wolfgang Albrecht
Thomas Albrecht
Estefania Alcaraz
Soo Alem
Leigh Alexander
Sarah Ali
Naim Alkhouri
Manon Allaire
Alina Allen
Samantha Allen
Michael Allison
Laura Almale del Barrio
Cristina Alonso
Marta Alonso-Peña
Laurent Alric
Gema Alvarez Nieto
Carmen Alvarez-Navascués
Domenico Alvaro
Carlos Alventosa Mateu
Yuichiro Amano
Adam Amaral
Philip Ambery
Naseem Amin
Javier Ampuero
Igor Anastasiy
Malena Anders
Birgitte Andersen
Jesper Andersen
Mark Anderson
Annelli Andersson
Anne-Christine Andréasson
Fausto Andreola
Pietro Andreone
Massimo Andreoni
Konstantina Andresaki
Carmen Andreu-Oller
Paolo Angeli
Yesseinia Anglero-Rodriguez
Piekarzka Anna
Quentin Anstee
Maja Antolic
Deana Antoniello
Masood Anwar
Myriam Aoudad
Katsumi Aoyagi
Douglas Applegate
Filipa Aragão
Manuela Arbune
Vijay Are
Vic Arendt
Andre Arizpe
Matthew Armstrong
Enara Arretxe
Yasuhiro Asahina
Mertxell Ascaino
Amir Ashique
Fred Askari
Patricia Aspichueta
Tarik Asselah
Alice Assinger
Christophe Aubé
Salvador Augustin
Daren Austin
Francisco Averhoff
Emma Avitabile
Mads Axelsen
Turgay Ayer
Oyekoya Ayonrinde
Walid S Ayoub
Sarah Ayton
Faroq Azam
Amy Azania
Karim Azer
James B Lorens
Henrik B. Hansen
Bert Baak
Fredrik Backhed
Ho S Bae
Si Hyun Bae
Adriano Baez-Ortega
Ru Bai
Jassoohan S Bajaj
Anna Bakardjiev
Barbara Bakker
Anu Balaji
Anand Balakrishnan
Sruthiyaa Balasubramanian
Alejandro Balbin
Kemal Balic
Scott Balsitis
David Baltimore
Jesus Maria Banales
Rafael Bañares
Rajarshi Banerjee
Marina Barcena-Varela
Stephen Barclay
Edouard Bardou-Jacquet
Malene Barfod O’Connell
Romain Barnault
Disclosures

Eleanor Barnes
Tamara Barnett
Ana Barreira
Thijs Barten
Sofia Bartlett
Mustafa Bashir
Ahmed Ba-Ssalamah
Melanie Bathon
Sara Battistella
David JM Bauer
Ulrich Baumann
Thomas Baumert
Vipul Baxi
Michel Bazinet
Andrew Beck
Svea Becker
Mark Becker
Sonja Beckmann
Philipp Bedard
Pierre Bedossa
Alex Befeler
Danny Bega
Elke Behaeghel
Cynthia Behling
Leonid Beigelman
Claudia Beisel
Pierre Bel Lassen
Mehdi Belkhodja
Mattia Bellan
Francesco Bellanti
Najib Ben Khaled
Elias Benabadji
Leda Bencheva
Flemming Bendsen
William Bernal
Merav Ben-Yehoyada
Christian Benzing
Rudolf Beran
Michael D. Bereket
Marina Berenguer
Thomas Berg
Christoph Berg
Ellen Berg
Irina Bergamin
Mattias Bargentall
Annika Bergquist
Tatiana Bering Bering
William Bernal
Mauro Bernardi
Barbara Bernardo
Antonio Beretoletti
Juliette Besombes
Dominik Bettinger
Maria Beumont-Mauviel
Cayden Beyer
Simon Beyer
Jorge Bezerra
Abhi Bhagat
Shrijad Bhagwat
Bal Raj Bhandari
Punam Bharania
Ilaria Biancacci
Vadim Bichko
Charles Biddle-Snead
Manuela Bieri
Michael Biermer
Joanna Bilak
Griffiths Bill
Andrew Billin
Marc Bilodeau
Julien Bissonnette
Niklas Björkström
Sarah Blach
Jean-Frédéric Blanc
Charlotte Blanc
Antje Blank
Lawrence Blatt
Bruce Blazar
Alfonso Blázquez-Moreno
Rob Blissett
Magnus Bötz
Sami Blom
Patricia Bloom
David Blue, Jr
Qingyan Bo
Hans Bock
Ravan Boddu
Jayasl Bodhani
Caroline Boeke
Klaus Boeker
Alina Bogdanov
Carri Boiselle
Jörg Bojunga
Selin Bolca
Galina Boldina
Jacques Bollékins
Ralf Bollhagen
James Bolognese
Maurizio Bonacini
Machao Bonafede
Ferruccio Bonino
Herbert L Bonkovsky
Britta Bonn
Odile Bonnin
Andre Boonstra
Brian Borg
Sergio Borgia
Salvador Borrós
Triijnie Bos
Jaime Bosch
Martina Bosnar
Mohamed Bouattour
Sihem Bouadina
Stéphane Bouée
Stéphane Bouët
Thomas Bouquin
Stefan Bourgeois
Marc Bourliere
Jerome Boursier
Karim Bouzakri
Christopher Bowlus
Adam Boyd
Kelli Boyd
Kaan Boztug
Chiara Braconi
John Michael Brady
