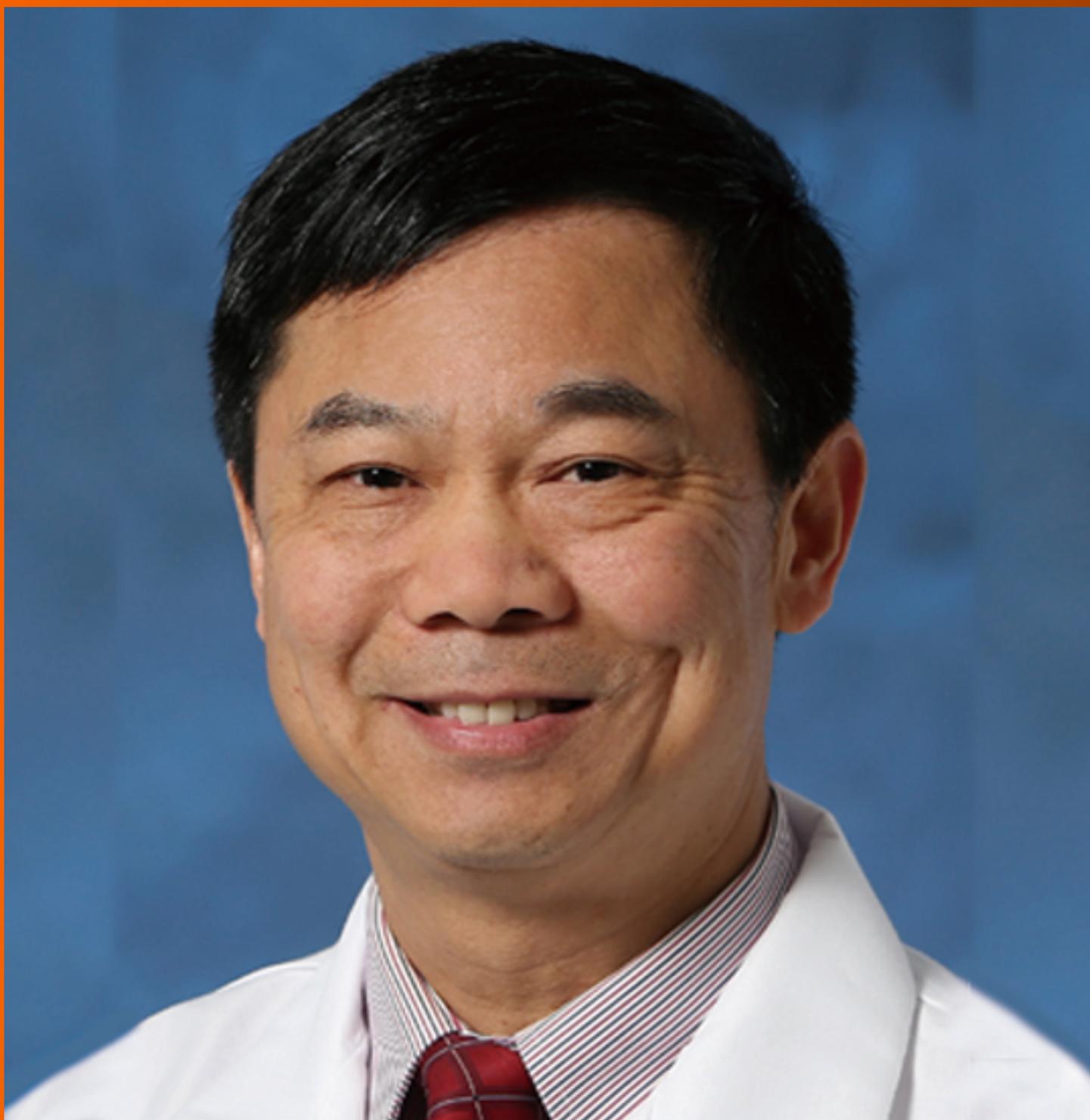


World Journal of *Hepatology*

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ABOUT COVER

Editor-in-Chief of *World Journal of Hepatology*, Dr. Ke-Qin Hu is Director of Hepatology Services and Professor of Medicine in the Division of Gastroenterology and Hepatology, University of California, Irvine School of Medicine (United States). Dr. Hu's career efforts emphasize bridging research advances to bedside patient care. His clinical research has focused on the natural history and outcomes of various liver diseases and healthcare disparity. His basic science research has focused on molecular virology and diagnosis of hepatitis B and C virus infection, and chemoprevention of liver cancer. Dr. Hu has coauthored more than 150 research papers, book chapters, and review articles. He is Deputy Editor-in-Chief for *Frontiers of Medicine*. He is dedicated to community outreach, public health education, and reduction of healthcare disparity. (L-Editor: Filipodia)

AIMS AND SCOPE

The primary aim of *World Journal of Hepatology* (*WJH*, *World J Hepatol*) is to provide scholars and readers from various fields of hepatology with a platform to publish high-quality basic and clinical research articles and communicate their research findings online.

WJH mainly publishes articles reporting research results and findings obtained in the field of hepatology and covering a wide range of topics including chronic cholestatic liver diseases, cirrhosis and its complications, clinical alcoholic liver disease, drug induced liver disease autoimmune, fatty liver disease, genetic and pediatric liver diseases, hepatocellular carcinoma, hepatic stellate cells and fibrosis, liver immunology, liver regeneration, hepatic surgery, liver transplantation, biliary tract pathophysiology, non-invasive markers of liver fibrosis, viral hepatitis.

INDEXING/ABSTRACTING

The *WJH* is now abstracted and indexed in PubMed, PubMed Central, Emerging Sources Citation Index (Web of Science), Scopus, Reference Citation Analysis, China National Knowledge Infrastructure, China Science and Technology Journal Database, and Superstar Journals Database. The 2022 edition of Journal Citation Reports® cites the 2021 Journal Citation Indicator (JCI) for *WJH* as 0.52. The *WJH*'s CiteScore for 2021 is 3.6 and Scopus CiteScore rank 2021: Hepatology is 42/70.

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New Year's greeting and overview of *World Journal of Hepatology* in 2021

Ke-Qin Hu, Koo Jeong Kang, Nikolaos Pyrsopoulos, Xiang Li

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Ke-Qin Hu, Division of Gastroenterology and Hepatology, University of California, Irvine Medical Center, Orange, CA 92868, United States

Koo Jeong Kang, Division of Hepatobiliary Pancreatic Surgery, Department of Surgery, Keimyung University Dong-San Medical Center, Daegu 41931, South Korea

Nikolaos Pyrsopoulos, Medicine-Gastroenterology and Hepatology, Rutgers-New Jersey Medical School, Newark, NJ 07103, United States

Xiang Li, Production Department, Baishideng Publishing Group Inc, Pleasanton, CA 94566, United States

Corresponding author: Xiang Li, BSc, Director, Production Department, Baishideng Publishing Group Inc, 7041 Koll Center Parkway, Suite 160, Pleasanton, CA 94566, United States. x.li@wjgnet.com

Abstract

The *World Journal of Hepatology* (WJH) was launched in October 2009. It mainly publishes articles reporting research findings in the field of hepatology, covering a wide range of topics, including viral hepatitis B and C, non-alcoholic fatty liver disease, alcoholic liver disease, autoimmune and chronic cholestatic liver disease, drug-induced liver injury, cirrhosis, liver failure, hepatocellular carcinoma, coronavirus disease 2019-related liver conditions, etc. As of December 31, 2020, the WJH has published 1349 articles, among which, the total cites is 18995 and the average cites per article is 14. In celebrating the New Year, we are pleased to share with you special a New Year's greeting from the WJH Editors-in-Chief, along with a detailed overview of the journal's submission, peer review and publishing metrics from 2020. In all, we are appreciative for the substantive support and submissions from authors worldwide, and the dedicated efforts and expertise provided by our invited reviewers and editorial board members.

Key Words: *World Journal of Hepatology*; New Year's greeting message; Editors-in-Chief; Editorial Board; Highly influential scientists; Baishideng Publishing Group Inc

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Core Tip: The *World Journal of Hepatology (WJH)* mainly publishes articles reporting research results obtained in the field of hepatology and covering a wide range of topics, including a variety of different liver diseases, cirrhosis, hepatocellular carcinoma, and more recently coronavirus disease 2019-related liver conditions and management, and so on. Since its launch in October 2009, the *WJH* has published 1349 articles. As of December 31, 2020, the total cites among these articles is 18995 and the average cites per article is 14. The enthusiastic and excellent support and submissions from authors worldwide, complemented by the dedicated efforts and expertise of our invited reviewers, Editorial Board members, and Editorial Office staff, have been invaluable.

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INTRODUCTION

The *World Journal of Hepatology (WJH)*, ISSN 1948-5182, <https://www.wjgnet.com/1948-5182/index.htm> is a high-quality, monthly, online, open-access, single-blind peer-reviewed journal published by the Baishideng Publishing Group Inc (BPG). The primary aim of *WJH* is to provide scholars and readers from various fields of hepatology with a platform to publish high-quality basic and clinical research articles and communicate their research findings online. The *WJH* is abstracted and indexed in PubMed, PubMed Central, Emerging Sources Citation Index (Web of Science), and Scopus.

Since its launch in October 2009, the *WJH* has published 1349 articles[1]. As of December 31, 2020, the total cites among these articles is 18995 and the average cites per article is 14.

A NEW YEAR'S GREETING FROM THE *WJH* EDITORS-IN-CHIEF

For all of us, 2020 was a very tough year due to coronavirus disease 2019 (COVID-19). As Editors-in-Chief of *WJH*, it is now our great pleasure to take this opportunity to wish all our authors, readers, Editorial Board members, independent expert referees, and staff of the Editorial Office a very Happy New Year. On behalf of the Editorial team, we would like to express our gratitude to all authors who contributed their valuable manuscripts, as well as all independent referees and readers for their continuous support, dedication, and encouragement. Together with an excellent team effort by our Editorial Board members and staff of the Editorial Office and BPG, *WJH* was able to advance in 2020 despite the ongoing COVID-19 pandemic.

As the chief editors, we strive to work with the journal's Editorial Office and BPG staff to make the manuscript submission process as simple as possible and ensure an efficient communication with the authors to provide our support and answer their questions. We are also open to any suggestions that could improve *WJH*'s operation and publication. Please feel free to contact us at (editorialoffice@wjgnet.com) with any question on your submission or suggestions for the journal in general.

OVERVIEW OF THE *WJH* IN 2020

In celebrating *WJH*'s 12-year anniversary and the 2021 New Year, we are very proud to share with you that we completed the following endeavors in submission, peer review and publishing in 2020.

Submission and acceptance

From 2013 to 2020, the *WJH* has received 2302 manuscripts, including invited manuscripts and unsolicited manuscripts, and the average submissions per year is 288. The submissions of unsolicited manuscripts are stable in recent years (Figure 1).

In 2020, we received 204 submissions from authors around the world and published 112 articles in 12 issues. Among those 112 articles, 57 (50.9%) were original articles, 31 (27.7%) were review articles, 1 was an editorial (0.9%), 15 (13.4%) were case reports and 8 (7.1%) were articles of 'other' types (Figure 2). The authors hailed from 32 countries, including 32 (28.6%) from the United States, 10 (8.9%) from Brazil, 6 (5.4%) each from Italy, Japan and Spain, and 5 (4.5%) each from the United Kingdom and France; the remaining 26 (23.2%) were from various individual countries (Figure 3).

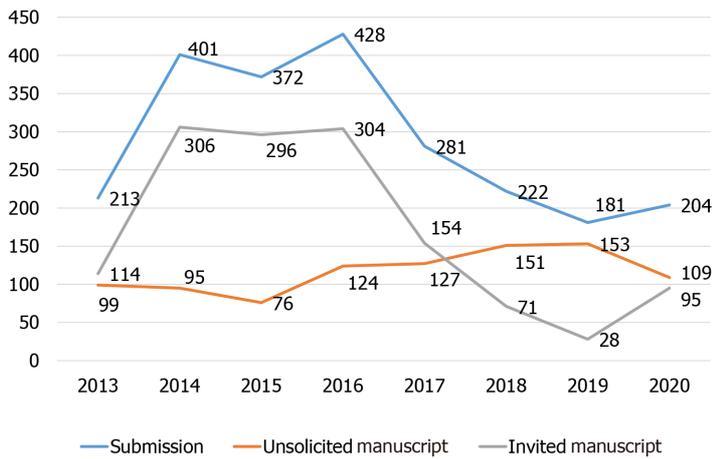


Figure 1 Annual submissions of *World Journal of Hepatology* from 2013 to 2020.

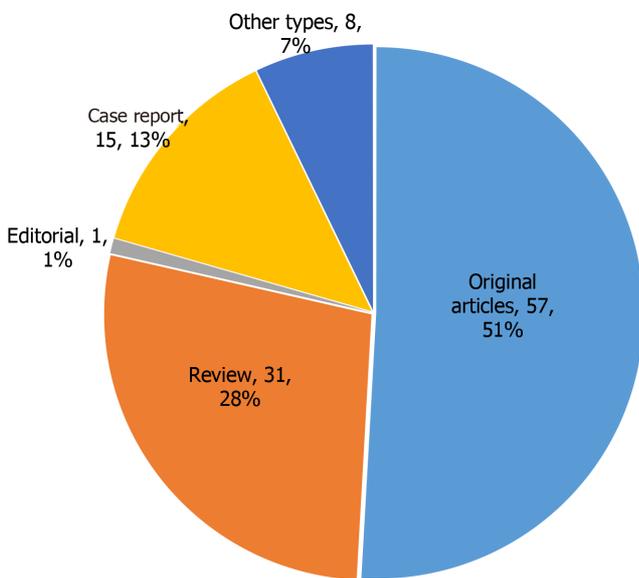


Figure 2 Article types among the 112 manuscripts published by *World Journal of Hepatology* in 2020.

Invitation for 2021

In November and December, invitations to contribute high-quality articles to *WJH* were sent out to distinguished scientists in the field of hepatology. As of December 31, 2020, *WJH* has accepted a total of 327 proposed titles for those invited manuscripts; these articles, to be submitted for publication in 2021, include 85 (26.0%) original articles, 215 (65.7%) review articles, 15 (4.6%) editorials, and 12 (3.7%) ‘other’ types (Figure 4). We are currently inviting highly influential scientists to submit Topic Highlight articles, commenting on and discussing hot topics in the field of hepatology. As of December 31, 2020, we have already received 14 submissions online.

Conducting peer review statistics

As of December 31, 2020, *WJH* had sent out 6120 invitations to peer reviewers and Editorial Board members to conduct peer review of manuscripts. Among the peer reviewers and Editorial Board members who accepted the invitation, 428 (35.0%) submitted the peer review report on time, 425 (34.7%) failed to submit the peer review report on time, and 370 (30.3%) have not submitted the peer review report yet.

Editorial Board members of *WJH*

The 2020 Editorial Board of *WJH* was composed of 195 members[2]. Among them, 3 were Editors-in-Chief (Professor Ke-Qin Hu, Professor Koo Jeong Kang, and Professor Nikolaos Pyrsopoulos), 5 were Associate Editors, and 187 were Editorial Board Members. The members were based in 45 countries and areas, including 23 (11.8%) in China, 22 (11.3%) in Italy, 19 (9.7%) in the United States, 18 (9.2%) in Turkey, 11 (5.6%) in Egypt, and 102 (52.3%) in various other countries (Figure 5). A total of 86 (44.1%) of

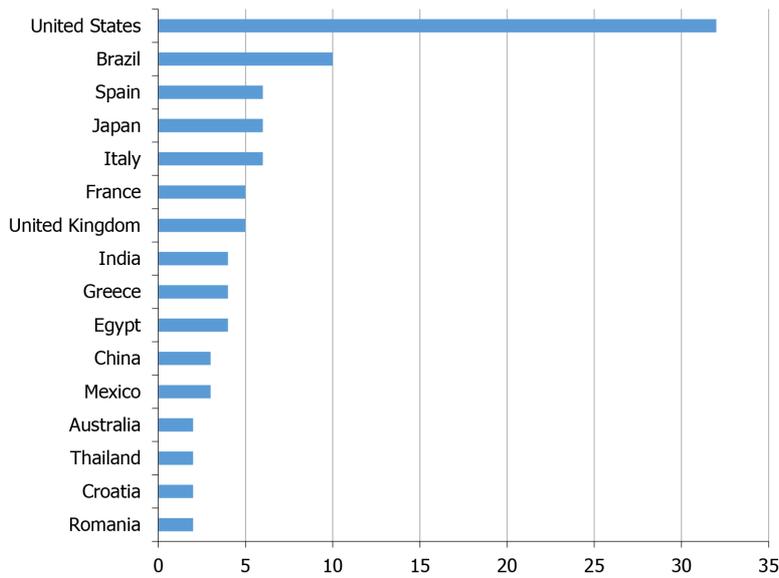


Figure 3 Top 16 countries by number of *World Journal of Hepatology* published manuscripts in 2020.

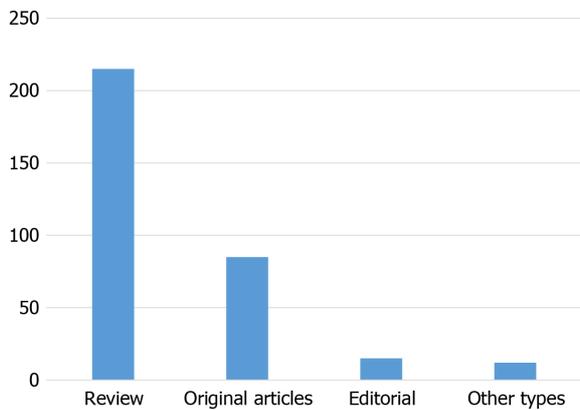


Figure 4 Article types of *World Journal of Hepatology* invited manuscripts for 2021.

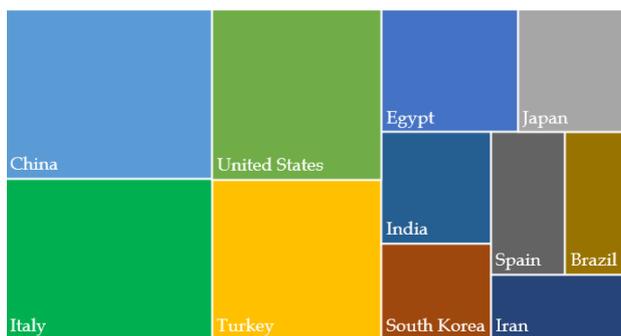


Figure 5 Countries of *World Journal of Hepatology* Editorial Board Members in 2020. Top 11 countries by the number of editorial members, where no less than five members are located in each country.

the Editorial Board Members served as peer reviewers in 2020.

We are pleased to have received 71 applications for Editorial Board membership (up to December 2020), which are currently under evaluation.

Journal metrics

According to data from the Web of Science (up to January 4, 2021), *WJH* published 258 articles between 2017 and 2018. These articles were cited 830 times in 2019, with a mean citation of 3.217 for each. On

behalf of *WJH*, BPG will submit an application to Clarivate Analytics for abstracting and indexing in Science Citation Index Expanded (SCIE), in the near future. *WJH*'s Scopus CiteScore for 2019 is 5.8, ranking 22/61 in the category of Hepatology.

Accurately pushing *WJH* articles and authors ahead

To enable more peers to read, share, and cite *WJH* authors' published research results and to help enhance their global academic influence and reputations, thereby also promoting the overall development of the field of hepatology, BPG sends *WJH*'s published articles to 1000-10000 highly influential experts in a topically-accurate manner. After completing this outreach activity, BPG formally notifies the paper's authors of the number of experts to whom their manuscript was sent *via* email. As of December 31, 2020, *WJH* articles included in the push email campaign were sent to 19905 in October, 5308 in November, and 11023 in December.

Challenges facing *WJH* in 2021

The development and growth of *WJH* rely on a large amount of high-quality manuscripts. We appreciate and encourage all authors to submit their topically-relevant manuscripts to *WJH*, to enjoy the benefits of this great platform and sharing resource in disseminating their medical research results. Our Editorial Board members are encouraged to continue their support by actively serving as peer reviewers, authors contributing articles, and journal representatives inviting high-quality articles from others. *WJH* Editorial Board members are also encouraged to communicate with the Editors-in-Chief actively, provide suggestions and analyze discipline hotspots to promote their academic influence through the *WJH*.

CONCLUSION

In 2021, *WJH* will publish more high-quality original and review articles, consistently improving its academic influence and moving closer towards its next goal of inclusion in the SCIE as soon as possible, which will ultimately promote the overall development of the field of hepatology. *WJH*'s Editors-in-Chief and Editorial Office staff expect to be more productive and have committed to working diligently with all of you to raise the academic rank of *WJH* in 2021. In order to achieve these goals, we recognize the importance of substantive support and submissions from authors like you in tandem with the dedicated efforts and expertise of our invited reviewers, many of whom also serve on our Editorial Board. Please feel free to contact our Editorial Office (editorialoffice@wjgnet.com) if you have further questions, need support, or wish to share your suggestions.

FOOTNOTES

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Country/Territory of origin: United States

ORCID number: Ke-Qin Hu 0000-0003-3377-6553; Koo Jeong Kang 0000-0003-1385-8308; Nikolaos Pyrsopoulos 0000-0002-6950-8174; Xiang Li 0000-0002-3585-4159.

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P-Editor: Wang LL

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- 2 **The 2020 Editorial Board of *World Journal of Hepatology*.** Available from: www.wjgnet.com/1948-5182/editorialboard.htm

Autophagy in liver diseases

Elias Kouroumalis, Argyro Voumvouraki, Aikaterini Augoustaki, Dimitrios N Samonakis

Specialty type: Gastroenterology and hepatology

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Elias Kouroumalis, Liver Research Laboratory, University of Crete Medical School, Heraklion 71110, Greece

Argyro Voumvouraki, 1st Department of Internal Medicine, AHEPA University Hospital, Thessaloniki 54636, Greece

Aikaterini Augoustaki, Dimitrios N Samonakis, Department of Gastroenterology and Hepatology, University Hospital of Crete, Heraklion 71110, Greece

Corresponding author: Dimitrios N Samonakis, FAASLD, MD, Chief Physician, Doctor, Department of Gastroenterology and Hepatology, University Hospital of Crete, Voutes, Heraklion 71110, Greece. dsamonakis@gmail.com

Abstract

Autophagy is the liver cell energy recycling system regulating a variety of homeostatic mechanisms. Damaged organelles, lipids and proteins are degraded in the lysosomes and their elements are re-used by the cell. Investigations on autophagy have led to the award of two Nobel Prizes and a health of important reports. In this review we describe the fundamental functions of autophagy in the liver including new data on the regulation of autophagy. Moreover we emphasize the fact that autophagy acts like a two edge sword in many occasions with the most prominent paradigm being its involvement in the initiation and progress of hepatocellular carcinoma. We also focused to the implication of autophagy and its specialized forms of lipophagy and mitophagy in the pathogenesis of various liver diseases. We analyzed autophagy not only in well studied diseases, like alcoholic and nonalcoholic fatty liver and liver fibrosis but also in viral hepatitis, biliary diseases, autoimmune hepatitis and rare diseases including inherited metabolic diseases and also acetaminophene hepatotoxicity. We also stressed the different consequences that activation or impairment of autophagy may have in hepatocytes as opposed to Kupffer cells, sinusoidal endothelial cells or hepatic stellate cells. Finally, we analyzed the limited clinical data compared to the extensive experimental evidence and the possible future therapeutic interventions based on autophagy manipulation.

Key Words: Autophagy; Lipophagy; Mitophagy; Fatty liver disease; Fibrosis; Liver sinusoidal cells

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Core Tip: Extensive investigation of autophagy is mostly based on experimental data. However there is now enough evidence to support the notion that autophagy is not only the waste recycling mechanism of the hepatocyte, but is strongly involved in the pathogenesis of almost all liver diseases. It can be either a defensive mechanism against various insults or a detrimental machinery aggravating the underlying disease. Modulation of autophagy has different consequences in the hepatocyte than in the liver macrophages, the sinusoidal endothelium or the hepatic stellate cells. There is also an opportunity for future treatment applications of autophagy manipulation.

Citation: Kouroumalis E, Voumvouraki A, Augoustaki A, Samonakis DN. Autophagy in liver diseases. *World J Hepatol* 2021; 13(1): 6-65

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INTRODUCTION

Autophagy in the liver

Autophagy (from the Greek self-eating) is a process crucial for cell survival[1,2]. Autophagy is a lysosomal degradation pathway that controls the disposition of intracellular waste including damaged organelles or invading pathogens. It can be characterized as the recycling energy system of the cell.

Under basal conditions autophagy degrades 1.5% of total hepatic protein per hour but in starvation, protein degradation increases to 4.5% of liver protein per hour[3]. When rodents are starved for 48 h, autophagy degrades up to 40% of liver protein[4].

Although it is accepted that the term “autophagy” was introduced in 1963 by the Belgian researcher Christian René de Duve, in fact the term autophagy was used almost a century earlier by Anselmier in a French journal[5].

However the modern era of autophagy started with the pioneer work of de Duve and Novicoff in the 1950s when acid phosphatase positive lysosomes were described in the rat liver[6-9] and the term lysosome was used for the first time[10]. Later de Duve introduced the term autophagosome and Arstila and Trump proved that the autophagosomes originate from the endoplasmic reticulum (ER)[11]. The next important progress came when Takeshige *et al*[12] identified approximately fifteen Autophagy related genes (Atgs) involved in *Saccharomyces cerevisiae* autophagy[12-14]. Today, more than 40 Atgs in various animal and human cells have been identified and unified[15-17]. The importance of autophagy was recognized by the award of two Nobel Prizes for Physiology or Medicine, the first to Cristian De Duve in 1974 and the second to Yoshinori Ohsumi in 2016[18,19]. Landmarks of autophagy were recently described[20]. During the period 2008-2018 more than 33000 papers related to autophagy were published[21,22].

Autophagy has certain discrete stages including induction, phagophore formation, autophagosome formation, autolysosome formation and degradation[23-25]. Atg molecules are involved in various complexes essential for autophagy induction and autophagosome formation[26]. Initiation starts with activation of the unc-51-like kinase 1 complex (ULK1, Atg1 in yeast) followed by beclin 1 (Atg6 in yeast) and a subsequent cascade of Atg proteins leading to autophagosome formation where LC3 (Atg8 in yeast) is implicated[27]. LC3 is further processed to form initially LC3-I and then LC3-II[28]. Once the autophagosome is formed, a blockage of autophagic flux at late steps will downregulate the clearance of autophagosomes. A blockage of autophagic flux finally results in autophagy dependent cell death[29]. Detailed descriptions of the complex molecular steps of each stage of autophagy were recently published[20,28,30].

A commonly used marker for estimating autophagosome formation is the fusion protein green fluorescent protein-LC3 (GFP-LC3)[31]. Of the three members LC3A, LC3B, and LC3C of the human LC3 gene family, LC3B and LC3-II are mostly used for autophagy assays[32-34]. Autophagic flux into the lysosomes is estimated by measuring p62/SQSTM1 degradation. p62/SQSTM1 is a protein complex that binds to LC3 and is efficiently degraded by autophagy[35]. The total cellular level of p62/SQSTM1 inversely correlates with autophagic activity. Thus in autophagy-deficient cells, p62/SQSTM1 levels are increased after starvation in contrast to cells with normal autophagy[36].

It should be stressed that the level of LC3 is related to the induction of autophagy but might not reflect the final stages of autophagy and should not be used as a general marker of autophagy[34-36]. Further progress of autophagy is detected by a low level of p62 since p62 degradation depends on the function of the autophagosome-lysosome fusion[37]. Therefore an increase of both LC3 and p62 indicates formation of autophagosomes without lysosomal degradation[38].

As mentioned before, a major breakthrough in autophagy was the identification of Atgs. Evidence for the importance of autophagy in liver homeostasis was provided by the generation of Atgs-knockout mice models[39]. Livers of mice with deletion of the autophagy gene Atg7 were markedly enlarged, up

to 30% of the body weight of the animal and hepatocytes were characterized by structural alterations of mitochondria and peroxisomes and aggregation of ubiquitinated proteins. These aggregates disappeared when the ATg7- knockout mouse was bred to a mouse null for SQSTM1/p62 indicating that SQSTM1 is important to direct damaged cytosolic proteins into the autophagic pathway[40,41].

To date, three major types of autophagy, namely, macroautophagy, microautophagy, and chaperone-mediated autophagy (CMA), have been described[22,42,43].

Macroautophagy is the classical pathway that engulfs the cytosolic components targeted for lysosomal degradation. Initiation of autophagy is controlled by two metabolic sensors the mammalian target of rapamycin complex 1 (mTORC1) and the AMP-activated protein kinase (AMPK). mTORC1 negatively regulates autophagy by direct phosphorylation of ULK1 thus inhibiting ULK1. AMPK suppresses mTORC1 activity by phosphorylation of tuberous sclerosis 2 and raptor, two essential regulators of mTORC1[44,45]. Recently it was reported that the final step in this activation process of mTOR is dependent on Rheb, a small GTPase that binds to mTOR and allosterically activates its kinase activity[46]. The long-term regulation of autophagy is carried out by transcription factor EB (TFEB)[47], the main regulator of lysosomal biogenesis and autophagy. Under nutrient-rich conditions, mTORC1 phosphorylates TFEB and retains TFEB in the cytosol[48-50]. Nutrient deprivation on the other hand leads to mTORC1 inhibition, dephosphorylation of TFEB and its translocation to the nucleus to initiate the rapid transcription of autophagy genes[51,52]. All subsequent series of complex events leading to the final degradation in lysosomes have elegantly been described[2,24,53].

A simplified scheme of macroautophagy is presented in **Figure 1**.

Microautophagy is the least studied type of autophagy where compounds or membranous vesicles are directly taken up by lysosomes[54]. Microautophagy is important during amino acid starvation[55, 56] and possibly three different types can be recognized[57].

Chaperone Mediated Autophagy (CMA) is a selective engulfment process of substrates containing the pentapeptide "Lys-Phe-Glu-Arg-Gln" (KFERQ) motifs. They are recognized by, the cytosolic chaperone heat-shock cognate protein of 70 kDa (HSC70), and transported into the lysosomes through the lysosomal membrane protein 2A (LAMP2A)[58,59]. CMA is induced by DNA damage, hypoxia and oxidative stress, among others[60-65].

Today macroautophagy is also divided into non selective autophagy and selective macroautophagy targeting special organelles or specific compounds for degradation[43,66,67]. Thus new names have appeared according to the compounds involved: Ribophagy (ribosomes)[68], pexophagy (peroxisomes)[69], ferritinophagy (iron-based compounds)[70] and most importantly reticulophagy (ER) [71] lipophagy (lipids)[72] and mitophagy (mitochondria)[73]. The last two are practically involved in every form of fatty liver.

Reticulophagy: Multiple receptors directly interact with LC3 and form autophagosomes during reticulophagy, a very important form of macroautophagy that preserves the size and function of the ER in different conditions like starvation, non-alcoholic fatty liver disease (NAFLD), viral infections and fibrosis[74-79].

Lipophagy: Lipophagy is implicated in lipid homeostasis and metabolism in liver diseases. It is usually down-regulated in steatosis of either alcoholic or non-alcoholic liver disease[80-84], but it is up-regulated when fibrosis, cirrhosis or hepatocellular carcinoma are evolving[85-87]. Comprehensive reviews of lipophagy in liver disease were recently presented[88-91].

Mitophagy: The first step of mitophagy in mammals requires the induction of canonic Atg-dependent autophagy with either mTOR suppression induced by mitochondrial generated reactive oxygen species (ROS), or AMPK activation induced by adenosine triphosphate (ATP) depletion. The second step is the priming of the mitochondria involving molecular modifications leading to their recognition by the autophagosomes[92,93]. Even in the healthy liver, worn out mitochondria with a half-life of 10 to 25 d are removed by mitophagy[94,95]. Elimination of aged or damaged mitochondria protect cells from release of pro-apoptotic proteins, generation of toxic ROS and non proper hydrolysis of ATP[96-99]. When oxidative stress appears, autophagy rapidly acts to remove oxidized proteins or damaged mitochondria that generate more ROS. Recent data show that in autophagy deficiency there is accumulation of ROS and p62 probably mediated by the loss of FOXO1/3. It has been reported that the p62-FOXO1/3 axis is the molecular basis for the reduction of antioxidant defense in autophagy deficiency [100]. Three different types of mitophagy have been described based in the different molecular pathways involved[101,102]. An extensive review of molecular mechanisms of mitophagy in liver diseases has been recently published[103].

New players in liver autophagy: It is clear today that apart from the known pathways regulating liver autophagy, there are additional mechanisms involved. The most important are the long non-coding RNAs (lncRNAs), microRNAs (miRNAs) and exosomes. Many recent studies have presented strong evidence that ncRNAs influence autophagy by regulating various autophagy pathways[104-110]. Equally, miRNAs regulate autophagy influencing the core autophagy pathways[111].

Evidence from experimental animals with liver specific deletions of Atgs has demonstrated the role of High mobility group box 1 (HMGB1)[112] and Yes-associated protein (YAP)[113] in the pathological

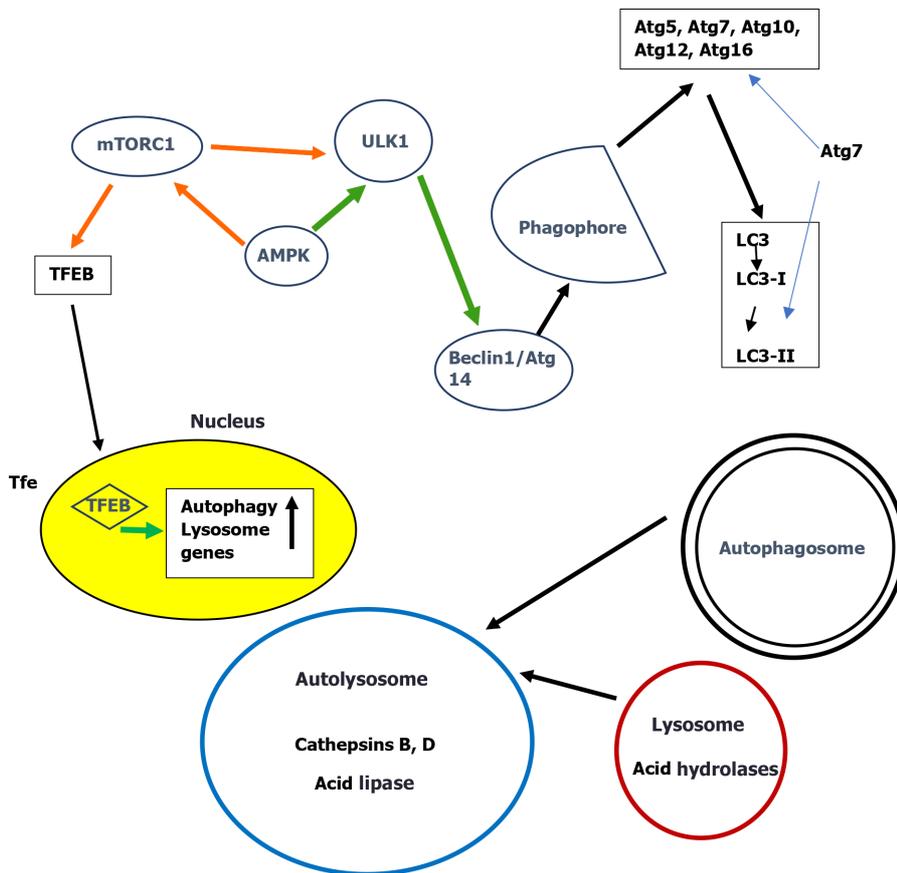


Figure 1 A simplified scheme of the macroautophagy pathways in the liver. Initiation starts with activation of the unc-51-like kinase 1 complex (ULK1, Atg1 in yeast) followed by beclin 1 (Atg6 in yeast) and a subsequent cascade of Atg proteins leading to autophagosome formation where LC3 (Atg8 in yeast) is implicated. LC3 is further processed to form initially LC3-I and then LC3-II. Fusion of the autophagosomes with lysosomes form the autolysosome where acid proteases (among which cathepsins are important) and lipases degrade proteins and lipids. Initiation of autophagy is controlled by two metabolic sensors the mammalian target of rapamycin complex 1 (mTORC1) and the AMP-activated protein kinase (AMPK). mTORC1 negatively regulates autophagy inhibiting ULK1. AMPK suppresses mTORC1 activity. The long-term regulation of autophagy is carried out by transcription factor EB (TFEB), the main regulator of lysosomal biogenesis and autophagy. Under nutrient-rich conditions, mTORC1 phosphorylates TFEB and retains TFEB in the cytosol. Orange arrows: Inhibition. Green arrows: Positive regulation. For details see Ref.[21,29,31]. mTORC1: Mammalian target of rapamycin complex 1; TFEB: Transcription factor EB; ULK1: Unc-51-like kinase 1 complex.

changes induced by autophagy. Nuclear receptors were also reported to control autophagy. Activation of the farnesoid X receptor (FXR), occurs during feeding and suppresses Atgs expression. On the other hand during starvation, fasting-activated nuclear receptors, the peroxisome proliferator-activated receptor alpha (PPAR), and the cAMP response element-binding protein (CREB), induce expression of Atgs and therefore increase autophagy[114-116].

An association of autophagy with the formation and function of exosomes has also been described. Exosomes are extracellular vesicles originating from late endosomes, which do not fuse with lysosomes but are released extracellularly by exocytosis. Exosomes can either activate autophagy pathways or transfer extracellular vesicles to the lysosomes[117].The interplay between autophagy and exosome biogenesis has been recently described[118].

Most researchers have studied either the early or the late stages of autophagy. However equally important is the final stage, namely the lysosome reformation (ALR), leading to regeneration of functional lysosomes from autolysosomes. A series of proteins including clathrin, the motor protein KIF5B, and dynamin 2 are sequentially involved up to the maturation of functional lysosomes. Early lysosomes are pH-neutral but eventually they gain acidity and luminal proteins[119-122]. Accumulating evidence suggests that most, if not all, components of the molecular machinery for autophagy also mediate autophagy-independent functions. Autophagy is involved in various cell functions like endocytosis, phagocytosis, DNA repair, centrosome function, cell proliferation, cell death and immunological response including memory. Details were recently reported[123].

Autophagy and immunity: The implication of autophagy with the immune system has been investigated in the last few years[124-131]. Non-canonical forms of macroautophagy were described, resulting in the formation of autophagosomes that fuse with the lysosomes[132]. Only a subset of the Atgs machinery is used. Among these, LC3-associated phagocytosis (LAP) has been extensively studied because of its implication in immune regulation. LAP recruits LC3-II to the phagosomal membrane[133-

[135] and is taken up by macrophages through innate immune receptors such as Toll-like receptors. In contrast to autophagy the LAPosome is a single membrane vacuole. In contrast to autophagy, ULK1 is not required for LAP[133]. Chaperone-mediated autophagy has also attracted attention because of its central role in antigen presentation and aging[136,137]. Autophagy is also implicated in the function of innate immunity interfering with macrophage autophagy. There is interplay between autophagy and innate immunity as interferon (IFN)- γ promotes autophagy in macrophages[138]. Mice fed with high fat diet had impaired autophagy in bone marrow-derived macrophages and peritoneal macrophages[139]. Mice with Atg5 deficient macrophages, developed hepatic inflammation when stimulated with lipopolysaccharide (LPS) after a high fat diet feeding. Acquired immunity is primarily a defense function against specific pathogens and is brought about by the different subsets of T cells and B cells. Interestingly there is evidence that high autophagic activity maintains the differentiation and function of important T-cell subsets such as regulatory T (Treg)-cells[140] and $\gamma \delta$ T-cells[141].

Autophagy and cell death: It has been proven that autophagy can be either a protective mechanism or a contributor to cellular death in certain instances[142-144]. Autophagy is involved in cellular death mostly by its effects on apoptosis. Autophagy is connected to apoptosis and these two cellular destructive phenomena are affecting each other[145-148]. This is particularly important in hepatic cell death[149].

Generally autophagy blocks the induction of caspase-dependent apoptosis, and apoptosis-associated caspase activation stops the autophagic process. Yet, in special cases, autophagy may induce apoptosis or necrosis, and autophagy has been shown to degrade the cytoplasm, leading to 'autophagic cell death' [150-152].

Autophagy is also implicated in caspase-independent cell death, leading to necrosis and necroptosis [153]. Induction of apoptosis eliminates cells damaged through the action of the tumor suppressor gene p53[154]. Apoptosis is counteracted, among others, by the mTOR/AKT pathway also involved in autophagy. The balance between p53 and AKT/mTOR is crucial for the fate of injured cells[155,156]. In addition, autophagy induces a particular mechanism of cell death named ferroptosis. It was initially reported as a specific iron-dependent form of malignant cell death. It soon became clear that ferroptosis is a more general form of cell death[157,158]. Many proteins implicated in autophagy (like Atgs and BECN1) were also involved in ferroptosis. Moreover activators of ferroptosis, like erastin, induced autophagosome accumulation and activation of autophagy led to ferroptotic cell death possibly by the turnover of ferritin through ferritinophagy[159-161].

A recent study has shown that ferroptosis is also interconnected with lipophagy. Lipids released during lipophagy and subsequent peroxidized increase ferroptosis. Therefore it might be that ferroptosis is a mechanism of cellular death in NAFLD[162].

Autophagy and inflammation: Autophagy is also closely associated with the inflammatory response in the liver. Inflammasome and autophagy regulate each other by the same inhibitory mechanisms which however are controlled by different input pathways. The NLRP3 inflammasome activation, usually through the stimulation by pathogen- and/or danger-associated molecular patterns[163,164], induces procaspase-1 activation which promotes interleukin interleukin (IL)-1 β and IL-18 production leading to pyroptotic cell death. These events are counteracted by caspase-1-mediated activation of autophagy. In addition autophagy reduces inflammasome activation degrading the inflammasomes in the autophagosomes but also eliminating damaged cytoplasmic organelles that otherwise would produce DAMPS increasing activation of inflammasomes[165,166].

On the other hand, the negative correlation between inflammasomes and autophagy[167-169] leads to an increased production of the pro-inflammatory IL-1 β [170] when autophagy is decreased[128]. However, the relationship between NLRP3 and autophagy has not been fully clarified, and recent studies have reported that nuclear factor-kappa beta (NF- κ B) activation can modulate the NLRP3 and autophagy towards the same direction[171].

In view of the above is not surprising that many reviews on autophagy use the term "double-edged sword" stressing the fact that autophagy may have opposite effects on the same biological phenomenon [172]. Prominent general paradigms are cancer[173,174] and viral infections[175].

Another characterization pertinent to the liver is that autophagy behaves like Jekyll and Hyde depending on the cells involved. In hepatocytes, macroautophagy [in NAFLD and alcoholic liver disease (ALD)] and CMA (in NAFLD) is protective. It reduces fat accumulation and oxidative stress, it removes damaged mitochondria and favors regeneration. In macrophages, macroautophagy inhibits liver inflammation and fibrosis but it enhances fibrosis activated stellate cells. It is protective in early phases of hepatocellular carcinoma, but may be detrimental in late phases[176,177].

Autophagy in hepatocytes but also in the non-parenchymal sinusoidal cells of the liver is a key for liver physiology[178,179] and defects of autophagy are implicated in the pathophysiology of most liver diseases[180]. Both common diseases like alcoholic and non-alcoholic fatty liver or viral hepatitis and rare entities like Wilson's disease and α 1 antitrypsin deficiency are related to autophagy defects[30,41, 57,181-184]. Defective autophagy also leads to accumulation of detrimental hepatocyte byproducts due to the fact that hepatocytes have a long half life of 6-12 mo [143]. Moreover, the liver is responsible for handling of a large number of xenobiotics and autophagy is a cytoprotective mechanism[99,185]

(Figure 2).

OBESITY, STEATOSIS AND NAFLD

NAFLD is the commonest liver disease worldwide. Recently it was suggested that it should be renamed as metabolic dysfunction-associated fatty liver disease (MAFLD)[186,187]. Pathological lesions in the liver vary from simple steatosis to non-alcoholic steatohepatitis (NASH) and cirrhosis. Current pathogenesis of NASH is mainly focused on the effects of insulin resistance and lipotoxicity in hepatocytes[188]. The abnormalities reported in Kupffer cells, stellate cells and endothelial cells are regarded as secondary events[189,190].

Obesity and insulin resistance are well documented risk factors for NAFLD development. Defects in liver autophagy have been established as fundamental abnormalities in both conditions.

Hepatic autophagy in obesity and insulin resistance

In the hepatocyte, lipids are catabolized by two major pathways. The first involves cytoplasmic neutral lipases and the second is lipophagy and acid lipases and hydrolases of the lysosomes. The end result is the production of free fatty acids that are further broken down by β I-oxidase in the mitochondria[191].

Lipid droplets have a core of lipids enwrapped in a phospholipid layer characterized by proteins called perilipins directing them to the autophagosome[72]. A crucial protein mediating lipolysis and autophagy is the adipose triglyceride lipase (ATGL). Cytoplasmic lipolysis and lipophagy are interconnected. The degradation of perilipins by autophagy facilitates actions of ATGL which in turn induces autophagy *via* sirtuin1 deacetylation of certain Atgs and activation of the transcription factors FoxO1 and FoxO3 thus promoting autophagy[192-194].

Lipophagy can prevent lipid accumulation in hepatocytes, while the inhibition of lipophagy promotes lipid droplets (LDs) accumulation, resulting in hepatocellular steatosis[195].

Characteristic changes of the metabolic syndrome like obesity, hyperglycemia, and dyslipidemia have been shown to exert a negative effect on autophagy because the regulatory control of forkhead box O1 (FoxO1) on the expression of *Atg* genes is lost leading to autophagy malfunction[196]. Macroautophagy and CMA are also down-regulated by increased intracellular lipids due to either interference with the lysosomal stability of the CMA receptor or to the reduction of the ability of autophagosomes to fuse with lysosomes leading to the reduction of macroautophagic flux[196-198].

The severity of steatosis is related to the expression of three proteins, the damage regulated autophagy modulator (DRAM), BAX and p53. In mice livers, p53 expression increased in mild and severe steatosis. A DRAM expression increase was observed in mild hepatosteatosis, whereas high BAX expression was identified in severe hepatosteatosis[199].

A clinical study has confirmed the link between induction of autophagy and liver steatosis[200]. Autophagy-related genes (*Atg5*, *LC3A*, and *LC3B*) were overexpressed in obese patients compared with non obese patients.

Experimental evidence also suggests that defective autophagy is crucial in the development of obesity, oxidative stress, and the metabolic syndrome[201-203].

Insulin is intimately involved in autophagy regulation as the mTOR inhibitor of the FoxO and TFEB controllers of the transcription of autophagic genes is insulin-inducible[204]. Overactivation of mTOR in turn leads to insulin resistance[205,206]. Several mechanisms might explain this defect in obesity. Obesity increases calpain-2 by a still unknown signal pathway. Calpain is a protease that degrades *Atg7* and modulates autophagy[201]. Autophagosome-lysosome fusion is also defective in livers of obese mice due to alterations of the lipids in cellular membranes induced by the high-fat diet[198]. A defective liver autophagy and the associated decrease of lysosomal degradation contribute to an additional increase in the ER stress which leads to insulin resistance and a vicious circle is completed[201,207,208]. Hyper-insulinemia decreases liver autophagy and reduced hepatic autophagy aggravates ER stress and insulin resistance.

An additional mechanism is a defect in acidification of lysosomes. Impaired substrate degradation in autolysosomes has also been reported for obese *ob/ob* mice. Activities of lysosomal cathepsins were implicated in obesity. Cathepsin L was decreased in obese adipose tissue, while Cathepsin B was significantly elevated. Interestingly in obese adipose tissue inflammasomes were activated and further upregulation of cathepsin B resulted in additional activation of inflammasomes[209-212].

A study of the expression of 322 lysosomal/autophagic genes was recently reported in adipose tissue of lean and obese patients. Among 35 significantly expressed genes, 34 were upregulated. In isolated murine cells, tumor necrosis factor alpha (*TNF α*) stimulation resulted in upregulation of lysosomal/autophagic genes accompanied by upregulation of the autophagy associated SQSTM1/p62 receptor leading to increased degradation of perilipin 1. It seems that local inflammatory cytokines may impair lipid storage *via* autophagy induction[213].

An extensive review of lysosomal enzyme abnormalities in both adipose and liver tissue was recently published[214]. A recent report suggests an additional mechanism contributing to obesity-associated abnormalities. Obesity increases lysosomal iNOS and NO production leading to exacerbation of

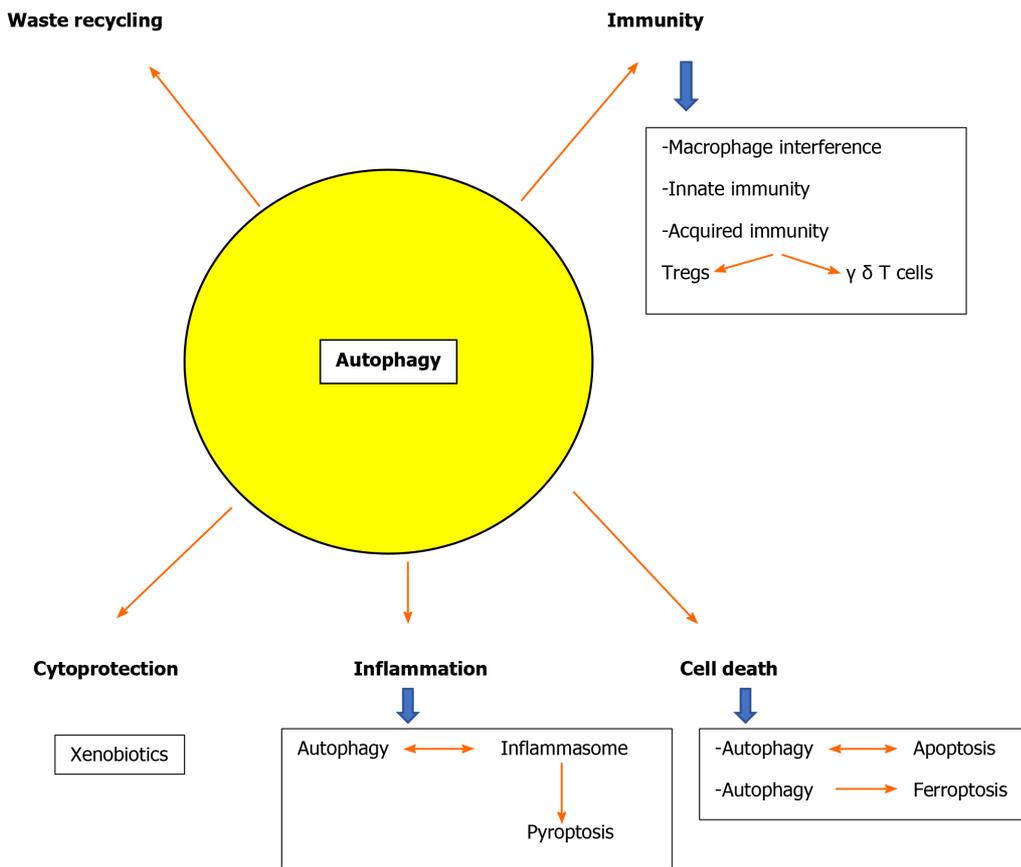


Figure 2 Implications of autophagy in critical cellular functions in the liver. For details see text.

lysosomal nitrosative stress, impairment of lysosomal function, defective autophagy and insulin resistance[215].

There is also evidence that mitophagy is negatively regulated by liver insulin resistance. Mitophagy can promote mitochondrial fatty acid oxidation to inhibit hepatic fatty acid accumulation and improve hepatic insulin resistance. Fundc1 is a recently characterized mitophagy receptor and mice lacking this receptor develop severe obesity and insulin resistance when maintained in a high-fat diet[216,217].

However, when autophagy is defective an alternative mechanism protects the liver from steatosis. An induction of fibroblast growth factor 21 (FGF21) was reported in mice with subsequent amelioration of insulin resistance and decreased diet-induced obesity[218,219]. This has been corroborated in a clinical study of overweight NAFLD patients, where increased FGF21 levels were correlated with steatosis grade, fibrosis and lobular inflammation. NASH patients had the highest levels[220]. An analogue of FGF21 has been tested in experimental animals and obese diabetic patients with promising results[221-223]. Nevertheless, the control of adipose tissue biology is very complex and is elegantly described in a recent publication[224].

NAFLD-NASH

Not surprisingly autophagy is strongly associated with NAFLD pathogenesis[179]. Diet-induced NAFLD in mice blocks hepatic autophagy and leads to oxidative stress and mitochondrial dysfunction [225], also reducing thyroid hormone-induced mitophagy[226]. The potential molecular pathways and possible therapeutic implications of thyroid hormones in NAFLD have been recently reviewed[227].

Mitophagy abnormalities are strongly implicated in NAFLD[228-230]. In particular an impairment of mitophagy seems to activate the NLRP3 inflammasome favoring the progression of NAFLD to NASH [38]. Accordingly, recent evidence indicates that restoration of mitophagy may improve NAFLD[231-234].

In addition to mitophagy, reticulophagy is also implicated in NAFLD. An extensive reticulophagic response is evident in hepatocytes after induction of NAFLD by oleic acid[228,235]. It is suggested that reticulophagy and mitophagy are independent, events involved in NAFLD progression[228].

Impaired lipophagy and lipotoxicity are also strongly involved in NAFLD[72,192,236,237]. Lipid accumulation in hepatocytes blocks autophagic flux and impaired autophagic flux favors the progress of

NAFLD[30].

This impaired flux and the subsequent ER stress can be improved by inhibition of the sterol regulatory element-binding protein 2 (SREBP-2) whose activation promotes accumulation of cholesterol in NAFLD. This improvement is associated with upregulation of autophagy genes[238].

Intracellular lipid trafficking is also regulated by store operated calcium entry and enhanced lipophagy is observed in cells defective in this system[239]. Moreover, the detrimental effects of diets rich in saturated FFA were increased by siRNA-3, which enhanced lipotoxicity, reducing the autophagic flux[240]. The effect of lipophagy in liver steatosis is further supported by experimental evidence that various chemicals are involved in steatosis by interfering with autophagy. Caffeine reduces lipid content and stimulates beta-oxidation in hepatocytes through autophagy in mammalian liver cells in NAFLD[17]. In essence caffeine protects against fatty liver through the co-ordination of the induced lipophagy and mitochondrial β -oxidation[241,242]. Epidemiologic studies demonstrated that coffee consumption reduced the development of fatty liver, fibrosis, and hepatocellular carcinoma in NAFLD patients[243,244] supporting thus the experimental evidence.

Methionine is a well known inactivator of autophagy and lipophagy. The correlation between lipophagy and methionine in the liver from patients with liver steatosis has been studied. Increased levels of methionine inhibit autophagic catabolism of lipids and contribute to liver steatosis in NAFLD [83]. Mice fed with a methionine/choline deficient diet developed steatosis, inflammation, fibrosis and ER stress associated with mitochondrial dysfunction. The administration of the autophagy enhancer rapamycin ameliorated these lesions while chloroquine, a well established autophagy inhibitor, aggravated the liver injury[245]. Resveratrol, another autophagy activator, also attenuated liver lesions induced by a similar diet[246,247]. Consistent with these findings is a recent report that a traditional Chinese herb increased autophagy and considerably improved steatohepatitis induced by methionine/choline deficient diet in rats[248].

Other diet-supplied molecules affect autophagy and are possibly beneficial in NAFLD including the purple sweet potato color[249]. Likewise, the caffeic acid of vegetables has been reported to ameliorate hepatic steatosis[250] while curcumin, an antioxidant polyphenol of *Curcuma longa*, has been shown to inhibit apoptosis and induce autophagy with a potential protective effect on hepatocellular carcinoma [251].

A finding that might be useful in future treatment of NAFLD was recently reported. Celecoxib, a COX-2 inhibitor, attenuated steatosis and restored autophagic flux in cells treated with palmitate and rats fed a high fat diet[252].

Other lipids like the sphingolipid ceramide may be implicated in NAFLD as it is increased in Atg7 knockout mouse liver in parallel with the impaired autophagy[253]. Autophagy increased when sphingolipid de novo synthesis was upregulated, indicating that lipid degradation was activated to prevent excessive sphingolipid accumulation.

Interestingly, autophagic activity seems to be upregulated when the renin angiotensin system is overexpressed. The underlying mechanisms and its role in NAFLD have yet to be clarified as there are many controversial issues to be solved[254]. Overall there is extensive evidence that inhibition of lipophagy is detrimental for the liver in NAFLD[198,222,238,255].

Summarizing the above studies, a therapeutic approach against NAFLD would be the activation of lipophagy[90]. However, it is noteworthy that there is one study indicating the opposite, as suppression of autophagy through inhibition of c-Jun N-terminal Kinase (JNK) ameliorates insulin resistance in a rat NAFLD model[256].

Extensive reviews on the mechanisms of autophagy deregulation in NAFLD were recently published [183,257,258]. Not only impaired macroautophagy but also reduced liver chaperon mediated autophagy (CMA) favors steatosis due to failure in the timely removal of perlipins[259,260] and therefore an increase in lipogenic enzymes. When oxidative stress is increased in the liver, an upregulation of CMA occurs to selectively remove damaged proteins[62]. Loss of CMA leads to impairment of proteostasis and accumulation of oxidized protein aggregates perpetuating thus chronic oxidative stress[261].

Autophagy and NASH

Involvement of autophagy in the progression of NAFLD to NASH has not yet been clarified and molecular mechanisms are not fully understood.

One of the histological characteristics of NASH used in diagnosis and scoring systems is the formation of Mallory-Denk bodies (MDB)[262-264]. There is experimental evidence that inhibition of autophagy and accumulation of p62 is related to their formation while autophagy activation with rapamycin leads to their resolution[265]. Further support of the involvement of autophagy in NAFLD evolution to NASH was reported in a clinical and experimental study where a decrease of autophagic flux in parallel with an increase in ER stress was demonstrated both in the livers from NAFLD patients and mice models of NAFLD, and in lipid-overloaded human hepatocytes[266]. However tests for measurements of autophagic flux used in this paper are not full-proof as they can be influenced by autophagy independent factors. Therefore these findings should be corroborated in a different set up.

Patients with NASH and murine models of steatotic inflammation had reduced expression of Atg7 and TFEB while the autophagy inhibitor rubicon was increased[139,177,255].

In contrast, steatosis and liver injury were improved in parallel with restoration of autophagy and reduction of ER stress in mice with a deletion of the Rubicon or adenoviral delivery of Atg7[202,251]. Recent evidence also indicates that impaired mitophagy may contribute to liver injury during progression of NAFLD and formation of megamitochondria[229].

Transition of NAFLD to NASH also implicates Kupffer cells. These cells, constitute 80%-90% of tissue macrophages in the body and are critical cells in liver inflammation[20]. They are the main site of NLRP3 inflammasome activation and production of the pro-inflammatory cytokines compared to hepatocytes and stellate cells[267,268]. Activation of the NLRP3 inflammasome plays an important role in the transition from NAFLD to NASH[269].

An earlier report demonstrated that cathepsin B, a lysosomal cysteine protease, is released in the cytosol in response to FFAs and that this redistribution of cathepsin B is present in the liver of patients with NAFLD related to disease severity. Importantly in a dietary mouse model of NAFLD, inhibition of Cath B significantly decreased steatosis, liver inflammation and insulin resistance[270].

These findings were recently elaborated in more detail as it was reported that cathepsin B and activation of the NLRP3 inflammasome are interconnected in a murine model of NASH but also in isolated Kupffer cells stimulated with palmitate. Expression of cathepsin B and activation of NLRP3 inflammasome were increase in NASH animals. Moreover, an inhibition of Cathepsin B decreased liver inflammation, ballooning, and the pro-inflammatory cytokines IL-1 β and IL-18. *In vitro* stimulation of Kupffer cells showed identical results in inflammasome activation, expression of Cath.B and cytokine production before and after Cath.B inhibition. These results indicate that NASH pathogenesis probably depends in part to inflammasome activation which in turn is regulated by the activity of a protease tightly connected to autophagy[271].

Additional supporting evidence for the role of autophagy in NASH pathogenesis is the fact that impaired autophagy in obese mice is critical for macrophage polarization. M2 macrophage polarization relies on energy provided by FFA oxidation, suggesting a potential implication of autophagy in this process. Macrophages change to a pro-inflammatory phenotype due to both increased M1 and decreased M2 polarization[132] with a resultant upregulation of liver inflammation, a prominent feature of NASH.

The situation is controversial when adipose tissue macrophages from obese mice are concerned. Increased rather than decreased autophagy of macrophages has been demonstrated in adipose tissue [272,273]. Another cathepsin mostly found in Kupffer cells seems to be implicated in NASH. Lysosomal cholesterol accumulation inside murine Kupffer cells leads to increased liver Cathepsin D activity which is related to liver inflammation[274]. Kupffer cell cathepsin D may therefore be an additional key player in hepatic inflammation of NASH[275]. The impairment of macrophage autophagy with aging may explain in part the increased prevalence of the metabolic syndrome and steatohepatitis of older age in humans[276,277].

The oxidative stress is also involved in the progression to NASH. Hepatocytes exposed to palmitate concentrations similar to those found in patients with the metabolic syndrome and NAFLD showed mitochondrial membrane permeabilization and production of ROS. Similarly, an inhibition of Cathepsin B ameliorated mitochondrial dysfunction and oxidative stress, indicating an additional mechanism of NASH progression[229,278].

Under normal conditions, damaged mitochondria are removed through mitophagy. In certain cases of NAFLD however mitophagy is defective and the oxidation of biomolecules by mitochondrial ROS starts a vicious cycle of increasing mitochondrial dysfunction and aggravation of hepatocellular oxidative damage. This ultimately leads to hepatic inflammation and liver failure[279,280], since impaired mitophagy triggers liver NLRP3 inflammasome activation *in vivo* and *in vitro* in isolated murine hepatocytes[38].

Impairment of autophagy in other liver sinusoidal cells may also participate in the progression of NAFLD to NASH. Decreased autophagy has been observed in the liver endothelial cells of patients with NASH or in mice with endothelial deletion of Atg5 and features of inflammation[180,190,281]. A very recent study has convincingly shown that impaired autophagy of liver endothelial cells (LSECs) occurs in NASH patients but not in simple steatosis. Deficiency in autophagy in LSECs induces endothelial inflammation ultimately leading to liver inflammation and fibrosis. This defective autophagy, in part due to inflammatory mediators of the portal blood, might well be one of the missing links of the progression of simple steatosis to NASH and cirrhosis[282].

A further mechanisms leading to NASH involves multivesicular bodies (MVBs), a form of endosomes, whose contents are transported into lysosomes[283]. The MVB-lysosomal pathway was shown to participate in the development of steatohepatitis through lysosomal degradation of Toll-like receptor 4 reported to be critical for the progression of NASH[284].

Finally a role of the chemokine CXCL10 in the development of steatohepatitis has been proposed. Upregulation of CXCL10 impairs autophagic flux decreasing thus autolysosome formation. Autophagic protein degradation is inhibited followed by the accumulation of ubiquitinated proteins with ultimate development of steatohepatitis[285].

ALD

The liver is the organ mostly responsible for ethanol metabolism. Oxidation of ethanol happens through three pathways namely alcohol dehydrogenase in the cytosol, cytochrome P450 (CYP2E1) in the ER and microsomes and the enzyme catalase in peroxisomes[286]. Ethanol oxidation also produces ROS, including superoxide anion, and hydroxyl radicals that may damage hepatocytes[287].

Ethanol induces autophagosome formation in the liver. Reduction of autophagy results in the accumulation of lipid droplets and apoptosis of hepatocytes[288]. On the other hand activation of autophagy by rapamycin attenuates steatosis and injury induced by a combination of ethanol and lipopolysaccharide[289].

Induction of autophagy by acute ethanol exposure is mediated through many mechanisms Ethanol-induced autophagy requires ethanol oxidation to acetaldehyde and ROS generation[290,291]. ROS activates autophagy by suppressing mTOR and proteasome activity[292,293] and inactivation of Atg4 [294].

Oxidants differentially influence the activities of the proteasome (the other major pathway of protein degradation.) Proteasomes are reduced when autophagosomes are increased[295]. Proteasome inhibition further triggers ER stress activates autophagy through JNK activation. Ethanol may also suppress Akt and mTOR through the upregulation of PTEN[296,297]. Metals, like zinc, are also implicated in autophagy alterations after ethanol treatment[298].

A caution should be exercised on CYP2E1 ethanol oxidation as oxidative products resulting from the expression of CYP2E1 may in fact impair autophagy leading to lipid accumulation in the liver. In cells expressing CYP2E1, hepatocyte lipids and generation of ROS were increased by an inhibitor of autophagy and decreased when a stimulator of autophagy was used[299]. Similar results were found after acute alcohol in CYP2E1 knockout mice[291]. These findings also support the idea that autophagy protects against ethanol/CYP2E1-dependent hepatic injury.

It has also been shown that hepatic autophagy depends on the level of acetaldehyde produced during ethanol metabolism. Mice expressing the ALDH2 isoenzyme, clear acetaldehyde more rapidly and have increased autophagy and lower levels of hepatic triglycerides[300]. Cannabinoid receptor 2 can also induce macrophage autophagy to protect from alcoholic liver damage[301].

It should be stresses however that acute and chronic ethanol exposure may have different effects in liver autophagy[302]. Increased autophagosome formation and autophagy flux were shown in cultured hepatocytes after short term incubation with ethanol or in livers of mice after acute alcohol administration[288,302]. Enhanced autophagy parallel a higher hepatocyte nuclear content of TFEB, the main transcriptional regulator of genes involved in lysosome biogenesis[49,50].

Alcohol also has an effect on the transcription factor forkhead box O3a (FoxO3a) that modulates liver autophagy[303]. The activity of FoxO3a is largely controlled by multiple post-transcriptional modifications, including phosphorylation and acetylation[304]. Acute ethanol exposure increases nuclear translocation of FoxO3a inducing its dephosphorylation and acetylation.

However, results are not uniform for the chronic ethanol effect. Chronic ethanol administration (Lieber-DeCarli model) for 4 wk or 10 wk increased autophagosome numbers in murine livers, suggesting the induction of autophagy[305]. In another similar murine model, mice were given gradually increasing ethanol ethanol concentrations for 10 d and autophagic flux was reduced[302].

The discrepancy seems to be solved by the report that autophagy response was dependent on the alcohol concentration used. In a murine model on Lieber-DeCarli diet with different levels of alcohol for 4 wk, autophagy is increased by a lower dose of alcohol (29% of the caloric need), but decreased by a higher dose (36% of the caloric need). Liver injury was aggravated by further reduction of autophagy and attenuated by autophagy activation[306].

Earlier studies have also demonstrated that chronic alcohol exposure disrupts lysosome function [307]. Overall results have demonstrated that autophagy is suppressed in chronic alcohol consumption due to either the defect of lysosomal function and biogenesis from TFEB suppression[302,308] or to a reduction in AMPK activity and inhibition of autophagosome formation[309,310].

After ethanol-induced reduction of autophagy, there is accumulation of aggregated proteins and SQSTM1/p62, leading to activation of nuclear factor erythroid 2-related factor 2 (Nrf2) and damage to the mitochondria and cell death[309,311].

How the other autophagy-related transcriptional factors, such as TFEB and farnesoid X receptor (FXR) are interconnected with FoxO3a in the expression of autophagy genes is unknown. Moreover, how ROS generation in acute or chronic alcoholic condition systematically affects the mTORC1 activation or TFEB translocation is unclear.

Autophagy is also protective against CYP2E1-dependent liver lesions in a chronically ethanol-fed murine model[312]. Autophagy in ALD can be further affected by additional factors identified in various experimental models. Augmenter of liver regeneration (ALR) is a factor that can promote liver growth. It was reported to protect mice from ethanol-induced liver injury through inhibition of mTOR and therefore activation of autophagy[313]. Moreover an interesting recent study used many genetic models of autophagy impairment, with different functional levels and different alcohol regimens. Deficiencies of either Atg7 or Atg5 demonstrated variable responses to ethanol feeding according to the timing of autophagy dysfunction, the gene being affected, and the alcohol scheme used[314].

It should be stressed that in acute alcohol administration, ethanol-induced autophagy may protect the liver by three basic mechanisms namely mitophagy[80,102,315,316], lipophagy[72,293,317] and clearance of Mallory-Denk bodies by proteophagy[265,318,319].

However, chronic alcohol exposure impairs autophagy and lipophagy[308,320] most likely due to the activation of mTOR signaling and a decrease in lysosomal biogenesis. Administration of the mTOR inhibitor Torin-1 restores lysosomal biogenesis and attenuates liver lesions[308]. An additional pathway through which chronic alcohol exposure could reduce liver autophagy is the inactivation of the guanosine triphosphate Rab7 and reduction of dynamin 2 activity leading to depletion of lysosomes and inhibition of hepatocyte lipophagy[320,321].

Ethanol Induced steatosis activates mitophagy by elevating PINK1 expression on mitochondria[305]. PINK1-dependent mitophagy was correlated with the mitochondrial expression of Parkin and the level of an indicator of oxidative mtDNA damage[322-325]. Mitophagy has a dominant role in protection of the hepatocyte from alcohol-induced hepatic injury as evidenced by a report that enhancement of mitophagy by quercetin, a natural flavonoid, attenuated ethanol-induced mitochondrial damage[326].

Regulation of mitophagy is related to three receptors namely FUN14 domain containing 1 (FUNDC1), BCL2 interacting protein 3 (Bnip3), and Parkin[327].

DNA-dependent protein kinase catalytic subunit (DNA-PKcs) is a newly described housekeeper of liver mitochondrial fission. DNA-PKcs is overexpressed in murine livers after exposure to ethanol and was positively correlated with steatosis, mitochondrial damage and fibrosis. On the other hand this over expression repressed FUNDC1-required mitophagy[328].

An additional significant point is the effect that ethanol might have on the different sinusoidal cell subpopulations. There is strong evidence that autophagy in macrophages is crucial to protect the liver from ethanol-induced damage. Investigations were mostly performed in macrophage specific deletions of either Atg7 or Atg5. The cannabinoid CB2 receptors of macrophages were found to have a protective role in ALD, which was abrogated by Atg5-deletion in macrophages[301]. Increased mortality in Atg5 deleted mice was also demonstrated after chronic ethanol feeding plus LPS challenge[329]. Similar findings were reported after Atg7 deletion[330]. Both studies demonstrated an activation of the inflammasome and an augmented IL-1 production.

In contrast to hepatocytes and macrophages the effect of autophagy in hepatic stellate cells after ethanol exposure has not been clarified. A recent study in immortalized rat stellate cells demonstrated that autophagy could contribute to ethanol-induced stellate cell activation[331]. Induction of fibrosis by alcohol in current murine models is not feasible unless accompanied by steatosis induced by a high-fat diet[332].

Most autophagy studies in ALD are focused on the involvement of macroautophagy. Recent evidence however indicates that CMA is also important in alcoholic liver disease through the CMA negative regulator sorting nexin 10 (snx10). Snx10 knockout mice fed with Lieber-DeCarli diet were resistant to alcohol-induced liver injury associated with an increase of lysosome-associated membrane protein 2A (LAMP2A) and CMA activation through inhibition of the enzyme Cathepsin A which is responsible for LAMP2A degradation[333]. Deficiency therefore of a CMA negative regulator, protects animals from ALD. Deficiency of another CMA negative regulator, Lipocaline-2 (LCN2), also maintains hepatic CMA activity in murine livers after chronic alcohol administration[334] verifying the idea that impaired CMA may be responsible at least in part in alcohol-induced liver injury.

Involvement of miRNAs is an additional factor in the regulation of autophagy in ALD that has emerged from recent evidence. Several miRNAs were reported to alter autophagy and alcoholic steatosis[335]. miR-26a ameliorates alcohol-induced acute liver injury by two MAPKs inhibitors thus inducing Beclin-1 expression and autophagy[335]. Another report provided evidence that miR-155 is a mediator of alcohol-related exosome production and autophagy impairment in both hepatocytes and macrophages[336]. Deletion of miR-155 protected mice from alcoholic steatosis and inflammation. Interestingly in this study serum levels of exosomes were increased in ALD patients and alcohol exposed mice, whereas miR-155 deficient mice had significantly reduced exosome release from both hepatocytes and Kupffer cells. It was suggested therefore that autophagy is an atypical promoter of exosome release in ALD.

Clinically important observations indicate that withdrawal of ethanol from ethanol-fed rats resolves steatosis[337] suggesting that removal of ethanol oxidation and restoration of lipophagy may be the mechanism of steatosis resolution observed in humans after ethanol abstinence[338,339]. Informative reviews of autophagy in ALD were recently published[90,181,182,340-342].

In view of the fundamental role of lipophagy in the pathogenesis of ALD, it is not surprising that pharmacological inducers of lipophagy like carvamazepine, rapamycin, resveratrol and simvastatin were tested in alcohol-fed animals with a resultant attenuation of liver lesions. By contrast chloroquine exacerbated hepatic steatosis[312,343,344]. Recently plant-derived agents were also used to activate lipophagy. Thus, corosolic acid[345], quercetin[346] and Salvianolic acid A[347] all had a favorable result on alcohol-induced liver lesions activating lipophagy through different pathways.

Summarizing, it is evident that whether ethanol causes an increase or decrease of autophagy depends on the duration of ethanol consumption/exposure, the amount of alcohol given, and the manner in which it is administered[290,302]. Moreover, lipophagy and mitophagy cannot act as defensive mechanisms in the long term as they do in acute ethanol consumption as they are inhibited by chronic

alcohol exposure[102,348].

VIRAL HEPATITIS

In the past decade, hepatic autophagy has been implicated in viral infection with either hepatitis B (HBV) or hepatitis C (HCV).

HBV

Recent studies have shown that autophagy is involved in the life cycle of Hepatitis B. Inhibition of autophagosome formation could reduce HBV production, while stimulation of autophagy could significantly contribute to HBV production[349,350].

However, the mechanism by which HBV activates autophagy is not clear. Previous reports have implicated either the HBx[351,352] the large HBsAg protein[353] or a mutant with a deletion in the preS2 region[354,355] as inducers of ER stress which in turn increases autophagy.

In contrast it was shown that HBx does not play a significant role in the induction of autophagy compared to the small HBsAg protein also increasing autophagy *via* the induction of ER stress. An HBV genome unable to express small HBsAg does not activate autophagy[356]. To reconcile the discrepancy, it has been suggested that autophagy can be stimulated both by HBx and the small surface HBsAg protein through upregulation of beclin-1 expression[357,358]. In addition HBx induces autophagy through its effect on the cytoplasmic high-mobility group box 1 (HMGB1), identified as a positive regulator of autophagy. HBx binds to HMGB1 and triggers autophagy in hepatocytes[359]. This observation may be clinically relevant. Spontaneous and induced autophagy of peripheral Treg cells from 98 patients with chronic hepatitis B were assessed[360]. No difference of spontaneous autophagy was found between patients and normal controls but induced autophagy was significantly higher in patients. It was also related to HMGB1 as it was significantly decreased when HMGB1 was blocked with a neutralizing antibody.

HBx further impairs lysosomal acidification with a final result the accumulation of immature lysosomes. Moreover immature lysosomal hydrolase cathepsin D was shown in human liver tissues with chronic HBV infection suggesting that a repressive effect of HBx on lysosomes may be responsible for the inhibition of autophagic degradation[350]. Interestingly, although HBV could impair lysosomal acidification it was unable to induce autophagic protein degradation, due to the inability of HBV to increase the sequestration of proteins destined for degradation by autophagy[350]. Therefore, it is usually stated that HBV induces incomplete autophagy. In addition, it was clearly shown that HBV specifically targets damaged mitochondria and mitophagy. Either the whole HBV genome or HBx alone were able to induce Parkin-mediated mitophagy[361,362]. In addition, HBx-induced autophagy inhibited mitochondrial apoptosis increasing the survival of HBV DNA-transfected cells[349]. Another clinically important observation is that different HBV genotypes have a variant effect on autophagy. HBV genotype C was a more potent inducer of autophagy than HBV genotype B. HBV-C is associated with more severe disease than HBV-B but however attractive such an association between autophagy and severity of liver disease may be, it has to be verified[363,364].

It is important to realize that many viruses, including HBV, have developed strategies to hijack autophagy to benefit their replication and dissemination[356,365,366]. So far, HBV is the only DNA virus known to exploit autophagy for its own replication as it is RNA, but not DNA viruses, that commonly use autophagic function to promote replication[367].

HBV infection induced the early-stage formation of autophagic vacuoles increasing the PI(3)K enzyme activity to promote HBV DNA replication. HBx can directly bind and activate the PI3KC3 complex[368,369]. Ablation of Atg5 has been shown to inhibit autophagy and impair nuclear localization of the HBV core protein. HBV DNA level in sera was decreased by more than 90% accompanied by practically undetectable levels of the HBV DNA replicative intermediate in the liver [370].

Autophagy was responsible for the degradation of an oncogenic microRNA-224 in the liver of HBV patients with hepatocellular carcinoma (HCC) and HBx-transgenic mice. In HCC patients, the combination of low-Atg5 expression and high miR-224, was significantly correlated with a poor overall survival rate[371]. The list of the mechanisms used by HBV to subvert autophagy and the detrimental consequences in the liver is by no means complete as new factors are constantly reported including release of pro-inflammatory cytokines and chemokines and inhibition of neutrophil extracellular trap [372-375].

Further evidence of autophagy subversion by HBV was recently reported. In HBV-replicating hepatocyte cultures, the silencing of Atg5, Atg12, and Atg16L1, interfered with viral core/nucleocapsid (NC) formation/stability and significantly reduced virus yields. It was further demonstrated that a covalent conjugation of Atg12 to Atg5 was essential for HBV replication. In addition the virus required Atg10 and Atg3 which are necessary for Atg5-12 conjugation. Deletion of Atg10 and Atg3 decreased HBV yields, while Atg3 overexpression increased virus production. HBV was associated with the Atg5-12/16L1 *via* interaction of HBV core protein with the Atg12 unit of the complex. Subsequent autophagy

gosome maturation events were not necessary for HBV replication. These data indicate that HBV subverts early, non degradative autophagy components avoiding thus autophagosomal destruction[178, 376,377].

Death receptors of TNFSF10 (tumor necrosis factor superfamily member 10) participate in the immune defense against several viruses by promoting apoptosis. HBx impairs TNFSF10 receptor signaling through autophagy mediated lysosomal and not proteasomal degradation. Importantly a significant reduction of the protein TNFRSF10B was demonstrated not only in cell lines but also in the liver of chronic HBV patients[378].

It was very recently reported that the hepatitis D virus also utilizes autophagy to assist its life cycle as it increases autophagosome accumulation and impairs autophagic flux. Both the small HDAG and large HDAG proteins are capable to disturb the autophagy machinery, in particular the proteins Atg7, Atg5, and LC3 involved in the early elongation stage of autophagy. Unexpectedly, deletion of Atg5 and Atg7 reduced the intracellular HDV RNA level in hepatocyte cell lines without an effect on HDV secretion [379]. Reviews of autophagy in HBV have recently been published[366,380].

HCV

Reported data have shown that HCV could induce autophagy to support its own replication[381,382]. Several mechanisms for HCV induction of autophagy have been investigated using hepatocyte cell lines [383,384]. HCV infection initiates the formation of phagophores after induction of the localization of Atg5 to the ER. Phagophores fuse to form autophagosomes. HCV-induced autophagosomes were further reported to be required for viral RNA replication as the autophagosomal membrane provided a platform containing HCV NS5A, NS5B, and viral RNA for replication[385-387] but subsequently HCV blocks the fusion of autophagosomes and lysosomes through Rubicon overexpression. As a result autophagosomes accumulate and HCV RNA replication and assembly of infectious virions[385,388,389, 390,391] are supported.

However, several studies have contradicted the need for co-localization of viral proteins in the autophagosomal membrane suggesting that this is not a necessity for viral replication[392-395].

Autophagy favors HCV replication with an additional mechanism. The entire autophagic process may be manipulated leading to the suppression of the HCV associated innate antiviral response[393, 396]. After silencing different Atgs, HCV viral infectivity was suppressed in parallel with an upregulation of interferon-stimulated gene expression[390]. Moreover, HCV seems to activate autophagy to degrade the tumor necrosis factor receptor -associated factor 6 (TRAF6), thus subverting innate host immunity[389,397-399]. HCV induced unfolded protein response strongly activates autophagy to sustain viral replication through inhibition of cellular apoptosis[396]. Different HCV genotypes may have variable influence on autophagy[391,400].

HCV was also found to selectively activate lipophagy to counteract the HCV induced lipid abnormalities. This may be clinically important as the levels of autophagy in the liver of chronic HCV patients were inversely correlated to steatosis[401]. Inhibition of autophagic degradation of lipophagy may account for the characteristic occurrence of hepatic steatosis in chronic HCV infection. Mitophagy is also selectively activated *via* the PINK1-Parkin axis in infected cells, thereby promoting HCV viral RNA replication[361,402]. Virus-activated mitophagy further attenuates apoptosis and favors persistent viral infection[403]. In agreement with this finding, the viral non-structural protein 5A (NS5A) was shown to disrupt mitochondrial dynamics, thus increasing ROS production and mitophagy[404].

On the other hand, the viral core protein interacts with Parkin inhibiting its translocation to mitochondria. Mitophagy is suppressed and mitochondrial injury of infected hepatocytes is sustained and viral persistence is maintained[405].

Syntaxin 17 is an autophagosomal protein required for the fusion of autophagosomes with lysosomes and also the release of HCV. The amount of syntaxin 17 was reduced in HCV-replicating cells indicating that HCV impairs the late stages of autophagy affecting the equilibrium between the release and the lysosomal degradation of viral particles[406].

Recently CMA was also demonstrated to be activated by HCV leading to degradation of IFN-alpha receptor-1[407]. Moreover the HCV NS5A was found to interact with Hsc70, recruiting Hsc70 to hepatocyte nuclear factor 1 alpha thus targeting HNF-1 α for CMA degradation[408]. Taken together these studies indicate that HCV induced CMA also facilitate HCV replication.