J Michael Brady
Emre Brady
Sylvia Brakenhoff
Clifford Brass
Marius Braun
David Breckinridge
Dominique Brees
Birgit Bremer
Natalia Breynner
Francois Briand
Paul Brinkman
Christian Briëkko
Jens Brodbeck
Jan Christian Brønd
Jean-Pierre Bronowicki
Craig Brooks-Rooney
Pierre Broqua
M. Julia Brosnan
Kenneth Brown
Joanne Brown
Robert Brown
Elizabeth Brown
Sarah Bowne
Jonathan Frederik Brozat
Jordi Bruix
Helmut Brunar
Maurizia Brunetto
Tony Bruns
Ksenia Brusilovskaya
Hrvoje Brzica
Arno Bucker
Grant Budas
Peter Buggisch
Elisabetta Bugianesi
Sherry Bullens
Stuart Bunting
Xabier Buque
Vinod Burade
Dara Burdette
Christophe Bureau
Lucas Burghart
Michela Emma Burlone
Rani Burm
Patrizia Burra
Sue Burrell
Maria Buti
Bryony Butler
Marcus Butler
Isabel Butrymowicz
Giuseppe Cabibbo
Edward Cable
Valle Cadahía-Rodrigo
Jean-François David Cadranel
Dachuan Cai
Stephen Gedwell
Paul Cales
Carlemi Calitz
Roberto Calle
José Luis Calleja Panero
Alberto Calleri
Vincenzo Calvaruso
Calogero Camma
Francesca Campanale
Fiona Campbell
Stephanie Campbell
Eda Canales
Harriet Cant
Helena Cantero
Shengtian Cao
Maria Domenica Cappellini
Paolo Caraceni
Valentina Carapella
Lorena Carballo-Folgoso
Marco Carbone
Michael Carleton
Michal Carmiel
Disclosures

Getachew Debas Belew
José Debes
Martin Decaris
Elisabetta Degasperi
Oliver Degerstedt
Luca Degli Esposti
Clayton Dehn
Arnaud Del Bello
Jared Delhaye
William Delaney
Philippe Delatour
Oliver Dillen
Jonas Demant
Münevver Demir
Guohong Deng
Douglas Denham
Gerald Denk
Andrea Dennis
Alex DePaoli
Laura D’Erasmo
Supriya Desai
Todd Z. DeSantis
Marc Deschenes
Katia Deterding
Sylvie Deuffic-Burban
krishnadas devadas
Jerome Deval
Carole Devaux
Sebastien Dharancy
Tony Dhillon
Romano Di Fabio
Tommaso Di Maira
Vito Di Marco
Francesca Di Stasi
Moises Diago
Álvaro Díaz-González
Francisco Diaz-Mitoma
Amy Dickey
Christopher Dickman
Michel Didier
Lauri Diehl
Douglas T Dieterich
John Dillon
Dessislava Dimitrova
Amreen Dinani
Dora Ding
Yanhua Ding
Luciana Dini
Luciana Diniz Silva
Vanessa Ditt
Bharat Dixit
Emmanuel Dauda Dixon
Son Do
Stephen Dodge
Sowjanya Dokku
Leona Dold
Lourdes Dominguez
Raquel Domínguez-Hernández
Gregory Donadio
Hélène Donnadieu-Rigole
Claire Donoghue
Gregory Dore
Lucy Dorrell
Kate Dorrington
Michael Doukas
Joseph Doyle
Michael Drage
vera dreizin
J.P.H. Drenth
Sandra Droese
Shunda Du
Shuyan Du
Andres Duarte Rojo
Ravi Dugvala
Jacques Dumas
Aurore Dumond
Jérôme Dumortier
James Duncan
Julien Dupin
David Durante
Geoffrey Dusheiko
Lea Duwe
Athena Dworakowski
Doug Dylla
Jessica Dyson
Lucile Dzen
Richard E Prattley
Matthias Ebert
Julien Edeline
Elazer Edelman
Hannah Edenbaum
Lindsey A Edwards
Erika Egal
Richard L. Ehman
Ursula Ehmer
Beate Eichelberger
Nicole Eichert
Petros Eiladiis
Mona El Awady
Ioannis Eleftheriou
Timothy Eley
Magdy Elkhoshab
Laure Elkrief
Emad El-Omar
Ahmed Elsharkawy
Robert Elston
Birol Emir
Grupo del Registro Col-Hai Enfermedades autoinmunes y colestásicas
Bastian Engel
AAron Engel
Hans-Peter Erasmus
Lauren Erdman
Trépo Eric
Olaf Eriksson
Megan Ermpler
Hannah Esser
Whitney Essex
Rafael Esteban
Roger Esteban-Fabró
Chris Estes
Ohad Etzion
Tom Evans
Kimberley Evasion
Greg Everson
Ondrej Fabian
Stefano FAGIOLI
Christine Falk
Kitt Falk Petersen
Jonathan Fallowfield
Kristi Fan
Daiming Fan
Fabrizio Fanelli
Marie C. Fanget
Hooman Farhang Zangneh
Marti Färkkilä
Ronald Farquhar
Brian Faegan
Molly Feder
Denise Federico
Becket Feierbach
Michael Feigh
Leighland Feinman
Jeanette Feizi
Jordan Feld
Vicente Felipo