However, an opposite less permissive effect of the manipulation of autophagy by HCV has been suggested as a result of recent studies. Atg10 is critical for autophagy as it promotes the Atg5-Atg12 complex formation. Two isoforms of the Atg10 protein were described, namely Atg10 (a longer one) and Atg10S. They have a similar amino acid sequence except for an absence of a 36-amino acid fragment in Atg10S. Yet they differ in their effects on HCV genome replication. Atg10 with deleted or mutated two cysteines, (Cys⁴⁴ and Cys¹³⁵) could trigger the expression of anti-HCV immunological genes combating the HCV replication[409,410].

Taken together these results indicate that autophagy is required for initiation of the HCV replicative phase but not for further replication[393]. However this might not be entirely true, as chloroquine an inhibitor of lysosomal acidification inhibits HCV replication offering an additional evidence for the permissive role of autophagy in HCV infectivity in the late phase[411].

Autophagy may additionally be involved in HCV replication through the regulation of the exosomal pathway[390] and apolipoprotein transport[412], both critical steps in the egress of the HCV virion. The virion is associated to apolipoprotein E (ApoE) and its infectivity is enhanced. Autophagy has a central role in the trafficking of ApoE in HCV-infected cells leading to partial autophagic degradation of ApoE, but also to the interaction between ApoE and the viral protein E2 to increase the production of infectious viral particles[412]. Molecular details of how HCV is using autophagy to its own advantage were recently published[380,413].

In summary, the life cycles of HBV and HCV in liver cells can be subdivided into 7 steps: Endocytosis, uncoating, genome replication, translation, envelopment, assembly and release. Both HBV and HCV drive autophagy largely by the ER stress response resulting from uncontrolled translation of viral proteins[414-416]. In addition HBx modulates autophagy for the benefit of HBV replication[357], while multiple HCV proteins including p7, NS3/4A and NS4B, modulate autophagy by direct or indirect association with moieties of the early autophagy machinery in favor of its replication[417-419]. Pharmacological or genetic manipulation of autophagy may limit the viral yield[183,369,420], making autophagy a feasible target for HBV and HCV treatment.

FIBROSIS-CIRRHOSIS

The liver responds to practically any insult with only a limited number of pathological lesions: Hepatitis (hepatocyte death), cholestasis, fibrosis-cirrhosis or a combination of the three. Autophagy participates in all liver pathological responses.

Liver fibrosis is a complex and dynamic cellular process implicated in the evolution of the majority of chronic liver disease towards cirrhosis. Most review articles have broadly concentrated on the role of autophagy in liver diseases, with restricted information on cell types implicated in liver fibrosis. Not unexpectedly, most research has focused on hepatic stellate cells (HSCs) and myofibroblasts, because they are the central elements in extracellular matrix production[421]. However, other liver cells, including hepatocytes, macrophages, sinusoidal endothelial cells (LSECs), infiltrating immune cells and the so-called ductular reaction (DR) are also important[422,423]. DR significantly correlates with the degree of fibrosis and involves cholangiocyte-like cells that dominate an interplay of extracellular matrix and inflammatory infiltrate[424-427].

HSC and autophagy

The fundamental event in fibrosis is the transformation of hepatic stellate cells into myofibroblasts and this is closely related to autophagy. Typical autophagosomes that contained LDs were found in cultured HSCs indicating a connection of liver fibrosis and lipid autophagy[428]. Increasing evidence supports the notion that inhibition of lipophagy in hepatocytes reduces HSC activation and fibrosis progression [429,430]. Inhibition of the activation of HSCs and the formation of autophagosomes have been reported and these seem to be connected with the downregulation of transforming growth factor beta 1/Smads pathway as an increase in TGFb/Smad3 Leads the transcription of Beclin-1, which is a critical player in the autophagy process[431-433].

In rat-derived HSCs, cytoplasmic LDs are degraded followed by fibrogenic genes expression. Moreover induced lipid accumulation by an alkaloid, was associated with quiescent HSCs due to autophagy blockade[434]. Inhibition of autophagy by chloroquine improved CCl4-induced liver fibrosis affecting the activation of hepatic stellate cells as expected[435]. On the other hand, dihydroceramide an inhibitor of autophagy promoted the progression of liver steatosis to fibrosis[436]. Similarly, inhibition of YAP degradation also led to liver fibrosis[113].

In addition, it has been suggested that the IL-17A/STAT3 signaling pathway is important in the evolution of liver fibrosis through suppression of hepatocellular autophagy since neutralization of IL-17A promotes the resolution of experimental fibrosis[437].

Based therefore on current evidence, it has been stated that autophagy at least in murine hepatocytes is a selective survival mechanism through clearance of excessive fat leading to attenuation of lipotoxicity [438]. This is certainly not the case for HSCs autophagy where lipid droplets are digested to supply energy for the activation of HSCs, promoting thus liver fibrosis. Non specific inhibition of stellate cell autophagy or specific inhibition of Atg5 or Atg7, blocked HSCs activation[439-441]. Lipophagy in HSCs is induced by ER stress[442] and is mediated through Rab25 in a ROS dependent manner as antioxidants were effective in stopping autophagy[87]. In agreement with experimental data, clinical research found that cirrhotic patients had significantly increased levels of several autophagy- related genes compared with non cirrhotics accompanied by increased maturation of lysosomal cathepsin D[85]. Furthermore, serum lipids were evaluated in patients with cirrhosis of viral etiology and compared to non cirrhotics. Low serum lipids were found in HCV and HBV cirrhosis which were negatively correlated with lipophagy[443].

Micro-RNAs interfere with the activation of stellate cells. miR-16 inhibits the expression of guanine nucleotide-binding -subunit 12 (G12) which is overexpressed during fibrogenesis and facilitates Atg12-5 formation, thus activating stellate cells[444]. Also miR-181-5p transferred to mouse HSCs *via* exosomes

from engineered adipose derived stem cells led to inhibition of fibrosis[445].

Several signals can induce autophagy in HSCs[180], including hypoxia-inducible factor-1alpha[446], transforming growth factor 1[447], as well as the danger-associated pattern molecule high-mobility group box-1 (HMGB-1)[448]. Additional signals like ROS-JNK1/2 and the XBP1 arm of the Unfolded Protein Response have also been identified as necessary requirements of HSCs activation through autophagy[449,450]. TGF- β 1 has also been reported to mediate autophagy[440]. Similarly, HSCs in cell culture with depleted Atg2A fail to spontaneously trans-differentiate[451]. Quercetin attenuated hepatic fibrosis in mice through inhibition of hepatic HSC activation and autophagy[452].

Selective activation of mitophagy in HSCs also favors fibrosis. PM2.5 is an air pollutant that activates HSCs and initiates liver fibrosis. This is due to increased ROS production and induction of mitophagy through activation of the Pink1/Parkin pathway[453]. In contrast, inhibition of mitophagy was shown to promote inflammation[454] due to dissemination of inflammatory signals from HSCs production of inflammatory cytokines[455]. However very recently it was reported that selective inhibition of mitophagy in macrophages attenuates fibrosis. Mice Kupffer cells from CCL4-induced acute injury showed increased ROS production, activated mitophagy and increased TGF- β 1 secretion. T-cell immunoglobulin domain and mucin domain-4 (TIM-4) interference in Kupffer cells inhibited Akt1-mediated ROS production and decreased mitophagy and TGF- β 1 secretion through suppression of PINK1/Parkin, to ameliorate CCL4-induced hepatic fibrosis[456]. Seemingly in disagreement with this notion, is the finding that the autophagic protein p62/SQSTM1, a negative controller of HSC activation is downregulated in trans-differentiating HSCs associated with hepatocellular carcinoma. P62 ablation increases fibrogenesis but this is not related to autophagy but rather to the reduction of p62-dependent activation of the vitamin D receptor (VDR) and the resultant loss of repression of HSC by VDR agonists [457,458].

Even in HSCs the characterization of autophagy as a double-edged sword has been justified. A novel molecular mechanism of selective autophagy in HSCs indicates that autophagy may also protect from liver fibrosis. The RNA-binding protein ELAVL1/HuR plays a crucial role in regulating ferroptosis in liver fibrosis. ELAV1 enhances ferritinophagy leading to ferroptosis of HSCs and attenuation of liver fibrosis[459]. Despite this report, most existing evidence indicate that activation of HSCs autophagy is pro-fibrogenic, therefore a selective block of autophagy in fibrogenic cells might be an attractive future anti-fibrotic therapy[90].

The opposite seems to happen in hepatic macrophages[55] where activation of autophagy is anti-fibrogenic[460]. Mice macrophages with specific deletion of atg5, secreted increased levels of ROS-induced IL-1A and IL-1B. In addition, liver myofibroblasts incubated with the conditioned medium of Atg5(-/-) macrophages expressed increased pro-fibrogenic genes. Attenuation of fibrosis was achieved after IL-1 neutralization indicating that IL1A/B are critical mediators of the profibrotic effects of autophagy inhibition in macrophages[461-463]. Autophagy in Kupffer cells is counteracted by the enzyme monoacylglycerol lipase catalyzing the production of arachidonic acid leading to inflammatory macrophage activation and fibrosis[464].

On the other hand deletion of Atg7 in sinusoidal endothelial cells (LSECs) demonstrated that the selective loss of their autophagy led to cellular dysfunction and decreased intrahepatic nitric oxide. Impairment of autophagy after CCL4-induced acute liver injury in rats, also impaired handling of oxidative stress by LSECs and amplified liver fibrosis[465].

Similarly, autophagy defective sinusoidal endothelial cells (LSECs) as demonstrated in patients with NASH favor advancement of fibrosis[282]. At the same time, even excessive autophagy activation may lead to caveolin-1 degradation, thus worsening the LSECs defenestration and ultimately promoting fibrosis[466]. Therefore, any dysregulation of autophagy in LSECs may aggravate liver fibrosis[467].

An elegant immunofluorescence study of cirrhotic livers linked autophagy with an additional population of fibrogenic cells other than HSCs, the reactive ductular cells (RDC) which were characterized as cholangiocyte-like epithelial cells positive for cytokeratin 19[85]. They are responsible for ductular reaction (DR), a common response to various insults of the liver implicated in the pathogenesis of cirrhosis[432]. Administration of chloroquine, reduced the expression of CK19 positive RDC and blunted liver fibrosis[86]. DR parallels HSC activation in many liver diseases[430]. Reactive ductular cells secrete soluble pro-fibrogenic factors targeting HSCs and myofibroblasts[468]. Recently it was demonstrated that in cirrhotic human livers, RDCs with activated autophagy also had upregulated expression of TGF and fibroblast specific protein-1[469] making autophagy a necessary requirement during the DR process. The role of autophagy in liver fibrosis is therefore complex and the end result depends on the cell population involved. In general, HSCs and RDCs have a pro-fibrogenic effect. On the contrary, autophagy counteracts fibrogenesis acting in hepatocytes, macrophages and LSECs[470].

HCC

The role of autophagy in tumor cell biology has not been fully elucidated. Autophagy has both pro-and anti-tumorigenic roles. For example, it can either inhibit inflammation acting as an anti-oncogen or protect tumor cells from ROS damage acting as a pro-oncogen[471,472].

Opposing effects have been reported. Activated Ras requires autophagy to maintain oxidative metabolism and tumorigenesis[473]. On the other hand, Ras-induced expression of two proteins Noxa and Beclin-1 promotes autophagic cell death, limiting thus the oncogenic potential of deregulated Ras signals[474]. Drugs like ursodexocholic acid can efficiently eliminate resistant to other drugs cancer cells through induction of autophagic death[475].

HCC is one of the most common types of liver cancer[476]. Most of the HCC cases are accompanied by cirrhosis that results from long-standing chronic inflammation due to viral hepatitis or non-viral etiologies including heavy alcohol intake, NAFLD, autoimmune hepatitis, primary biliary cholangitis, and hemochromatosis[477].

Mice with impaired autophagy are unable to develop HCC even after of strong challenge. This was related to the induction of tumor suppressors like p53[478]. However, after initiation of HCC, the presence of autophagy is required to degrade tumor suppressors promoting thus the development of HCC[86]. Both macroautophagy and CMA are implicated as a double edge sword in liver tumorigenesis [479].

Autophagy has a dual role in hepatocellular carcinoma (HCC). It is an anti-cancer mechanism in the dysplastic stage of HCC initiation, while it favors HCC development and confers resistance to treatment [480,481]. This is possibly due to the maintenance of mitochondrial integrity and protection of cells against oxidative stress during HCC initiation, followed by the downregulation of tumor suppressors to promote the development of HCC[86,482].

In a study of 156 HCC patients increased levels of the autophagy marker LC3B are associated with a dismal prognosis[483]. Higher levels of LC3-II were associated with lymph nodes metastasis, higher vascular invasion and reduced 5-year survival[484].

Macroautophagy may also have an anti-oncogenic function, as reduction of either Atg5 or Atg7 Levels lead to appearance of multiple liver tumors[485]. Similarly, low levels of autophagic proteins and activity are associated with bad prognosis of human HCC[486,487]. Beclin-1 Levels are lower in HCC tissue samples compared to normal tissue from the same patient. Beclin-1 expression was studied in 300 HCC patients. A correlation with disease-free survival and overall survival was found only in the Bcl-xL+ve patients. It was suggested therefore that a synergy of defective autophagy and altered apoptotic activity lead to tumor progression and reduced survival[488].

Inhibition of autophagy leads to the accumulation of SQSTM1/p62. Accumulation of p62 on the one hand may protect from HCC initiation as it blocks the antioxidant functions of nuclear factor erythroid-2-related factor 2 (Nrf2)[489-492]. On the other hand, accumulation of p62 also contributes to carcinogenesis through persistent activation of Nrf2[493]. Nrf2 expression promotes the development of HCC [493]. Deletion of p62 in autophagy defective livers counteracts tumorigenesis. Therefore an accumulation of p62 is partly responsible for the increase in hepatic tumors, *via* the activation of Nrf2[492-494]. The activation of Nrf2 turns glucose and glutamine into anabolic pathways supporting tumor cell proliferation[176,495]. In addition, autophagy inhibits malignant transformation in the liver through Yes associated protein 1 (YAP1) degradation, a protein with a crucial role in hepatic oncogenesis[113,496].

Aberrant activation of the Wnt/ β -catenin signaling is another critical pathway in the onset and development of HCC. A recent study reported that the Wnt/ β -catenin inhibitors exert anti-tumor effects on HCC cells by regulating autophagy[497]. However this is in disagreement with a previous report where interfering with Wnt secretion in HCC cell lines does not affect autophagy or the level of β -catenin signaling despite cell growth suppression indicating that other mechanisms might underlie the growth-suppressive effect[498].

Furthermore, the activation of autophagy was shown to mediate inhibition of proliferation and induction of apoptosis of hepatoma cell through several mechanisms[499-506]. The induction of autophagy by concanavalin A or different chemotherapeutic drugs in murine livers inhibit hepatoma cell growth and prolongs survival[507-519]. On the other hand suppression of autophagy was reported to enhance the susceptibility of hepatocellular cancer cells towards a variety of chemotherapeutic agents [108,520-529].

Several microRNAs (mirRNAs) have been implicated in HCC tumorigenesis. miR-204 reduces tumor autophagy in HCC[530]. Moreover autophagy degradation of miRNA-224 suppressed the growth of HBV-related HCC[371], while miR-375 which is downregulated in HCC was reported to inhibit autophagy by decreasing the expression of Atg7 and autophagic flux. Up-regulation of miR-375 inhibits mitophagy of HCC cells, reduces the elimination of damaged mitochondria, and decreases cell viability [99]. miR-26 could inhibit autophagy and enhance chemosensitivity of HCC cells[531].

LncRNAs are another set of ncRNAs with a length exceeding 200 nucleotides without translation into proteins[109]. Several lncRNAs, like Hnf1a-as1, Hotair and Huc promote autophagy and function as oncogenes in HCC[106-109].

The role of mitophagy and lipophagy is also important in HCC growth acting as a double edge sword. Increased mitophagy by concanavalin A, adriamycin or curcumin was shown to suppress hepatoma cell growth[507,510,517,530] while melatonin increased the sensitivity of human hepatoma cells to sorafenib by triggering mitophagy[532]. A recent study also demonstrated that inhibition of inflammasome activation and induction of mitophagy suppressed HCC growth[533]. On the other hand it has been demonstrated that increased mitophagy may facilitate HCC cell survival either through ROS production or attenuation of p53 activity[534,535].

Lipophagy can also act both ways. On the one hand, it can allow tumor cells to have access to a supply of energy critical to their growth[536] and on the other hand, lysosomal acid lipase, the lipase that facilitates lipophagy, exhibits tumor suppressor activity[537]. Lipophagy was also reported to induce apoptosis *in vitro*, via induction of ER and mitochondrial stress[538]. CCAAT enhancer binding protein a, a protein that is upregulated in HCC patients, increases resistance to energy starvation and favors carcinogenesis through lipophagy[539].

In addition to the general characteristics of autophagy implication in HCC, there are certain points to be mentioned in specific liver disease associated HCC. As mentioned before, autophagy is activated by the HBx protein[357,369] and this may be related to HBV carcinogenesis. Increased autophagosome formation by HBx was accompanied by decreased degradation of LC3 and SQSTM1/p62 and greatly impaired lysosomal acidification and accumulation of immature Cathepsin D. These data may indicate that repression of lysosomal function by HBx could be important for the initiation and progress of HBV-associated HCC[350].

CMA and cancer metabolism are also interconnected. Once malignant transformation occurs, CMA activity is significantly increased in cancer cells so that the new metabolic requirements are maintained [64]. Blockade of CMA which is upregulated in several cancers reduces progression and metastatic potential of solid tumors because the characteristic increased rates of aerobic glycolysis are reduced in a p53-dependent manner[540]. Macroautophagy and CMA seems to be interconnected and often substitute for one another as in the case of HCC. Under physiological conditions there is no expression of p62 in normal livers pointing to macroautophagy as the main mechanism facilitating cell survival. However in a recent study of 46 cirrhotic livers it was shown that p62 was increased indicating an impairment of macroautophagy, but LAMP-2A and heat shock protein 70 were uniformly increased indicating that an upregulated CMA was trying to compensate for the reduced macroautophagy and therefore promote HCC survival. Moreover, hydroxychloroquine inhibition of lysosomal degradation led to induction of the tumor suppressor p53 and promotion of apoptosis[541]. HCV is also an inducer of HCC. During HCV infection, increased cellular stress has been reported. Severe stress promotes Nrf2 transcription which in turn is responsible for CMA activation resulting in the suppression of hepatic innate immunity and possible degradation of tumor suppressors. The subsequent oncogenic cell programming initiated by a cytoplasmic virus like HCV, has been recently described in detail[542].

Defective autophagy is linked to MAFLD-related HCC, because the accumulated p62/SQSTM1, induces the oncogenic NF- κ B activity while retained damaged mitochondria and produced ROS to damage cellular DNA[543]. A novel mechanism was recently reported in ethanol induced liver disease and HCC. Tumor necrosis factor- α -induced protein 8 (TNFAIP8) has been associated with tumor progression in several cancer types including the initiation of HCC. TNFAIP8 induced autophagy in liver cancer cells through blocking of AKT/mTOR signaling and direct interaction with ATg3-Atg7 proteins. This mechanism is operative in alcohol related liver disease in mice and humans but not in high-fat-fed obese mice or patients with MAFLD[544]. Details of the molecular mechanisms of autophagy in both protection and promotion of HCC were recently published[545-547].

An additional aspect of HCC biology where autophagy plays an important role is the involvement of tumor-associated macrophages and tumor microenvironment. They are polarized after implication of sensing factors from tumor environment and autophagy[130,548]. Deficiency of TLR2 decreased the liver production of TNF α , IFN gamma and IL1a/b accompanied by reduction of autophagy flux and increase in oxidative stress and p62 aggregates in liver tissue. These changes were associated with increased carcinogenesis and progression of HCC[549]. Enhancement of autophagy in tumor-associated macrophages leads to M1 polarization which reduces tumor progression while M2 polarization is permissive for tumorigenesis[550]. The mTOR-TSC2 pathway, a key negative regulator of autophagy, is crucial for macrophage polarization since its activation leads to M2 phenotype. It was recently shown that the coagulants tissue factor (TF) and factor VII (FVII) produced in tumor microenvironment, are implicated in HCC growth promotion by suppression of autophagy mediated through mTOR activation and Atg7[551].

In view of the variable functions of autophagy, there should be an individualized approach of autophagy manipulations for HCC treatment. Thus, various lysosomal inhibitors including chloroquine and hydroxychloroquine have been used as treatment either as sole agents or in combinations with other treatment modalities in a variety of murine HCC models[523,552,553]. Interference with autophagy may be a sound therapeutic option for the treatment of HCC[554,555]. Based on the fact that autophagy is upregulated in metastatic HCC[556] use of autophagy inhibitors like chloroquine and hydrochloroquine in combination with other drugs may be a better option for treating metastatic HCC in humans. A combination of a number of drugs with autophagy inducers have been used to target cancer cells. A combination of percutaneous transarterial chemoembolization with chloroquine, was associated with increased tumor cell necrosis and apoptosis[557] and might counteract the presence of residual hepatocellular carcinoma cells[558,559]. Sorafenib, a multikinase inhibitor approved for HCC treatment, induces autophagy[560] and data show that a combination with autophagy inhibitors increase tumor response[537,561].

Cholangiocarcinoma

Xenografts in nude mice are widely used models of cholangiocarcinoma (CCA). Activated autophagy has been reported in tumor cells from such a model and in specimens from CCA patients[562]. LC3B, Beclin 1, and p62/SQSTM1 expressions were additionally found to be increased at the initial stage of the multistep cholangiocarcinogenesis[563]. However, a lower Beclin 1 expression was associated with metastatic lymph node disease and poor survival of patients with intrahepatic CCA[564,565]. Apoptosis was induced in cholangiocellular cell lines and tumor development was suppressed in a mice xenograft model after interference with autophagy[562]. Similarly, suppression of autophagy by chloroquine increased the chemosensitivity of cisplatin-treated CCA cells[566] and increased apoptosis of CCA cells through ER stress[567]. Chloroquine blockade of autophagy inhibited the tumor growth in Kras/p53 intrahepatic CCA[568,569]. CCA is extremely resistant to chemotherapy. 5-fluorouracil (5-FU) induced autophagy in CCA cells[570] while autophagy inhibition by capsaicin was followed by repression of malignant cell growth[570], indicating that autophagy may be implicated in the multidrug resistance of this tumor. Autophagy was also induced after incubation of CCA cells with the sphingosine kinase 2 inhibitor, ABC294640. Inhibition of autophagy by chloroquine potentiated ABC294640-induced apoptosis[571]. Modulation of autophagy therefore may be helpful in CCA treatment.

INHERITED METABOLIC DISEASES

A1 antitrypsin deficiency and fibrinogen storage disease

Autophagy is also implicated in other types of liver injury like the inherited metabolic diseases. Alpha 1-antitrypsin deficiency is the most extensively studied. Alpha 1-AT is a glycoprotein inhibitor of destructive neutrophil proteases[572,573]. Several naturally occurring mutants of alpha1-AT, have been shown to participate in the pathogenesis of human diseases, such as chronic liver-associated diseases [574-576]. The Z mutation resulting from a single G->A transition in codon 342, generates a mutant protein that forms aggregates in the hepatocytes[577]. Liver injury is caused by the retention of this polymerized mutant alpha1-ATZ molecule in the ER of hepatocytes followed by an induction of autophagic response. Removal of the insoluble alpha-1 anti-trypsin by the autophagosome is the mechanism by which the activation of autophagy protects the liver in alpha1-antitrypsin deficiency[578-581]. In earlier studies, liver injury was associated with mitophagy indicating that the ER retention of alpha(1)-ATZ led to involvement of the mitochondria, with specific patterns of mitochondrial dysfunction and mitochondrial injury[582,583].

Genetic studies in mice have shown that deletion of Atg5 led to an increased retention of alpha 1-ATZ [584] and that deficiency of Atg6 and Atg14 in yeasts inhibited alpha1-ATZ degradation[585]. Similarly, the induction of autophagy in mice by rapamycin reduced liver alpha1-ATZ aggregation and liver injury[582,586-589]. These findings have been repeated and verified when enhancement of autophagy [590] with either carbamazepine[591], gene transfer of the autophagy regulator TFEB[592] or an analog of glibenclamide[593] reduced the toxic protein. Recent preclinical studies have also demonstrated that an exogenous bile acid like norursodeoxycholic acid may be clinically useful in this condition[594,595].

Fibrinogen storage disease is a very rare autosomal-dominant ER storage disease presented with hypofibrinogenemia, elevated transaminases, accumulation of fibrinogen aggregates in the ER of hepatocytes and several fold increase of autophagocytic vacuoles. Some patients progress to cirrhosis similar to alpha-1-AT deficiency. A clinical study of eight patients has showed that administration of carbamazepine at low anticonvulsive dosage led to rapid normalization of alanine-aminotransferase indicating a critical role of autophagy in this disease[596].

Wilson's disease

Wilson disease is an inherited disease of copper metabolism linked to hundreds of mutations in the ATP7B gene[597]. Recent evidence based on studies from hepatocytes of patients and ATP7b deleted mice has shown the presence of an increased number of autophagosomes, indicating the activation of an autophagic response to prevent copper associated cell death[598]. Moreover, inhibition of autophagy accelerated hepatocyte death whereas increased autophagy by either starvation or TFEB overexpression had a cytoprotective effects[598]. Autophagy therefore seems to be a major protective mechanism for hepatocytes in copper accumulation. These findings may lead to the use of autophagy inducers like carbamazepine as a future potential treatment of Wilson's disease.

Glycogen storage disease

Glycogen storage disease type 1a (GSD1a) is an inherited hepatic disease associated with decreased autophagic flux as a consequence of defects in the glucose-6-phosphatase a, that converts glucose-6-phosphate into glucose. These abnormalities lead to glycogen and lipid accumulation in hepatocytes [599]. GSD1a is associated with the down regulation of several components of the autophagy machinery [600].

GSD1a has also been associated with defective sirtuin 1 (SIRT1) signaling leading to impairment of TFEB activity. As in other storage diseases, pharmacological or genetic activation of autophagy reduces the accumulation of glycogen and lipids in cellular and animal models[601].

VARIOUS DISEASES

Autophagy in the liver is implicated in other diseases as well. An important point that should always be remembered is that the liver is the site of almost 80% of body macrophages and therefore innate immunity can be deeply involved in liver and other organ abnormalities through impaired autophagy of Kupffer cells. Sepsis is the main paradigm of this notion.

Sepsis and liver autophagy

Infection can lead to a systemic multi-organ inflammatory response. Macrophages, play a critical role as they are the most important cells of the innate immunity. Autophagy induction is protective in sepsis through regulation of macrophage polarization. Negative regulation of macrophage activation inhibits inflammasome activation[602]. Autophagy also interferes with macrophage apoptosis. Uncontrolled autophagy however may lead to autophagy death of macrophages with additional aggravation of inflammation and the so called cytokine storm[603]. A current example is possibly the SARS-Cov-2 pandemic[604]. Interestingly, autophagy-deficient macrophages after LPS stimulation over-secrete macrophage migration inhibitory factor and aggravate inflammation[605]. Other mechanisms are also involved including signaling pathways such as NF- κ B, mTOR, and PI3K/AKT[603].

Mitophagy and mitochondrial dysfunction seem to be also a fundamental factor in multiple organ failure caused by sepsis[606]. It has been shown that mtDNA liberated from damaged mitochondria, induces a cascade of inflammatory responses[607-609]. Mitophagy therefore is of great importance for the protection against oxidative stress during sepsis. It should be noted however that mitophagy defects in the liver, are not the only cause of organ or cell damage during sepsis[610]. Nonetheless, the liver is the main organ responsible for sepsis-induced damage[611]. Autophagy is an important protective mechanism in septic liver injury. Increased autophagy can play a protective role in liver function in septic conditions where the activation of autophagy is mediated through activating transcription factor 4 (ATF4). ATF4 is inhibited 48 h after LPS-induced acute liver injury and reversed after obeticholic acid treatment[612]. Autophagy inhibitors or AMPK inhibitors administration reduced the protective mitochondrial function in LPS-induced human hepatocyte injury[613,614]. Mitophagy is also involved in apoptosis of CD4⁺ve T cells which is the main mechanism of immune inhibition during sepsis. Mitofusin 2 (Mfn2) is a mitochondrial outer membrane protein and a negative regulator of autophagy which is increased in sepsis leading to inhibition of autophagy and increase in apoptosis of CD4⁺ve T cells[615]. Autophagy defects can affect antigen presentation by T cells leading to immunosuppression as in the case of Atg5 deficiency[616]. The role of autophagy in sepsis has been recently reviewed[617].

Acetaminophen liver damage

Autophagy is also implicated in acetaminophen induced liver disease. There is evidence that increased autophagy is protective against acetaminophen (APAP)-induced liver damage[618,619]. Pathogenetically, APAP was reported to form APAP-protein adducts in hepatocytes of mice and humans[620]. Adducts localized in mitochondria contribute to APAP-induced mitochondrial dysfunction and subsequent oxidant stress[621,622]. Therefore, it is plausible that removal of APAP-adducts will help to ameliorate APAP-induced mitochondrial damage and maintain hepatocyte integrity[41,623,624]. Experimental evidence indicates that autophagy is mostly responsible for the removal of APAP-adducts[625]. Moreover administration of adiponectin was found to attenuate APAP-induced injury activating AMPK mediated autophagy[626]. Activation of autophagy by rapamycin also attenuates APAP-induced liver injury, whereas inhibition of autophagy by chloroquine or deletion of Atg7 in hepatocytes deteriorates liver damage[153,627]. There is also evidence that autophagy is activated after APAP overdose in specific liver zones[53].

Somewhat different results were recently presented. Unc-51-like autophagy activating kinase 1 and 2 (Ulk1/2) are important autophagy initiation regulators. Unexpectedly, Ulk1/2 double knockout mice have normal autophagic activity after fasting, but are exceptionally resistant to APAP-induced liver injury possibly indicating that autophagy-dependent and independent ULK1/2 pathways have opposing effects in APAP-induced liver injury[628].

Reduction of ROS and repression of apoptosis by autophagy is also essential for hepatic regeneration after APAP-induced acute liver failure[520,627]. A very recent report confirmed that increased autophagy by rapamycin protects mice against APAP hepatotoxicity while chloroquine enhanced liver injury. Importantly it was demonstrated that APAP overdose activated PINK1/Parkin-mediated mitophagy and increased the expression of NF- κ B and NLRP3 inflammasome signaling. These findings were reversed by rapamycin and augmented by chloroquine indicating the critical role of mitophagy in APAP hepatotoxicity[629].

Interestingly it was reported that infusion of human amniotic mesenchymal stromal cells ameliorated the APAP liver injury through promotion of Kupffer cell M2 polarization and reduction of Kupffer cell autophagy. These results suggest that Kupffer cell autophagy has an opposite effect on APAP hepatotoxicity compared to hepatocytes. This last observation may be useful for future therapeutic exploitation [630].

Acute liver failure

Acute liver failure (ALF) is a serious syndrome of different etiologies with high mortality[631]. HSCs implication is significant in ALF. Temporarily increased fibrosis in ALF is probably beneficial serving as scaffolding that maintains regenerating hepatocytes and hepatic integrity[437,632,633]. Data from a murine APAP induced ALF model have demonstrated that mortality was significantly increased in HSCs depleted animals[633]. HSCs cannot usually regenerate during ALF due to the submassive necrosis. Autophagy seems to be implicated[634]. The significance of HSCs survival has been verified in a study of patients with HBV induced acute liver failure. ALF was accompanied by fibrosis and HSCs activation and autophagy induction. It was shown for the first time that the High Mobility Group Box 1 (HMGB1) protein is a powerful inducer of autophagy responsible for HSCs survival[635].

As mentioned before, autophagy is crucial for HSCs activation which in turn maintains the liver architecture thus preventing the liver scaffold collapse during ALF.

Nitric oxide induces HSCs apoptosis through generation of ROS[636]. There is evidence however that nitric oxide is also involved in the regulation of autophagy in ALF. Observations in human liver tissue showed an inhibition of autophagy in HSCs while further *in vitro* experiments demonstrated that nitric oxide inhibited autophagy and increased apoptosis of HSCs. These findings were reproduced by chloroquine and reversed by the autophagy inducer rapamycin. Therefore, nitric oxide impairment of HSCs survival may be a decisive factor for the devastating effects of ALF[637].

An additional clinical and experimental study verified the significance of intact mitophagy in ALF. One of the measurements of oxidative stress is the level of superoxide dismutase (SOD). The serum superoxide dismutase was significantly increased in ALF patients, correlating with the MELD-Na score. SOD levels returned to normal in the remission stage of ALF. In liver tissue from ALF patients and mice models, manganese-dependent SOD was overexpressed and mitophagy in HSCs was inhibited by ROS. Inhibition of mitophagy promoted inflammation in HSCs which was reversed by a mitophagy inducer [454].

Acute liver damage

Autophagy also protects hepatocytes from acute liver injury, a characteristic of viral hepatitis and acute alcoholic and non-alcoholic steatohepatitis. Mechanisms and cells involved are different as both direct and indirect effects on hepatocytes and macrophages are implicated. Direct effects include autophagy dependent inhibition of caspase 8 in hepatocytes[638], while indirect effects on macrophages involve limitation of NF- κ B-mediated inflammation and inflammasome-dependent IL-1 β production through p62-dependent mitophagy[462,639]. Reduced macrophage autophagy can induce pro-inflammatory macrophage polarization and increase the immune mediated acute damage in obese mice[131]. The TAM family of RTKs (receptor tyrosine kinases), which is expressed in macrophages, has been reported to alleviate inflammation. AXL is the only member of the TAM family that induces autophagy in macrophages and ameliorates hepatic inflammatory responses inhibiting the NLRP3 inflammasome activation in murine macrophages[640].

The role of Kupffer cells (Kcs) is significant in the pathogenesis of acute liver injury. In a murine model of thioacetamide induced acute liver injury it was shown that hyperglycemia aggravated the liver lesions activating the NLRP3 inflammasome of Kupffer cells *via* inhibition of AMPK/mTOR-mediated autophagy. Interestingly, AMPK activation or mTOR signaling deletion restored autophagy and subsequently inhibited inflammasome activation in Kupffer cells[641]. Spermine is an anti-oxidative polyamine with autophagy induction properties. In a model of acute liver injury, spermine pre-treatment ameliorated liver injury and intrahepatic inflammation by promoting M2 polarization of Kupffer cells.

Furthermore, spermine increased autophagy in KCs. Deletion of Atg5 in spermine treated KCs greatly increased pro-inflammatory cytokines and reduced the anti-inflammatory cytokine IL-10[642].

LSECs are also involved in acute liver injury. Selective impairment of autophagy in liver endothelial cells increases oxidative stress, thus leading to fibrosis in acute injury[465].

Ischemia/reperfusion injury

The central role of autophagy in ischemia/reperfusion injury (I/R) injury has been verified by the fact that pharmacological or genetic stimulation of autophagy ameliorate the liver reperfusion injury[643-645].

I/R impairs hepatocellular autophagy[646] through I/R-induced ATP depletion leading to energy shortage and malfunction of the autophagic machinery. Moreover Ca²⁺ overloading during I/R results in calpain overproduction and ultimate loss of key autophagy proteins like Atg7. Interestingly the autophagy suppressor chloroquine attenuated liver injury when administered in early phases of I/R but aggravated the lesions, as expected, when given in late phases[647].

Hepatic encephalopathy

Ammonia is an important mediator of hepatic encephalopathy. Increased ammonia levels rapidly induce an autophagic response that preferentially targets mitophagy[648-650]. Ammonia induced autophagy may in fact be a protective mechanism against encephalopathy as suggested by a recent report. Deletion of Atg7 or loss of functional TFEB deteriorated ammonia detoxification in mice. By contrast activation of liver autophagy either by rapamycin administration or genetic TFEB expression reduced ammonia levels in acquired hyperammonaemia[651].

Autoimmune hepatitis

The role of autophagy in autoimmune hepatitis (AIH) has not been adequately studied. It is suggested that autophagy is implicated in AIH through its involvement in antigen processing and presentation to T cells[652] and its well proven role in liver fibrosis[653], but the exact pathways have not been delineated.

Concanavalin A-induced hepatitis is an extensively used model for immune-mediated liver injury. Comparative proteomic results in this model have shown that the activation of immune system resulted in hepatitis with deregulation of autophagy as indicated by an increase in p62 and LC3B. Arctigenin is a biologically active lignan with antioxidant and anti-inflammatory properties. Pretreatment with arctigenin alleviated autophagy as well as apoptosis verifying that immunity and autophagy are interconnected in AIH pathogenesis[654].

A group of researchers recently used the same model of concanavalin (conA) induced experimental hepatitis to clarify the role of autophagy in AIH. Methyl prednisolone (MP) treatment significantly decreased inflammation in the liver and activated the Akt/mTOR pathway to inhibit hepatocyte apoptosis and autophagy. Reduced numbers of autophagosomes were present in the MP treated group compared to the conA group. It was further shown that MP attenuated the mitochondria-mediated autophagy and apoptosis[655]. In a second report on the same experimental model, accumulation of mature conventional dendritic cells (cDCs) was observed in the liver. *In vitro*, ConA treatment induced the expression of autophagy proteins and the formation of autophagosomes in dendritic cells. A further blockade of autophagy flux inhibited the maturation of DCs and the proliferation and differentiation of CD4+ T cells when ConA-induced DCs were co-cultured with CD4+ T cells. Taken together these studies elegantly showed that autophagy is critically implicated in AIH and aberrant autophagy and defective maturation of cDCs are involved in AIH immunopathogenesis[656].

A recent clinical study using immunohistochemistry in liver biopsy samples from chronic HCV and AIH patients confirmed the central role of autophagy in AIH. Activated but impaired autophagy and less efficient elimination of damaged mitochondria were demonstrated in AIH as compared with HCV. Increased p62 levels significantly correlated with necroinflammation in AIH[657].

Biliary disease

The mechanisms of liver damage in cholestasis are incompletely understood. Autophagy and protein degradation were shown to be impaired in cholestasis induced in bile duct ligated mice[658-660]. Moreover, defective autophagy after chloroquine inhibition or deletion of Atg7 and Atg5 led to increased cholestatic liver injury[661,662].

Accumulated toxic bile acids lead to ER stress, mitochondrial dysfunction with increased oxidative stress, inflammasome activation and apoptosis leading to liver fibrosis[663]. These events should in fact activate autophagy in cholestasis but instead, at least in mice, it appears that autophagy is inhibited in cholestasis[664,665]. Bile acids can inhibit autophagy in mice either *via* the farnesoid X receptor (FXR) during the feeding-fasting cycle[114,115] or independently of FXR[666]. How autophagy is affected in human cholestasis is under investigation.

In human disease autophagy was initially associated with the pathogenesis of primary biliary cholangitis (PBC)[667-669]. As mentioned before autophagy is also involved in the processing and presentation of various antigens. It is only logical therefore that an interesting hypothesis implicating deregulated cholangiocyte autophagy connected to cholangiocyte senescence has been proposed to explain not only the pathogenesis of PBC but of the other fibrosing cholangiopathies including primary sclerosing cholangitis (PSC) and biliary atresia as well[670].

An upregulation of autophagy was reported along with senescence in PBC[668,671]. LC3B and p62 proteins were accumulated in damaged bile ductular cells in association with senescence markers[68, 125] suggesting that autophagy could induce and facilitate cholangiocyte senescence[664,665,671-674]. Mitophagy may be specifically involved in PBC as granular expression of the mitochondrial protein PDC-E2 was co-localized with LC3[667].

Autophagy has also been implicated in the treatment of PBC. Ursodeoxycholic acid (UDCA) is still the first line treatment of PBC while obeticholic acid (OCA) is a second-line treatment[675-677]. Hydrophobic bile acids, such as glycochenodeoxycholic acid impair autophagy *in vitro* and induce abnormal expression of mitochondrial antigens and cellular senescence in cholangiocytes, possibly through induction of ER stress. Pretreatment with UDCA reduced ER stress and partially restored deregulated autophagy and cellular senescence[678]. It is not clear how UDCA stimulates autophagy. UDCA has been reported to be an FXR antagonist[679] but this may not be the explanation[680]. On the

contrary, OCA is a semi-synthetic FXR agonist with anti-cholestatic functions including the suppression of endogenous bile acid synthesis and interference with hepatocellular bile acid transporter systems [681]. OCA impairs autophagic flux *in vitro* and also *in vivo*. A favorable effect of treatment with OCA in a cholestatic disease like PBC would be incompatible with data, indicating that cholestasis progresses when autophagy is blocked[661,662]. However, the other potent, anti-cholestatic properties of OCA can overcome the negative effects of reduced autophagy.

A recent paper offers an interesting explanation. Autophagy seems to be also impaired in human cholestatic conditions where accumulated bile acids induce Rubicon in an FXR-dependent fashion. Rubicon induction suppresses autophagosome-lysosome fusion and inhibits proper autophagolytic breakdown. Rubicon was also induced after treatment with the FXR agonist OCA. Genetic inhibition of Rubicon reversed the impairment of autophagic flux. In contrast, UDCA reduced Rubicon levels, enhanced autophagic flux and autophagolysosome formation independently of FXR[680].