Shibao Feng
Daphna Feyyes
Beatrice Bois De Fer
Peter Ferenci
Guillermo Fernández Varo
Isabel Fernández-Lizaranzu
Giovanna Ferriani
Pasquale Ferraro
Carlos Ferreira
Sofía Ferreira-Gonzalez
Philip Ferstl
James Fettplace
Friedrich Feuerhake
Bart Ferey
Katia Fiaschetti
Marco Fidalgo
Isaac Finberg
Peter Finkelman
Fabian Finkelmeier
Sarah Finnegan
Jesse Fishman
Megan Fitzgerald
John F. Flaherty
Simon Fletcher
Robert Flisak
Amarasara Floreani
Friedrich Foerster
Pelagia Foka
Erica Fong
Sylvia Fong
Helene Fontaine
Mariana Fontana
Corinne Foo-Atkins
Stuart Forbes
Alejandro Forner
Xavier Forns
Aino Forsten
Robert Foster
Eriin Foster
Robert Foster
Graham Foster
John Foster
Robert Foster
Fayssoil Fouad
Slim Fournier
Céline Fournier
Claire Fournier
Céline Fournier
Kathryn Fowler
Miguel Fraile
Sven Francque
Sona Frankova
Chris Fraser
R. Todd Frederick
Peder Frederiksen
Alice Freer
Bradley Freilich
Lars Frelin
Disclosures
Disclosures

Bettina Hansen
Scott Hansen
Christina Hanson
Shaorui Hao
Olaf Harth
M. Scott Harris
Stephen Harrison
Lukas Hartl
Tarek Hassanein
Ziad Hassoun
Kelly Haston
Angelos Hatzakis
Anna Hauptmann
Liat Hayardeny
Jennifer Hayden
Peter Hayes
Kelly Hayward
Brendan Healy
Christy Hebner
Christina Heeke
Gavin Heffernan
Johannes Kolja Hegel
Brian Heglar
Zeev Heimanson
Femke Heindryckx
Margaret Hellard
Steve Helmk
Louise Henderson
Julie Henderson
Michael Heneghan
Mark Henkemeyer
Jim Hennan
Roland Henrar
Eugenia Henry
Jeong Heo
German Hepatitis C-Registry
Julian Hercunc
Pernille Hermann
Heike Hermanns
Candido Hernández
Manuel Hernández Guerra
Virginia Hernandez-Gea
Kerstin Heurling
Helen Heymann
Matthew Hickman
Lindsey Hibert
Hayato Hikita
Karl Hillebrandt
Jan Hinrichs
Andreas Hintz
Gideon Hirschfield
Sara Toftegaard Hjuler
Gideon Ho
Erwin Ho
Khanh Hoang
Todd Hobbs
Paul Hockings
Linn Hodneland
Lisa Hoelting
Christoph Hoener zu Siederissen
Benedikt Hofer
Sara Hoffman
Charlotte Hoffmann
Alexander Hofmann
Sarah Hofmann
Wolf Peter Hofmann
Malcolm Hogan
Kurt Højlund
Meghan Holdorf
Adriaan C. Holleboom
David Hollenback
Julius Hollnberger
Dan Holmberg
Ben Holmes
Curtis Holt
Taus Holtug
Jin Hong
Kristian Honnens de Lichtenberg
Adelina Horhat
Patrick Horn
Maria Hörnberg
Patrick Horne
Stephen Horrigan
Raquel Horrillo
Nigel Horscroft
Thomas Horvatits
Yujin Hoshida
Moigan Hosseini
Jinlin HOU
Inbal Houri
Michael House
Anne Hout
Johannes R. Hov
Rob Howard
Laura Howe
Yao-Chun Hsu
Heather Hsu
J-X Huang
Yan Huang
Daniel Huang
Chung-Feng Huang
Yi-Hsiang Huang
Chung-Feng Huang
Jee-Fu Huang
Genevieve Huard
Jaroslav A. Hubacek
Yvonne Huber
Samuel Huber
Sanne Hulsps
Dean Hum
Philip Hunt
Philippe Huot-Marchand
Dietrich Hüppe
Ryan Huss
Tanweer Hussain
Sharon Hutchinson
Simon Hutter
Carey Hwang
Seong Gyu Hwang
Anastasia Hyrina
Marco Iafolla
Matteo Iannacone
P Ibrahim
Adam Igloi-Nagy
Arfan Ikram
Kamran Ikram
Hasan Imam
Giuseppe Indolfi
Patrick Ingiliz
Takako Inoue
Jun Inoue
Pietro Invernizzi
Christina Iqbal
Shahed Iqbal
Marta Iruarrizaga-Lejarreta
William Irving
Gemma Iserse
Yuji Ishida
Mohamed Ismail
Robert Israel
Yoshito Itoh
Timo Itzel
Tommy Ivanics
Elena Ivanova
Sowmya Iyengar
Janani Iyer
Namiki Izumi
Alan Jaap
Mathias Jachs
Akil Jackson
Ira M Jacobson
Emmanuel Jacquemin
Vasant Jadhav
Jørgen Jahnk
Vipul Jairath
Ruchika Jaiswahani
Rajiv Jalan
Reza Jalili
Joyce James
Khurram Jamil
Ewa Janczewska
Arun Jandor
Maria João Janeiro
Se Young Jang
Naveed Janju
Giulia Jannone
Harry Janzen
Harry LA Jansen
Ronald Janzen
Maximilian Jara
Jerzy Jaroszewicz
Arjun Jayaswal
Fahnaz Jazaeri
Makuza Jean Damascene
Andreas Jekle
Robert Jenders
Rachel Wen-Juei Jeng
Craig Jenne
Dahn Jeong
Nakcheol Jeong
Mirjana Jerkic
Lutz Jermutus
John Jerzorwski
Arun Jesudian
Kartik Jhaveri
Fanpu Ji
Linong Ji
Ji-Dong Jia
Li Jian
Jing Jiang
Li Jiang
Lijuan Jiang
Li Jie
Wladimiro Jiménez
Elena Jimenez Mutiloa
Maria Jimenez Ramos
Feng Jin
Milan Jirska
Quinian Johanson
Lars Johansson
Edvin Johansson
Katharina John
Binu John
Disclosures

Christopher Jones
David Jones
Catherine Jones
Andrew Jones
Heidi Jones
Kelsey Jordan
William Jordan
Kristin Jorgensen
Juan Jose Perez Ruixo
Zhang Juan
Alina Jucov
Perinlle Juhl
Gillmore Julian
Tom Jun
Birgit Jung
Eun Sun Jung
Jean-Louis Junien
Marzena Jurek
Meriam Kabbaj
Kajetan Kubat
Nandita Kachru
Mohammad Kadivar
Shaui Kadosh
Apichat Kaeawdech
Thomas Kakuda
George Kalamitsis
Nina Kallin
Ronald Kalmeijer
Jibrin Kama
Severin Donald Kamdem
C.Omar Kamlin
Tania Kamphaus
Atsushi Kaneko
Shuichi Kaneko
Don Kang
Ramesh Kangarajan
Aimo Kannt
Tatsuya Kanto
Jia-Horng Kao
David Kaplan
Leonard Kaps
Theofanis Karaletos
Eirini Karamichali
Chitira Karki
Saui J. Karpen
Morten Karsdal
Nikolaos Kartalis
Nino Katchiuri
Lorn Kategaya
Naoya Kato
Sarah Kattakuzhy
Goutham Reddy Katukuri
Helena Katzman
Stefan Guntther Kauschke
Ankita Kaushik
Maryam Kavousi
Norifumi Kawada
Matt Kelly
Deirdre Kelly
Scott Kelly
George Kemble
Bradley Kendall
Tim Kendall
Stuart Kendrick
Patrick Kennedy
Carla Kettler
Cassandra Key
Shameer Khader
Jaafar Khaled
Faisal Khan
Tanweer Khan
Tipu Khan
Ambreen Khan
Saifuddin Kharawala
Aditya Khosla
Kamlesh Khunti
Steven Kiddle
Alexander Killer
Alastair Kilpatrick
Jae Heon Kim
Hyun Jung Kim
Meel Kim
Yoon Jun Kim
Won Kim
W. Ray Kim
Benjamin Kim
Kyung Mo Kim
Jung-Hee Kim
Ryou Ho Kim
Chang Min Kim
Yele King
Kathryn K M Kitrinos
Ligia Akemi Kiyuna
Mette Kjaer
Maria Kjergaard
Lise Kjems
Hartwig Klinker
Markus Klinkicht
Kevin Klucher
Heinz Josef Klumpen
Maximilian Knapp
Cornelis Knetsch
Percy A. Knolle
Steven J Knox
Andreas Dehlbæk Knudsen
Hin Hln K
Jossy George Kochuparampil
Takahiro Kodama
Jan Köhler
Anita Kohli
Daphne Koller
Loreta Kondili
Philipp Königshofer
Dennis Koob
Maria Kopsida
Miroslaw Kornek
Konstantin Koro
Ioannis-Georgios Koskinas
Radina Kostadinova
Cory Kostrub
Kris Kowdley
Kris V. Kowdley
Kris Kowdley
Aleksander Krag
Filip Krag Knop
Johanne Kragh Hansen
Mel Krajden
Niels Krapup
Marcin Krawczyk
Wolfgang Maximilian Kremer
Andreas E Kremers
Felix Krenzien
Vijayanthi Krishnan
Konstantin Kroniger
Carrot Kruse
Simon Krzysztof
Iwona Ksiazek
Reinhard Kubale
Masatoshi Kudo
Patrizia Kuengler
Mary Kuhns
Folkert Kuipers
Santosh Kulkarni
Anand Kulkarni
Joel Kullberg
Parag Kumar
Ravi Kumar
Sonal Kumar
Yong-Fang Kuo
Masayuki Kurosaki
Tatyana Kushner
David Kuter
Manik Kuvalekar
Martin Kveton
Paul Vienu Kw
Christian Labenz
Eternity Labio
Florence Lalcaill
Alain Lachaux
Olivier Lada
Hermann Laferl
Juan Lafuente-Barquero
Felix Lai
Jennifer Lai
Gerond Lake-Bakaar
Wim Laiemam
Jacob P Lalezari
Angela Lam
Angela Lamarca
Tom Lambechh
Twan Lammers
Frank Lammert
Pietro Lampertico
Tian Lan
Tina Landsvig Berentzen
Marcia Lange
Christian M. Lange
Miriam Langelaar
Taro Langner
Dominique Larrey
Guillaume Lassailly
Audrey H. Lau
Daryl Lau
Chi Lau
Stefan Laufur
Caroline Laurendeau
Volker Lauschke
Juliette Lavaux
Matthew Law
Adelayo Lawal
Eric Lawitz
Jeffrey Lazarus
Patrice Lazure
Kha Le
Quang Le
Bertrand Lebouche
David Lebwohl
Chee Seng Lee
Lois Lee
Yun Bin Lee
Jeong-Hoon Lee
Yeongju Lee