An overview of autophagy abnormalities is presented in [Table 1](#).

CONCLUSION

Autophagy is an important process through which intracellular parts are degraded in the lysosomes. It is a fine example of effective cellular recycling mechanism, connecting cellular quality control with energy saves. There are three types of autophagy with various pathways of delivery to the lysosomes: Macroautophagy (which is further divided into non selective autophagy and selective macroautophagy targeting special organelles or specific compounds for degradation), microautophagy and chaperon-mediated autophagy. Autophagy is related to major physiologic processes as cell death, inflammation and immunity. It is increasingly recognized that it is implicated in almost every aspect of liver diseases, and this can be the basis for future pathophysiologically based and targeted management.

Table 1 Overview of autophagy abnormalities in liver disease

Disease	Abnormalities of autophagy	Results	Ref.
Obesity	↓Autophagy; Hepatocytes: ↓Mitophagy, ↓Lipophagy; HSCs: ↓Autophagy	↑ER stress, →↑Lipids, ↑Insuline resistance, → Anti-fibrotic	Liu <i>et al</i> [203], Lavallard <i>et al</i> [204], Gual <i>et al</i> [205], Tremblay <i>et al</i> [206]
NAFLD	↓Lipophagy; ↓CMA	Lipotoxicity, ↑Lipogenic enzymes	Madrigal-Matute <i>et al</i> [30], Zhou <i>et al</i> [234], Niso-Santano <i>et al</i> [235], Singh <i>et al</i> [236]
NASH	Hepatocytes: ↓Autophagy, ↓Mitophagy; Kupffer cells: ↓Autophagy; LSECs: ↓Autophagy	↑Mallory-Denk bodies, ↑Inflammasome activation; ↑Cathepsins B,D, ↑M1 polarization, ↓M2 polarization; ↑Inflammation, fibrosis	Xu <i>et al</i> [272], Noureddin <i>et al</i> [277], Zhang <i>et al</i> [285], Dey <i>et al</i> [287]
Alcoholic liver disease	Acute ETOH administration: ↑Autophagy, ↑Mitophagy, ↑Lipophagy, ↑Proteophagy; Chronic ETOH administration: ↑Autophagy (low dose), ↓Autophagy (high dose); Kupffer cells: ↓Autophagy, ↑Autophagy; HSCs: ↓Autophagy, ↑Autophagy	Protection, protection, protection, →Clearance of Mallory-Denk bodies; →Protection, →Mitochondrial damage, Cell death; Liver damage, protection; Reduced fibrosis, increased fibrosis	Chao <i>et al</i> [308], Komatsu <i>et al</i> [311], Yan <i>et al</i> [314], Harada <i>et al</i> [318]
HBV	↑Autophagy, ↓Lysosomal acidification, ↑Mitophagy	↑Virus replication, ↓HBV degradation	Li <i>et al</i> [356], Tang <i>et al</i> [357], Luo <i>et al</i> [372], Wang <i>et al</i> [383]
HCV	↑Autophagy, ↓Lipophagy, ↑Mitophagy; ↑CMA	↑Virus replication, steatosis, ↑Virus replication, ↓Apoptosis, persitent infection, ↑Virus replication	Ferraris <i>et al</i> [387], Paul <i>et al</i> [395], Jassey <i>et al</i> [404], Ren <i>et al</i> [406]
Fibrosis-Cirrhosis	Hepatocytes: ↓Autophagy, ↓Lipophagy; Kupffer cells: ↓Mitophagy, or, ↑↑Mitophagy; HSCs: ↓Mitophagy, ↓Lipophagy, or, ↑Lipophagy, ↑Mitophagy; LSECs: ↑↓Autophagy; Ductular reaction: ↑Autophagy	↑Fibrosis, ↑Lipotoxicity, ↑TGFb, ↓Fibrosis; ↑TGFb, ↑Fibrosis; Pro-inflammatory anti-fibrotic: →Pro-fibrotic, →Pro-fibrotic, ↑Fibrosis, ↑Fibrosis	Zhang <i>et al</i> [437], Singh <i>et al</i> [438], Li <i>et al</i> [448], Sun <i>et al</i> [463]
HCC, "Double edge sword"	Induction stage: ↑CMA, ↑Autophagy; Late stages: ↑Autophagy, or, ↓Autophagy, ↑Mitophagy, ↑Lipophagy	Anti-oncogenic: ↓YAP1, ↓proliferation, ↑Apoptosis→Anti-oncogenic, ↓Tumor suppressors; ↑Tumor progression, ↓↑Progression↑↓Progression	Wang <i>et al</i> [558], Zhao <i>et al</i> [559], Prieto-Domínguez <i>et al</i> [560]; Niture <i>et al</i> [544], Yang <i>et al</i> [547]; Lin <i>et al</i> [549], Chen <i>et al</i> [550], Chen <i>et al</i> [551]
Cholangiocarcinoma	↑Autophagy	↑Tumor progression	Marciniak <i>et al</i> [580], Teckman <i>et al</i> [581]
A1 antitrypsin deficiency	↓Autophagy		Yamamura <i>et al</i> [590], Pastore <i>et al</i> [592]
Fibrinogen storage disease	↓Autophagy		Hu <i>et al</i> [609]
Wilson'S disease	↓Autophagy		Oami <i>et al</i> [611]
Glycogen storage disease	↓Autophagy		Xing <i>et al</i> [613]
Sepsis	Kupffer cells: ↑Autophagy, ↑↑Autophagy, ↓Mitophagy	M2 polarization, ↓Inflammasome activation; Kupffer cell apoptosis→Cytokine storm, ↓Apoptosis of CD4+ve T cells	Ying <i>et al</i> [615], Neumann <i>et al</i> [616], Sun <i>et al</i> [628], Shan <i>et al</i> [629]
Acetaminophene liver damage	↓Autophagy, ↓Mitophagy, ↑Kupffer cell autophagy	↑APAP-Protein adducts	Sydor <i>et al</i> [618], Kim <i>et al</i> [643], Biel <i>et al</i> [644]
Acute liver failure	↑Autophagy, ↓Autophagy, ↓HSCs Mitophagy	HMGB1→HSCs activation (protective); ↑NO,ROS→↓HSCs→Devastation	Cheong <i>et al</i> [649], Sridhar <i>et al</i> [652]
Ischemia/reperfusion injury	↓Autophagy		Kwak <i>et al</i> [658], Huang <i>et al</i> [659]
Hepatic encephalopathy	↑Autophagy (NH4)	Protection	Woolbright <i>et al</i> [663], Manley <i>et al</i> [666]

Autoimmune hepatitis	↑Autophagy, ↓ Mitophagy	Defective maturation of dendritic cells	Sasaki <i>et al</i> [671], Sasaki <i>et al</i> [672], Young <i>et al</i> [673]
Biliary disease (experimental)	↓Autophagy	Possibly through increased bile acids	Sasaki <i>et al</i> [665], European Association for the Study of the Liver[675], Lindor <i>et al</i> [676], Panzitt <i>et al</i> [680]
Primary biliary cholangitis	Deregulated autophagy	Cholangiocyte senescence	Van de Graaf <i>et al</i> [669], Sasaki <i>et al</i> [665], Sasaki <i>et al</i> [674]

Note the double edge sword behaviour of autophagy, particularly evident in hepatocellular carcinoma. Autophagy refers to macroautophagy. HSCs: Hepatic stellate cells; LSECs: Liver sinusoidal endothelial cells; CMA: Chaperone mediated autophagy; ER: Endoplasmic reticulum; ASH: Acute alcoholic hepatitis.

FOOTNOTES

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Country/Territory of origin: Greece

ORCID number: Elias Kouroumalis 0000-0002-6875-906X; Argyro Voumvouraki 0000-0002-2725-6028; Aikaterini Augoustaki 0000-0001-8490-3618; Dimitrios N Samonakis 0000-0003-0418-4620.

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Irina Boeva, Petko Ivanov Karagyozov, Ivan Tishkov

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Irina Boeva, Ivan Tishkov, Department of Interventional Gastroenterology, Acibadem City Clinic Tokuda Hospital, Sofia 1407, Bulgaria

Petko Ivanov Karagyozov, Department of Interventional Gastroenterology, Clinic of Gastroenterology, Acibadem City Clinic Tokuda Hospital, Sofia 1407, Bulgaria

Corresponding author: Petko Ivanov Karagyozov, MD, PhD, Chief Doctor, Department of Interventional Gastroenterology, Clinic of Gastroenterology, Acibadem City Clinic Tokuda Hospital, 51B N. Vapzarov Blvd, Sofia 1407, Bulgaria. petko.karagyozov@gmail.com

Abstract

Liver transplantation is the current standard of care for end-stage liver disease and an accepted therapeutic option for acute liver failure and primary liver tumors. Despite the remarkable advances in the surgical techniques and immunosuppressive therapy, the postoperative morbidity and mortality still remain high and the leading causes are biliary complications, which affect up to one quarter of recipients. The most common biliary complications are anastomotic and non-anastomotic biliary strictures, leaks, bile duct stones, sludge and casts. Despite the absence of a recommended treatment algorithm many options are available, such as surgery, percutaneous techniques and interventional endoscopy. In the last few years, endoscopic techniques have widely replaced the more aggressive percutaneous and surgical approaches. Endoscopic retrograde cholangiography is the preferred technique when duct-to-duct anastomosis has been performed. Recently, new devices and techniques have been developed and this has led to a remarkable increase in the success rate of minimally invasive procedures. Understanding the mechanisms of biliary complications helps in their early recognition which is the prerequisite for successful treatment. Aggressive endoscopic therapy is essential for the reduction of morbidity and mortality in these cases. This article focuses on the common post-transplant biliary complications and the available interventional treatment modalities.

Key Words: Post-transplant biliary complications; Endoscopic retrograde cholangiopancreatography; Cholangioscopy; Percutaneous biliary interventions; Liver transplantation; Living-donor liver transplantation

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Core Tip: Liver transplantation is the current standard of care for end-stage liver disease. Biliary complications are the leading cause of morbidity and mortality among recipients and despite the advances in surgical techniques they are seen in up to 25% of cases. Surgery, interventional endoscopy and percutaneous approaches are the available therapeutic options. Endoscopic retrograde cholangiography when possible is the most recommended therapeutic modality, replacing more aggressive surgical interventions. New techniques such as cholangioscopy overcome many of the limitations of conventional endoscopy. This article discusses the most common post-transplant biliary complications and the advances in treatment modalities.

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INTRODUCTION

Liver transplantation (LT) is the widely endorsed method for treatment of end-stage liver disease, acute liver failure and primary liver cancer. The advances in surgical techniques, postoperative care, immunosuppression, and antiviral therapy have led to remarkable progress in survival of these patients. The currently reported 5-year survival rate is 70%-75% [1,2].

Biliary complications are a significant source of morbidity in the early and long-term period after LT (Table 1). Their overall incidence ranges between 15% and 25%. With associated mortality of 10%, they remain a major problem in post-transplant patients. Timely identification and treatment play a significant role in preserving the graft and improving the overall survival rate of patients [3,4].

The most common current treatment is focused on interventional endoscopic (ERC) and percutaneous (PTC) procedures [4-6].

ERC provides minimal invasion with great long-term results and is a preferred method when surgical reconstruction allows this. ERC has been proven to be safe and highly effective in dealing with most of the early as well as late post-LT biliary complications. Procedural-related adverse events in post-LT cases are comparable with those among the general population [6].

The complication rate in patients after living donor liver transplantation (LDLT) in particular is about 10%, which is 2-fold higher than the standard [7,8].

PTC is an effective alternative in patients with altered anatomy which impedes endoscopy access. There is growing evidence that cholangioscopy could be a beneficial tool in the diagnostics and therapy of selected cases [9].

Surgery is available for cases when endoscopic and PCT methods have failed.

Biliary reconstruction techniques

The two major options for biliary reconstruction are bilio-enteric (hepatico-jejunostomy or choledocho-jejunostomy) and duct-to-duct anastomosis. Duct-to-duct anastomosis is the method of choice for biliary reconstruction in any type of transplantation: Cadaveric liver transplantation (DDLT), split transplantations, LDLT (left lobe or right lobe) transplantations [10,11].

Hepatico-jejunostomy is currently used only for selected cases such as those with primary sclerosing cholangitis, prior bilio-digestive surgery, significant ductal size mismatch, and insufficient length of recipient bile ducts [12].

Many benefits motivate the preference for direct duct-to-duct suturing: Preserved sphincter-of-Oddi function, lower risk of cholangitis, and reduction in the number of anastomoses. Besides, the preserved intestinal continuity ensures an endoscopic access to the biliary tree in case of potential complications [13,14].

T-tube placement has been widely abandoned over the last decades [15]. It has been proven that its usage increases the rate of biliary complications. A single-center retrospective review of 1041 transplantations reported that cholestatic liver disease, Roux-en-Y anastomosis, donor risk index > 2, and T-tubes were independent predictors of post-LT complications [16].

LDLT and DDLT

The rising number of LTs augments the need for liver grafts. This has led to the widespread tendency of LDLT. Multiple factors related to LDLT techniques contribute to the increased incidence of biliary complications [11].

Hepatic resection of the donor liver in LDLT requires dissection of the hilum, which could cause bile duct devascularization or subsequent bile leak from the cut surface of the liver. Excessive use of coagulation diathermy is another risk factor for the occurrence of bile leak. On the other hand, the need

Table 1 Risk factors for the most common biliary complications

	Anastomotic	Non-anastomotic
Strictures	Advanced recipient age; Female donor; Failure to flush the donor duct; Preceding bile leakage; Acute rejection; Chronic rejection; Hepaticojejunostomy reconstruction	HAT; Chronic ductopenic rejection; Blood type ABO incompatibility; PSC, autoimmune hepatitis prolonged warm and cold ischemia times prolonged donor exposure to vasopressors
Leaks	Active bleeding at the bile duct end excessive dissection of periductal tissue tension on ductal anastomosis	T-tube tract, excessive use of electrocautery incorrect suture of the cystic duct stump
Stones and clots	Ischemia, stricture, infection	
Biliary cast syndrome	Acute cellular rejection, bile stasis, ischemia, infection, sepsis, HAT	
Haemobilia	Alcoholic liver disease, high body mass index of recipient; Iatrogenic: PTC, liver biopsy	

PSC: Primary sclerosing cholangitis; PTC: Percutaneous; HAT: Hepatic artery thrombosis.

for dissection of the recipient's left or right hepatic duct could prolong the ischemic time. Bringing the recipient's hepatic duct to the graft's hilum to ensure tension-free anastomosis could cause additional disturbance of the blood supply. In general, the reported biliary complication rate is 2-3-fold higher in LTLD than in DDLT. Furthermore, the treatment is usually more complicated due to the smaller size of the ducts or the presence of multiple anastomoses. Therefore, the success rate of treatment for complications is lower in LDLT[14,17-19].

Classification

The most common complications are strictures, leaks, and biliary stones. According to the timeframe of their occurrence, post-LT complications can be divided into early (occurring within the first 4 wk after transplantation) and late. Biliary leaks are the most common complication in the early postoperative period, while biliary strictures are the predominant complication as a whole. According to the lesion location, strictures and leaks are divided into anastomotic and non-anastomotic[20-22].

It is appropriate to make a distinction between biliary stricture and biliary obstruction. While the obstruction can be caused by external compression (biloma, haematoma), luminal cast, stones or tube remnants, the stricture is narrowing of the duct lumen, causing bile outflow disturbance.

Multiple factors can play a role in the occurrence of biliary complications. Anastomotic lesions are mostly due to technical issues, while non-anastomotic lesions are the result of ischemia or immune reactions[23].

With respect to the etiology, some authors divide the complications into five groups[21]: (1) Hepatic artery thrombosis-related; (2) Technical biliary complications; (3) Ischemic-type biliary lesions; (4) Infectious biliary complications; and (5) Uncommon: Sphincter of Oddi dysfunction (SOD), bile cast syndrome, haemobilia, lymphoproliferative disease, and other neoplasms.

Biliary strictures

Up to 50% of post-LT biliary complications consist of biliary strictures[24]. They are divided into two major morphological types: Anastomotic (AS) and non-anastomotic (NAS).

Most frequently, the strictures are anastomotic. AS appear more often in LDLT than in DDLT. They are short, single narrowings, located at the anastomotic site. The incidence ranges between 5%-15% in DDLT and 13%-36% in LDLT[21-26]. They occur mostly during the first year after transplantation within a mean time of 5-8 wk[23,27].

The most common factors associated with AS are surgical issues over the first months and ischemia leading to fibrous healing at the later stages. Additionally, ABO incompatibility, advanced recipient age, small bile duct caliber, prolonged warm and cold ischemia time, and cytomegalovirus infection are reported to be significant risk factors[25,28-30].

Endoscopic retrograde cholangiography (ERCP) is the standard of care for AS treatment, whenever anatomy allows it. The overall reported success rate ranges between 70%-100%[31-33].

For patients with hepatico-jejunostomy, different scopes such as single or double balloon enteroscope, spiral enteroscope or pediatric colonoscope are used. These techniques are time-consuming and complex; they require additional expertise and are related to higher risk and higher cost[32,34-37].

For all these reasons, PTC is a widely accepted approach in cases of altered anatomy[38]. Surgical therapy is now used as salvage therapy and is required in about 1% of cases[39].

AS treatment aims to normalize bile outflow through the anastomosis. The endpoint of ERC is lack of narrowing during occlusive cholangiography or free contrast outflow during fluoroscopy (Figure 1). Clinical and laboratory resolution of cholestasis are the most reliable measures of successful treatment.

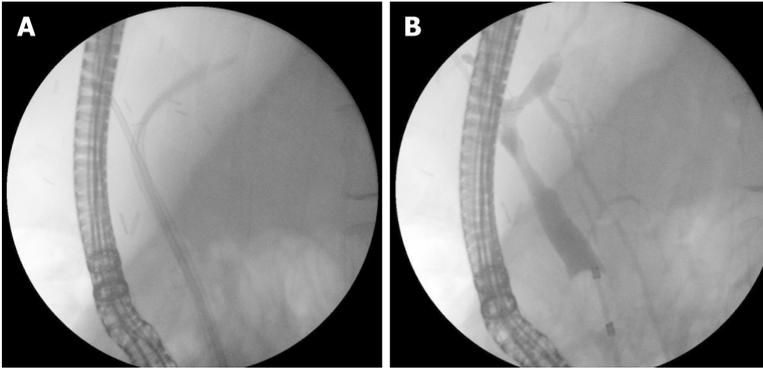


Figure 1 Endoscopic treatment of anastomotic stricture after living donor liver transplantation. A: Two plastic stents; and B: Occlusive cholangiogram after treatment.

The standard treatment includes guidewire insertion across the stricture, followed by balloon dilation and stent insertion. Most commonly 10Fr or 7Fr plastic stents are used. These stents can be easily removed or replaced. Balloon dilation in itself is effective as a non-invasive technique, which has shown less than promising long-term results with a 30%-40% success rate[34,40] (Figure 2).

Numerous large studies have proven that the combination of balloon dilation plus stent placement is more effective than dilation or stenting alone[41].

Several endoscopic strategies are applied in the management of anastomotic strictures. The most frequently used technique is balloon dilation with placement of a maximum number of 10Fr plastic stents with subsequent stent exchange until full resolution of the stricture on fluoroscopy (Table 2).

The initial dilation requires 4-10 mm balloons. In rare cases of tight strictures a Soehendra catheter can be used to overcome the stricture. The progressive increase in the number of stents with every subsequent procedure has ensured more sustained resolution of the stricture[42,43].

Different time intervals between stent exchanges were investigated. In a study from 2008, a short-term stent exchange of every 2 wk was investigated. The reported resolution rate was 87%, achieved for a mean period of 107 d and a mean number of stents inserted of 2.5. More often stents are replaced every three months to prevent occlusion and cholangitis. The reported success rate in many large studies is 80%-95% [39,41-43]. In a review of 440 post-LT patients with AS, the success rate of stent therapy was 84%. The resolution rate was established to be dependent on therapy duration and was highest (94%-100%) when therapy lasted 12 mo or more[44].

The time it takes for the structure to evolve has also been proved to be a predictive factor for healing. Strictures manifested within the first 6 mo after LT have better prognosis for sustained resolution[25,31, 45].

Due to elevated rupture risk, it is preferable for ERC to be postponed at least one month after the transplantation. When necessary, a 7-8.5 Fr stent is applied without balloon dilation. In tight strictures, a 4 mm angioplasty balloon may be considered[46].

Some new dilation balloons have been tested in order to improve bile stricture resolution. There are few published data on the usage of peripheral cutting balloons[47].

Paclitaxel-eluting balloons have been investigated, due to the fact that paclitaxel can suppress fibrotic proliferation[48]. The latter two are not in common use.

An available alternative to the standard multiple-plastic-stent therapy is the placement of fully covered self-expanding metal stents (fSEMS). Their major benefits are a reduction in the number of procedures and cost-effectiveness[49-52].

In a substantive study with 200 cases, the reported success was 80%-95% [51]. Eight and 10 mm SEMS are available according to the stricture size. FSEMS are not considered suitable for AS smaller than 5 mm[24].

Stent migration is the major limitation of this technique. The main strategies to prevent migration include skipping dilation of the stricture, using stents with flaps, and leaving the stent in the duodenum for a long period[49-51].

A large systematic review, published in 2013, reported a migration rate of fSEMS of 16%; the authors also mentioned a low risk of stent ingrowth and stent impaction. The comparison analysis in that study showed that neither technique was superior[49,53].

Management in LDLT is more challenging due to the frequent presence of multiple anastomoses with a smaller size (Figure 3). According to Coté *et al*[24], significant risk factors for treatment failure in LDLT are higher LT recipient age, longer operation duration, and a pouched morphology of the AS.

Non-anastomotic strictures consist of one or more duct narrowings proximal to the anastomosis. They are longer, complex, and usually multiple, and can affect intra- and extrahepatic ducts. NAS are more rarely observed: 5%-10% of biliary complications[54]. Ischemia and immunological reactions are the main aetiological mechanisms. The most common risk factors reported in the literature are hepatic

Table 2 Studies on the effectiveness of maximal stent therapy in post-operative biliary strictures

Ref.	Patients	Treatment duration	Mean number of stents	Number of ERCPs	Success rate
Costamagna <i>et al</i> [41], 2001	45	12.1 mo (range 2-24 mo)	3.2 (range 1-6)	4.1 (range 2-8)	89% (40/45)
Hsieh <i>et al</i> [23], 2012	41	5.3 (range 3.8-8.9)	7.0 (range 4-10)	4.0 (range 3.0-5.3)	100% (41/41)
Morelli <i>et al</i> [43], 2008	38	107 d (range 20-198 d)	2.5 (range 1-6)	3.4 (range 2-6)	87% (33/38)
Pasha <i>et al</i> [90], 2004	25	3.3 mo (range, 2.2-7 mo)	2.0 (range 1-4)	3.5 (range 1-9)	88% (22 of 25)
Tabibian <i>et al</i> [42], 2010	69	15 mo (range 12-60 mo)	3.0 (range 2-7)	2.5 (range 2-5)	94% (65/69)

ERCP: Endoscopic retrograde cholangiography.

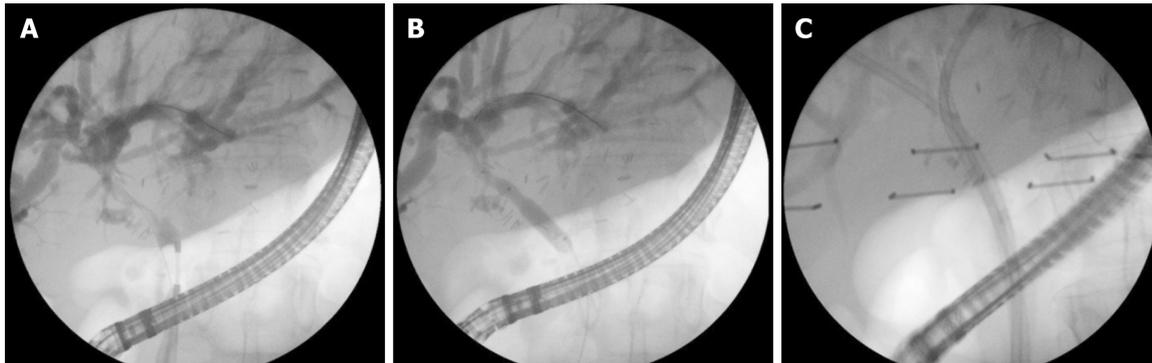


Figure 2 Anastomotic stricture. A: Cholangiogram; B: Balloon dilation; and C: Multiple stent treatment.

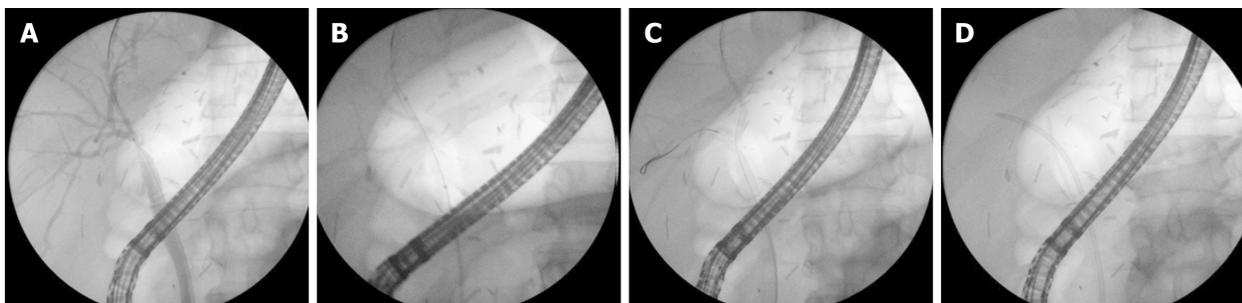


Figure 3 Anastomotic stricture after living donor liver transplantation (right lobe). A: Guidewire insertion; B: Balloon dilation; C: Second guidewire insertion; and D: Stent placement (7Fr + 5Fr).

artery thrombosis, prolonged cold and warm ischemia, prolonged exposure to vasopressors of the donor, ABO incompatibility, chronic ductopenic rejection, PSC or autoimmune hepatitis in the recipient [55,56]. In the case of acute hepatic artery thrombosis, early revascularization therapy is required to prevent multiple stricture formation.

Cases with NAS could benefit from mini-invasive (endoscopic and percutaneous) treatment, but the estimated results are significantly worse than in cases with AS. In cases with dominant strictures and extrahepatic localization ERC is the first treatment option. Endoscopic access to NAS is much more challenging due to the small caliber and relatively proximal location[53]. Cases with angulated, complex strictures, not suitable for ERC passage benefit from percutaneous approaches, followed by hybrid procedures such as the rendezvous technique. When intrahepatic strictures are present, PTC with direct radiology-guided percutaneous stent insertion could be in order[57,58].

Stricture recurrence and continued stricture formation are possible even after successful endoscopic therapy. Long-term observation (MRCP and laboratory) of these patients is required to evaluate the disease course and the response to treatment. Cases resistant to stent treatment, or those with diffuse bile duct injury, must be listed for re-transplantation. Percutaneous drainage could be a bridging therapy to the operation[54,58].

The reported success rate of stenting therapy in the literature is 50% to 75% for DDLT and 33%-50% for LDLT[26,50]. In most NAS cases, the treatment process also takes longer than with AS[11,59].

Passing a guidewire through the stricture is considered the most critical moment. Occlusion balloons and swing-tip catheters for selective cannulation are used for this purpose[54]. The rendezvous technique could also be used to deal with this issue[59,60].

After successful cannulation, the standard technique of balloon dilation followed by plastic stent insertion is performed. For this type of stricture, 4-6 mm balloons with a subsequent increase in caliber are used. Even when cannulated, the width, angulation and proximal location of the strictures often limit the stent insertion. The stents used are usually 7 or 8.5Fr and carry a high migration risk due to rigidity of the plastic[58,59].

A working group from Minnesota reported their treatment for NAS with long (12-20 cm), 10Fr flexible stents with side fenestration. They provide better bile drainage through the stent and through the side holes and could be inserted higher due to their flexibility[61].

Cholangioscopy provides direct visualisation of the biliary tree. This allows visual assessment of the biliary epithelium at the stricture and tissue sampling if needed. In cases of strictures, not suitable for standard cannulation, cholangioscopy enables guidewire insertion under visual control (Figure 4). This facilitates guidewire placement in tight, angulated strictures. Cholangioscopy has been proven to increase the stricture cannulation rate and the success rate of endoscopy treatment as a whole (Figure 5). The implementation of cholangioscopy in stricture therapy could spare the need for percutaneous drainage and surgical interventions[62,63].

Bile leaks

Bile leaks are the second most frequent biliary complication after LT. Bile leaks are also divided into anastomotic and non-anastomotic. Most of them are anastomotic and occur early - within the first 4 wk after LT[8,10,64].

The reported incidence in the literature ranges from 2% to 25%[13,22].

Their occurrence is slightly higher in patients with bilio-enteric reconstruction than with cases of duct-to-duct anastomosis. A systematic review, including data from 61 studies, reported the incidence of bile leaks to be 9.5% in LDLT and 7.8% in DDLT[64]. The presence of a bile leak is an independent risk factor for further development of a stricture[65].

Early bile leaks are usually caused by technical issues related to surgery, such as tension of the anastomosis, incomplete cystic stump suture, excessive use of diathermy, bleeding from the cut ends of ducts, premature T-tube extraction, and the cut surface of the graft. Ischemic injury is the other major cause of bile leaks[8,18,19,52]. Large studies have shown double and triple hepatico-jejunostomy and warm ischemia time as independent risk factors for the occurrence of bile leaks[17,18].

Bile diversion is the key to bile leak healing. Therapeutic options include ERC followed by stenting or nasobiliary drainage, percutaneous drainage, and surgical revision. Sphincterotomy with endoscopic stenting leads to reduction in the transpapillary pressure, usually followed by fast lesion closure. Stent placement leads to successful treatment in over 90% of cases with early leaks (Figure 6)[13,66]. Simple defects like T-tube exit, cystic duct remnant or small anastomotic leaks usually close in 2-5 wk. The biliary stent is usually extracted after no less than 3 mo due to potentially delayed tissue healing on account of immunosuppression. Some centers prefer the placement of nasobiliary drainage for early small defects. This allows close fluoroscopic follow-up of the defect closure and avoids the need for a second stent extraction procedure. Given the low patient tolerance, displacement risk, and prolonged hospital stay, this practice is currently of limited use[19,66].

In cases with defects, refractory to plastic stent treatment, fcSEMS usage could be considered. Small studies have reported good closure success rate[67-69].

According to a study including 35 cases treated with 8 mm and 10 mm fcSEMS, the achieved leak resolution was 94%[68].

In some studies, a high incidence of stricture was observed after stent removal[70].

In cases with bilio-enteric anastomosis, percutaneous access to the biliary tree is used for bile diversion. An internal-external drainage placement for 3-6 mo is an effective alternative to the endoscopic approach. A technique with EUS-guided gastrostomy, used for ERCP access, is also reported in a small study from 2011[33].

In cases with a T-tube, drainage unclamping is sufficient. When bile juice is diverted outside the body (nasobiliary, percutaneous, T-tube drainage), the level of immunosuppression medication, in particular cyclosporine, should be closely monitored. If a significant collection is formed, the latter must be drained to prevent infection, sepsis, and late adhesion. Large or complex leaks often require surgical revision due to a high probability of intra-abdominal abscess formation[54,55].

Bile stones and sludge

Formation of sludge, clots, casts and stones can cause bile obstruction. The reported incidence after LT ranges widely between 4%-10%[71,72].

Cyclosporine therapy, mucosal damage due to ischemia or infection and cholesterol supersaturation (often seen post-LT) could predispose to lithogenesis. In many cases, there is an underlying stricture. Usually, an ERC and sludge/stone extraction procedure is sufficient for definitive treatment with a success rate over 90%[72-76].

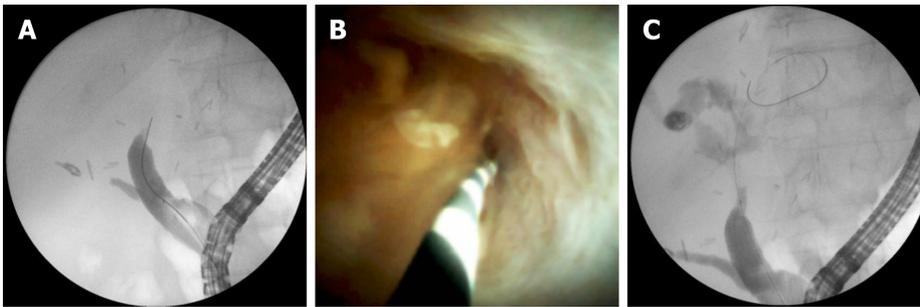


Figure 4 Complex anastomotic stricture. A: Impossible insertion of guidewire through a stricture; B: Guidewire insertion under direct visual control; and C: Guidewire inserted above anastomosis.

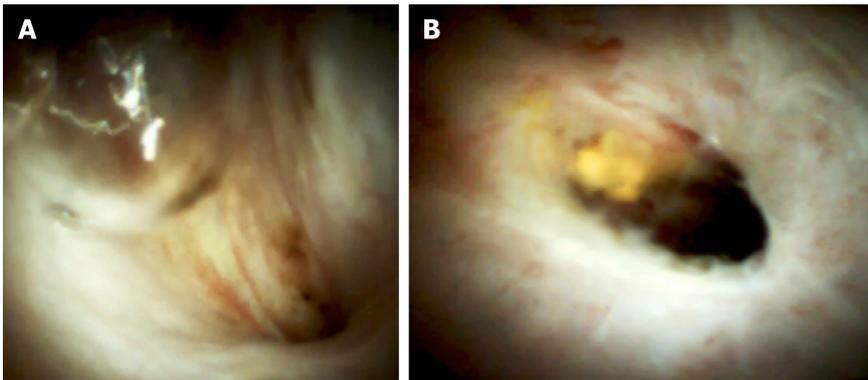


Figure 5 Digital cholangioscopy image of an anastomotic stricture.

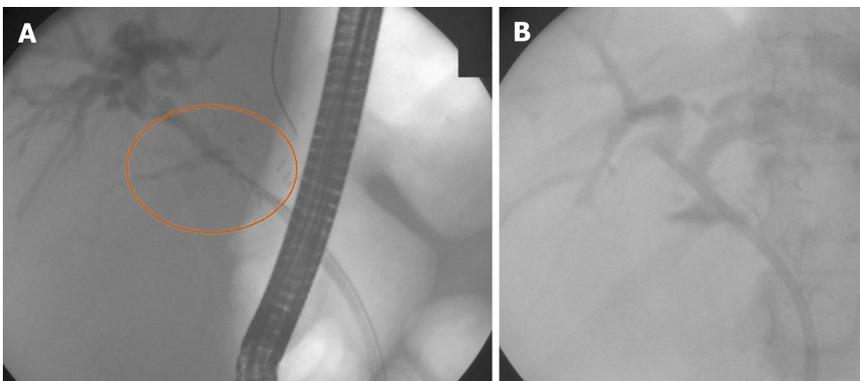


Figure 6 Anastomotic leak. A: Guidewire insertion; and B: Stent placement (10Fr).

According to Alazmi *et al*[45], there is a 17% incidence rate of recurrence within the first 6 mo after the procedure.

Well-known techniques, such as large balloon dilation and mechanical lithotripsy, are used in cases of large stones. In cases of difficult lithiasis such as multiple, large or intrahepatic stones, as well as stones over the stricture, extracorporeal lithotripsy could be applied. A study in 2015 reported six cases of difficult lithiasis that could not be treated with standard ERCP. Five of the six cases were managed with ECSL with no reported adverse events[77].

The limitations of endoscopic therapy can be overcome by means of digital cholangioscopy. Cholangioscopy provides an opportunity for visually controlled fragmentation of large biliary stones with little risk of biliary injury. Advanced intraductal techniques such as Holmium laser or Electrohydraulic lithotripsy achieve outstanding results in difficult cases, not suitable for ERC treatment (Figure 7)[62,78,79].

A research team from South Korea (Nam *et al*[79]) reported a case series of 15 patients (intrahepatic lithiasis $n = 10$, biliary cast syndrome $n = 3$, stones over the stricture $n = 2$) treated with percutaneous intrahepatic cholangioscopy. Eleven patients were successfully managed and no procedure-related adverse events were observed[79].

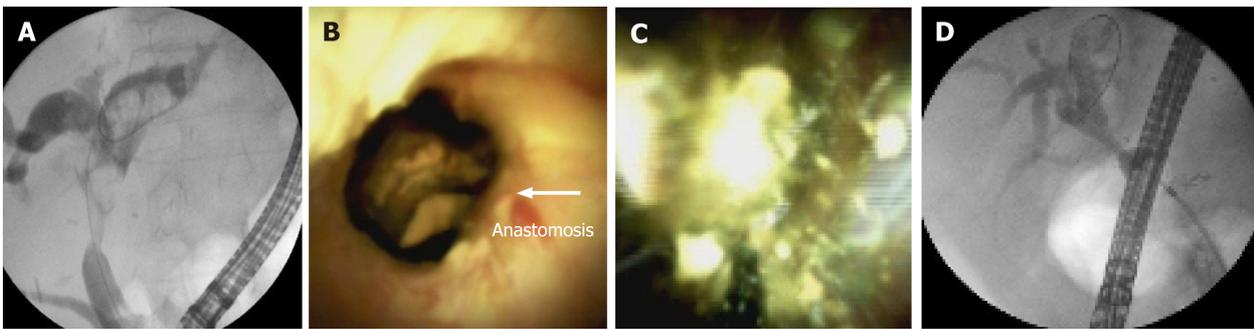


Figure 7 Multiple intrahepatic stones above anastomotic stricture. A: Fluoroscopic image; B: Digital cholangioscopic image; C: Electrohydraulic lithotripsy performance; and D: Fluoroscopic image after treatment.

Biliary cast syndrome

This disorder represents multiple filling defects in intra- and extrahepatic bile ducts, caused by casts adherent to the biliary epithelium. The reported incidence varies between 2.5% and 18%[80,81].

The pathogenetic mechanism is considered to be cell injury as a result of ischemia, acute cellular rejection, chronic rejection, infection, or bile stasis. The desquamated epithelial cells combined with bile components may form hard casts[82].

ERC with bile tree flushing and cast extraction will suffice in many cases. Balloon extractors and Dormia baskets are used for this purpose[81]. In cases of extended intrahepatic involvement or altered anatomy, a percutaneous procedure could be needed. In a study of 10 patients with biliary cast syndrome, mini-invasive (endoscopic/percutaneous) treatment was successful in 60% of cases[83].

Several studies noted good outcomes following cholangioscopy-guided therapy of bile cast syndrome (Figure 8). Nam *et al*[79] reported three cases, treated by percutaneous cholangioscopy.

Ursodeoxycholic acid is considered to have a role in the prophylaxis of bile cast syndrome. In cases refractory to mini-invasive therapy, surgery is required.

Sphincter of Oddi dysfunction

Chronic injury, denervation of the recipient's common bile duct (CBD), or fibrotic tissue formation could cause impaired ampullary relaxation and hypertension of the papilla of Vater. The role of biliary manometry in the diagnosis of SOD after transplantation is uncertain. Sphincterotomy is usually sufficient to resolve the obstruction[27,29]. In cases of firm fibrosis, stent placement could be in order[8, 21].

Mucocele

In rare cases, the donor's cystic duct could be incorporated in the suture line of the anastomosis. As a consequence, a blind mucosa-lined sac is formed. Due to accumulation of mucin, this sac can increase in size and cause bile obstruction due to external compression. Endoscopy could not provide sustainable resolution in such cases. Percutaneous drainage or surgical resection are effective treatment options. The differential diagnosis of mucocele is made with any type of fluid collection such as biloma, abscess, hemorrhage, and aneurysm[8,84,85].

Redundant CBD

The excessive length of the donor's common hepatic duct could lead to a sigmoid-shaped deflection of the CBD. This could entail bile outflow deterioration. The reported incidence is 1.6% in all LT. ERC with long plastic stent placement usually resolves cholestasis. In very rare cases, surgery with a new biliodigestive anastomosis is needed[86].

Haemobilia

Spontaneous haemorrhage in the biliary tree after LT occurs rarely with a reported frequency of 1.2%. There are reported cases of haemobilia associated with large biliary stones over the stricture. More often, haemobilia is iatrogenic, *i.e.* subsequent to percutaneous biliary drainage or liver biopsy. Rupture of a hepatic artery pseudoaneurysm can cause severe biliary haemorrhage. Recipient high BMI and alcoholic liver disease were significant risk factors for spontaneous haemobilia reported in a study including 2701 post-LT patients[87].

ERC with clot extraction and nasobiliary drainage placement is the first-choice therapy. Nasobiliary drainage ensures an opportunity for biliary lavage, which prevents the development of cholangitis and indicates the presence of recurrent bleeding. In most cases, the combination of endoscopic desobstruction therapy, coagulation correction, and supportive medication yields good results. In cases of severe haemorrhage, selective embolization techniques are reported to be successful. Plastic biliary stents or fSEMS were reported to be effective haemostatic tools in studies of non-transplant patients

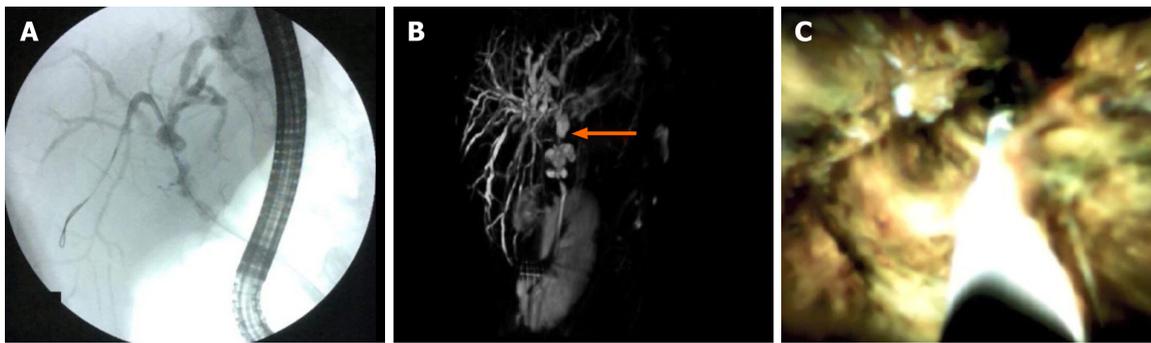


Figure 8 Biliary cast syndrome. A: Fluoroscopic image; B: Magnetic resonance cholangiopancreatography; and C: Digital cholangioscopic image.

with significant haemobilia[88-90].

Due to low incidence, there are not enough data regarding post-transplant patients with severe haemobilia.

Foreign bodies

Suture materials or T-tube remnants could form a nidus for bile sediment and stones. ERC and PTC are effective methods for detection and clearance of bile duct remnants[59].

CONCLUSION

Known as the Achilles' heel of liver transplantation, biliary complications are observed in one quarter of all patients. Their prevalence has increased due to the worldwide increase in liver transplantation. Living donor liver transplantations have a higher complication rate and presuppose more complicated treatment scenarios with lower success rates. Endoscopic stent insertion is the key treatment for most biliary complications. Percutaneous or EUS-guided puncture and cholangioscopy are feasible options for biliary access when standard fluoroscopic cannulation fails. A wide variety of accessories have been developed to overcome the complexity of living donor liver transplantation complications, but the treatment success rate remains unsatisfactory. Early recognition and aggressive management are essential for the reduction of morbidity and mortality in patients with biliary complications.

FOOTNOTES

Author contributions: All authors contributed equally to this paper.

Conflict-of-interest statement: Petko Karagyozov has received fees for proctoring SpyGlass DS procedures from Boston Scientific Corp.

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Country/Territory of origin: Bulgaria

ORCID number: Irina Boeva 0000-0001-6381-0949; Petko Ivanov Karagyozov 0000-0002-2297-547X; Ivan Tishkov 0000-0002-6175-7272.

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Shifting perspectives – interplay between non-alcoholic fatty liver disease and insulin resistance in lean individuals

Ines Bilic-Curcic, Maja Cigrovski Berkovic, Lucija Virovic-Jukic, Anna Mrzljak

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Ines Bilic-Curcic, Department of Pharmacology, Faculty of Medicine, University of J. J. Strossmayer Osijek, Osijek 31000, Croatia

Ines Bilic-Curcic, Clinical Hospital Center Osijek, Osijek 31000, Croatia

Maja Cigrovski Berkovic, Department of Kinesiological Anthropology and Methodology, Faculty of Kinesiology, University of Zagreb, Zagreb 10000, Croatia

Maja Cigrovski Berkovic, Clinical Hospital Dubrava, Zagreb 10000, Croatia

Lucija Virovic-Jukic, Department of Medicine, Division of Gastroenterology and Hepatology, Sisters of Charity University Hospital, Zagreb 10000, Croatia

Lucija Virovic-Jukic, Anna Mrzljak, School of Medicine, University of Zagreb, Zagreb 10000, Croatia

Anna Mrzljak, Department of Medicine, Merkur University Hospital, Zagreb 10000, Croatia

Corresponding author: Anna Mrzljak, FEBG, MD, PhD, Associate Professor, Department of Medicine, Merkur University Hospital, Zajčeva 19, Zagreb 10000, Croatia.

anna.mrzljak@gmail.com

Abstract

Non-alcoholic fatty liver disease (NAFLD) has become a significant public health burden affecting not only obese individuals but also people with normal weight. As opposed to previous beliefs, this particular subset of patients has an increased risk of all-cause mortality and worse outcomes than their obese counterparts. The development of NAFLD in lean subjects seems to be interconnected with metabolic phenotype, precisely visceral fat tissue, sarcopenia, and insulin resistance. Here, we summarize available data focusing on the co-dependent relationship between metabolic phenotype, insulin resistance, and development of NAFLD in lean individuals, suggesting more appropriate tools for measuring body fat distribution for the screening of patients at risk.

Key Words: Non-alcoholic fatty liver disease; Metabolic phenotype; Lean individuals; Insulin resistance; Visceral fat tissue; Sarcopenia

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Core Tip: The prevalence of non-alcoholic fatty liver disease among non-obese (overweight or lean) individuals seems to be much higher than previously reported, affecting almost 20% of the non-obese population. Non-alcoholic fatty liver disease is no longer considered solely an obesity-related disorder since non-obese individuals participate significantly in this entity. The metabolic phenotype is the key role-player in the development of non-alcoholic fatty liver disease in lean individuals. The detection of lean patients with non-alcoholic fatty liver disease is particularly challenging since the body-mass index is not a good indicator of metabolic health.

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INTRODUCTION

Non-alcoholic fatty liver disease (NAFLD), recently known as metabolic-associated fatty liver disease [1], is one of the most common causes of chronic liver disease. NAFLD was traditionally associated with metabolic syndrome encompassing obesity, insulin resistance, hypertension, and atherogenic dyslipidemia [2]. Recently, a new clinical entity, including NAFLD in non-obese/lean individuals has emerged. It soon became apparent that the existence of NAFLD in non-obese subjects should not be neglected since its prevalence has significantly increased. According to a recently published meta-analysis, up to 40% of NAFLD patients are non-obese, with the highest prevalence in western countries as opposed to previous findings dominantly allocating this entity in Asian regions [3]. The clinical consequences of NAFLD can be detrimental; for instance, progression to significant fibrosis remains uncertain as well as long-term cardiometabolic complications and mortality [4-7]. However, prevalence data and terminology are quite variable since definitions used to determine lean and obese patients differ among various studies, depending on Asian or Caucasian cutoff values. In addition, a body mass index (BMI) cutoff value of 25 kg/m² is frequently used to differ between lean and obese individuals, thus excluding the overweight population (Table 1). Here, we decided to use terms “non-obese” or “lean NAFLD” depending on the study in question and definitions used.

The recognition of NAFLD in lean individuals is associated with a concept known as the metabolic phenotype. There are separate subgroups of individuals divided according to their phenotype and metabolic profile to metabolically unhealthy normal weight (MUHNW) and metabolically healthy obese (MHO), the latter being disputable due to higher incidence of cardiovascular disease (CVD) in long-term studies [8]. Distinguishing between those phenotypes is based on BMI, an inadequate surrogate marker for determining the quantity of skeletal muscle mass and adipose tissue, especially in the visceral area [9]. As a consequence, a MUHNW individual could be a person with sarcopenia and a high proportion of fat tissue, with a high probability of developing insulin resistance and/or metabolic syndrome (MetS), subsequently leading to the development of NAFLD [10]. In addition, other factors could be involved in the pathogenesis of NAFLD in lean subjects such as genetics [*e.g.*, patatin-like phospholipase domain-containing 3 (PNPLA3) variant (rs738409 C/G)] [11], environmental factors including dietary habits [12,13] and physical activity [14], changes in gut microbiota [15], and secondary causes such as hypothyroidism or polycystic ovary syndrome.

Lean NAFLD patients were traditionally considered to have milder metabolic disturbances, thus carrying a lower risk for the development of CVD and progression to non-alcoholic steatohepatitis (NASH) and fibrosis [6,16,17]. However, recent data suggest that progression to diabetes as well as NASH and fibrosis is higher in lean NAFLD individuals, undoubtedly linking visceral fat tissue with undesirable consequences of MUHNW phenotype [5,10,18,19]. Still, a contribution of specific components of MetS to fibrosis remains unclear, although insulin resistance seems the most probable culprit [20-22], Table 1.

In this critical review, we summarized available data and addressed practical issues of whether it is time to shift perspectives away from the scale and how to screen for non-obese patients with a metabolically unhealthy profile.

METABOLIC PHENOTYPE – THE KEY ROLE PLAYER IN THE DEVELOPMENT OF NAFLD IN LEAN INDIVIDUALS

Obesity is generally associated with severe health consequences, mainly related to increased

Table 1 Prevalence, characteristics, and outcomes in lean/non-obese individuals with non-alcoholic fatty liver disease

Author, year	Population, study design, sample size	Prevalence of NAFLD in lean subjects	Main findings
Zou <i>et al</i> [4], 2020	Mixed population, 1999-2016 NHANES databases	32.3% overall NAFLD prevalence; 22.7% obese and 9.6% non-obese; Amongst NAFLD patients, 29.7% were non-obese (Caucasian BMI 25-30 kg/m ² , Asian BMI 23-27 kg/m ²), of which 13.6% had lean NAFLD (Caucasian BMI < 25 kg/m ² , Asian BMI < 23 kg/m ²)	Non-obese NAFLD individuals had higher 15-year cumulative all-cause mortality (51.7%) than obese NAFLD (27.2%) and non-NAFLD (20.7%)
Huang <i>et al</i> [20], 2020	2483 Asian participants, community based study	44.5% NAFLD and 15.8% MetS prevalence; Among NAFLD subjects, 48.8% were obese (BMI ≥ 24 kg/m ²)	IR is predictive of NAFLD irrespective of BMI; CV risk calculated by Framingham Risk Score may exist in lean NAFLD subjects
Tobari <i>et al</i> [18], 2020	Asian, biopsy-proven 762 NAFLD patients, cross sectional study	Over 25% men and almost 40% women were non-obese, but most of them had visceral fat obesity and/or IR; BMI cutoff 25 kg/m ²	NAFLD was not milder in non-obese patients; Histological steatosis was associated with BMI; Advanced fibrosis was not associated with BMI and showed a significant sex difference
Kim <i>et al</i> [10], 2020	664 Asian subjects with biopsy-proven NAFLD and controls, cross sectional study	542 subjects with biopsy-proven NAFLD (132 non-obese NAFLD (BMI < 25 kg/m ²); 410 obese NAFLD (BMI > 25 kg/m ²); 122 controls	Non-obese subjects with NAFLD displayed a similar severity of histological liver damage; Sagittal abdominal diameter was independently associated with significant fibrosis among subjects with non-obese NAFLD
Alferink <i>et al</i> [71], 2019	4609 elderly European, population based study	1623 had NAFLD (<i>n</i> = 161 normal-weight and <i>n</i> = 1462 overweight, BMI cutoff 25 kg/m ²)	Both high fat mass and low SMI were associated with normal-weight NAFLD; Fat distribution (assessed by AGR) could best predict NAFLD prevalence
Denkmayr <i>et al</i> [19], 2018	European, 466 patients diagnosed with NAFLD, cross sectional study	Lean (BMI ≤ 25.0 kg/m ² , <i>n</i> = 74); Overweight (BMI > 25.0 ≤ 30.0 kg/m ² , <i>n</i> = 242); Obese (BMI > 30.0 kg/m ² , <i>n</i> = 150)	Lean NAFLD patients had a histological picture similar to obese patients but more severe compared to overweight patients.
Gonzalez-Cantero <i>et al</i> [21], 2018	European, cross-sectional study 113 non-obese, non-diabetic individuals	55 patients diagnosed with NAFLD; NAFLD defined as hepatic triglyceride content > 5.56% (quantified by 3T H1-MRS); BMI cutoff 25 kg/m ²	Lean-with-NAFLD group had significantly higher HOMA-IR and lower serum adiponectin than the overweight-without-NAFLD group; IR was independently associated with NAFLD but not with waist circumference or BMI
Hagström <i>et al</i> [5], 2017	European, prospective cohort study of 646 patients with biopsy-proven NAFLD	19% lean NAFLD; 52% overweight NAFLD; 29% obese NAFLD; BMI cutoff 25 and 30 kg/m ²	Lean NAFLD had lower stages of fibrosis and higher risk for severe liver disease development compared to patients with NAFLD and a higher BMI, independent of available confounders (follow-up 19.9 years)
Leung <i>et al</i> [6], 2017	Asian, prospective, 307 NAFLD patients	23.5% were non-obese; BMI cutoff 25 kg/m ²	Non-obese NAFLD patients have less-severe disease and may have a better prognosis than obese patients; Hypertriglyceridemia and higher creatinine are the key factors associated with advanced liver disease in non-obese patients
Fracanzani <i>et al</i> [11], 2017	European, retrospective cohort study of 669 patients with biopsy-proven NAFLD	143 patients had BMI < 25 kg/m ² and NAFLD	20% of patients with lean NAFLD have NASH, fibrosis scores of 2 or higher, and carotid atherosclerosis
Feldman <i>et al</i> [22], 2017	Caucasian, cross sectional, 187 subjects with hepatic steatosis on ultrasound	Lean healthy (BMI ≤ 25 kg/m ² , no steatosis, <i>n</i> = 71); Lean NAFLD (BMI ≤ 25 kg/m ² , steatosis, <i>n</i> = 55); obese NAFLD (BMI ≥ 30 kg/m ² , steatosis; <i>n</i> = 61)	Lean NAFLD have impaired glucose tolerance, low adiponectin concentrations and an increased rate of PNPLA3 risk allele carriage
Feng <i>et al</i> [7], 2014	Asian, population based, 1779 participants	The prevalence of NAFLD was 18.33% in the lean group and 72.90% in the overweight-obese group BMI cutoff 24 kg/m ²	Lean-NAFLD was more strongly associated with diabetes, hypertension, and MetS than overweight-obese-NAFLD; NAFLD patients were more likely to have central obesity especially in lean groups
Younossi <i>et al</i> [17], 2012	Mixed population, 1988-1994 NHANES databases	2185 (18.77% ± 0.76%) of subjects had NAFLD; 7.39% ± 0.65% had lean NAFLD; 27.75% ± 1.00% had overweight/obese NAFLD BMI cutoff 25 kg/m ²	Lean NAFLD was independently associated with younger age, female sex, and a decreased likelihood of having IR and hypercholesterolemia
Margariti <i>et al</i> [16], 2012	European, cross sectional, 162 NAFLD patients	Normal BMI was present in 12% of patients; BMI cutoff 25 kg/m ²	Lean NAFLD patients do not have IR-associated metabolic disorders, but they have higher levels of ALT/AST than the overweight or obese NAFLD patients

3T H1-MRS: 3Tesla H1-magnetic resonance spectroscopy; ALT: Alanine aminotransferase; AGR: Android gynoid ratio; AST: Aspartate aminotransferase; BMI: Body mass index; CV: Cardiovascular; IR: Insulin resistance; MetS: Metabolic syndrome; NAFLD: Non-alcoholic fatty liver disease; NASH: Non-

alcoholic steatohepatitis; SMI: Skeletal muscle index.

cardiovascular risk[8]. However, a subset of obese patients will never develop cardiovascular disease and is therefore considered an MHO. Conversely, metabolically unhealthy patients exist even in the group of normal-weight people, the category known as the MUHNW. People with this phenotype seem to have 1.5 to 3-times higher risk for cardiometabolic complications than metabolically healthy normal-weight people and even higher risk than MHO[23,24], but unfortunately often go under the radar for cardiovascular screening and primary outcome prevention.

Generally, the assessment of cardiovascular risk, regardless of the patient's BMI, was historically mainly based on the presence of the MetS. However, according to data from prospective studies, only a smaller proportion of individuals in the normal-weight category with cardiovascular events have MetS compared to patients with cardiovascular events who were overweight or obese (20% compared to 52% and 76%, respectively)[25]. Although MetS as such might not be an accurate predictor of CV risk in normal-weight individuals, its components, especially, lipids and glucose level, as well as waist circumference and waist-to-hip ratio might be useful for risk stratification[9,26,27]. On the other hand, up to 30% of normal-weight individuals can be classified as metabolically obese normal weight having an increased cardiometabolic risk.

It seems that the distribution and health of fatty tissue, rather than its amount, is likely the major determinant of disease risk. For example, higher amounts of visceral fat compared to peripheral and subcutaneous fat comprise a higher metabolic risk and are directly linked to both liver inflammation and fibrosis, independently of insulin resistance and hepatic steatosis[24,28-30].

Some previously published studies have failed to show an association of insulin resistance and NAFLD in lean individuals[16,17]. However, more recently published studies have demonstrated the opposite, linking insulin resistance with the development of NAFLD, irrespective of BMI[10,20-22].

In a study published by Kim *et al*[10] comparing non-obese with MetS and obese without MetS, the ratio of visceral adipose tissue area-to-subcutaneous adipose tissue area (VAT/SAT) was independently linked with NASH or fibrosis in a dose-dependent manner, confirming that metabolic phenotype is crucial in the progression of liver disease, irrespective of the presence of obesity. Lean with MetS were non-obese, had insulin resistance, and an increased VAT area[10]. Another community-based study in the Asian population demonstrated that insulin resistance was a significant predictive factor for NAFLD in both obese and lean subjects[20].

Obviously, metabolic disturbances are responsible for disease progression, with insulin resistance being a key role player (Figure 1). The mechanisms involved seem to be similar as in obese individuals [22]. Higher levels of free fatty acids, enhanced adipose tissue lipolysis, and decreased fat storage capacity of subcutaneous fat tissue overcome fatty acid oxidation and triglyceride secretion leading to the accumulation of triglycerides in hepatocytes[23,31]. An increase in lipotoxicity causes pronounced oxidative stress[32], whereas chronic inflammation is continuously being fueled by changed adipokine secretion from visceral adipocytes, primarily decreased adiponectin secretion together with mitochondrial dysfunction leading to further liver injury[23,31].

Some of the major game-changers determining the nature of metabolic profiles are dietary intake and physical activity. To date, published data indicate a correlation between weight gain in non-obese individuals with the development of NAFLD[12,13], suggesting that calorie intake and modest weight gain in non-obese individuals have deleterious effects on metabolic disturbances primarily through an increase in visceral adipose tissue. Conversely, waist circumference and body weight reduction achieved through lifestyle intervention were independent predictors of NAFLD resolution in lean subjects[33]. Furthermore, sarcopenia is positively correlated to insulin resistance in obese patients and is considered one of the major factors responsible for the obesity paradox[14]. The potential mechanisms involved are the accumulation of intramyocellular lipid and intermuscular adipocytes, chronic inflammation, and loss of insulin sensitivity to protein synthesis preceding insulin resistance to glucose metabolism[34]. Thus, we could hypothesize that the unfavorable ratio of skeletal muscle mass and visceral adipose tissue in non-obese individuals is one of the main determinants of insulin resistance. Indeed, it has been shown that physical activity increases skeletal muscle mass, thus improving sarcopenia and lean/fat tissue mass ratio advancing metabolic health in non-obese individuals through the reduction of insulin resistance[18,35].

OTHER RISK FACTORS INVOLVED IN THE DEVELOPMENT OF NAFLD IN LEAN INDIVIDUALS

Compared to obese and overweight NAFLD patients, some clinical, biochemical, and histological distinctions have been observed in lean NAFLD subjects, going far beyond the simple differences in the BMI. Specifically, low adiponectin levels and high concentrations of proinflammatory cytokines suggest a pronounced degree of adipose tissue dysfunction and distinct metabolic and gut microbiota profiles

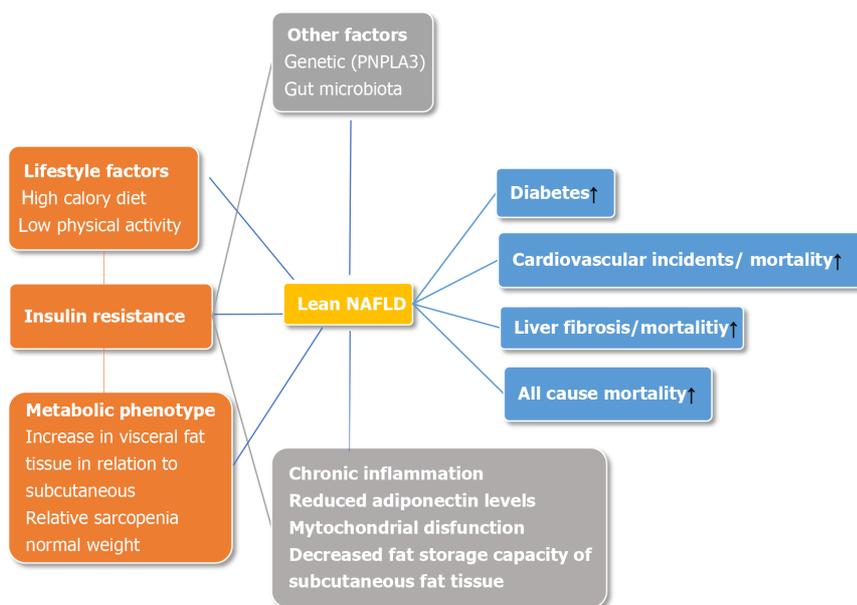


Figure 1 Pathophysiological mechanisms and outcomes of non-alcoholic fatty liver disease in non-obese individuals. NAFLD: Non-alcoholic fatty liver disease.

[11,19,36-38]. Additionally, impaired glucose metabolism and carriage of the *PNPLA3* minor allele was seen in lean Caucasian NAFLD patients[22].

Genetic factors

Several genes and single-nucleotide polymorphisms (SNPs) associated with NAFLD have been identified, of which transmembrane 6 superfamily member 2 (*TM6SF2*)[39-41] and the patatin like *PNPLA3*[42-44] are the most investigated ones.

The rs58542926 genetic variant of *TM6SF2* gene, which encodes the E167K aminoacidic substitution and determines neutral fat accumulation in the liver, has been implicated in NAFLD development. Previous studies suggested a significant association between the *TM6SF2* polymorphism and disease severity and/or progression[39,41].

The rs738409 genetic variant of the *PNPLA3* gene, which takes part in lipid transformation, is now recognized as the major genetic determinant of NAFLD. A meta-analysis based on 23 case-control studies involving 6071 NAFLD patients and 10366 controls showed that *PNPLA3* rs738409 polymorphism is associated with disease severity and progression and that these changes were not influenced by the ethnicities or age of subjects[45]. In addition, Shen and al. demonstrated that the G allele in *PNPLA3* rs738409 increases the risk of NAFLD, especially in subjects without MetS, independent of dietary pattern and metabolic factors[46].

Genetic background for developing NAFLD in the absence of obesity has also been investigated in different populations. Initial reports on NAFLD in lean individuals originated mostly from an Asian background[7,47,48], and implicated Asian ethnic preponderance. However, “non-obese” NAFLD makes just over 40% of the NAFLD population and is common in both eastern and western countries[3].

Earlier studies in Asian populations found that the G allele at the *PNPLA3* rs738409 mutation has been more common in lean than obese NAFLD patients (78.4% vs 59.8%; $P = 0.001$)[49]. However, a study investigating the prevalence of metabolic co-morbidities and *PNPLA3* risk alleles (GG) in the Japanese population did not confirm the difference among the non-obese, obese, and severely obese groups of both sexes[18]. Similarly, a recently published study in the Chinese population found no difference in the SNPs of several genes (*SIRT1*, *APOC3*, *PNPLA3*, *AGTR1*, and *PPARGC1A*) between lean subjects with and without NAFLD[50].

In the Caucasian population, Feldman *et al*[11] showed a high rate of *PNPLA3* risk alleles (CG/GG) in the lean NAFLD group compared with lean controls (odds ratio [OR] 2.676, $P = 0.007$), but at a comparable rate to obese NAFLD subjects (OR 0.759, $P = 0.464$)[22]. Another study investigating gene polymorphisms in the Caucasian population demonstrated that in lean NAFLD subjects, the only independent variable associated with NASH and significant fibrosis (≥ 2) was the GG *PNPLA3* polymorphism[11]. In addition, in lean NAFLD patients, a significantly higher prevalence of *TM6SF2* E167K variant carriers was associated with more severe steatosis, inflammation, and NASH.

Gut microbiota

The human gut microbiota (GM) forms a complex ecosystem involving different microorganisms

(bacteria; dominated by four bacterial phyla: Bacteroidetes, Firmicutes, Proteobacteria, and Actinobacteria[51], viruses, uni/pluricellular eukaryotes) that have been implicated in various physiological processes[52]. The impact of diet on GM composition and function is well established, and alterations in the microbiome composition have been associated with the development of obesity, diabetes, MetS and NAFLD[15,53,54]. Previous studies have identified that NAFLD patients have altered microbiome with fewer proportions of Bacteroidetes and higher proportions of Porphyromas and Prevotella than healthy individuals[55,56]. Moreover, an increase in *Lactobacillus*, *Escherichia*, *Streptococcus* abundance, decrease in *Ruminococcaceae*, and *Faecalibacterium prausnitzii*, have also been identified in NAFLD patients[57-59].

In addition, substantial differences in fecal and blood microbiota profiles between obese and lean individuals with NAFLD have been identified in the Asian population[18]. Similarly, a Brazilian study confirmed a specific gut microbiota composition in lean NASH patients, showing a lower abundance of *Faecalibacterium* and *Ruminococcus*, and a deficiency in *Lactobacillus* compared with overweight and obese NASH patients[60]. These differences in microbiota composition between lean and obese NAFLD patients may serve as biomarkers for identifying the specific metabolic NAFLD phenotype.

AVOIDING PITFALLS IN THE DIAGNOSIS OF LEAN NAFLD

After publishing a meta-analysis on metabolic health, which suggested the highest CV risk among individuals of normal weight who are metabolically unhealthy (response rate [RR] 3.14, 95% confidence interval [CI] 2.36-3.93)[61], Kramer *et al*[61] raised the need to phenotype metabolically unhealthy individuals.

Currently, definitions of metabolic health are not unique (Table 2). Sometimes they include either the absence of insulin resistance[62,63], or the absence of insulin resistance and low C-reactive protein (CRP) levels as a surrogate marker for inflammation, in combination with up to any two parameters of MetS[64,65]. In clinical practice, only the latter are used[66,67].

The study by Stefan *et al*[23] (2017) was the first head-to-head comparison of cardiometabolic risk phenotypes suggesting that metabolically unhealthy lean people mainly have insulin secretion failure, insulin resistance, and increased carotid intima-media thickness. Among the aforementioned, insulin resistance is the most widely used cardiovascular risk marker. Metabolically unhealthy normal-weight subjects (defined by a BMI < 25 kg/m² and presence of insulin resistance), compared to their healthy counterparts, in addition to elevated CV risk, have an elevated risk of colorectal cancer (OR = 1.59, 95%CI: 1.10-2.28)[68].

As already mentioned, BMI is an inadequate surrogate marker of metabolic health, especially in determining the ratio of visceral and subcutaneous fat tissue, the most important risk factors of NAFLD's insulin resistance and progression in lean individuals[10]. In addition, data on muscle mass are missing, thus providing no information on sarcopenia[69], which is clinically relevant in the development of NAFLD in lean patients. Thus waist circumference and/or waist-to-hip ratio might be a better tool. However, waist circumference is mostly dependent on BMI, meaning that normal-weight patients could have waist circumference in the normal range, but still have higher visceral fat tissue and increased cardiometabolic risk[9]. This issue could be avoided by using waist circumference adjusted for BMI, which has shown a strong linear increase in risk for cardiovascular mortality[70], but no data are available on the association of adjusted waist circumference and NAFLD in lean individuals.

Additionally, in an elderly population-based study, both high-fat mass and low skeletal muscle index were associated with normal-weight NAFLD, although fat distribution assessed by the android gynoid ratio was the best predictor of NAFLD prevalence[71].

CLINICAL AND THERAPEUTIC IMPLICATIONS OF NAFLD IN LEAN INDIVIDUALS ASSOCIATED WITH INSULIN RESISTANCE

The liver-related and general outcomes of patients with NAFLD depend on a number of factors including the presence of metabolic risk factors, especially type 2 diabetes mellitus and hypertension, severity of fibrosis, genetic predisposition, age, diet and other environmental factors.

Metabolic consequences

Regarding metabolic health and clinical outcomes, cardiometabolic complications take the most prominent place in driving the mortality. It seems that metabolically unhealthy, regardless of BMI, including individuals within the normal range of BMI category, have the highest risk of cardiometabolic consequences[72]. Moreover, in a recently published study, normal-weight patients with central adiposity and coronary artery disease had a worse survival rate than normal, overweight, or obese subjects without central obesity[73]. However, long term studies in lean NAFLD patients and cardiovascular health are lacking. In a retrospective study of lean Caucasian patients with biopsy-

Table 2 Definitions of metabolic health in non-obese

Definitions of metabolic health in non-obese individuals:	
Absence of insulin resistance	Meigs <i>et al</i> [62]; Stefan <i>et al</i> [63]
Absence of insulin resistance and low CRP levels as a surrogate marker for inflammation, in combination with up to any two parameters of metabolic syndrome	Wildman <i>et al</i> [64]; Karelis <i>et al</i> [65]
Combination with up to any two parameters of metabolic syndrome	Stefan <i>et al</i> [66]; Phillips[67]
Definition of metabolically unhealthy non-obese individuals:	
BMI < 25 kg/m ² and presence of insulin resistance	Stefan <i>et al</i> [23]
Waist circumference adjusted for BMI and/or android gynoid ratio and presence of insulin resistance	Suggested by authors

BMI: Body mass index; CRP: C-reactive protein.

proven NAFLD *vs* obese or overweight individuals, 20% of patients who were lean developed NASH, significant fibrosis, and carotid atherosclerosis[11].

A study by Feng and coauthors addressed the question of metabolic consequences and laboratory discrepancies in lean subjects with NAFLD. Compared to obese and overweight NAFLD counterparts, lean Chinese NAFLD individuals had a higher risk of developing diabetes (OR = 2.47, 95%CI: 1.14-5.35), hypertension (OR = 1.72, 95%CI: 1.00-2.96) and MetS (OR = 3.19, 95%CI: 1.17-4.05), making them prone to the development of cardiovascular disease[7].

In terms of mortality, the higher fat mass could be associated with better nutritional state associated with higher survival rates (also known as obesity paradox); thus, lean individuals with the more severe and advanced liver disease could have a poor prognosis, especially if sarcopenia is present[74]. This was confirmed in a recently published meta-analysis, encompassing 93 studies including lean NAFLD individuals, demonstrating that all-cause mortality, liver-related mortality, and cardiovascular-related mortality in non-obese individuals with NAFLD was higher than that of obese individuals with NAFLD (12.1 *vs* 7.5 per 1000 person-years; 4.1 *vs* 2.4 per 1000 person-years; 4.0 *vs* 2.4 per 1000 person-years respectively)[3].

In addition, NHANES based study demonstrated that non-obese NAFLD individuals had increased 15-year cumulative all-cause mortality (51.7%) compared to obese NAFLD (27.2%) and non-NAFLD (20.7%) patients[4].

Therefore it seems that NAFLD in lean individuals has serious cardiometabolic complications leading to an increase in mortality, even higher than in their obese counterparts.

Liver consequences - fibrosis, cirrhosis and cancer

Non-alcoholic fatty liver disease encompasses a spectrum of histological changes with different evolution and outcomes, ranging from simple steatosis to NASH with varying degree of fibrosis. The later entity is characterized by lobular inflammation and hepatocyte ballooning degeneration accompanied by various stages of fibrosis that more often progresses to cirrhosis. However, fibrosis can be found in liver biopsy specimens in the absence of significant inflammation; in a recent multicenter study from Italy and Finland, 34% of patients with significant fibrosis did not have NASH and 10.0% had no inflammation[75].

Currently there are no published data on the specific inflammatory pathways or hepatic stellate cells activation pathways that would be unique to the development of NASH in lean patients as opposed to obese NASH patients. It is therefore believed that progression of NASH in lean individuals follows pathways similar to those demonstrated in obese patients with NASH, and that rate of progression probably depends on the similar risk factors as in their obese counterparts[76].

In general, NAFLD is a slowly progressive disease, but more rapid progression occurs in 20% of patients[77]. In a meta-analysis of over 400 patients with paired liver biopsy, 34% of NAFLD patients had fibrosis progression, 43% had stable fibrosis, and 22% showed an improvement in the fibrosis stage during follow-up[77]. The rate of progression was doubled in the presence of arterial hypertension[77]. The data on the natural history and prognosis of lean patients with NAFLD remains conflicting. Although better or similar metabolic and histological profiles than in obese NAFLD patients are mainly suggested, long term liver related outcomes remain an open question[5,6,19].

In a retrospective cohort study from Italy, significantly lower proportions of lean NAFLD patients had NASH (17% *vs* 40% of obese or overweight patients), and significant fibrosis of F2 or more (17% *vs* 42% for obese/overweight NAFLD patients)[11]. However, lean patients with high waist circumference had increased risk of significant fibrosis of F2 or more, compared to overweight/obese subjects with the same waist circumference[11]. A study from two university centers from Sweden with a median follow-up of 20 years reported that 50% of lean patients had NASH compared to 65% and 80% of overweight

and obese subjects[5]. Yet, lean patients with NAFLD had slightly more events of severe liver disease (defined as decompensated liver disease, liver failure, hepatocellular carcinoma, or cirrhosis) compared to overweight patients (16% *vs* 9%), but similar to obese patients (14%)[5]. The main finding of the study was that although lean patients had a better prognostic profile at baseline with less advanced fibrosis and NASH, an increased risk for the development of severe liver disease was found compared to patients with a higher BMI[5].

In a study from Hong Kong, non-obese patients had lower NAFLD activity score and lower fibrosis stages compared to obese patients[6]. In a recently published meta-analysis, 39% of non-obese or lean NAFLD patients had NASH (compared to 53% of obese individuals), 25% had significant lobular inflammation (compared to 36% of obese), 29% had significant fibrosis of F2 or more (compared to 38% of obese individuals), and 3% had cirrhosis in one study[3]. However liver related mortality was higher in non-obese NAFLD subjects compared to obese equivalents (4.1 per 1000 person-years *vs* 2.4 per 1000 person-years)[3].

Additionally, in a study published by Kim *et al*[10] progression to NASH and fibrosis was equally present in non-obese patients with MetS and obese patients without MetS (55%-60%) linking metabolic phenotype with the liver disease progression.

Cirrhosis of any etiology is a well-known risk factor for the development of hepatocellular carcinoma (HCC); the same is true for NAFLD-induced cirrhosis. The reported incidence of HCC development in patients with NAFLD varies significantly depending on the study population, ranging from 0.25% to 11% after 5 years[78,79]. Furthermore, in a significant proportion of patients, ranging from 23% to 46%, HCC has been reported to develop in the earlier stages of the disease, before the development of cirrhosis[80,81]. Except for the study of Hagström *et al*[5] where the incidence of hepatocellular carcinoma was collectively reported with other liver-related outcomes, no data on the incidence and risk of HCC development in the subgroup of lean patients with NAFLD has been published. Until new data becomes available, no conclusions can be drawn on the risk for HCC development in lean individuals with NAFLD.

MANAGEMENT

As 3%-25% of lean/non-obese and non-diabetic individuals are diagnosed with NAFLD, with potential for progression to NASH and subsequently liver fibrosis with metabolic dysfunction, it is of interest to find pharmacological modalities and lifestyle interventions to treat this specific phenotype[82-84]. Animal studies on obese rats and mice showed significant reductions in hepatic steatosis and oxidative stress when glucagon-like peptide-1 receptor agonists (GLP-1RAs) were used to treat liver steatosis with no or mild fibrosis[85,86]. Moreover, randomized control trial investigating the role of liraglutide (daily GLP-1RA) reported on histological resolution of NASH after 48 wk of treating obese and overweight NASH patients[87]. Data on lean NAFLD/NASH counterparts are lacking, but recently published animal study gave promising results. Ipsen and colleagues reported on liraglutide effects in reducing both inflammation and hepatocyte ballooning in advanced NAFLD in an animal model. The treatment was more effective than dietary intervention, and when the two were combined, they led to rapid weight loss[88].

Still, available data on the treatment and management of lean subjects with NAFLD are practically non-existent, and further studies are needed to evaluate the effects of lifestyle changes and pharmacotherapy in this vulnerable population.

CONCLUSION

NAFLD in lean individuals presents a severe global burden with detrimental clinical consequences. Determining metabolic phenotype is crucial for detecting normal-weight patients at risk of developing NAFLD and preventing possible long-term complications, such as the cardiometabolic, liver, and all-cause mortality, which may be even more pronounced than in the obese individuals. The main characteristic of MUHNW seems to be insulin resistance associated with visceral adiposity; thus, waist circumference or the android gynoid ratio along with HOMA IR could be better predictors of NAFLD in lean subjects than traditionally used BMI and other components of metabolic syndrome. Insulin resistance is undoubtedly associated with the development of NAFLD in lean individuals irrespective of BMI and the presence of MetS; however, is it causality or correlation remains an open question.

FOOTNOTES

Author contributions: Bilic-Curcic I made contributions to the conception and design of the study, involved in drafting and revising the manuscript critically; Cigrovski Berkovic M, Virovic-Jukic L and Mrzljak A were involved

in collecting the data, and drafting and writing the manuscript; All authors read and approved the final manuscript.

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Country/Territory of origin: Croatia

ORCID number: Ines Bilic-Curcic 0000-0002-8861-5987; Maja Cigrovski Berkovic 0000-0003-0750-9785; Lucija Virovic-Jukic 0000-0002-6350-317X; Anna Mrzljak 0000-0001-6270-2305.

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Basic Study

Integrative analysis of layers of data in hepatocellular carcinoma reveals pathway dependencies

Mamatha Bhat, Elisa Pasini, Chiara Pastrello, Sara Rahmati, Marc Angeli, Max Kotlyar, Anand Ghanekar, Igor Jurisica

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Mamatha Bhat, Elisa Pasini, Marc Angeli, Multi Organ transplant Program, University Health Network, Toronto M5G2N2, Canada

Chiara Pastrello, Sara Rahmati, Max Kotlyar, Igor Jurisica, Osteoarthritis Research Program, Division of Orthopedic Surgery, Schroeder Arthritis Institute, University Health Network and Krembil Research Institute, University Health Network, Toronto M5T 0S8, Canada

Anand Ghanekar, Surgery, University Health Network, Toronto M5G 2C4, Canada

Igor Jurisica, Departments of Medical Biophysics and Computer Science, University of Toronto, Toronto M5T 0S8, Canada

Corresponding author: Mamatha Bhat, MD, MSc, PhD, FRCPC(C) Assistant Professor, Staff Physician, Multi Organ transplant Program, University Health Network, 585 University avenue 11th floor, PMB, rm 183, Toronto M5G2N2, Canada. mamatha.bhat@uhn.ca

Abstract**BACKGROUND**

The broader use of high-throughput technologies has led to improved molecular characterization of hepatocellular carcinoma (HCC).

AIM

To comprehensively analyze and characterize all publicly available genomic, gene expression, methylation, miRNA and proteomic data in HCC, covering 85 studies and 3355 patient sample profiles, to identify the key dysregulated genes and pathways they affect.

METHODS

We collected and curated all well-annotated and publicly available high-throughput datasets from PubMed and Gene Expression Omnibus derived from human HCC tissue. Comprehensive pathway enrichment analysis was performed using pathDIP for each data type (genomic, gene expression, methylation, miRNA and proteomic), and the overlap of pathways was assessed to elucidate pathway dependencies in HCC.

RESULTS

We identified a total of 8733 abstracts retrieved by the search on PubMed on HCC

for the different layers of data on human HCC samples, published until December 2016. The common key dysregulated pathways in HCC tissue across different layers of data included epidermal growth factor (EGFR) and β 1-integrin pathways. Genes along these pathways were significantly and consistently dysregulated across the different types of high-throughput data and had prognostic value with respect to overall survival. Using CTD database, estradiol would best modulate and revert these genes appropriately.

CONCLUSION

By analyzing and integrating all available high-throughput genomic, transcriptomic, miRNA, methylation and proteomic data from human HCC tissue, we identified EGFR, β 1-integrin and axon guidance as pathway dependencies in HCC. These are master regulators of key pathways in HCC, such as the mTOR, Ras/Raf/MAPK and p53 pathways. The genes implicated in these pathways had prognostic value in HCC, with Netrin and Slit3 being novel proteins of prognostic importance to HCC. Based on this integrative analysis, EGFR, and β 1-integrin are master regulators that could serve as potential therapeutic targets in HCC.

Key Words: Hepatocellular carcinoma; Gene expression; miRNA; Methylation; Proteomics; High throughput data

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Core Tip: Analyzing all available high-throughput genomic, transcriptomic, miRNA, methylation and proteomic data from human hepatocellular carcinoma tissue, we identified master regulators of key pathways in hepatocellular carcinoma, such as the mTOR, Ras/Raf/MAPK and p53 pathways.