Samuel Lee
Soon Kyu Lee

Journal of Hepatology 2022 vol. 77(S1) | S1065–S1079  S1071
Disclosures

Dong Ho Lee
Misun Lee
Justin Lee
Gil Won Lee
Sanghyeok Lee
Jina Lee
Alicia Lee
Diana Leening
Ann Leen
Eric Lefebvre
Sander Leferre
Vanessa Legry
Rory Leisengang
Martin Leivers
Frédéric Lemaigre
Maud Lemoine
Florian Lempp
Hans Lennernas
Sabela Lens
Oliver Lenz
Alvin Leong
Stefano Leporatti
Jack Leslie
Paul Lessenich
Will Lester
Cynthia Levy
Itzchak Levy
Sharon Levy
Jing Li
Ruidong Li
Li Li
Yizhao Li
Hai Li
Ming Li
Hai Li
Wei Li
Jun Li
Hongming Li
Qian Li
Tan Li
Lewyn Li
Tao Liang
Xi Liang
Yun-Fan Liaw
Stephanie Liebig
Hsiao Lieu
Young-Suk Lim
Seng Gee Lim
Young-Suk Lim
Joseph Lim
Tse-I Lin
Jaw-Town Lin
Chuan-Hao Lin
MingDe Lin
Katherine E. Lindblad
Anna Lindblom
Kajsa Lind
Daniel Lind
Björn Lindkvist
Erik Lindström
Lei Ling
Mattias Lissing
Yang Liu
Shangbin Liu
Weijian Liu
Jiemic Liu
Yang Liu
Peidi Liu
Yang Liu
Tian Liu
Yan Liu
Boya Liu
Jing Liu
Cheng Liu
Yen-Chun Liu
Wenhu Liu
Yunpeng Liu
Su Liu
Yang Liu
Yen-Chun Liu
Neus Llarch
Jose Luis Lledó
Ana Lleo
Josep M. Llovet
Andrew Lloyd
Emily Lloyd
Andrew Lloyd
Jonathan Lloyd
Stephen Locarnini
Khalida Ann Lockman
Mark Lockwood
Juergen Loeffler
Alessandro Loglio
David Lomas
Stephen Lombardelli
Sara Lonardi
María Carlota Londoño
Edward Long
Jiang Long
Thomas Longerich
Louise Longworth
Isabelle Lonjon-Domanec
Ida Lønsmann Lønsmann
Rohit Loomba
Katharina Malinowsky
Maryse Malysiak
Kwan Man
Prasad Manchem
Mittias Mandorfer
Alessandra Mangia
Komal Kant Mangla
Savrina Manhas
Nagraj Mani
Derek A Mann
Jelena Mann
Derek A Mann
Michael P. Manns
Spilios Manolakopoulos
Hank Mannshoek
Dmitry Manuilov
Antonio Manzur
John Mao
Panagiota Maravelia
Julian Marchesi
John Marcinak
Christelle Marcou
Maya Margalit
Silke Marhenke
Montserrat Marí
Rui Marinho
Zoe Marinho
Ed G. Marins
Jonathon Marioneaux
Christelle Marcou
Maria Carlota Londoño
Edward Long
John Mao
Panagiota Maravelia
Julian Marchesi
John Marcinak
Christelle Marcou
Maya Margalit
Silke Marhenke
Montserrat Marí
Rui Marinho
Zoe Marinho
Ed G. Marins
Jonathon Marioneaux
Jessica Markby
denis marleau
Tonya Marmon
Xavier Marniquet
Christine Marotta
Laura Marquez Perez
Fabio Marra
Mark Ma
Shenglin Ma
Benjamin Maasoumy
Leigh MacConell
Graeme Macdonald
Kelli MacDonald
Guilherme Macedo
Rocío IR Macias
Cara L. Mack
Donald Mackenzie
Alison MacKinnon
Iain Macpherson
Kairat Madin
David Madoff
Andreas Nygaard Madsen
Mindy Magee
Anna Mageras
Sanjiv Mahadeva
Sangeetha Mahadevan
Anadi Mahajan
Tobias Maharaj
Chinthaka Mahesh Udamulle Gedara
Hassan Mahmood
Nadim Mahmud
Jiajia Mai
Mala Maini
Michael Maitland
Ozren Majstorović
Sara Malcús
Elizabeth Malecha
Harmeet Malhi
Deepa Malhotra
Mark Ma
Tian Liu
Yan Liu
Boya Liu
Jing Liu
Cheng Liu
Yen-Chun Liu
Wenhu Liu
Jiemic Liu
Yang Liu
Tian Liu
Yan Liu
Boya Liu
Jing Liu
Cheng Liu
Yen-Chun Liu
Wenhu Liu
Yunpeng Liu
Su Liu
Ye Liu
Ye Liu
Yen-Chun Liu
Neus Llarch
Jose Luis Lledó
Ana Lleo
Josep M. Llovet
Andrew Lloyd
Emily Lloyd
Andrew Lloyd
Jonathan Lloyd
Stephen Locarnini
Khalida Ann Lockman
Mark Lockwood
Juergen Loeffer
Alessandro Loglio
David Lomas
Stephen Lombardelli
Sara Lonardi
María Carlota Londoño
Edward Long
Jiang Long
Thomas Longerich
Louise Longworth
Isabelle Lonjon-Domanec
Ida Lønsmann Lønsmann
Rohit Loomba
Katharina Malinowsky
Maryse Malysiak
Kwan Man
Prasad Manchem
Mattias Mandorfer
Alessandra Mangia
Komal Kant Mangla
Savrina Manhas
Nagraj Mani
Derek A Mann
Jelena Mann
Derek A Mann
Michael P. Manns
Spilios Manolakopoulos