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INTRODUCTION

The molecular basis of hepatocellular carcinoma (HCC) has been elusive, given the significant heterogeneity of this tumor that arises in the context of various chronic liver diseases[1]. HCC remains a high-fatality cancer, despite large-scale efforts to better characterize and therapeutically target this malignancy. Since prevalence of cirrhosis due to hepatitis C and fatty liver disease is increasing in North America, HCC continues to rise[2]. Five-year survival remains poor at 18% due to late diagnosis and inability to tolerate chemotherapy in patients with cirrhosis[2]. Consequently, there is an urgent need to better understand the molecular basis of this highly fatal cancer.

Clinical management of HCC is optimized based on disease stage[3]. Curative treatment with resection, radiofrequency ablation or transplantation is possible in early stage disease[4]. When HCC is diagnosed at a later stage, sorafenib is the first-line chemotherapy, which is directed against the Ras/Raf/MAPK pathway[4]. This is associated with a very modest improvement in overall survival of 3 additional months as compared to placebo (10.7 mo *vs* 7.9 mo)[5].

The cancer genome atlas (TCGA) is a large-scale project that has enabled improved characterization of cancers with several layers of data. The TCGA multi-platform analysis of 196 HCC tumors described this cancer as highly heterogeneous and difficult to characterize, although certain key pathways did emerge including the Ras/Raf/MAPK, mTOR, Wnt/B-catenin, and Sonic Hedgehog pathways[1,6]. Integration of various types of data has previously been performed to map interaction networks. By integrating genomic, transcriptomic and proteomic data, one can understand potential interactions that contribute to a disease condition or process[7,8]. These interactions may otherwise not be uncovered, on the basis of a single type of data. This systems biology approach has been especially important in cancer, given that alterations in one gene can have a ripple effect on proteins in the rest of a protein-protein interaction network. Therefore, elucidating the layers of data in a disease can provide additional insights into the pathways that drive cancer[9].

In the current study, we aim to characterize the landscape of high-throughput data profiling in HCC and determine the patterns in key dysregulated genes and pathways across these different layers of data. The patterns that emerge could help in better understanding the pathways that drive HCC and

could be considered as therapeutic targets.

MATERIALS AND METHODS

Data collection, analysis and database compiling

We downloaded all available high-throughput genomic, transcriptomic, microRNA, methylation, and proteomic datasets related to human HCC samples from published datasets (PubMed, <http://www.ncbi.nlm.nih.gov/PubMed> and Gene Expression Omnibus (GEO), <https://www.ncbi.nlm.nih.gov/geo>).

Using PubMed, the following search was performed for whole exome sequencing data on HCC: ("carcinoma, hepatocellular" [MeSH Terms] OR ("carcinoma" [All Fields] AND "hepatocellular" [All Fields]) OR "hepatocellular carcinoma" [All Fields] OR ("hepatocellular" [All Fields] AND "carcinoma" [All Fields])) AND (whole [All Fields] AND ("exome" [MeSH Terms] OR "exome" [All Fields]) AND sequencing [All Fields]). The following MeSH terms were used to identify gene expression papers: ("carcinoma, hepatocellular" [MeSH Terms] OR ("carcinoma" [All Fields] AND "hepatocellular" [All Fields]) OR "hepatocellular carcinoma" [All Fields] OR ("hepatocellular" [All Fields] AND "carcinoma" [All Fields])) AND ("gene expression" [MeSH Terms] OR ("gene" [All Fields] AND "expression" [All Fields]) OR "gene expression" [All Fields]) AND ("humans" [MeSH Terms] OR "humans" [All Fields]) AND English [All Fields] NOT ("review" [Publication Type] OR "review literature as topic" [MeSH Terms] OR "reviews" [All Fields]). To identify suitable papers regarding methylation in HCC, we used the following terms: ("methylation" [MeSH Terms] OR "methylation" [All Fields]) AND ("carcinoma, hepatocellular" [MeSH Terms] OR ("carcinoma" [All Fields] AND "hepatocellular" [All Fields]) OR "hepatocellular carcinoma" [All Fields] OR ("hepatocellular" [All Fields] AND "carcinoma" [All Fields]) AND ("humans" [MeSH Terms] AND English [lang]). Proteomics papers were retrieved using the following search: [("proteomics" [MeSH Terms] OR "proteomics" [All Fields]) AND high [All Fields] AND throughput [All Fields]] AND ("carcinoma, hepatocellular" [MeSH Terms] OR ("carcinoma" [All Fields] AND "hepatocellular" [All Fields]) OR "hepatocellular carcinoma" [All Fields] OR ("hepatocellular" [All Fields] AND "carcinoma" [All Fields])). MicroRNAs reported in HCC were identified using these MeSH terms: ("micrnas" [MeSH Terms] OR "micrnas" [All Fields] OR "mirna" [All Fields]) AND profile [All Fields] AND ("carcinoma, hepatocellular" [MeSH Terms] OR ("carcinoma" [All Fields] AND "hepatocellular" [All Fields]) OR "hepatocellular carcinoma" [All Fields] OR ("hepatocellular" [All Fields] AND "carcinoma" [All Fields])).

We considered for inclusion all datasets available in PubMed.

The datasets publicly available on the GEO, a public functional genomics data repository of high-throughput array data (<https://www.ncbi.nlm.nih.gov/geo>) were retrieved and analyzed using GEO2R (<https://www.ncbi.nlm.nih.gov/geo/info/geo2r.html>), a web tool available on the portal, identifying genes differentially expressed between samples of HCC and the non-tumoral liver portion. GEO2R compares original submitter-supplied processed data tables using the GEOquery and limma R packages from the Bioconductor project. Following instructions available online at (<https://www.ncbi.nlm.nih.gov/geo/info/geo2r.html>), we retrieved all dysregulated genes. Only those with an adjusted *P* value < 0.05, and expression fold change value below ≤ 0.5 or above ≥ 1.5 were considered for further analysis (Table 1, Supplementary Table 1). The genes included in our list from WES papers were reported as affected by nonsynonymous mutations, and synonymous mutations were not considered. Putative microRNA gene targets were identified using an online database, mirDIP 4.1 [10], (<http://ophid.utoronto.ca/mirDIP>). The most stringent predictive search option (top 1%) was used to obtain the list of putative targets of all differentially expressed miRNAs.

From the selected 11 methylation datasets, raw data from eight studies were available on the GEO website (<https://www.ncbi.nlm.nih.gov/geo/>). We selected the CpG sites or genes reported to be hyper- or hypo- methylated in these publications. The genomic region was considered differentially methylated between HCC tissue and the adjacent non-tumoral sample, if the FDR corrected *P* value < 0.01. Furthermore, we filtered out everything that did not satisfy the criteria: $\Delta\beta \geq 0.20$ or $\Delta\beta \leq -0.20$, where $\Delta\beta = \beta_{\text{HCC}} - \beta_{\text{adjacent}}$ was the difference in methylation between above specified groups. When the CpG sites were considered, the Illumina HumanMethylation450K and 27K platforms were used for mapping to the genes. When multiple sites or genes were found to have the same sense of differential methylation, the mean value of $\Delta\beta$ was calculated. Only the CpGs in the 5'UTR, 1st Exon, TSS200, TSS1500 or in CpG islands were considered in our analysis. Proteomic results were retrieved and included only if protein abundance was reported as different in HCC liver samples compared to control samples.

Figure 1 outlines our study workflow. Papers were excluded from each specific search for the following reasons: Data from cell lines, or animal models, studying efficacy or drugs, or the presence of long non-coding RNA, mechanistic studies not performing high-throughput or evaluating the role of one molecule, papers focused on liver diseases but not HCC or liver tissue, not original data such as review articles, or those studies using already selected datasets, not reporting the modulation of the molecules, and papers without data available.

Table 1 List of the final 85 selected publications for each layer of data. For each publication the number of hepatocellular carcinoma samples and controls and the platform used for the analysis are reported

Gene expression					
No.	year	PMID	HCC (n)	Controls (n)	GEO dataset
1	2004	17393520	35	13	GSE6764
2	2008	18504433	11	2	GSE6222
3	2008	18923165	80	82	GSE10143
4	2009	19098997	47	58	GSE14323
5	2009	19861515	16	47	GSE17967
6	2011	21320499	34	34	GSE20140 (GSE10141, GSE10140)
7	2011	21712445	40	40	GSE28248
8	2013	23691139	15	15	GSE17548
9	2013	23800896	GSE36376_276; GSE25097_211	GSE36376_247; GSE25097_283	GSE36376, GSE25097
10	2014	24498002	46	46	GSE47595
11	2014	24564407	45	45	GSE45114
12	2014	25093504	39	40	GSE57958
13	2014	25141867	11	11	GSE55092
14	2014	25376302	18	18	GSE60502
15	2014	25536056	72	72	GSE39791
16	2015	25666192	132	132	GSE54236
17	2015	25645722	228	168	GSE63898
18	2016	27499918	60	60	GSE64041
19	2016	25964079	26	20	GSE54238
Proteomics					
No.	year	PMID	HCC (n)	Controls (n)	
1	2004	14726492	8	8	
2	2008	19003864	12	12	
3	2005	15759316	10	10	
4	2005	16097030	14	14	
5	2007	17627933	12	12	
6	2014	23621634	3	3	
7	2009	19562805	3	3	
8	2016	26709725	24	12	
9	2013	23589362	20	20	
10	2012	22813877	10	10	
11	2012	22082227	11	11	
12	2011	21631109	69	123	
13	2010	20230046	5	5	
14	2010	19956837	20	20	
15	2009	19715608	18	18	
16	2009	19535095	3	3	
17	2009	19161326	80	80	

18	2004	15221772	20	20	
19	2003	14673798	21	21	
20	2003	14654528	21	21	
21	2002	12481271	11	11	
22	2013	23462207	7	7	
23	2005	16335951	8	8	
24	2006	16342242	10	10	
25	2011	22034872	3	3	
26	2005	15852300	7	7	
27	2011	21913717	3	3	
28	2007	17203974	25	28	
29	2007	17586277	10	10	
Whole exome sequencing					
No.	year	PMID	HCC (n)	Controls (n)	GEO dataset
1	2013	23912677	3	3	N/A
2	2014	24055508	4	7	N/A
3	2017	28323123	5	5	N/A
4	2014	24798001	231	231	GSE54504
5	2012	22561517	24	24	N/A
Epigenetic_miRNAs					
No.	year	PMID	HCC (n)	Controls (n)	GEO dataset
1	2015	26190160	9	7	N/A
2	2014	24789420	10	9	GSE31383
3	2014	24564407	45	45	GSE10694
4	2011	21298008	73	73	GSE21362
5	2008	18649363	78	10	N/A
6	2012	22135159	20	20	N/A
7	2011	21319996	94	94	N/A
8	2009	19473441	20	20	N/A
9	2009	19173277	35		N/A
10	2007	18171346	10	10	N/A
11	2006	16331254	25	25	N/A
12	2015	26062888	30	30	N/A
13	2015	26046780	327	43	N/A
14	2015	25861255	66	66	GSE54751
15	2015	25500075	6	6	GSE54537
16	2014	24875649	24	24	
17	2013	23812667	166	166	GSE31384
18	2013	23390000	9	17	GSE40744
19	2012	23082062	18	18	N/A
20	2014	24586785	29	29	N/A
21	2013	24417970	78	78	N/A
Epigenetic methylation					

No.	year	PMID	HCC (n)	Controls (n)	GEO dataset
1	2011	21500188	13	12	N/A
2	2014	24306662	45	45	N/A
3	2014	25376292	22	22	N/A
4	2015	25945129	8	8	GSE59260
5	2011	21747116	12	12	GSE29720
6	2010	20165882	20	20	GSE18081
7	2012	22234943	62	62	GSE37988
8	2013	24012984	20	8	GSE44970
9	2013	23208076	66	66	GSE54503
10	2014	25093504	59	59	GSE57956
11	2014	25294808	27	27	GSE60753

HCC: Hepatocellular carcinoma; GEO: Gene Expression Omnibus; N/A: Not applicable.

Available patient data, including etiology of liver disease (hepatitis C, hepatitis B, alcohol, fatty liver disease) on the basis of which the HCC tumors developed, presence of cirrhosis, the Model for End-stage Liver Disease score (MELD score, an assessment of the severity of liver dysfunction), tumor histology, stage of cancer, alpha-fetoprotein level, overall and recurrence-free survival following treatment were also documented (Supplementary Table 2).

Pathway enrichment analysis

The key dysregulated genes from each type of data (genomic, miRNA, methylation, transcriptomic, and proteomic) were fed into the Integrated Interactions Database[11] (IID, <http://ophid.utoronto.ca/iid>), to obtain a list of the protein-protein interactions. For the miRNA dataset, we determined the target genes of the differentially expressed miRNAs in tumors using the miRNA Data Integration Portal mirDIP v4.1 [10]. The individual lists derived from each type of data were then fed into the pathway Data Integration Portal, pathDIP v3.0 (<http://ophid.utoronto.ca/pathDIP>)[12], in order to determine the significantly dysregulated pathways in HCC. pathDIP integrates data from 20 major pathway databases, and computationally predicts gene association to curated pathways using protein-protein interactions from IID significance of their connectivity[12]. We used this comprehensive pathway enrichment analysis portal to obtain a list of significantly enriched pathways using literature curated (core) pathway memberships *P* value (FDR: BH-method) less than 0.05.

The lists of pathways from each type of data were then assessed for overlap using Venny 2.1, an online tool for Venn diagram design (<http://bioinfogp.cnb.csic.es/tools/venny/index.html>).

Retrospective validation on independent dataset

In order to determine whether key differentially expressed genes along the overlapping pathways had prognostic value, we used KMplotter, a web-based tool that enables survival analysis across multiple cancers and datasets[13]. Patient samples were split into two groups per autoselection of the best cutoff for each gene, in order to assess its prognostic value. We ran multivariate overall survival analysis based on the high *vs* low expression of each gene in HCC tumors. The two groups were compared by a Kaplan-Meier survival plot, and the hazard ratio with 95% confidence intervals and log-rank *P* value were calculated.

Drug identification by CTD

The identification of putative therapeutic agents able to revert the modulation of genes of interest based on their modulation associated with a worse prognosis was obtained using the online Comparative Toxicogenomics Database <http://ctdbase.org>[14]. This database provides manually curated information about chemical-gene/protein interactions, chemical-disease and gene-disease relationships.

RESULTS

We identified a total of 8733 abstracts retrieved by the search on PubMed on HCC for the different layers of data on human HCC samples, published until December 2016. The flow chart outlining the selection process is detailed in Figure 1.

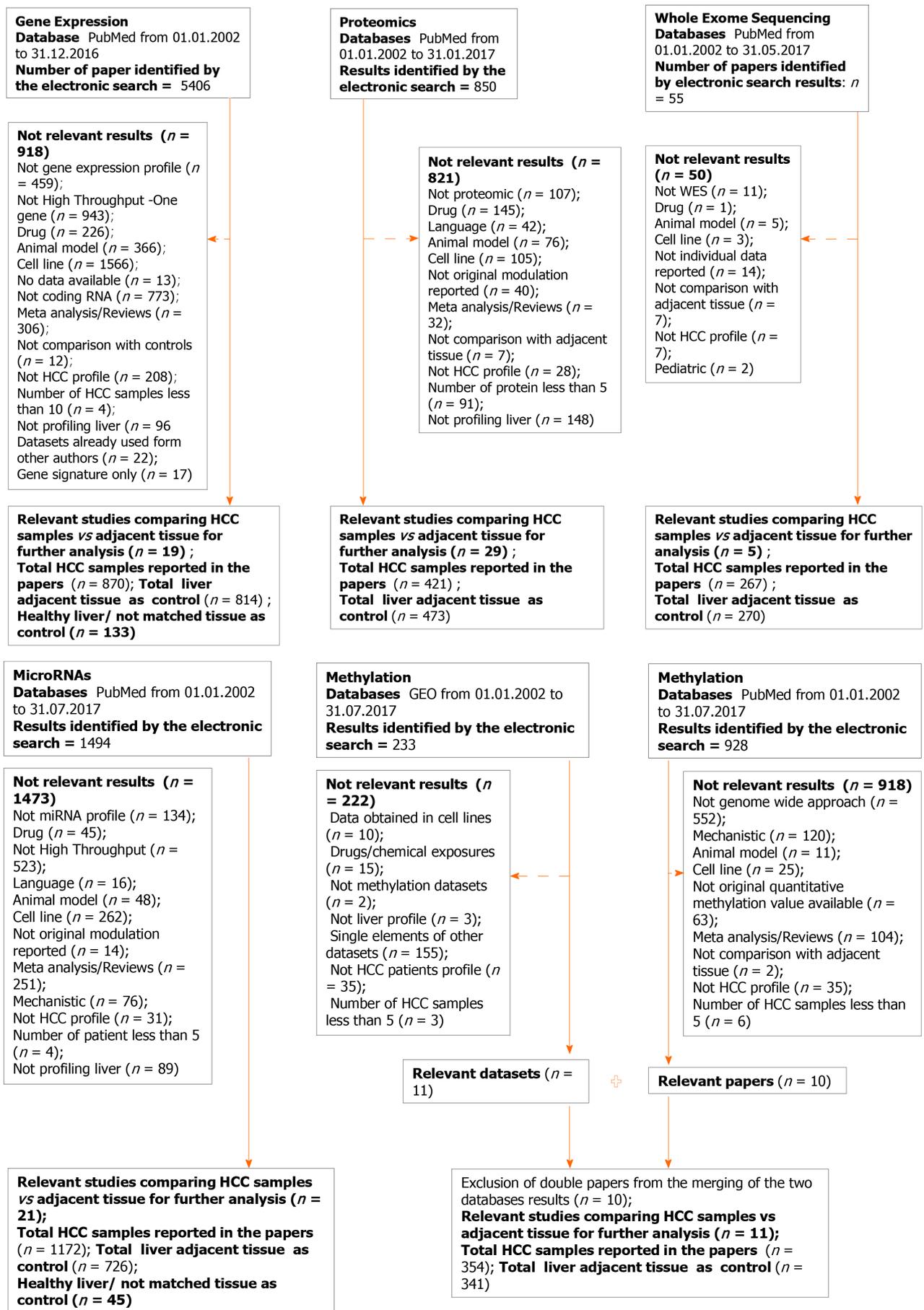


Figure 1 Flow chart showing the paper selection process and exclusion criteria for each data type: Gene expression, proteomics, whole

exome sequencing, microRNAs and methylation.

The number of samples included in our analysis are as follows: (1) Whole exome sequencing: 267 HCC and 270 control samples; (2) Gene expression: 870 HCC and 814 control samples; (3) miRNA: 1172 HCC and 771 control samples; (4) Methylation: 354 HCC and 341 control samples; and (5) Proteomics: 421 HCC and 473 control samples. The methodologies and platforms used to obtain these high-throughput data are reported by type of data (genomic, transcriptomic, miRNA, methylation and proteomic) in [Table 1](#). Clinical data, regarding etiology of liver disease (hepatitis C, hepatitis B, alcohol, fatty liver disease) were frequently reported, on the other side serum levels of liver enzymes, AST and ALT, frequently used to assess liver functions were not available. Pathological details relative to differentiation or stage were frequently absent as well as other crucial variables in the clinic setting, such as Child Pugh/MELD score ([Supplementary Table 2](#)).

Integrative analysis reveals most important pathways in HCC

There were 188 overlapping dysregulated genes/proteins across the different types of data. Independently for each type of data, we obtained a list of pathways using pathDIP. We merged the list of dysregulated pathways in miRNA and methylation, given that these epigenetically regulate gene expression, in order to assess for overlapping pathways across the datasets.

This resulted in a list of 3 common, overlapping pathways among the different types of data: EGFR, β 1-integrin, and axon guidance pathways, as depicted in [Figure 2](#). From the previous list of 188 common dysregulated elements in all different layers of data ([Figure 3](#)), we were able to identify 35/188 genes that were involved in these 3 shared pathways across the layers of data ([Supplementary Table 1](#)).

Prognostic value of pathways in HCC

We then examined the prognostic value of the deregulated genes associated to pathways of interest in HCC using TCGA RNA seq dataset, as listed in [Table 2](#). Median survival of 364 patients in the TCGA, which was used for validation purposes regarding the prognostic value is reported. KMplotter HR results from TCGA RNA seq data reflected the altered modulation identified for these 9 genes in the 19 HCC papers relative to the gene expression data ([Table 2](#)). Among the five upregulated genes associated with positive HR values, CDK5, was reported with the highest HR value (1.85, $P = 0.0035$) and involved in cell cycle ([Table 3](#)). The other 4/9 genes reported as upregulated, COL2A1, LAMC1, RPS6KA3 and ITGB1 were identified with positive HR value by KM plotter analysis and involved in cellular migration ([Table 2](#) and [Table 3](#)).

Four out of 9 genes were reported as downmodulated in the 19 HCC gene expression papers. Among these four, two genes, FGA and FGG, were identified as the top statistically significantly ($P = 0.0009$) associated with a protective role in HCC (HR values 0.52 and 0.59, respectively). FGA and FGG were consistently reported as downmodulated in about 45% of our 19 selected gene expression papers ([Table 3](#)). The other two downmodulated genes, EPHB1 and EFGR with negative HR values ([Table 2](#)) are reported to be affected by missense mutation leading to a loss of their protective role against cell migration.

Estradiol is a therapeutic agent that appropriately targets HCC genes

Using CTD, we found that estradiol was able to appropriately down- or upmodulate 4 out of 9 cancer-related genes ([Table 2](#)). Particularly, CTD reported estradiol capabilities to upregulated FGA, FGG and EGFR reported downmodulated in HCC ([Table 2](#)) and counteracting the upregulation of RPS6KA3 in HCC, suggesting a possible role for this hormone in HCC treatment.

DISCUSSION

In this study, we evaluate the molecular pathogenesis of HCC using a unique approach, that of combining all publicly available high-throughput data from patient HCC tumors. This encompasses all miRNA, methylation, genomic, transcriptomic and proteomic profiling data present in the literature, and represents the first effort to derive a consensus molecular model of HCC through analysis of these different types of data. Although these datasets originated from different patient cohorts, presented integrative analysis offers the opportunity to explore common key pathway dependencies of HCC. Starting with the initial generation of genomics and whole exome sequencing data, previous high-throughput studies have brought forth different lists of dysregulated genes, depending on the type of data evaluated. Dysregulated genes may affect different parts of a pathway. Therefore, a pathway-based approach when evaluating different types of high-throughput data offers the ability to assess the pathways most commonly affected in a given cancer. Additionally, the integrative analysis in our study encompasses a large number of patient samples.

Table 2 Prognostic value of the 9 dysregulated genes associated with the 3 common dysregulated pathways (EGFR, epidermal growth factor, β 1-integrin and axon guidance) among the 4 types of data in obtained with KMplotter

Gene	Modulation in the 19 HCC papers	Probe-ID	HR	CI	Log-Rank P value	Median survival low (mo)	Median survival high (mo)	Estradiol gene modulation predicted by CTD
COL2A1	Up	1280	1.49	1.05-2.11	0.0229	61.7	54.1	N/A
FGA	Down	2243	0.52	0.35-0.77	0.0009	49.7	70.5	+
FGG	Down	2266	0.56	0.39-0.79	0.0009	38.3	70.5	+
LAMC1	Up	3915	1.43	0.98-2.09	0.06	56.5	38.3	N/A
CDK5	Up	1020	1.85	1.22-2.81	0.0035	81.9	6.2	N/A
EPHB1	Down	2047	0.72	0.048-1.08	0.1135	54.1	70.5	N/A
RPS6KA3	Up	6197	1.2	0.8-1.78	0.3743	54.1	56.5	-
EGFR	Down	1956	0.61	0.43-0.89	0.0085	31	70.5	+
ITGB1	Up	3688	1.37	0.95-1.97	0.0924	82.9	49.7	N/A

CTD based prediction identified Estradiol to efficiently affect the expression of the 4/9 genes based on their hazard ratios values. HR: Hazard ratios; HCC: Hepatocellular carcinoma; CI: Confidence interval; N/A: Not applicable.

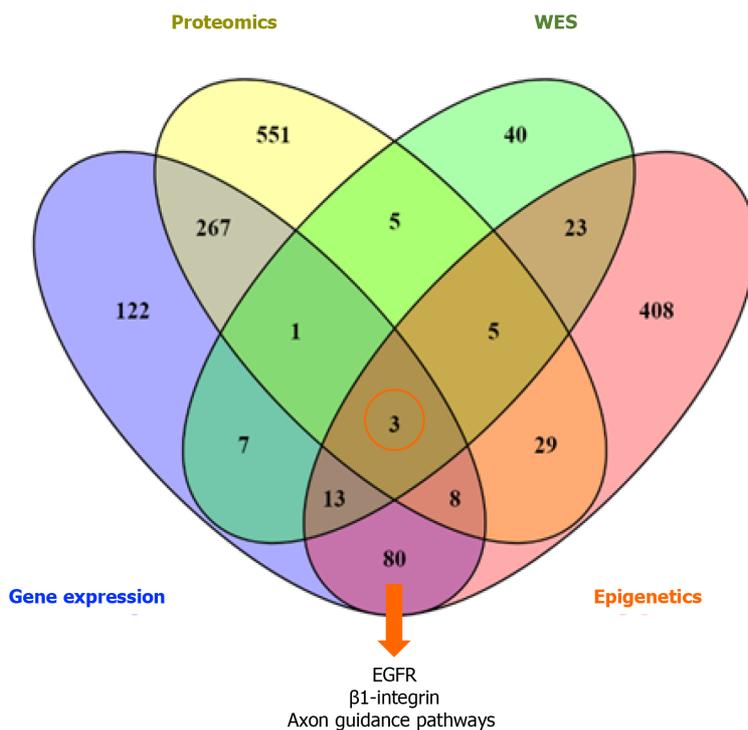


Figure 2 Venn diagram shows the three common pathways (EGFR, epidermal growth factor, β 1-integrin, and axon guidance pathways) across the four different types of data.

Using this integrative approach, we confirm the importance of EGFR, β 1-integrin and axon guidance as pathways critical in hepatocarcinogenesis. EGFR activates the signaling cascades of the Ras/Raf/MAPK and mTOR pathways, two pathways that were identified as key to HCC pathogenesis in the TCGA study[6]. The identification of β 1-integrin as being commonly dysregulated in HCC is novel, and its significance is confirmed through its consistent dysregulation across types of data. β 1-integrin is a cell surface receptor that senses the extracellular matrix, thereby modulating the hallmarks of cancer such as proliferative signaling with continuous activated cell replication, evasion of growth suppressors, resistance to angiogenesis as well as cancer cell invasion and metastasis[14].

Table 3 Modulation of the 9 dysregulated genes associated with the 3 common dysregulated pathways (EGFR, epidermal growth factor, β 1-integrin and axon guidance) identified in the 19 hepatocellular carcinoma gene expression papers. Their genetic alteration in hepatocellular carcinoma and their mechanism in cancer are reported

Gene	Modulation in the 19 HCC papers	PMID	Mutation in HCC (PMID)	Role in cancer (PMID)
COL2A1	Up (2/19)	23800896/25666192	(rs3917) polymorphism is associated with higher risk of HCC (21665180)	COL2A1 promotes migration in HCC (29858962)
FGA	Down (9/19)	21320499/23800896/25093504/25536056/25141867/25376302/25666192/25645722/25666192	Deleted in HCC patients (27511114)	FGA is a positive predictor of survival in gastric cancer patients (15756001)
FGG	Down 8/19	21320499/23800896/25093504/25536056/25141867/25376302/25645722/24498002	Allelic loss (16980951)	FGG is involved in amino acid and redox metabolism pathway in HCC (28089356)
LAMC1	Up (4/19)	23800896/25536056/25141867/25645722	Not identified	LAMC1 promotes tumor cell invasion and migration in HCC (28928891)
CDK5	Up (2/19)	25141867/25376302	Not identified	CDK5 promotes proliferation in HCC (29312535)
EPHB1	Down (2/19)	23800896/25141867	Missense mutation (19469653)	EPHB1 inhibits cell migration (22242939)
RPS6KA3	Up 1/19	25141867	Somatic mutation and copy number variations (22561517)	RPS6KA3 increases cell proliferation (15833840)
EGFR	Down (2/19)	19098997/25141867	Missense mutation (26436086)	EGFR promotes cell adhesion (31465839)
ITGB1	Up (1/19)	25141867	Somatic number variations (24512821)	ITGB1 promotes migration (30664185)

HCC: Hepatocellular carcinoma.

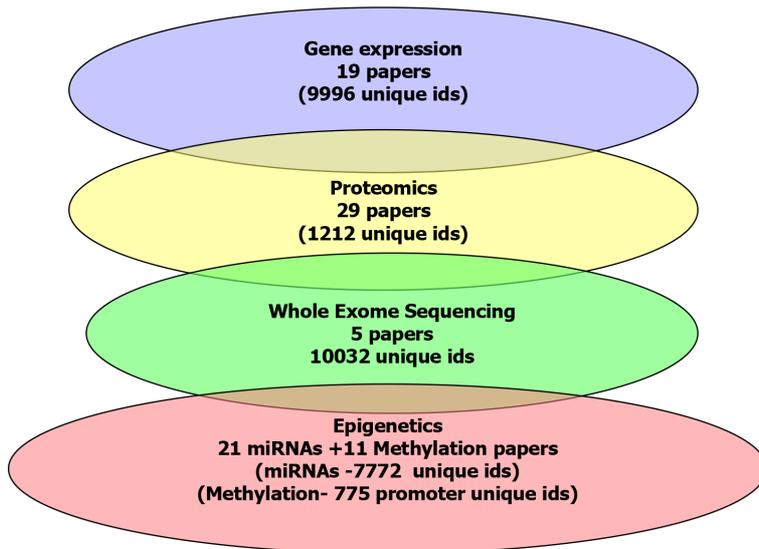
Ras/Raf/MAPK and mTOR are established pathways in hepatocarcinogenesis, and are integrin-dependent signaling pathways[15]. Additionally, β 1-integrin is known to crosstalk with EGFR. In fact, the downregulation of β 1-integrin was found to decrease phosphorylation of EGFR and c-Met in hepatocytes during liver regeneration[16]. A synergistic relationship between integrins and EGFR has also been demonstrated in tumor progression[17]. The finding of axon guidance pathway-related proteins as being dysregulated across types of data, thereby establishing consistent dysregulation of this pathway in HCC, is also novel. Netrin-1 is the best studied protein in the axon guidance pathway, and is known to be overexpressed in various cancers[13]. It is responsible for regulation of apoptosis, with increased presence of netrin-1 leading to inhibition of apoptosis. The tumor suppressor p53, frequently mutated in the TCGA HCC study, regulates the cell cycle through netrin-1. The axon guidance pathway has previously been identified as a pathway that is significantly mutated in HCC based on integration of all genomic data in HCC[18]. This analysis revealed mutations along the axon guidance pathway as being prognostic of a higher rate of HCC metastasis. We were able to additionally validate the prognostic importance of dysregulated proteins in these pathways proteins using TCGA data.

HCC is a cancer that develops in the context of various chronic liver diseases, which may influence the molecular characteristics of HCC. Additionally, the underlying cirrhosis and liver dysfunction that are often concurrent may influence HCC development and behavior[2]. Patients are often diagnosed at an advanced stage of disease, when it is too late for curative treatment. A unique consideration in HCC is the inability to tolerate hepatotoxic chemotherapy in patients with liver dysfunction, as it is often patients with cirrhosis who develop HCC[19,20]. Therefore, liver function must be considered prior to, during, and after any form of treatment for HCC.

Thus, especially for HCC, it has been suggested that a multi-pronged approach to HCC therapy jointly targeting different pathways be adopted.

Omics technologies are essential in the progress towards elucidating the molecular basis of HCC. The current study represents the largest integration of all publicly available genomic, gene expression, methylation, miRNA and proteomic data in HCC, covering 85 studies and 3355 patient sample profiles. We identified consistently deregulated pathways associated with hepatocarcinogenesis across different types of data using integrative analysis tools, thereby confirming the importance of these genes in HCC pathogenesis. EGFR (activator of Ras/Raf/MAPK and mTOR) and β 1-integrin (also modulator of the

A



B

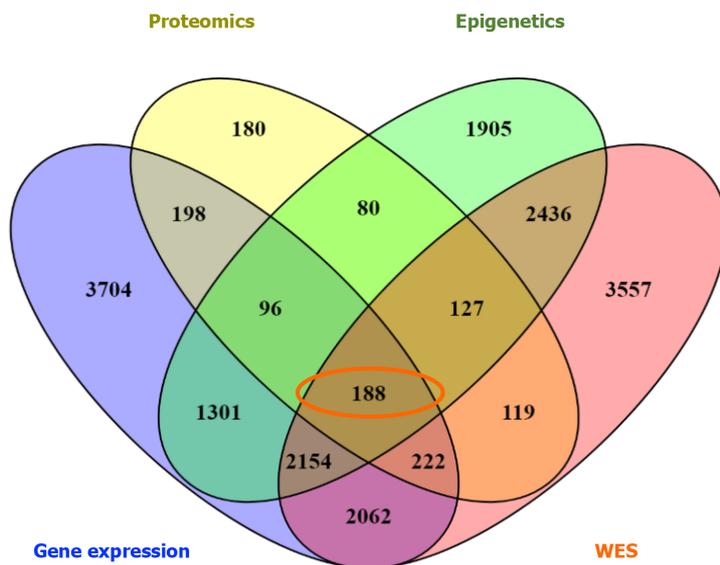


Figure 3 From the previous list of 188 common dysregulated elements in all different layers of data. A: Number of genes/proteins identified in each data type; B: Venn diagram showing the 188 genes identified as commonly deregulated across the 4 different type of data.

aforementioned pathways) were clearly identified as pivotal to HCC[5,21-23]. This is in keeping with the efficacy of the Ras/Raf/MAPK inhibitors sorafenib and regorafenib in HCC[24].

Even beyond this, we found these consistently deregulated genes across pathways to be appropriately modulated by estradiol. HCC is less common in women, and there have been clinical studies demonstrating that hormone therapy and female sex are protective against HCC as described earlier in this thesis.

Other integrative multi-omics studies have been recently performed for other tumors with high mortality such as breast and ovarian cancer[6,25]. Several breast cancer studies emphasizing how data integration of genomic/transcriptomic and proteomic has improved the molecular characterization of subtypes of breast cancer and elucidate its heterogeneity and its interaction with the microenvironment and aggressiveness[26,27]. A single source of data was used in the ovarian cancer multi-omics mathematical integration performed by Bhardwaj *et al*[25]. Copy number variation gene expression and methylation data from TCGA data portal were integrated using mathematical algorithm and identified 32 co-expressed genes and 6 pathways associated with survival.

The main limitation of our study is the different patient samples represented by the various types of data. Nonetheless, there is a large amount of high-throughput data, which allowed us to detect pathway dependency patterns that are compatible with the current HCC literature. Additionally, HCC tumors

arise in the setting of various chronic liver diseases. We could not assess for etiology-specific genes and pathways in this study, given that the clinical and genetic data to evaluate these differences were not fully available for all the studies. Therefore, we could only evaluate gene differences over whole datasets, rather than individual patients, due not complete individual annotation of the samples available on GEO for each specific dataset. The HCC samples in this integrative analysis all came from patients who had undergone hepatectomy. There were no specimens from patients who were candidates for ablation therapy (early stage), those who were undergoing liver transplantation, or those with advanced HCC. One might anticipate that the molecular features of such tumors differ, given the different stages of HCC captured, but there is unfortunately scarcity of data in this regard.

CONCLUSION

In conclusion, our study represents the largest integrative analysis of all publicly available data in HCC, spanning different types of high-throughput data. Pathway enrichment analysis elucidated EGFR, β 1-integrin and axon guidance as pathway dependencies in HCC. These are proteins known to serve as master regulators of key pathways in HCC such as Ras/Raf/MAPK, Wnt/ β -catenin and mTOR[28], and may serve as potential overarching therapeutic targets in HCC. The axon guidance pathway was identified as being of potential importance to HCC for the first time, with prognostic value suggested in patient sample validation with TCGA. Estradiol affects a large number of deregulated genes across data with appropriate modulation and may be a therapeutic agent that helps in HCC. A combined therapeutic approach conjointly targeting different pathways may be more optimal in the treatment of HCC, especially when underlying hepatic dysfunction compromises the ability to tolerate optimal chemotherapeutic doses.

ARTICLE HIGHLIGHTS

Research background

Hepatocellular carcinoma (HCC) is highly heterogeneous, difficult to characterize and the molecular basis of HCC has been elusive.

Research motivation

The Cancer Genome Atlas is a large-scale project that has enabled improved characterization of cancers with several layers of data. Elucidating the layers of data in a disease can provide additional insights into the pathways that drive cancer.

Research objectives

A novel integrative approach of all publicly available high-throughput data from patient HCC tumors was used to delineate critical pathway dependencies in HCC.

Research methods

A comprehensive analysis and characterization of all publicly available genomic, gene expression, methylation, miRNA and proteomic data in HCC covered 85 studies and 3355 patient sample profiles and identified the key overlapping dysregulated genes and pathways affected.

Research results

We identified the prognostic value of these genes in HCC genes, specifically with Netrin and Slit3 being novel proteins of prognostic importance to HCC.

Research conclusions

Our large integrative analysis of all publicly available data in HCC and our pathway enrichment analysis has elucidated epidermal growth factor, β 1-integrin, and axon guidance as pathway dependencies in HCC.

Research perspectives

Based on our integrative analysis, epidermal growth factor, and β 1-integrin are master regulators that could be considered as potential therapeutic targets in HCC.

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FOOTNOTES

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Data sharing statement: Technical appendix, statistical code available from the corresponding author at mamatha.bhat@uhn.ca all data sets are publicly available.

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Country/Territory of origin: Canada

ORCID number: Mamatha Bhat 0000-0003-1960-8449; Elisa Pasini 0000-0002-1547-7077; Chiara Pastrello 0000-0002-1934-7472; Sara Rahmati 0000-0002-7054-3946; Marc Angeli 0000-0002-6809-8820; Max Kotlyar 0000-0002-1111-8667; Anand Ghanekar 0000-0003-0000-0000; Igor Jurisica 0000-0002-2507-946X.

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Case Control Study

Association of interferon lambda-4 rs12979860 polymorphism with hepatocellular carcinoma in patients with chronic hepatitis C infection

Jóice Teixeira de Bitencorte, Tássia Flores Rech, Vagner Ricardo Lunge, Deivid Cruz dos Santos, Mário Reis Álvares-da-Silva, Daniel Simon

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Jóice Teixeira de Bitencorte, Tássia Flores Rech, Vagner Ricardo Lunge, Daniel Simon, PPG Biologia Celular e Molecular Aplicada à Saúde, Universidade Luterana do Brasil, Canoas 92425-900, Rio Grande do Sul, Brazil

Deivid Cruz dos Santos, Mário Reis Álvares-da-Silva, Division of Gastroenterology, Hospital de Clínicas de Porto Alegre, Porto Alegre 90035-903, Rio Grande do Sul, Brazil

Corresponding author: Daniel Simon, PhD, Adjunct Professor, PPG Biologia Celular e Molecular Aplicada à Saúde, Universidade Luterana do Brasil, Av. Farroupilha, 8001 – Prédio 22-5º andar, Canoas 92425-900, Rio Grande do Sul, Brazil. daniel.simon@ulbra.br

Abstract

BACKGROUND

Hepatitis C virus (HCV) infection is a public health concern worldwide. Several factors, including genetic polymorphisms, may be evolved in the progression of HCV infection to liver diseases. Interferon lambdas (IFNLs) modulate the immune response during viral infections. IFNLs induce antiviral activity, interfering in the viral replication by promoting the expression of several genes that regulate immunological functions. The interferon lambda-4 (*IFNL4*) rs12979860 polymorphism, which is characterized by a C to T transition in intron 1, is associated with spontaneous and treatment-induced clearance of HCV infection and may play a role in the development of HCV-associated liver diseases, including hepatocellular carcinoma (HCC).

AIM

To investigate the association of *IFNL4* rs12979860 polymorphism with fibrosis, cirrhosis, and HCC in patients with chronic HCV infection.

METHODS

This study was comprised of 305 chronic HCV-infected patients (53 fibrosis, 154 cirrhosis, and 98 HCC cases). The control group was comprised of 260 HCV-negative healthy individuals. The *IFNL4* rs12979860 polymorphism was genotyped using the TaqMan assay. Fibrosis was diagnosed based on liver biopsy findings, while cirrhosis was diagnosed through clinical, laboratory, anatomo-

pathological, and/or imaging data. HCC was diagnosed through imaging tests, tumor, and/or anatomopathological markers.

RESULTS

The T allele was observed in the three groups of patients (fibrosis, cirrhosis, and HCC) at a significantly higher frequency when compared with the control group ($P = 0.047$, $P < 0.001$, and $P = 0.01$, respectively). Also, genotype frequencies presented significant differences between the control group and cirrhosis patients ($P < 0.001$) as well as HCC patients ($P = 0.002$). The risk analysis was performed using the codominant and dominant T allele models. In the codominant model, it was observed that the CT genotype showed an increased risk of developing cirrhosis in comparison with the CC genotype [odds ratio (OR) = 2.53; 95% confidence interval (CI): 1.55-4.15; $P < 0.001$] as well as with HCC (OR = 2.54; 95% CI: 1.44-4.56; $P = 0.001$). A similar result was observed in the comparison of the TT vs CC genotype between the control group and cirrhosis group (OR = 2.88; 95% CI: 1.44-5.77; $P = 0.001$) but not for HCC patients. In the dominant T allele model, the CT + TT genotypes were associated with an increased risk for progression to cirrhosis (OR = 2.60; 95% CI: 1.63-4.19; $P < 0.001$) and HCC (OR = 2.45; 95% CI: 1.42-4.31; $P = 0.001$).