Hank Mannshoek
Dmitry Manuilov
Antonio Manzur
John Mao
Panagiota Maravelia
Julian Marchesi
John Marcinak
Christelle Marcou
Maya Margalit
Silke Marhenke
Montserrat Marí
Rui Marinho
Zoe Marinho
Ed G. Marins
Jonathon Marioneaux
Jessica Markby
denis marleau
Tonya Marmon
Xavier Marniquet
Christine Marotta
Laura Marquez Perez
Fabio Marra
K. Tao Pun
Massimo Puoti
Lisa A. Purcell
Antonella Putignano
Nikolaos T. Pyrsopoulos
Yuquan Qian
Lei Qin
Hisam Qosa
Xiujuan Qu
Dongmei Quan
Geoff Quinn
Huma Qureshi
Zuzana Rabekova
Pascaline Rabiega
Liane Rabinowich
Pierre Raboisson
Daniel Rader
Andrew Radley
Pompilia Radu
David Rafei-Shamsabadi
Shaimaa Ragab
Syedia Rahman
Maruthi Raja
Ravi Rajagopalan
Vivek Rajwanshi
Prakash Ramachandran
Rakesh Raman
Ricardo Ramirez
Alnoor Ramji
Savita Rangarajan
Navpreet Ranu
Joanna Raszeja-Wyszomirska
Vlad Ratziu
Monika Rau
Pierre-Emmanuel Rautou
Micol Rava
Natarajan Ravendran
Avijit Ray
Homie Razavi
Devin Razavi-Shearer
Kathryn Razavi-Shearer
Christopher Recknor
Nageshwar Reddy
Gili Regev
Helen Regnault
Thomas Reiberger
Maria Reig
Dag Henrik Reikvam
Tanja Reineke-Plaaß
Florian P Reiter
Kristina Reksyte-Matiene
André-Jean Remy
Kaili Ren
keke ren
Hong Ren
Yayun Ren
Murray Resnick
Peter Revill
Archie C. Reyes
Tadeja Rezen
Christopher Rhodes
Carlota Riba
Andrea Ribeiro
Rasmus Ribel-Madsen
Anna Richards
Holly Richardson
Armin Rieger
Elena Riester
Cristina Rigamonti
Lorenza Rimassa
Jordi Rimola
Anthony Rinaldi
Mercedes Rincón
Mary Rinella
Cristina Ripoll
Jen Rito
Timothy Ritter
Mar Riveiro Barciela
Giuliano Rizzardini
Scot Roberts
Lewis Roberts
John Robertson
Darren Robertson
Adriana Rocca-Fernandez
Michael Roden
Christoph Roderburg
Kyle Rodney
Christophe Rodriguez
Manuel Rodriguez
Miguel Ángel Rodríguez Sagrado
Tamara Rodriguez-Castaneda
Manuel Rodríguez-Perálvarez
Sergio Rodriguez-Tajes
Angela Rojas Alvarez-Ossorio
Benjamin Rolland
Tim Rolph
Renato Romagnoli
Krista Rombouts
Manuel Romero Gomez
Martin Renn Madsen
Maxime Ronot
James Roper
Manuel Roqueta-Rivera
Silvia Rosati
Valerio Rosato
Jenny Rosenquist
Elana Rosenthal
Philip Rosenthal
Trenton Ross
Jean-Francois Rossignol
Celine Rossignol
Françoise Roudot-Thoraval
Dominique Roulot
Mackenzie Rowe
Ian Rowe
Nichola Royal
Damjana Rozman
Peter Ruane
Aileen Rubio
Luong Ruiz
Isaac Ruiz
Maria Grazia Rumi
Valgerdur Runarsdottir
Jana Rupp
Matthew Russell
Chris Russell
Francesco Paolo Russo
Vinod Rustgi
Erica Rutherford
Guy Rutter
Pablo Ryan
John Ryan
Anna Saborowski
Jonah Sacha
Hesham Sadek
Shakhllo Sadirova
Kourosh Saeb-Parsy
Diego Saenz de Urturi
Olga Sagalova
Brad Saget
Ebada Said
Andreas Sailer
Ryotaro Sakamori
Magdalena Salcedo
Matti Sällberg
Romina Salpini
Ayan Samanta
Anthony Samir
Demetrious N. Samonakis
Sumeyye Samur
Javier San Martin
Jose Sanchez
Katarzyna Sanchez
Rubén Sánchez-Aldehuelo
Lisa Sandmann
Louis Sandra
Marco Sanduzzi Zamparelli
Bruno Sangro
Jessica Santana
Armando Santoro
Sandra Santos
Alvaro Santos-Laso
Arun Sanyal
Gonzalo Sapisochin
Margherita Saracco
Samantha Sarognato
Souvik Sarkar
Christoph Sarrazin
Janeli Sarv
Santhosh Satapati
Romil Saxena
Katia Sayaf
Pietro Scaffaro
Ute Schaepker
Martina Scharitzer
Hubert Scharnagl
Jörn Schattenberg
Johanna Schaub
Bernhard Scheiner
Stacey Scherbakovsky
Eugene R. Schiffr
Michael Schilsky
Franklin Schlerman
Thomas Schlupe
Moritz Schmelzle
Michael A. Schmid
Ingo G. Schmidt-Wolf
Bernd Schnabl
Stephan M Schneeweiß
Carolin Victoria Schneider
Kai Markus Schneider
Guenther Schneider
David Schoeler
Katrin Schöneweis
Jeffrey Schouten
Philipp Schuetz
Martin Schulz
Julian Schulze zur Wiesch
Dietlef Schuppan
Andrew Schwab
Christian Schwabe
Philipp Schwabl
Disclosures

Xiaohong Wang  
xiao-hao Wang  
Bing Wang  
Hee Jung Wang  
Guoqiang Wang  
Bin Wang  
Ilan Wapinski  
John Ward  
Suzan Warner  
Matthew Warr  
Elaine Watkins  
Tim Watkins  
Hugh Watson  
Michiel Weber  
Sabine Weber  
Heiner Wedemeyer  
Yishuang Wei  
Frank Weilert  
Ilan Wapinski  
John Ward  
Suzan Warner  
Matthew Warr  
Michelle Weber  
Nina Weis  
Ilan Weisberg  
Carl Heinz Weiss  
Markus Weissbach  
Karin Weissenborn  
Lisa Weissfeld  
Bo Wen  
Charlotte Wernberg  
Christopher Westland  
Jochen Wettengel  
Victoria Wharton  
Kristen Wheeden  
Darren Wheeler  
Nicole White  
Thomas Wiersma  
Signe Wiese  
Philippe Wiesel  
Bernard Willems  
Philippe Willems  
Jorke Willemse  
Caroline Williams  
Catherine Williamson  
Todd Willis  
Arnulf Willms  
Wendy Winckler  
Karim Wisserkinchen  
Magdalena Witschi  
Jennifer Witt  
Melanie Wittner  
Owens Wiwa  
Maciej Wójcicki  
Armin Wolf  
Danny Ka-Ho Wong  
C Wong  
Robert Wong  
Steven Wong  
Simon Wong  
Robert Wong  
Vincent Wai-Sun Wong  
Grace Lai-Hung Wong  
Danny Ka-Ho Wong  
Alexander Wong  
Robert Wong  
Yu Jun Wong  
David Wong  
Darren Wong  
Grace Wong  
Wing Yen Wong  
Kristy Wood  
Jinny Woolgar  
Xavier Woot de Trixhe  
Thomas Wollard  
David Wraith  
Min Wu  
Wenqiang Wu  
Jinzi Wu  
Xiaoqin Wu  
Tongfei Wu  
Wei Wu  
Tiffany Wu  
Tianzhuo Wu  
Jamie Wu  
Torsten Wuestefeld  
Jay Wustner  
Verheist Xavier  
Ningshao Xia  
Tian Xiao  
Yao Xie  
Qing Xie  
Lin Xie  
Jiaoqiao Xin  
Shaojie Xin  
Cheng-jian Xu  
Simin Xu  
Jianfeng Xu  
Simin Xu  
Yuaxin Xu  
Jun Xu  
Qingqing Xu  
Deming Xu  
Zenghui Xue  
Kitty Yale  
Leo Yamamoto  
Ran Yan  
Yuemei Yan  
Wen Hao Yan  
Ju Dong Yang  
Qiang Yang  
Yongping Yang  
Xinye Yang  
Hwai-l Yang  
Yuan Yang  
Genren Yang  
Junlin Yang  
Heng Yao  
David Yardeni  
Hiroaki Yashiro  
Bridget Yates  
Hiroshi Yatsuhashi  
Tahmíneh Yazdí  
Lei Ye  
Leland Yee  
Alon Yehoshua  
Yee Hui Yeo  
Jian Yeo  
Min Yi  
Hyung Joon Yim  
Terry Cheuk-Fung Yip  
Masato Yoneda  
Zhao Yongliang  
Jeongin Yoo  
Jung-Hwan Yoon  
Hitoshi Yoshiji  
Shaoli You  
Shihyun You  
Ramy Younes  
Ziad H. Younes  
Ramy Younes  
Liam Young  
Vincent B. Young  
Zohair Younossi  
Amir Youssef  
W Yu  
Zhou Yu  
Qifeng Yu  
Meng Yu  
Ming-Lung Yu  
Yun Suk Yu  
Yuan Yuan  
Zheng Yubo  
Man-Fung Yuen  
Carla Yunis  
Cihan Yurdageldi  
Aziz Zaanan  
Giacomo Zacherini  
Syeda Zahida Sarwar  
Ane Zamballo  
Floriana Zanderigo  
Alberto Zanetto  
Alexandra Zanin-Zhorov  
Illaria Zanotto  
Dorota Zarębska-Michaluk  
Anna Zehnder  
Lars Zender  
Ni Zeng  
Alithia Zetter  
Fredrick Zetterberg  
Stefan Zeuzem  
Jiping Zha  
Guofang Zhang  
Yong-Yuan Zhang  
Tai-Hua Zhang  
Yi Zhang  
Dong Zhang  
Qingling Zhang  
Ningning Zhang  
Xiaodong Zhang  
Jiliang Zhang  
Mengnan Zhang  
Yingjun Zhang  
Haiting Zhang  
Linwen Zhang  
Ke Zhang  
Wen Zhang  
Yuchen Zhang  
Hong Zhang  
Dong Zhang  
George Zhang  
Yanhua Zhang  
Qingling Zhang  
Yibo Zhang  
Jun Zhang  
Lening Zhang  
Hua Feng Zhang  
Xuchen Zhang  
Shu Zhang  
Caroline Zhao  
Jiang Zhigan  
Jingye Zhou  
Yuanping Zhou  
Linghua Zhou  
Kali Zhou  
Yuhong Zhou  
Qian Zhou  
Julie Zhu  
Qianru Zhu
We express our deepest appreciation to the following people, who have given us generous and invaluable help as abstract reviewers for the ILC 2022.