CONCLUSION

These findings suggest that the T allele of *IFNL4* rs12979860 polymorphism is associated with the development of cirrhosis and HCC in chronic HCV-infected patients.

Key Words: Hepatitis C; Hepatitis C virus; Cirrhosis; Hepatocellular carcinoma; Genetic polymorphism; Interferon-lambda

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Core Tip: Hepatitis C virus (HCV) infection is a major public health problem worldwide as the infection progresses to severe chronic liver diseases in many patients. Interferon lambdas modulate the immune responses against infections, including the antiviral activity by promoting the expression of several genes related to immunological functions. The interferon lambda-4 rs12979860 (C/T) polymorphism, which is associated with spontaneous and treatment-induced clearance of HCV, plays a pivotal role in the host response to HCV-associated liver diseases. In this case-control study, the rs12979860 T allele was found to be associated with the development of cirrhosis and hepatocellular carcinoma in chronic HCV-infected patients.

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INTRODUCTION

Hepatitis C virus (HCV) infection is a public health concern worldwide as it is associated with increased morbidity and mortality[1,2]. HCV, a hepatotropic virus, is the etiological factor for chronic hepatitis C. Patients with HCV infection can develop cirrhosis and hepatocellular carcinoma (HCC) and may need liver transplantation[2-4]. According to the World Health Organization report on viral hepatitis, 71 million people were infected with hepatitis C in 2015[2].

Generally, acute HCV infections are clinically silent infections. Among the patients with HCV infection, 15%-45% can eliminate the virus spontaneously, with the highest recovery rates observed in children and young women[5]. However, a vast majority of infected patients develop chronic hepatitis C, which is characterized by the persistence of HCV in the serum for more than 6 mo. Chronic HCV infection is associated with slow progression, and the patients may remain asymptomatic for several decades. Thus, the persistence of HCV in the organism can cause continuous damage to the liver and can progress to fibrosis, cirrhosis, and HCC[5,6].

HCC, which accounts for 80% of all primary liver cancers, is associated with high mortality rates. Globally, HCC is the third leading cause of cancer-related deaths. HCC is a complex disease with a variety of etiologies and may be associated with different risk factors, such as chronic hepatitis B virus (HBV) and HCV infections, alcoholic liver disease, and nonalcoholic steatohepatitis[7,8]. HCV infection,

which is the second most common risk factor for HCC, accounts for 10%-25% of all HCC cases. Additionally, 80%-90% of HCC cases are reported in patients with cirrhosis[9,10].

The pathogenesis of HCV infection and its progression to chronic liver disease vary among individuals. Several factors, including viral, environmental, and host characteristics, such as age, sex, ethnicity, and genetic factors, contribute to the pathogenesis of HCV[11]. The immune system-related genes, such as interferon lambdas (IFN- λ s), are directly related to modulate viral infections with the ability to induce antiviral activity in target cells and interfere with HCV replication within the host cells. The binding of IFN- λ to its receptor activates the signal transducer and activator of transcription phosphorylation-dependent signaling cascade, inducing hundreds of IFN-stimulated genes and consequently regulating various immune functions[12-14].

The interferon lambda-3 gene (*IFNL3*), which is located on chromosome 19q13.13, encodes IFN- λ 3 protein, a cytokine with antiviral properties. Genome-wide association studies have demonstrated the association of single nucleotide polymorphisms, such as rs12979860 and rs8099917, near the *IFNL3* gene (formerly known as interleukin-28B gene; *IL28B*), both with spontaneous virus elimination after acute infection and with sustained virological response in patients with chronic hepatitis C treated with pegylated interferon plus ribavirin combination therapy[15-18].

Prokunina-Olsson *et al*[19] demonstrated that the rs12979860 polymorphism, commonly referred as an *IL28B* or *IFNL3* variant, is in an independent loci and should be called an interferon lambda-4 (*IFNL4*) variant. The *IFNL4* gene is controlled by rs368234815 Δ G-TT polymorphism, in which the Δ G allele creates an open reading frame for *IFNL4*, while the TT allele does not. Furthermore, the Δ G allele (rs368234815) is reported to be in linkage disequilibrium with the T allele of rs12979860 polymorphism [13,19].

The rs12979860 polymorphism has a relevant and well-known role in the spontaneous and treatment-induced clearance of HCV infection[20]. However, the importance of this polymorphism in the progression of HCV-associated liver diseases is still unclear. Therefore, the objective of our study was to investigate the potential role of the variants from *IFNL4* rs12979860 polymorphism in the progression to hepatic fibrosis, cirrhosis, and HCC in chronic HCV-infected patients.

MATERIALS AND METHODS

Study population

This case-control study was conducted using a convenience sampling strategy. The case group was comprised of 305 patients who visited the outpatient clinic of the Gastroenterology-Hepatology Service of the Hospital de Clínicas de Porto Alegre in Brazil. HCV-positive patients diagnosed with fibrosis, cirrhosis, or HCC were included in the case group. Fibrosis (METAVIR F1-F3) was diagnosed based on liver biopsy findings, while cirrhosis was diagnosed based on liver biopsy or clinical evidence, such as liver imaging (abdominal ultrasonography, computed tomography, and magnetic resonance) abnormalities or endoscopic findings as well as current or past clinical evidence of decompensation, including Child-Pugh B or C classification (score of > 6), ascites on physical examination, hepatic encephalopathy, or variceal bleeding. HCC was diagnosed through liver biopsy (64/98; 65.3%) or in cirrhotic patients through dynamic computed tomography or magnetic resonance by the presence of a nodule of at least 1 cm featuring arterial phase enhancement with decreased enhancement during the portal venous phase as recommended by international guidelines. Patients with HCV/human immunodeficiency virus and/or HCV/HBV coinfection were excluded as well as patients with other causes of liver diseases such as HBV, metabolic associated fatty liver disease, alcohol abuse (more than 20 or 30 g daily consumption of ethanol for females and males, respectively), and/or hemochromatosis. The control group was comprised of 260 samples obtained from the donors at the Hospital de Clínicas de Porto Alegre blood bank. As Brazilian laws for blood donation requires, all have been tested negative for HBV, HCV, human immunodeficiency virus, syphilis, and Chagas disease. This study was approved by the Research Ethics Committee of the Hospital de Clínicas de Porto Alegre (protocol number: 15-0126). All participants provided their written informed consent to participate in the study.

Molecular analysis

DNA was extracted from the blood samples using the salting-out method as described previously[21]. The polymorphism was genotyped using the validated pre-designed real-time PCR TaqMan® Assays (Applied Biosystems Inc., Foster City, CA, United States; catalog 4351376, assay ID: C__7820464_10) in the StepOnePlus™ Real-Time PCR Systems (Applied Biosystems Inc.). PCR was performed in an 18 μ L reaction volume containing 10 mmol/L Tris-HCl (pH 8.5), 50 mmol/L KCl, 1.5 mmol/L MgCl₂, 0.0625 mmol/L dNTPs, 0.25 μ M of each primer, 0.045 μ M of each probe, 1 U Taq DNA polymerase (Cenbiot Enzimas, Porto Alegre, Brazil), and 1 μ L extracted DNA (10-200 ng). The PCR conditions were as follows: 95 °C for 10 min (initial DNA denaturation), followed by 40 cycles of 95 °C for 15 s (denaturation) and 60 °C for 1 min (annealing and extension).

Statistical analyses

All statistical analyses were performed using SPSS® software (Statistical Package for the Social Sciences 17.0 version, Chicago, IL, United States). The normal distribution of the quantitative variables was examined using the Kolmogorov-Smirnov test with Lilliefors correction. The quantitative variables, which were expressed as mean \pm SD, were analyzed using analysis of variance, followed by Tukey post-hoc test. For the categorical variables, the frequencies were calculated and expressed as percentages. Gene frequencies were determined by direct allele counting. Hardy-Weinberg equilibrium (HWE) deviation and the gene frequencies between groups were compared using the Chi-square test. Yates' correction for continuity was used to analyze the 2×2 contingency tables. Odds ratio (OR) was estimated with 95% confidence interval (CI). The differences were considered significant at $P < 0.05$ (two-tailed). Potential confounding factors were entered in the logistic regression models based on statistical criteria (only if the variable was associated with the study factor and with the outcome at $P < 0.20$). The statistical methods used in this study were reviewed by Dr. D. Simon from the Human Molecular Genetics Laboratory, Universidade Luterana do Brasil (Canoas, Brazil).

RESULTS

The sociodemographic and clinical characteristics of patients are described in Table 1. Patients were stratified into the following three groups: Fibrosis ($n = 53$), cirrhosis ($n = 154$), and HCC ($n = 98$). The mean age of the patients was 59.85 ± 8.83 years, with a statistically significant difference among the groups studied ($P = 0.019$). A significant statistical difference ($P = 0.024$) was also observed in the frequency of males in the HCC group (58.2%) when compared to the fibrosis (37.7%) and cirrhosis groups (43.5%). The mean value of body mass index presented a statistically significant difference between the groups with cirrhosis and HCC (27.80 ± 5.39 and 26.34 ± 4.15 kg/m², respectively; $P = 0.038$). Blood transfusion was the most frequent possible infection source among patients (41.0%). The frequencies of HCV 1 and 3 genotypes, which were the most common, were 40.7% and 36.7%, respectively.

Table 2 shows the allele and genotype frequencies of the *IFNL4* rs12979680 polymorphism in the patient and control groups. The success rate for genotyping *IFNL4* rs12979680 polymorphism was 100% in all studied groups. Statistically significant differences were observed regarding the allele frequencies, in which the frequency of the T allele was significantly higher in the three groups of patients analyzed when compared to the controls: [fibrosis group *vs* control group (OR = 1.57; 95%CI: 1.03-1.68; $P = 0.047$), cirrhosis group *vs* control group (OR = 1.75; 95%CI: 1.30-2.36; $P < 0.001$), and HCC group *vs* control group (OR = 1.57, 95%CI: 1.11-2.23; $P = 0.01$)].

Compared with those in the control group, the *IFNL4* genotype frequencies were significantly higher in the cirrhotic and ($P < 0.001$) HCC groups ($P = 0.002$). The genotype distribution in the control and fibrosis groups was in agreement with those expected from HWE ($P = 0.81$ and $P = 0.88$, respectively). In contrast, the genotype frequencies in the cirrhosis and HCC groups deviated from those expected from HWE ($P = 0.02$ and $P = 0.01$, respectively). When the genotype distribution was analyzed in the total sample of patients ($n = 305$), deviations from HWE were maintained ($P = 0.001$).

The risk of developing fibrosis, cirrhosis, and HCC was calculated using the following two genetic models: Codominant and dominant T allele models (Table 3). In the codominant model, it was observed that the CT *vs* CC genotype conferred an increased risk of developing cirrhosis in HCV patients when compared with the control group (OR = 2.53; 95%CI: 1.55-4.15; $P < 0.001$). Additionally, the CT *vs* CC genotype conferred an increased risk for HCC (OR = 2.54; 95%CI: 1.44-4.56; $P = 0.001$). A similar result was observed in the comparison of the TT *vs* CC genotype between cirrhosis patients and controls (OR = 2.88; 95%CI: 1.44-5.77; $P = 0.001$) but not for HCC. In the dominant T allele model, the CT + TT genotypes conferred an increased risk of developing cirrhosis (OR = 2.60; 95%CI: 1.63-4.19; $P < 0.001$) and HCC (OR = 2.45; 95%CI: 1.42-4.31; $P = 0.001$) when compared with the CC genotype. The observed associations remained significant when logistic regression models were analyzed controlling for potential confounding factors (data not shown).

Table 4 presents the distribution of the *IFNL4* rs12979680 polymorphism genotypes regarding clinical features of HCC patients. A significantly higher frequency of the T allele in the dominant T allele model was observed among patients with HCV genotypes 1 and 3 with a frequency of 92% and 67%, respectively ($P = 0.017$). In addition, a higher frequency of the TT genotype was observed among patients with hepatic encephalopathy ($P = 0.03$).

DISCUSSION

This study investigated the association of the *IFNL4* rs12979860 polymorphism with the development of fibrosis, cirrhosis, and HCC among patients with chronic HCV infection. The frequency of the T allele in the case group was higher than that in the control group. Additionally, the risk analyses indicated that

Table 1 Sociodemographic and clinical features of chronic hepatitis C virus positive patients

Characteristics	Total, n = 305	Fibrosis, n = 53	Cirrhosis, n = 154	HCC, n = 98	P value
Age in yr	59.85 ± 8.83	57.89 ± 10.43	59.29 ± 8.43	61.78 ± 8.22	0.019
Male	144 (47.2)	20 (37.7)	67 (43.5)	57 (58.2)	0.024
Ethnicity, Caucasian	218 (71.5)	35 (66.1)	110 (71.4)	73 (74.5)	0.547
BMI in kg/m ²	27.08 ± 4.85	26.39 ± 4.14	27.80 ± 5.39	26.34 ± 4.15	0.038
Level of education					0.366
Completed primary education or less	196 (62.0)	31 (56.6)	100 (62.3)	65 (64.3)	
Secondary or higher education	102 (24.9)	20 (34.0)	51 (25.3)	31 (19.4)	
Smoker	59 (19.3)	16 (30.2)	31 (20.1)	12 (12.2)	0.001
Alcohol consumption					0.004
No	260 (85.2)	49 (92.5)	137 (89.0)	74 (75.5)	
Former	45 (14.8)	4 (7.5)	17 (11.0)	24 (24.5)	
Illicit drug use					0.164
No	243 (79.7)	43 (81.1)	122 (79.2)	78 (79.6)	
Yes	9 (3.0)	4 (7.5)	4 (2.6)	1 (1.0)	
Former user	53 (17.4)	6 (1.1)	28 (18.2)	19 (19.4)	
Coffee drinker	213 (69.8)	39 (73.6)	112 (72.7)	62 (63.3)	0.226
Age at infection of HCV in yr	27.43 ± 9.75	28.47 ± 9.12	27.48 ± 9.77	26.64 ± 10.26	0.735
Age at diagnosis of HCV in yr	49.11 ± 11.11	46.88 ± 12.99	49.17 ± 10.97	50.24 ± 10.11	0.223
HCV infection <i>via</i> blood transfusion	125 (41.0)	24 (45.3)	64 (41.6)	37 (37.8)	0.706
HCV-RNA as log ₁₀ UI/mL	6.05 ± 0.86	-	6.11 ± 0.87	5.86 ± 0.78	0.141
HCV genotypes					0.060
1	124 (40.7)	-	86 (55.8)	38 (38.8)	
2	7 (2.3)	-	4 (2.6)	3 (3.1)	
3	112 (36.7)	-	61 (39.6)	51 (52.0)	
Antiviral treatment	178 (58.4)	-	115 (74.7)	63 (64.3)	0.077
Diabetes	85 (27.9)	-	50 (32.5)	35 (35.7)	0.595
Steatosis	24 (7.9)	-	13 (8.4)	11 (11.2)	0.431
Ascites	66 (21.6)	-	31 (20.1)	35 (35.7)	0.005
Portal hypertension	146 (47.9)	-	72 (46.8)	74 (75.5)	< 0.001
Esophageal varices	156 (51.1)	-	91 (59.0)	65 (66.3)	0.231
Upper gastrointestinal bleeding	49 (16.0)	-	26 (16.9)	23 (23.5)	0.184
Spontaneous bacterial peritonitis	13 (4.3)	-	7 (4.5)	6 (6.1)	0.568
Hepatic encephalopathy	24 (7.9)	-	13 (8.4)	11 (11.2)	0.431
Child-Pugh					0.083
A	137 (44.9)	-	95 (61.7)	42 (42.9)	
B	43 (14.1)	-	28 (18.2)	15 (15.3)	
C	9 (3.0)	-	3 (1.9)	6 (6.1)	
Number of tumors					
1		-	-	62 (63.37)	
2		-	-	17 (17.35)	
≥ 3		-	-	18 (18.37)	

Tumor size in cm	-	-	2.8 ± 1.81
Portal vein thrombosis	-	-	10 (10.20)
Extrahepatic metastases	-	-	7 (7.14)
Liver transplantation	-	-	47 (47.96)
Deaths	14 (4.59)	8 (5.19)	6 (6.12) 0.754

Characteristics expressed as number and percentage or mean ± SD. BMI: Body mass index; HCC: Hepatocellular carcinoma; HCV: Hepatitis C virus.

Table 2 Allele and genotype frequencies of interferon lambda-4 rs12979860 polymorphism in patients with hepatitis C virus-associated liver diseases and healthy control subjects

rs12979860	Control, n = 260	Total patients, n = 305	Fibrosis, n = 53	Cirrhosis, n = 154	HCC, n = 98	P value				
							Fibrosis vs Control	Cirrhosis vs Control	HCC vs Control	Fibrosis vs Cirrhosis
Allele						0.047	< 0.001	0.010	0.708	0.618
C	345 (66.3)	331 (54.3)	59 (55.7)	163 (52.9)	109 (55.6)					
T	175 (33.7)	279 (45.7)	47 (44.3)	145 (47.1)	87 (44.4)					
Genotype						0.113	< 0.001	0.002	0.541	0.665
CC	115 (44.2)	76 (24.9)	16 (30.2)	36 (23.4)	24 (24.5)					
CT	115 (44.2)	179 (58.7)	27 (50.9)	91 (59.1)	61 (62.2)					
TT	30 (11.6)	50 (16.4)	10 (18.9)	27 (17.5)	13 (13.3)					

Variables expressed as number (percentage). HCC: Hepatocellular carcinoma; HCV: Hepatitis C virus.

patients with HCV infection harboring the T allele were more susceptible to develop cirrhosis and HCC.

The studies on the role of *IFNL4* rs12979860 polymorphism in HCV-related liver diseases have yielded controversial results. A recent meta-analysis of 18 studies involving different ethnicities attempted to elucidate the global association of this polymorphism with HCV and HBV[22]. The meta-analysis revealed that the *IFNL4* rs12979860 polymorphism is a risk factor for both HCV-and HBV-related HCC. Although the meta-analysis enhanced our understanding of the role of *IFNL4* rs12979860 polymorphism in the outcomes of liver diseases with viral etiologies, the results must be carefully analyzed. Some limiting factors, such as ethnic differences, discrepancies in clinical characteristics among different studies, genotyping methods, HCV genotypes, nonuniform controls in case-control studies, and the influence of confounding factors should be considered.

Various studies have evaluated the role of *IFNL4* rs12979860 polymorphism in the development of HCC. De la Fuente *et al*[23] examined the association of rs12979860 polymorphism with the development of HCC in both chronic HCV infection and nonviral cirrhosis. The authors reported that the TT genotype is highly prevalent in cirrhotic patients infected with HCV genotype 1 who were subjected to liver transplantation. However, there was no significant association between polymorphism variants and hepatocarcinogenesis.

The risk of developing HCC in patients responding to pegylated interferon plus ribavirin treatment is lower than that in nonresponders. Chang *et al*[24] evaluated 800 patients who received pegylated interferon plus ribavirin combination therapy but did not respond to treatment to evaluate the risk factors for HCC. The CT + TT genotypes of rs12979860 polymorphism were an independent risk factor for the development of HCC in these patients, which further indicated the importance of this polymorphism in the progression to HCC. Similarly, a study on 200 patients with advanced fibrosis revealed that the *IFNL4* rs12979860 TT genotype was significantly associated with HCC development after direct-acting antiviral therapy for chronic hepatitis C[25].

Table 3 Genetic models of association between interferon lambda-4 rs12979860 polymorphism and hepatitis C virus-associated liver diseases

rs12979860	Fibrosis vs Control		Cirrhosis vs Control		HCC vs Control		Fibrosis vs Cirrhosis		Cirrhosis vs HCC	
	OR (95%CI)	P value	OR (95%CI)	P value	OR (95%CI)	P value	OR (95%CI)	P value	OR (95%CI)	P value
Codominant model										
CC	1.00 (Ref.)	-	1.00 (Ref.)	-	1.00 (Ref.)	-	1.00 (Ref.)	-	1.00 (Ref.)	-
CT	1.69 (0.82-3.54)	0.126	2.53 (1.55-4.15)	< 0.001	2.54 (1.44-4.56)	0.001	1.50 (0.67-3.28)	0.277	1.01 (0.52-1.95)	0.986
TT	2.40 (0.87-6.27)	0.053	2.88 (1.44-5.77)	0.001	2.08 (0.86-4.83)	0.068	1.20 (0.43-3.45)	0.702	0.72 (0.28-1.80)	0.447
T allele dominant model										
CC	1.00 (Ref.)	-	1.00 (Ref.)	-	1.00 (Ref.)	-	1.00 (Ref.)	-	1.00 (Ref.)	-
CT + TT	1.83 (0.94-3.71)	0.061	2.60 (1.63-4.19)	< 0.001	2.45 (1.42-4.31)	0.001	1.42 (0.66-2.97)	0.325	0.94 (0.50-1.79)	0.840

CI: Confidence interval; HCC: Hepatocellular carcinoma; HCV: Hepatitis C virus; OR: Odds ratio; Ref.: Reference.

A large international study involving 2916 patients, mostly the European Caucasian population, revealed that the increased number of the T allele was significantly associated with the prevalence of cirrhosis/transition to cirrhosis in patients infected with HCV genotype 1. This association was evident in Caucasian European patients but not in Asian, Latin American, or Middle Eastern patients infected with HCV genotype 1[26].

The genetic background of populations can contribute to variable results among different studies as the allele frequencies of *IFNL4* rs12979860 polymorphism vary among populations. In this study, the minor allele frequencies of the *IFNL4* rs12979860 polymorphism, represented by the T allele, in the case and control groups were 0.46 and 0.34, respectively. The minor allele frequencies reported for European, Japanese, and Chinese populations in the 1000 Genomes database were 0.28, 0.10, and 0.06, respectively.

The role of IFN- λ 4 in the pathophysiology of chronic HCV infection-mediated liver diseases is still under investigation. IFN- λ 4 activates interferon-stimulated genes, induces cell death, and inhibits cell proliferation[27]. In the IFN- λ 4-expressing cells, enhanced cell death may cause tissue inflammation, while the antiproliferative effect of IFN- λ 4 could decrease the capacity of tissue remodeling[27,28]. In this sense, our study may provide significant information about the association of the genetic variants of the *IFNL4* rs12979860 polymorphism with disease progression and clinical features of hepatitis C, demonstrating that this polymorphism has relevance in the HCV spontaneous and treatment-induced clearance of HCV infection. Also, the present study can stimulate the clarification of this issue by the analyses of large samples as well as the correlation of genetic variants with gene expression and protein interactions.

This study has some limitations. The sample size of this study is relatively small. A more representative sample could enhance the statistical power to detect genetic differences. In this study, the fibrosis group, which had the lowest sample number, exhibited a trend of association with the TT genotype and the T allele when compared with the control group. A larger sample size could clarify the role of this polymorphism in the development of fibrosis. In addition, some data are missing in the liver fibrosis group (such as HCV RNA, HCV genotype, number of patients on antiviral treatment, diabetes, and steatosis), which precluded a more detailed comparison with the other groups. Besides, the analysis of a nonfibrotic (F0) HCV-infected group would be important because it makes the study more comprehensive. The analysis of a single polymorphism is insufficient to fully explain the genetic basis of HCC. In the cirrhosis and HCC groups, the genotype frequencies of the *IFNL4* rs12979860 polymorphism did not concur with those expected from HWE. The deviations from HWE can be due to the population stratification and selection or may indicate disease association[29,30]. As population stratification may have caused disequilibrium among the cirrhosis and HCC groups, HWE analysis was performed on the case group. However, the genotype frequency in the case group deviated from that expected from HWE. Thus, the observed imbalance could be explained by the effective role of this polymorphism in the sample of patients with HCV-related liver diseases.

Table 4 Distribution of the interferon lambda-4 rs12979860 genotypes based on the clinical features of patients with hepatocellular carcinoma, *n* = 98

Variable	Genotypes			Codominant model	T allele dominant model
	CC, <i>n</i> = 24	CT, <i>n</i> = 61	TT, <i>n</i> = 13	<i>P</i> value	<i>P</i> value
HCV genotypes				0.052	0.017
1	3 (14.3)	27 (46.6)	8 (61.5)		0.004
2	1(4.8)	2 (3.4)	-		
3	17 (81.0)	29 (50.0)	5 (38.5)		0.007
Diabetes	10 (41.7)	19 (31.1)	6 (46.2)	0.463	0.484
Steatosis	1(4.2)	8 (13.3)	2 (16.7)	0.409	0.195
Ascites	10 (41.7)	20 (32.8)	5 (41.7)	0.679	0.511
Portal hypertension	17 (70.8)	48 (78.7)	9 (75.0)	0.741	0.469
Esophageal varices	17 (70.8)	39 (63.9)	9 (75.0)	0.682	0.646
Upper gastrointestinal bleeding	8 (33.3)	10 (16.4)	5 (41.7)	0.075	0.201
Spontaneous bacterial peritonitis	1 (4.2)	5 (8.2)	-	0.500	0.636
Hepatic encephalopathy	3 (12.5)	2 (3.3)	3 (25.0)	0.030	0.383
Child-Pugh				0.209	0.156
A	8 (61.5)	26 (63.4)	8 (88.9)		
B	2 (15.4)	12 (29.3)	1 (11.1)		
C	3 (23.1)	3 (7.3)	-		
Number of tumors				0.325	0.684
1	17 (70.8)	39 (65.0)	6 (46.2)		
2	3 (12.5)	12 (20.0)	2 (15.4)		
≥ 3	4 (16.7)	9 (15.0)	5 (38.5)		
Portal vein thrombosis	4 (16.7)	4 (6.6)	2 (16.7)	0.286	0.238
Extrahepatic metastases	1 (4.2)	5 (8.6)	1 (7.7)	0.780	0.487

Variables expressed as number (percentage). HCC: Hepatocellular carcinoma; HCV: Hepatitis C virus.

CONCLUSION

The findings of this study suggest that the T allele of *IFNL4* rs12979860 polymorphism is a potential genetic factor that determines the susceptibility to cirrhosis and HCC development among patients with chronic HCV.

ARTICLE HIGHLIGHTS

Research background

As a serious public health problem worldwide, hepatitis C virus (HCV) infection has unfavorable trends in morbidity and mortality. Due to high hepatotropic potential, HCV may cause chronic complications, such as fibrosis, cirrhosis, and hepatocellular carcinoma (HCC). Progression to chronic liver disease usually varies and is influenced by different factors, including genetic factors. The interferon lambda-4 (*IFNL4*) rs12979860 polymorphism, characterized by a C to T transition in the intron 1, has been associated with spontaneous and treatment-induced clearance of HCV infection and may play a role in HCV-associated liver diseases, including HCC.

Research motivation

Although the rs12979860 polymorphism has a relevant and well-known role in the spontaneous and treatment-induced clearance of HCV infection, the importance of genetic variants of this polymorphism

in the progression of HCV-associated liver diseases is still unclear.

Research objectives

We aimed to investigate the potential role of the variants in the progression to hepatic fibrosis, cirrhosis, and HCC in chronic HCV-infected patients. In addition, the distribution of the rs12979860 *IFNL4* genetic variants was analyzed in accordance with clinical features of patients.

Research methods

This case-control study included 305 patients with chronic HCV infection patients (53 with fibrosis, 154 with cirrhosis, and 98 with HCC), and 260 HCV-negative healthy individuals as controls. Diagnosis of fibrosis (METAVIR F1-F3) was performed by liver biopsy findings, while the diagnosis of cirrhosis was performed through clinical, laboratorial, anatomopathological, and/or imaging data. Lastly, diagnosis of HCC was performed through dynamic imaging tests, and/or anatomopathological markers. Patients with HCV/human immunodeficiency virus and/or HCV/ hepatitis B virus coinfection were excluded. Molecular analysis was performed using validated pre-designed real-time PCR TaqMan® Assays.

Research results

A higher frequency of the T allele was observed among the groups of patients (fibrosis, cirrhosis, and HCC) as compared to the controls: ($P = 0.047$; $P < 0.001$; and $P = 0.01$, respectively). Also, significant differences were observed concerning genotype frequencies between HCC ($P = 0.002$) and cirrhosis patients ($P < 0.001$) in comparison with controls. Two genetic models were tested in the risk analysis: Codominant model and dominant T allele model. In the codominant model, it was observed that the CT genotype was related to an increased risk of cirrhosis [odds ratio (OR) = 2.53; 95% confidence interval (CI): 1.55-4.15; $P < 0.001$] and HCC (OR = 2.54; 95%CI: 1.44-4.56; $P = 0.001$) as compared to CC genotype. In the comparison of the TT vs CC genotype, a significant difference was observed between the control group and cirrhosis group (OR = 2.88; 95%CI: 1.44-5.77; $P = 0.001$) but not the HCC group. In the dominant T allele model, the CT + TT genotypes confer an increased risk for the progression to cirrhosis (OR = 2.60; 95%CI: 1.63-4.19; $P < 0.001$) and HCC (OR = 2.45; 95%CI: 1.42-4.31; $P = 0.001$). Finally, a significant higher frequency of the T allele among patients with HCV genotypes 1 and 3 (92% and 67%, respectively; $P = 0.017$) and a higher frequency of TT genotype among patients with hepatic encephalopathy ($P = 0.03$) was observed.

Research conclusions

This study suggests that the T allele from *IFNL4* rs12979860 polymorphism is associated with the development of cirrhosis and HCC in chronic HCV-infected patients.

Research perspectives

As an important factor related to spontaneous and treatment-induced clearance of HCV infection, the analysis of *IFNL4* rs12979860 polymorphism in the present study may provide a better understanding of the genetic variants with disease progression and clinical features. In order to clarify this issue, large samples are needed to verify the association of genetic polymorphisms with hepatitis C as well as the correlation of genetic variants with gene expression and protein interactions.

FOOTNOTES

Author contributions: de Bitencorte JT, Álvares-da-Silva MR, and Simon D were involved with conception and design of the study; de Bitencorte JT, Rech TF, and dos Santos DC were involved with acquisition of the samples and data; de Bitencorte JT performed the molecular analysis; de Bitencorte JT, Rech TF, Lunge VR, and Simon D performed the statistical analysis and interpretation of data; de Bitencorte JT, Rech TF, and Simon D drafted the manuscript; All authors read and approved the final version of the manuscript.

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Country/Territory of origin: Brazil

ORCID number: Joice Teixeira de Bitencorte 0000-0002-0156-4225; Tássia Flores Rech 0000-0002-9530-7042; Vagner Ricardo Lunge 0000-0003-4012-8650; Deivid Cruz dos Santos 0000-0001-7300-422X; Mário Reis Álvares-da-Silva 0000-0002-5001-246x; Daniel Simon 0000-0003-1122-8468.

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Retrospective Study

Immunization status and hospitalization for vaccine-preventable and non-vaccine-preventable infections in liver-transplanted children

Palittiya Sintusek, Yong Poovorawan

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Infections and associated morbidity and mortality may be more frequent in children who have undergone liver transplant than in healthy children. Immunization strategies to prevent vaccine-preventable infections (VPIs) can effectively minimize this infection burden. However, data on age-appropriate immunization and VPIs in children after liver transplant in Asia are limited.

AIM

To evaluate the immunization status, VPIs and non-VPIs requiring hospitalization in children who have undergone a liver transplant.

METHODS

The medical records of children who had a liver transplant between 2004 and 2018 at King Chulalongkorn Memorial Hospital (Bangkok, Thailand) were retrospectively reviewed. Immunization status was evaluated *via* their vaccination books. Hospitalization for infections that occurred up to 5 years after liver transplantation were evaluated, and divided into VPIs and non-VPIs. Hospitalizations for cytomegalovirus and Epstein-Barr virus were excluded. Severity of infection, length of hospital stay, ventilator support, intensive care unit requirement, and mortality were assessed.

RESULTS

Seventy-seven children with a mean age of 3.29 ± 4.17 years were included in the study, of whom 41 (53.2%) were female. The mean follow-up duration was 3.68 ± 1.45 years. Forty-eight children (62.3%) had vaccination records. There was a significant difference in the proportion of children with incomplete vaccination according to Thailand's Expanded Program on Immunization (52.0%) and accelerated vaccine from Infectious Diseases Society of America (89.5%) ($P < 0.001$). Post-liver transplant, 47.9% of the children did not catch up with age-appropriate immunizations. There were 237 infections requiring hospitalization during the 5 years of follow-up. There were no significant differences in hospitalization for VPIs or non-VPIs in children with complete and incomplete immunizations. The risk of serious infection was high in the first year after receiving a liver transplant, and two children died. Respiratory and gastrointestinal systems were common sites of infection. The most common pathogens that caused VPIs were rotavirus, influenza virus, and varicella-zoster virus.

CONCLUSION

Incomplete immunization was common pre- and post-transplant, and nearly all children required hospitalization for non-VPIs or VPIs within 5 years post-transplant. Infection severity was high in the first year post-transplant.

Key Words: Children; Hospitalization; Immunization; Liver transplant; Thailand; Vaccine-preventable infection

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Core Tip: Incomplete age-appropriate immunization in children waiting for a liver transplant was expected, and nearly half of them had not caught up with age-appropriate vaccinations post-transplant. Though there was no significant difference in hospitalization from vaccine-preventable infections (VPIs) and non-VPIs in children with complete and incomplete immunizations. At least 13.1% required hospitalization within 5 years post-transplant, and $> 10\%$ were admitted to the intensive care unit and required respiratory support. The severity of infections was high during the first year post-transplant. Complete immunization and robust infection control should be prioritized in children both pre and post-liver transplant.

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INTRODUCTION

Infection after a liver transplant is a serious concern due to potential associated morbidity and mortality [1-4], as well as the standard complications and severe symptoms that can be experienced by immunocompetent patients. Such infections can give rise to graft rejection, thus affecting short- or long-term graft survival[4]. Accordingly, strategies to reduce overall post-transplant infection are warranted. Immunization is considered an effective, relatively noninvasive, and affordable way to reduce vaccine-preventable infections (VPIs)[5] such as measles, varicella, influenza, and viral hepatitis A and B, among others. The Infectious Diseases Society of America (IDSA)[6] and the American Society of Transplantation Infectious Disease Community of Practice[7] encourage accelerated vaccination, particularly with regard to live vaccines in immunocompromised children awaiting for solid organ transplantation.

Children awaiting a liver transplant can be at a disproportionate risk of VPIs because they tend not to have undergone a complete series of age-appropriate immunizations, because their serious illness has taken medical priority over vaccination[8]. Verma and Wade[9] reported that in their experience at King's College Hospital, only 20%-30% of children had undergone a complete series of age-appropriate immunizations prior to liver transplantation. Diana *et al*[10] reported that less than half of a cohort of children who underwent liver transplant at the Children's Hospital of Geneva in Switzerland had undergone a complete series of age-appropriate vaccinations, with rates of 43% for diphtheria-tetanus-acellular pertussis-polio vaccine, 44% for measles-mumps-rubella (MMR) vaccine, 13% for hepatitis B vaccine, and 5% for hepatitis A vaccine at the time of liver transplantation. Feldman *et al*[4,11] investigated morbidity, mortality, and costs associated with VPIs in children after solid organ transplants, and reported a significantly higher rate of VPIs in these children than in the general pediatric population.

Studies conducted in the United States and other western countries have highlighted the effects of VPIs in children after solid organ transplantation[4,9-11], but published data on VPIs in children after liver transplantation in the East are scarce. To improve the quality of life of liver-transplanted children by minimizing the serious complications associated with post-liver transplant infections, strategies to avoid VPIs based on strong evidence should be initiated worldwide, including in Asia.

The aim of the present study was to evaluate immunization status in Thai children at the time of liver transplantation, and for up to 5 years post-liver transplantation. The prevalence and effects of VPIs and non-VPIs during hospitalization were also assessed.

MATERIALS AND METHODS

The current study was a retrospective review of all children who received a liver transplant at King Chulalongkorn Memorial Hospital in Thailand from January 2004 to August 2018. Demographic data, patient characteristics, and immunization records from vaccination books were collated. Hospitalization records pertaining to the liver transplant operation and admission due to infections for up to 5 years post-transplant were included. Hospitalizations for Epstein-Barr virus (EBV) and cytomegalovirus were excluded from the study. Infection etiology and source were investigated by the doctors in charge. Culture from specimens was available for all bacterial origins, and immunological and molecular techniques were available for the diagnosis of both viral and bacterial infections, including polymerase chain reaction panel analysis for respiratory tract infections and gastrointestinal infections, and antibody titers for hepatitis A/B/E, dengue, and measles.

Infections were divided into VPIs and non-VPIs. Length of hospital stay, severity of infections, and mortality from infections were collated and classified into three groups: Intensive care unit (ICU) requirement, ventilator support, and death. Complete immunization was defined as that conducted in accordance with the Expanded Program on Immunization (EPI) in Thailand (Table 1) and the accelerated vaccination recommendations described in the 2013 IDSA Clinical Practice Guideline for Vaccination of the Immunocompromised Host[6], which notes: "... children aged 6-12 mo can receive MMR and varicella vaccine and the second dose should be administered at 12 mo for MMR and ≥ 3 mo apart for varicella vaccine. However, the last MMR or varicella vaccine injection should not be within 4 wk of a liver transplant schedule."

Statistical analysis

Continuous and categorical data are presented as the mean \pm SD, medians and interquartile ranges, proportions, or percentages as appropriate. The Mann Whitney *U* test and unpaired *t*-test were used to compare continuous data, and Fisher's exact test and the χ^2 test were used to compare discrete data. *P* < 0.05 was considered statistically significant. Data analyses were performed using Statistical Package for the Social Sciences version 24.0.0 (SPSS, Inc.; Chicago, IL, United States). A biomedical statistician employed at the Department of Statistics Science, Kasetsart University (Bangkok, Thailand) reviewed the statistical analyses conducted in the study.

RESULTS

Patient characteristics and history of immunization

Seventy-seven children with a mean age of 3.29 ± 4.17 years were included in the study, of whom 41 (53.2%) were female. The indications for liver transplantation were biliary atresia (*n* = 63), indeterminate acute liver failure (*n* = 3), progressive familial intrahepatic cholestasis (*n* = 2), Alagille syndrome (*n* = 2), cryptogenic cirrhosis (*n* = 1), citrin deficiency (*n* = 1), Budd-Chiari syndrome (*n* = 1), hepatoblastoma (*n* = 1), autoimmune hepatitis (*n* = 1), glycogen storage disease type IV (*n* = 1), and bile acid deficiency (*n* = 1). The mean follow-up time was 3.68 ± 1.45 years, and 32 children were followed up for a full 5 years after liver transplantation. Vaccinations were noted in the vaccination books of 48/77 children (62.3%). Substantial proportions of children did not have complete vaccinations in accordance with Thailand's EPI (*n* = 25, 52%) (Table 1) or accelerated vaccinations in accordance with the IDSA recommendations (*n* = 43, 89.5%) (*P* < 0.001). Post-liver transplant, 23 children (47.9%) could not catch up with the appropriate immunizations for age. All children were revaccinated with hepatitis B vaccine if hepatitis B surface antibody was < 10 mIU/mL. Other vaccines they received after liver transplantation included those for influenza (*n* = 12), invasive pneumococcal disease (*n* = 10), Japanese encephalitis (*n* = 6), diphtheria/ tetanus/ pertussis-inactivated polio vaccine (*n* = 6), and hepatitis A (*n* = 3). A minority of children were not up-to-date with influenza vaccination (*n* = 18, 37.5%) and pneumococcal conjugate vaccine (*n* = 22, 45.8%) post-liver transplant compared with pre-liver transplant (*n* = 30, 62.5% for influenza and *n* = 36, 75% for pneumococcal conjugate vaccine) (*P* < 0.001; Table 2). With regard to live vaccines, three individuals were inadvertently vaccinated with MMR at their local hospitals without any serious side effects.

Table 1 The immunization schedule in Thailand and accelerated vaccines by the Infectious Disease Society of America

	Vaccine	Birth	1 mo	2 mo	4 mo	6 mo	7 mo	9 mo	12 mo	18 mo	24 mo	4 yr	9 yr	11 yr	
Thai's EPI vaccines	BCG	1													
	HBV	1	(For positive maternal HBsAg)	2		3									
	DTP, OPV/IPV			1	2	3				4		5			
	MMR					Acc ¹		1	Acc ¹		2				
	JE							1			2				
	Influenza					1	2								
	Tdap														1
	HPV													Acc	1-2 ²
Optional vaccine in Thailand	Rota			1	2	(3)									
	PCV			1	2	3			4						
	Varicella					Acc ¹		Acc ¹	1	2					
	HAV								1	2					
	Dengue												1-3 ³		

¹Acc denotes accelerated vaccines from the 2013 Infectious Diseases Society of America Clinical Practice Guideline for Vaccination of the Immunocompromised Host in which measles-mumps-rubella (MMR) at 6 and 12 mo of age and varicella at 6 mo of age and 3 mo apart from the first dose.