Abdelmalek Manal
Adams Leon
Alazawi William
Aleman Soo
Alisi Anna
Andersson Emma
Armstrong Matthew
Asselah Tarik
Bansal Ruchi
Behrendt Patrick
Berg Thomas
Bernal William
Beuers Ulrich
Björnsson Einar
Bonilla Carolina
Böttler Tobias
Buti Maria
Cabibbo Giuseppe
Calderaro Julien
Castera Laurent
Cazzagon Nora
Childs Kate
China Louise
Ciesek Sandra
Coll Mar
Conti Filomena
Corey Kathleen
Corpechot Christophe
Culver Emma
D’Ambrosio Roberta
Dalekos George
de Lédinghen Victor
De Martin Eleonora
Degasperi Elisabetta
Deuffic-Burban Sylvie
Dietz Julia
Durand François
Elkrief Laure
Fabrellas Nuria
Faivre Sandrine
Ferraioli Giovanna
Flisiak Robert
Forner Alejandro
Forrest Ewan
Fraga Christinet Montserrat
Frances Ruben
Francoz Claire
Fraqquelli Mirella
Galle Peter
Ganne Carrie Nathalie
Gastaldelli Amalia
Gastaminza Pablo
Gerbes Alexander
Gilgenkrantz Helene
Gill Upkar

Gonzales Emmanuel
Graupera Isabel
Grebsky Jason
Gual Philippe
Gustot Thierry
 Hagstroem Hannes
Hernández-Gea Virginia
Hoener zu Siederdissen Christoph
Hofmann Maike
Huch Meri
Hydes Theresa
Iavarone Massimo
Jack Kate
 Komuta Mina
Kondili Loreta
Krag Aleksander
 Kuenzler-Huele Patricia
Lachenmayer Anja
Lemoine Maud
Lemoine Sara
Leo Ana
Loan Dao Thi Viet
 Long Michelle
Longrich Thomas
 Lotersztajn Sophie
Louvet Alexandre
 Luukkanen Panu
Makara Michael
Manolakopoulos Spilios
Mantovani Alessandro
Martin Natasha
Marzioni Marco
Mas Valeria
Maticic Mojca
Mauss Stefan
McPhail Mark
Merle Uta
Meuleman Philip
Minguez Beatriz
Moreau Richard
Moschetta Antonio
Nault Jean-Charles
Negro Francesco
Newsome Philip
Oude Elferink Ronald
Pais Raluca
Papatheodordis George
Papp Maria
Pérez-del-Pulgar Sofia
Petta Salvatore
Piano Salvatore
Pietrangelo Antonello
Pinzani Massimo
Pons Monica
Ponziani Francesca
Postic Catherine
Raggi Chiara
Ramachnadran Prakash
Ratziu Vlad
Reiberger Thomas
Reverter Enric
Rimassa Lorenza
Rinella Mary
Ripoll Cristina
Rodríguez-Peralvarez L. Manuel
Romeo Stefano
Romero Gomez Manuel
Rowe Ian
Sällberg Chen Margaret
Sarobe Pablo
Schulze-zur Wiesch Julian
Schwaibel Philipp
Scorletti Eleonora
Scott Charlotte
Semmler Georg
Serfaty Lawrence
Shiri Sverdlou Ronit
Spaan Michelle
Spee Bart
Stal Per
Steinmann Eike
Stickel Felix
Strick-Marchand Helene
Strnad Pavel
Tacke Frank
Taubert Richard
Thompsen Karen
Toniutto Pierluigi
Trebioka Jonel
Trepo Eric
Tritos Christos
Tschatzis Manolis
Ulrich Marschall Hans
Vacca Michele
Valenti Luca
van de Graaf Stan
van Mil Saskia
Vesterhus Mette
Vonghia Luisa
Wagner Martin
Waidmann Oliver
Webb Glynn
Wen-Juei Jeng Rachel
Westbrook Rachel
Williams Felicity
Wong Vincent
Yasuko Iwakiri
Yki-Järvinen Hannele