²Indicates 0 and 6 mo.

³Indicates 0, 6, 12 mo.

BCG: Bacillus Calmette-Guerin vaccine; DTP: Diphtheria-tetanus-pertussis; EPI: Expanded Program on Immunization; HAV: Hepatitis A vaccine; HBsAg: Hepatitis B surface antigen; HBV: Hepatitis B vaccine; HPV: Human papillomavirus vaccine; JE: Japanese encephalitis; OPV/IPV: Oral polio vaccine/inactivated polio vaccine; PCV: Pneumococcal conjugate vaccine; Tdap: Tetanus-diphtheria-acellular pertussis.

Infections during and after liver transplant

Infection severity and mortality were highest during the first year post-liver transplant. The respiratory and gastrointestinal systems were the most common sites of infection (Table 3). Two children died within 3 mo after liver transplantation, and both had underlying post-transplant lymphoproliferative disorder. One of these two children had mixed infection with bocavirus, mycoplasma, and parvovirus B19. The other exhibited EBV viremia that progressed to respiratory failure with an unidentified infectious origin. Of the 31 hospitalizations for VPIs recorded during the study period the median length of hospital stay was 6 d (range: 3-8 d), and in three cases ICU admission and ventilator support were required; two with influenza and one with *Streptococcus pneumoniae* infection. When the children were divided into complete and incomplete immunization groups based on Thailand's EPI, there were no significant differences in the numbers of hospitalizations for VPIs or non-VPIs (Table 4).

Table 2 Vaccination history in children at liver transplant and up to 5 years follow-up (n = 48)

Vaccines	Incomplete vaccination for age at transplantation		Incomplete vaccination for age after liver transplant, n (%)
	Thai EPI program, n (%)	Accelerated vaccine from IDSA, n (%)	
DTP-OPV/IPV	12 (25)	N/A	6 (12.5)
HBV	6 (12.5)		0
MMR	12 (25)	30 (62.5) ^b	27 (56.3) ^b
JE	16 (33.3)	N/A	10 (20.8)
Varicella	16 (33.3)	34 (70.8) ^b	34 (70.8) ^b
HAV	26 (54)		23 (47.9)
Influenza	30 (62.5)		18 (37.5) ^a
PCV	36 (75)		22 (45.8) ^b
Rota	37 (77)	N/A	37 (77)
All	25 (52)	43 (89.5) ^b	23 (47.9)
	(not included rota vaccine)		(not included lived vaccine)

^aP < 0.05 vs Thai Expanded Program on Immunization (EPI).

^bP < 0.001 vs Thai EPI program.

DTP: Diphtheria-tetanus-pertussis; HAV: Hepatitis A vaccine; HBV: Hepatitis B vaccine; IDSA: Infectious Diseases Society of America; JE: Japanese encephalitis; MMR: Measles-mumps-rubella; N/A: Not applicable; OPV/IPV: Oral polio vaccine/inactivated polio vaccine; PCV: Pneumococcal conjugate vaccine.

Pathogens causing hospitalization in children post-liver transplant

A total of 237 infections requiring hospitalization were recorded during the study period. The most commonly identified bacterial pathogens were *Escherichia coli* (13.1%), *Salmonella* sp. (8.1%), and *Klebsiella pneumoniae* (6.8%), and the most commonly identified viral pathogens were parainfluenza (5.9%), rotavirus (3.4%), and respiratory syncytial virus (3.4%). In cases of VPIs, the most common pathogens were rotavirus (3.4%), influenza virus (2.5%), and varicella-zoster virus (2.1%) (Table 5 and 6).

DISCUSSION

In this study, incomplete age-appropriate immunization before liver transplantation in children was common, particularly with regard to live vaccines that can be accelerated before liver transplantation. Post-liver transplant in nearly half of the children in the study did not catch up with all age-appropriate vaccines. At least 13.1% of the children in the study required hospitalization for VPIs during the 5 years post-liver transplant, and in these cases, the lengths of hospital stays were up to 1 wk. More than 10% of the children required admission to the ICU and respiratory support from VPIs, reflecting the burden of VPIs during the post-transplant period. With regard to non-VPIs, both bacterial and viral infections of the respiratory and gastrointestinal systems played major roles in hospitalizations with severe infections and mortality, especially during the first year post-transplant.

To the best of our knowledge, the current study is the first to investigate immunization status and infections requiring hospitalization in Asian children who underwent a liver transplant. Compared to previous studies in Europe^[9,10] and the United States^[4,11], in the present study, there was a higher rate of incomplete age-appropriate immunization before liver transplantation, particularly with respect to the accelerated MMR and varicella vaccination. However, the number of hospitalizations with VPIs (13.1%) was comparable to that in a study conducted in the United States by Feldman *et al*^[4,11] (11.3%). Moreover, the VPIs in that study were more severe and required longer hospital stays than those in the current study. Genetic risk factors may explain this phenomenon, as with the more contagious and severe coronavirus disease 2019 infections in Europe and the United States than in Thailand.

Prior to liver transplantation, physicians frequently do not offer patient immunization, particularly with respect to live vaccines^[8,12,13]. There is solid evidence of adequate immune responses to varicella and measles vaccination in children aged < 1 year^[14-16]; hence, the policy to promote accelerated vaccination in children before immunosuppressant therapy was initiated^[6,7,17,18]. It is probable that this is not standard practice in healthy children. Moreover, children waiting for a liver transplant may have had complex and serious illnesses that needed to be given priority. Some physicians may not be

Table 3 Characteristics of hospitalization from vaccine-preventable infections and non-vaccine-preventable infections up to 5 years follow-up

Time	Type of infections				Organ specific infections, n (%)						The severity of infections, n (%)		
	VPis		Non-VPis		RS	GI	Blood	Renal	Skin	Others	ICU	Ventilator dependence	Death
	Times, n (%)	LOS (d) ¹	Times, n (%)	LOS (d) ¹									
During transplant	4 (5.2)	51 (24,79)	73 (94.8) ^b	35 (27,49)	25 (35.2)	24 (31.2)	20 (26)	6 (7.8)	2 (2.6)	0	All	All	0
< 3 mo	2 (6.9)	3 (3,3)	27 (93.1) ^b	12 (7,28) ^a	13 (44.8)	10 (34.5)	2 (6.9)	2 (6.9)	1 (3.4)	1 (3.4)	6 (20.7)	5 (17.2)	2 (6.9)
3-6 mo	5 (17.9)	8 (5,39)	23 (82.1) ^b	10 (4,15)	11 (39.3)	13 (46.4)	2 (7.1)	1 (3.6)	0	1 (3.6)	8 (28.6)	6 (21.4)	0
> 6-12 mo	3 (8.3)	5 (3,5)	33 (91.7) ^b	7 (6,17)	15 (41.7)	11 (30.6)	6 (16.7)	0	2 (5.6)	2 (5.6)	10 (27.8)	6 (8.3)	0
> 12-24 mo	6 (15)	5 (4,9)	34 (85) ^b	7.5 (5,10)	18 (45)	12 (30)	1 (2.5)	1 (2.5)	4 (10)	4 (10)	11 (27.5)	9 (22.5)	0
> 2-5 yr	11 (40.7)	6 (3,8)	16 (59.3)	5 (4,9)	7 (25.9)	10 (37)	1 (3.7)	0	6 (22.2)	3 (1.9)	5 (18.5)	1 (3.7)	0
Total	31 (13.1)	6 (3,8)	206 (86.9) ^b	8 (5,15)	89 (37.6)	80 (33.8)	32 (13.5)	10 (4.2)	15 (6.3)	11 (4.6)	40 (16.9)	27 (11.4)	2 (0.84)

^a $P < 0.05$ vs vaccine-preventable infection (VPI) group.

^b $P < 0.001$ vs VPI group.

¹Data are presented as median (interquartile range).

GI: Gastrointestinal; ICU: Intensive care unit; LOS: Length of stay; RS: Respiratory system.

familiar with the accelerated immunization program[8,13], and therefore may decide to postpone vaccination. A specific protocol and concerted focus on educational interventions, or the development of specialized team care that is responsible for these issues is crucial to ensure that all candidates receive appropriate vaccinations to minimize complications associated with VPis[6]. One great benefit of pre-liver transplant vaccination is higher immunogenicity compared with revaccination post-liver transplant[18]. Moreover, pretransplant vaccination of children will likely lead to herd immunity that will be beneficial for other transplant children in inpatient and outpatient clinics during their visits[13].

In the present study, the rate of incomplete age-appropriate immunization after liver transplantation was high, and there was no significant difference between the pretransplant rate (52.0%) and the post-transplant rate (47.9%). In theory, children's vaccination schedules should be postponed for more than 2 mo after liver transplantation because of the possibility of an inadequate immune responses[6]. The high level of immunosuppressants is another factor to consider. In the present study almost half of the children were not up-to-date with their age-appropriate immunizations during up to 5 years of follow-up. The reasons might be relatively low concern over children in a stable condition post-transplant, and a level of immunosuppression that is not low enough to warrant immunization. Notably, only 62.3% of the children's guardians brought vaccination books to visits to the doctor. As well as unawareness, financial problems would likely be a major concern for the children's guardians, especially with regard to vaccines that are not included in Thailand's EPI such as pneumococcal conjugate vaccine, influenza vaccine, hepatitis A vaccine, and varicella vaccine. Fortunately the infectious diseases unit in our department conducted a campaign to promote the administration of pneumococcal conjugate vaccine

Table 4 Children with vaccination records who developed vaccine-preventable or non-vaccine-preventable diseases

Age-appropriate immunization	Thai's Expanded Program on Immunization				2013 Infectious Diseases Society of America			
	Infection and hospitalization, <i>n</i>			Total	Infection and hospitalization, <i>n</i>			Total
	None	VPIs and non-VPIs	Non-VPIs		None	VPIs and non-VPIs	Non-VPIs	
Complete immunization	5	5	12	22	9	9	25	43
Incomplete immunization	5	6	15	26	1	2	2	5
Total	10	11	27	48	10	11	27	48

VPIs: Vaccine-preventable infections.

and influenza vaccine to all immunocompromised children every year at no charge. This afforded the children in the present study the opportunity to access these vaccines, and there was a significant increase in the proportion of children that received these vaccines post-transplant ($P < 0.001$). Long-term provision of these high-cost vaccines by the authorities would be a worthwhile venture. With respect to live vaccines, there has been controversy about whether they should be administered to children after liver transplantation[17,19,20-23]. Thus, further reports and large cohort studies are required in order to clarify the safety of live vaccines in these vulnerable patients, before they are routinely vaccinated posttransplant.

In this study, the rate of hospitalization for VPIs up to 5 years post-transplant was similar to those reported in previous studies[9-11], but significantly higher than that in the normal population[9]. There was the mortality report of VPIs in children with immunocompromised hosts[1,2,22,24,25], but in this study, there was no mortality from VPIs. The VPIs requiring hospitalization in the current study were due to rotavirus, influenza, varicella, dengue fever, measles, *Streptococcus pneumoniae*, hepatitis B/E, and *Vibrio cholera*. These data should emphasize the value of complete immunization and robust infection control to physicians.

Viral hepatitis is endemic in Thailand, but interestingly in the present study there were no reports of hospitalization for hepatitis A post-liver transplant, and only one case of hepatitis E infection that required hospitalization. Viral hepatitis can be symptomatic and severe in older children and adults, and older children and adults may ingest more contaminated food and water than young children. Consequently, serology testing and immunization may be valuable in these groups. There is a reported case in which *de novo* hepatitis B infection was diagnosed 3 years after a liver transplant despite the recipient having undergone complete hepatitis B immunization pre-transplant[26]. This demonstrates that complete hepatitis B immunization pre-liver transplant does not guarantee post-transplant protection. That case prompted us to instigate a protocol for reimmunization and hepatitis B surface antibody monitoring every 3-6 mo to maintain a protective level of > 100 mIU/mL. *De novo* hepatitis B in the aforementioned boy who had hepatitis B surface antibody > 1000 mIU/mL pretransplant[26] may reflect waning immunity post-liver transplant. As well as vaccination, research evaluating the humoral and cellular immunity evoked by each vaccine should be conducted to determine vaccination schedules and the antibody parameters required to prevent VPIs more effectively. In the present study, the overall infection rate was high in the first year post-transplant, hence vaccination should be initiated as soon as possible after liver transplanted children are sufficiently stable. Predictors of high immunogenic responsivity to vaccination are needed to enable physicians to decide on optimal timepoints for reimmunization.

The current study had some limitations. It was a single-center study with a relatively small sample size. The true prevalence of VPIs may be lower than the frequency in the study, because the study only included children with severe enough illness to require hospitalization. Almost all children in the present study were referred from distant and rural areas, and it is possible that some of them subsequently attended more local hospitals due to infections. The main strength of the study was the reliable vaccination records obtained directly from the patients' vaccination books, which facilitated comparisons of vaccination status pre-transplant and post-transplant.

CONCLUSION

Incomplete immunization was common in children pre-liver transplant and post-liver transplant. Almost all of the children in the study required hospitalization due to VPIs or non-VPIs within 5 years post-liver transplant. The severity of infections was highest in the first year post-liver transplant.

Table 5 Pathogen causing hospitalization in children after liver transplantation

Time	The rank of the pathogen, n (%)			Total
	Bacteria	Total	Virus, fungus, and unidentified	
During transplant	<i>E. coli</i> (n = 19, 24.7), <i>K. pneumoniae</i> (n = 12, 15.6), <i>A. baumannii</i> (n = 11, 14.3), <i>Enterococcus/Staphylococcus</i> (n = 4, 5.2), <i>Salmonella</i> (n = 3, 3.9), <i>P. aeruginosa</i> (n = 2, 2.6), <i>B. cereus/Corynebacterium/S. pneumoniae/Elizabethkingia meningoseptica/Stenotrophomonas/Streptococcus mirabilis/C. difficile</i> (n = 1, 1.3)	62	Rotavirus/adenovirus/bocavirus (n = 2, 2.6), parainfluenza/fungus/varicella-zoster virus (n = 1, 1.3)	9 ^b
< 3 mo	<i>E. coli/K. pneumoniae/Enterococcus/Salmonella/Aeromonas</i> (n = 2, 6.9), <i>Corynebacterium/C. difficile/Plesiomonas</i> (n = 1, 3.4)	13	Parainfluenza (n = 3, 10.3), coronavirus (n = 2, 6.9), rotavirus/bocavirus/RSV/dengue/fungus/norovirus/rhinovirus/parvovirus B19 (n = 1, 3.4), unidentified (n = 6, 20.7)	19
3-6 mo	<i>Salmonella/E. coli</i> (n = 2, 7.1), <i>K. pneumoniae/Enterococcus/S. pneumoniae/Staphylococcus</i> (n = 1, 3.6)	8	RSV (n = 4, 14.3), influenza (n = 2, 7.1), rotavirus/parainfluenza/rhinovirus/measles/HHV6 (n = 1, 3.6), unidentified (n = 9, 32.1)	20
> 6-12 mo	<i>E. coli</i> (n = 4, 11.1), <i>Salmonella</i> (n = 3, 8.3), <i>A. baumannii/Enterococcus/mycoplasma/C. difficile</i> (n = 2, 5.6), <i>Stenotrophomonas/Staphylococcus/Aeromonas/Pseudomonas/Plesiomonas/P. jirovecii</i> (n = 1, 2.8)	21	Parainfluenza (n = 3, 8.3), norovirus/herpes simplex virus (n = 2, 5.6), fungus/RSV/rhinovirus/influenza/measles (n = 1, 2.8), unidentified (n = 3, 8.3)	15
> 12-24 mo	<i>Salmonella</i> (n = 8, 12.5), <i>E. coli</i> (n = 3, 7.5), <i>Aeromonas/Pseudomonas/mycoplasma/Plesiomonas</i> (n = 1, 2.5)	15	Parainfluenza (n = 6, 15), rotavirus (n = 2, 5), adenovirus/varicella-zoster virus/dengue/rhinovirus/influenza/measles/metapneumovirus/hepatitis E/coxakie AB (n = 1, 2.5) unidentified (n = 11, 27.5)	28
> 2-5 yr	<i>Salmonella/mycoplasma</i> (n = 2, 7.4), <i>E. coli/K. pneumoniae/Staphylococcus/Vibrio cholera/B. cereus</i> (n = 1, 3.7)	9	Varicella-zoster virus (n = 3, 11.1), rotavirus/RSV/dengue/influenza (n = 2, 7.4), fungus/norovirus/herpes simplex virus/hepatitis B (n = 1, 3.7), unidentified (n = 3, 11.1)	18
Overall	<i>E. coli</i> (n = 31, 13.1), <i>Salmonella</i> (n = 20, 8.1), <i>K. pneumoniae</i> (n = 16, 6.8), <i>A. baumannii</i> (n = 13, 5.5), <i>Enterococcus</i> (n = 9, 3.8), <i>Staphylococcus</i> (n = 8, 3.3), <i>mycoplasma</i> (n = 5, 2.1), <i>C. difficile</i> (n = 4, 1.7), <i>Plesiomonas Shigelloides/Aeromonas</i> (n = 3, 1.3), <i>Corynebacterium/S. pneumoniae/Stenotrophomonas/P. aeruginosa/Aeromonas</i> (n = 2, 0.8), <i>Bacillus/Elizabethkingia meningoseptica/Streptococcus mirabilis/P. jirovecii/Vibrio cholera/B. cereus</i> (n = 1, 0.4)	128	Parainfluenza (n = 14, 5.9), rotavirus/RSV (n = 8, 3.4), influenza (n = 6, 2.5), varicella-zoster virus (n = 5, 2.1), dengue/norovirus/fungus/rhinovirus (n = 4, 1.7), adenovirus/bocavirus/herpes simplex virus/measles (n = 3, 1.3), coronavirus (n=2, 0.8), HHV6/metapneumovirus/hepatitis E/coxakie AB/hepatitis B (n = 1, 0.4), unidentified (n = 32, 13.5)	109 ^b

^bP < 0.001; virus *vs* bacterial causes of infections at each time point. *A. baumannii*: *Acinetobacter baumannii*; *B. cereus*: *Bacillus cereus*; *C. difficile*: *Clostridium difficile*; *E. coli*: *Escherichia coli*; HHV6: Human herpes virus 6; *K. pneumoniae*: *Klebsiella pneumoniae*; *P. aeruginosa*: *Pseudomonas aeruginosa*; *P. jirovecii*: *Pneumocystis jirovecii*; RSV: Respiratory syncytial virus; *S. pneumoniae*: *Streptococcus pneumoniae*.

Table 6 Vaccine-preventable infections causing hospitalization in children after liver transplantation

Time	During transplant	< 3 mo	3-6 mo	> 6-12 mo	> 12-24 mo	> 2-5 yr	Overall
Rota	2	1	1	0	2	2	8
Influenza	0	0	2	1	1	2	6
Varicella	1	0	0	0	1	3	5
Dengue	0	1	0	0	1	2	4
Measles	0	0	1	1	1	0	3
<i>Streptococcus pneumoniae</i>	1	0	1	0	0	0	2
Hepatitis B	0	0	0	0	0	1	1
Hepatitis E	0	0	0	0	1	0	1
<i>Vibrio cholera</i>	0	0	0	0	0	1	1

ARTICLE HIGHLIGHTS

Research background

Infection after liver transplantation is a serious concern due to potential morbidity and mortality, thus strategies to reduce overall post-transplant infection are warranted. Immunization is an effective and relatively noninvasive and affordable way to reduce vaccine-preventable infections (VPIs).

Research motivation

There is strong evidence that VPIs and non-VPIs post-transplant cause high fatality and increase graft rejection, but published data on VPIs and their effects in children post-liver transplant in Asia are scarce.

Research objectives

To investigate immunization status in children at the time of liver transplantation and up to 5 years thereafter. The prevalence and impact of VPIs and non-VPIs during hospitalization were also evaluated.

Research methods

The current retrospective study included 77 children who underwent liver transplantation and were followed up for up to 5 years thereafter. Demographic data, patient characteristics, immunization details derived from vaccination records, and hospitalizations for VPIs and non-VPIs were analyzed.

Research results

The mean follow-up duration after liver transplantation was 3.68 ± 1.45 years. Of the 77 children in the study, 48 (62.3%) had vaccination records in their vaccination books. There was a significant difference in the proportion of children with incomplete vaccination according to Thailand's Expanded Program on Immunization ($n = 25$, 52%) and accelerated vaccine from Infectious Diseases Society of America recommendations ($n = 43$, 89.5%) ($P < 0.001$). Post-liver transplant, almost half of the children in the study did not catch up with appropriate immunizations for age. There were 237 infections requiring hospitalization during up to 5 years of follow-up post-liver transplant at our hospital. The risks of VPIs and non-VPIs were highest during the first year after liver transplantation, and 2 children died. Respiratory and gastrointestinal systems were common sites of infection. The most commonly identified pathogens that caused VPIs were rotavirus, influenza virus, and varicella-zoster virus.

Research conclusions

Incomplete age-appropriate immunization in children pre-liver transplant and post-liver transplant were common. At least 13.1% of the children in the study required hospitalization for a VPI during a follow-up period of up to 5 years post-transplantation. There was high morbidity, especially during the first year after transplantation. Hence, complete immunization and robust infection control should be considered in such children.

Research perspectives

The current study suggests that incomplete age-appropriate immunization is a major concern, because a large number of patients with VPIs requiring hospitalization were recorded. Interestingly, waning immunity post-liver transplant can evidently lead to VPIs, as evidenced by a case in which *de novo* hepatitis B infection developed 3 years postliver transplantation in a child who had a hepatitis B surface antibody titer of > 1000 mIU/mL pre-liver transplantation. As well as policies to increase pre- and post-

transplant immunization rates, studies investigating humoral and cellular immunity induced by vaccination after liver transplantation are needed.

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FOOTNOTES

Author contributions: Sintusek P designed and oversaw the study, drafted the manuscript, collected, interpreted, and analyzed the data, and made critical revisions related to important intellectual content; Poovorawan Y suggested critical intellectual content and approved the final manuscript.

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Country/Territory of origin: Thailand

ORCID number: Palittiya Sintusek 0000-0003-4441-0151; Yong Poovorawan 0000-0002-2337-6807.

Corresponding Author's Membership in Professional Societies: American Association for the Study of Liver Diseases, No. 174508.

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Observational Study

Endoscopic retrograde cholangiopancreatography and liver biopsy in the evaluation of elevated liver function tests after liver transplantation

Augustin Attwell, Samuel Han, Michael Kriss

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Abstract

BACKGROUND

Abnormal liver function tests (LFTs) in post-liver transplant (LT) patients pose a challenge in the timing and selection of diagnostic modalities. There are little data regarding the accuracy of endoscopic retrograde cholangiopancreatography (ERCP) and liver biopsy (LB) in diagnosing post-transplant complications.

AIM

To evaluate the diagnostic performance of ERCP and LB in patients with non-vascular post-LT complications.

METHODS

This single-center retrospective study evaluated patients undergoing both ERCP and LB for evaluation of elevated LFTs within 6 mo of LT from 2000 to 2017. Diagnostic operating characteristics including accuracy, sensitivity and specificity for various diagnoses were calculated for ERCP and LB. The R factor (ratio of alkaline phosphatase to alanine aminotransferase) was also calculated for each patient.

RESULTS

Of the 1284 patients who underwent LT, 91 patients (74.7% males, mean age of 51) were analyzed. Anastomotic strictures (AS, 24.2%), acute cellular rejection (ACR, 11%) and concurrent AS/ACR (14.3%) were the most common diagnoses. ERCP

carried an accuracy of 79.1% (95%CI: 69.3-86.9), LB had an accuracy of 93.4% (95%CI: 86.2-97.5), and the combination of the two had an accuracy of 100% (95%CI: 96-100). There was no difference between patients with AS and ACR in mean R factor (AS: 1.9 vs ACR: 1.1, $P = 0.24$). Adverse events did not differ between the two tests (ERCP: 3.1% vs LB: 1.1%, $P = 0.31$).

CONCLUSION

In patients with abnormal LFTs after LT without vascular complications, the combination of LB and ERCP carries low risk and improves diagnostic accuracy over either test alone.

Key Words: Liver transplantation; Endoscopic retrograde cholangiopancreatography; Liver biopsy; Abnormal liver tests; Acute cellular rejection; Anastomotic biliary stricture

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Core Tip: Patients commonly develop unexplained elevations in liver function tests after liver transplantation. After cross sectional imaging and basic lab tests, endoscopic retrograde cholangiopancreatography (ERCP) and liver biopsy (LB) are both performed in arbitrary fashion since the diagnostic capacity of each test remains unclear. In this study we found that ERCP and LB are both effective diagnostic tests in the setting of the 2 most common diagnoses, anastomotic biliary stricture and acute cellular rejection. Combining these tests increases the overall diagnostic accuracy to 100%, and both tests carried adverse event rates of < 5%. This study justifies combining ERCP and LB when the diagnosis remains elusive.

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INTRODUCTION

Since 2012, the number of liver transplants (LTs) performed annually in the United States has increased each year, reaching a record number of 8250 in 2018[1]. Just as the field of transplantation has evolved over the past 5 decades, so too have the nuances of post-transplant clinical care. Clinicians commonly face the conundrum of abnormal liver function tests (LFTs) soon after LT which often indicates a transplant-related complication. Practice guidelines provided by the American Association for the Study of Liver Diseases (AASLD), American Society of Transplantation, and the European Association for the Study of the Liver note that the frequency of monitoring LFTs after LT and the subsequent work-up should be individualized to the patient and time after LT, prior complications, stability of serial testing, and the suspected underlying pathology[2,3].

The underlying cause, however, can be challenging to discern. Depending on the pattern of abnormal LFTs, evaluation of the biliary system with transabdominal ultrasound, MRI, CT, and/or endoscopic retrograde cholangiopancreatography (ERCP) may be most appropriate when the LFT pattern is cholestatic, whereas liver biopsy (LB) should be performed first when parenchymal injury is suspected [2]. To date, there are insufficient data regarding the relative accuracy of ERCP and LB in diagnosing specific post-LT complications. Current societal guidelines strongly support both of these tests (Grade 1A recommendations) but provide little guidance on which should be performed initially[2]. The decision to choose LB, ERCP, or both (and in which order) is therefore left to the discretion of the transplant surgeon, hepatologist, or interventional endoscopist. The primary aim of this study was to evaluate the diagnostic performance of ERCP and LB in patients with non-vascular post-LT complications.

MATERIALS AND METHODS

This was a single-center, retrospective review of all patients who underwent LT followed by both LB and ERCP at the University of Colorado Hospital from January 2000 to June 2017.

Patients

Patients undergoing deceased or living donor LT at our center during the study period were identified

using the LT database. Inclusion criteria included adult patients post-LT who underwent both LB and ERCP within 6 mo after LT with a primary indication of elevated LFTs. Patients with a clearly identifiable cause of elevated LFTs—such as drug or medication-related hepatitis, vascular liver disease or infectious hepatitis based on the initial history, labs, or imaging studies—were excluded from the analysis. Patients who did not receive post-LT care at our institution were also excluded. Post-LT biliary anatomy types included duct-to-duct (DD) anastomosis and Roux-en-Y hepaticojejunostomy (RYHJ).

Patients with a mixed pattern of liver injury based on LFTs underwent either LB or ERCP initially at the discretion of the provider. ERCP was the first invasive diagnostic test performed when patients had symptoms suggestive of cholangitis or a predominantly cholestatic pattern of elevated LFTs. LB was performed after labs and cross-sectional imaging when hepatocellular disease was suspected. It is our practice to monitor immunosuppressant levels on all post-LT patients. Approval from the Colorado Multi-Institutional Review Board was obtained prior to beginning the study.

ERCP

ERCP was performed under conscious sedation, monitored anesthesia care, or general anesthesia by one of 7 advanced endoscopists who have performed > 1000 ERCPs each. Endoscopists utilized the standard technique in cannulating the bile duct and performing cholangiography. Occlusion cholangiography was used to visualize the entire native and donor biliary tree with particular attention paid to the anastomosis. Biliary sphincterotomy was performed in select cases at the discretion of the endoscopist. If present, strictures were treated with the placement of plastic or fully covered metal stents were placed across strictures according to the endoscopist's judgment. Dilatation of strictures *via* balloon or catheter was performed prior to stenting in select cases.

Conventional techniques such as balloon and basket sweeping were used to remove bile duct stones and/or casts, and single or multiple stents were placed across anastomotic bile duct leaks. For patients with DD biliary anastomosis, a standard duodenoscope was used to reach the ampulla. For patients with RYHJ anatomy either a pediatric colonoscope or small bowel enteroscope (single-balloon, double-balloon, or rotational overtube) was used to reach the biliary anastomosis.

LB

While percutaneous (ultrasound-guided) LB represented the preferred route of biopsy, transjugular LB was generally performed in patients with an International Normalized Ratio > 1.5, when intravascular pressure measurements were needed, or when the abdominal anatomy precluded a safe percutaneous approach. Both percutaneous and transjugular LB were performed under conscious sedation. LB techniques are described in detail in an AASLD position paper[4]. Board certified GI pathologists examined all histology samples.

Outcomes and definitions

The study's primary outcome was the accuracy of ERCP and LB in making the ultimate final diagnosis or diagnoses driving the abnormal LFTs, as determined by the GI and Hepatology services. Secondary outcomes included sensitivity and specificity for ERCP and LB in the final diagnosis. Acute cellular rejection (ACR) was defined and graded using a 1-9 scale based on histopathologic findings using the rejection activity index, which was based on inflammatory changes in the portal triads, bile ducts, and venous endothelium (with scores of 1-3 for each of the 3 categories)[5]. A score of 3 or more was classified as definite ACR (Figure 1)[5]. Recurrent hepatitis C infection (HCV) after LT was defined by detectable serum HCV RNA. Anastomotic stricture (AS) was defined as a benign-appearing narrowing in the region of the biliary anastomosis during ERCP, typically within 5-6 mm from the suture line, usually associated with delayed contrast drainage and/or moderate resistance to passage of an inflated 12 mm balloon (Figure 2).

True positive results for LB or ERCP were defined by findings supportive of at least one of the final diagnosis/es as defined above. True negative results were defined by ERCP or LB results that failed to support the final diagnosis/es with or without supporting an alternative diagnosis. For example, if LB showed signs of a large bile duct obstruction or cholangitis, this was considered a true positive for a final diagnosis of anastomotic stricture or cholangitis, respectively. Conversely, if ERCP did not show biliary pathology, this was considered a false negative when the final diagnosis was a hepatocellular disorder such as ACR or recurrent HCV.

Statistical analysis

Descriptive statistics were used to depict patient demographics, symptoms and laboratory data. An R factor was calculated as the ratio between the degree of elevation of alkaline phosphatase and the degree of elevation of alanine aminotransferase[6]. R factors > 5 were considered to be consistent with hepatocellular damage and R factors < 2 suggested cholestatic patterns of injury, with R factors between 2 and 5 suggesting a mixed pattern of injury. Diagnostic operating characteristics including sensitivity, specificity, and accuracy [(true positive + true negative)/(true positive + false negative + false positive + true negative)] were calculated for both ERCP and LB. Fisher's exact test or the chi square test were used to compare categorical variables between patients with ACR and AS. The student's *t*-test was used to

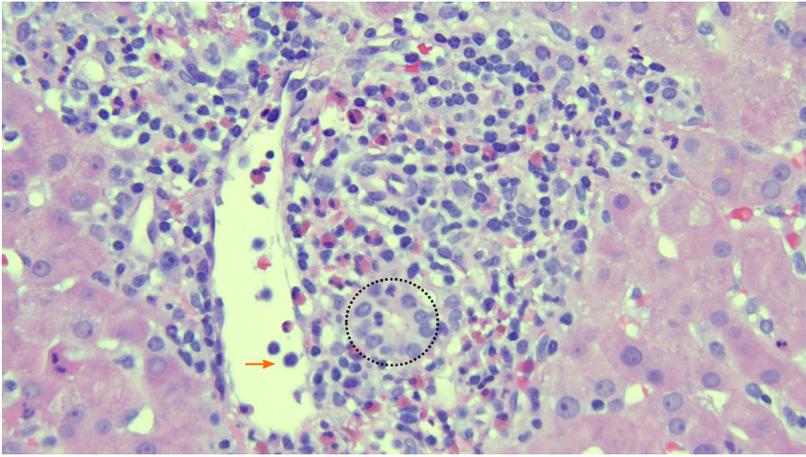


Figure 1 Photomicrograph of representative portal tract in acute cellular rejection. Mixed, lymphocyte predominant portal-based inflammation, bile duct inflammation characterized by lymphocyte infiltration (circle), and a large portal venule with subendothelial lymphocyte infiltration and intraluminal lymphocyte tethering[24] (hematoxylin and eosin stain, 40 ×).

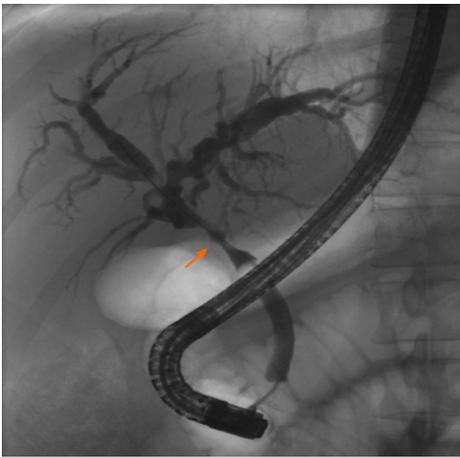


Figure 2 Cholangiogram during endoscopic retrograde cholangiopancreatography demonstrating an anastomotic stricture (arrow).

compare continuous variables between patients with ACR and AS. Adverse event rates were compared between ERCP and LB using the Fisher's exact test. All statistical analysis was performed using STATA 15.1 (StataCorp, College Station, TX, United States).

RESULTS

Patients

A total of 1284 patients underwent LT at our center during the study period (Figure 3). Of these, 96 patients (7.5%) received both an ERCP and LB for evaluation of persistently elevated LFTs within the first 6 mo after LT. Ninety-one patients received long-term follow-up at our institution and were included in the final analysis. The mean time interval between the 2 procedures was 9.1 d (SD 6.9).

The mean age of the cohort was 51 (SD 12.1) and 74.7% ($n = 68$) were male (Table 1). Deceased donor transplants ($n = 73$, 80.2%) accounted for the majority of transplants, and 73.6% ($n = 67$) had DD biliary anatomy. Presenting symptoms included jaundice (23.1%, $n = 21$), abdominal pain (15.4%, $n = 14$), and fever (12.1%, $n = 11$), and 21 (25%) patients were asymptomatic. Initial imaging consisted of ultrasound (74.7%), CT (18.7%), and magnetic resonance cholangiopancreatography (MRCP, 6.6%) with a mean donor bile duct diameter of 4.6 (SD 1.9) mm. Imaging revealed a dilated duct in 9 (9.9%, 8 with ultrasound, 1 with MRCP) of patients. LB was performed as the first of the 2 tests in 51 (56%) patients, and 71.4% ($n = 65$) of LBs were performed *via* the percutaneous route. Nearly 75% of patients were on dual immunosuppression therapy ($n = 68$) with 22% of patients on monotherapy ($n = 20$) with the combination of tacrolimus and mycophenolate sodium being the most common combination therapy ($n = 21$).

Table 1 Baseline characteristics reported as *n* (%) or mean (SD)

Variable	Overall cohort (<i>n</i> = 91)
Age	51 (12.1)
Sex (male)	68 (74.7)
Presenting symptom	
Jaundice	21 (23.1)
Fever	11 (12.1)
Abdominal pain	14 (15.4)
Asymptomatic	21 (25)
Liver biopsy performed first	51 (56)
Percutaneous liver biopsy	65 (71.4)
Bile duct diameter (mm)	4.6 (1.9)
R factor	2 (2.4), Range: 0.1-6.4
Alkaline phosphatase (international units/liter)	392.6 (248.4)
AST (units/liter)	200.5 (674.8)
ALT (units/liter)	205.4 (444.2)
Total bilirubin (mg/dL)	4.5 (5.4)
Deceased donor	73 (80.2)
Transplant biliary anatomy	
Duct-to-duct	67 (73.6)
Roux-en-Y hepaticojejunostomy	24 (26.4)
Tacrolimus	66 (73.3)
Sirolimus	20 (22.2)
Everolimus	6 (6.6)
Mycophenolate sodium	28 (31.1)
Mycophenolate mofetil	13 (14.4)
Cyclosporine	16 (17.8)
Prednisone	20 (22.2)
Immunosuppression monotherapy	20 (22)
Dual immunosuppression therapy	68 (74.7)
Triple immunosuppression therapy	3 (3.3)

AST: Aspartate aminotransferase; ALT: Alanine transaminase.

Technically, all LB and ERCP procedures were performed successfully. The most common single diagnosis ultimately was AS (34.1%), followed by ACR (11%) with all diagnoses displayed in [Table 2](#). A total of 29 (31.9%) patients had multiple concurrent diagnoses contributing to the elevation in LFTs (and included as final diagnoses), and the most common was a dual diagnosis of AS with ACR (14.3%, *n* = 13). Four (4.4%) patients had 3 concurrent diagnoses, all of which included ACR and AS ([Table 2](#)).

Diagnostic operating characteristics

The diagnostic operating characteristics of LB and ERCP are shown in [Table 3](#). The overall accuracy of ERCP was 79.1% (95% CI: 69.3-86.9). The overall accuracy of LB was 93.4% (95% CI: 86.2-97.5). Combined, the 2 tests had an overall accuracy of 100% (95% CI: 96-100).

For AS, ERCP had an accuracy of 100% (95% CI: 84.6-100) while LB had an accuracy of 72.7% (95% CI: 49.8-89.3). For ACR, LB had an accuracy of 100% (95% CI: 69.2-100) while ERCP had an accuracy of 0% (95% CI: 0-30.9). Sensitivities carried the same values as the accuracy in all cases due to the lack of false positive results. For the same reason, specificity could not be calculated for any of the diagnostic tests.

Table 2 Etiologies of liver function test elevation reported as *n* (%)

Single diagnosis	<i>n</i> (%)
Anastomotic stricture	31 (34.1)
Acute cellular rejection	10 (11)
Recurrent primary sclerosing cholangitis	6 (19.4)
Recurrent HCV	5 (5.5)
Biliary cast syndrome	3 (3.3)
Ischemic cholangiopathy	2 (2.2)
Papillary stenosis	1 (1.1)
Posterior reversible encephalopathy syndrome	1 (1.1)
Cholestatic hepatitis	1 (1.1)
Recurrent PBC	1 (1.1)
Venous outflow obstruction	1 (1.1)
Two diagnoses	
Anastomotic stricture and acute cellular rejection	13 (14.3)
Recurrent HCV and anastomotic stricture	6 (19.4)
Bile leak and acute cellular rejection	2 (2.2)
Congestive hepatopathy and anastomotic stricture	1 (1.1)
Anastomotic stricture and suprahepatic cava stenosis	1 (1.1)
Recurrent PBC and anastomotic stricture	1 (1.1)
CMV hepatitis and bile leak	1 (1.1)
Three diagnoses	
Acute cellular rejection, anastomotic stricture, and recurrent HCV	2 (2.2)
Acute cellular rejection, anastomotic stricture, and de novo autoimmune hepatitis	1 (1.1)
Acute cellular rejection, anastomotic stricture, and CMV hepatitis	1 (1.1)

HCV: Hepatitis C virus; PBC: Primary biliary cholangitis; CMV: Cytomegalovirus.

Table 3 Operating characteristics for endoscopic retrograde cholangiopancreatography and liver biopsy in diagnosing post-liver transplant complications

	ERCP	LB	ERCP + LB
Overall accuracy % (95%CI)	79.1 (69.3-86.9)	93.4 (86.2-97.5)	100 (96-100)
Overall sensitivity % (95%CI)	79.1 (69.3-86.9)	93.4 (86.2-97.5)	100 (96-100)
Acute cellular rejection accuracy % (95%CI)	0 (0-30.9)	100 (69.2-100)	100 (91.9-100)
Anastomotic stricture accuracy % (95%CI)	100 (84.6-100)	72.7 (49.8-89.3)	100 (89.4-100)

ERCP: Endoscopic retrograde cholangiopancreatography; LB: Liver biopsy.

Liver function tests

The mean R factor (ratio of alkaline phosphatase and alanine aminotransferase) was 2 (SD 2.4), with a mean alkaline phosphatase (AP) level of 392.6 (SD 248.4) IU/L and mean total bilirubin (TB) level of 4.5 (SD 5.4) mg/dL. The mean aspartate aminotransferase (AST) and alanine aminotransferase (ALT) levels were 200.5 (SD 674.8) and 205.4 (444.2), respectively. Between patients with AS and patients with ACR, there was no significant difference in R factor (AS: 1.9 vs ACR: 1.1, $P = 0.24$), AP (AS: 376.3 vs ACR: 452.2, $P = 0.48$), TB (AS: 4.1 vs ACR: 5.5, $P = 0.41$), AST (AS: 130.9 vs ACR: 127.9, $P = 0.94$), or ALT (AS: 203.1 vs ACR: 169.5, $P = 0.58$). There was also no difference between the 2 diagnoses in terms of bile duct diameter (AS: 4.8 mm vs ACR: 3.8 mm, $P = 0.36$). Patients with concurrent AS and ACR had a mean R

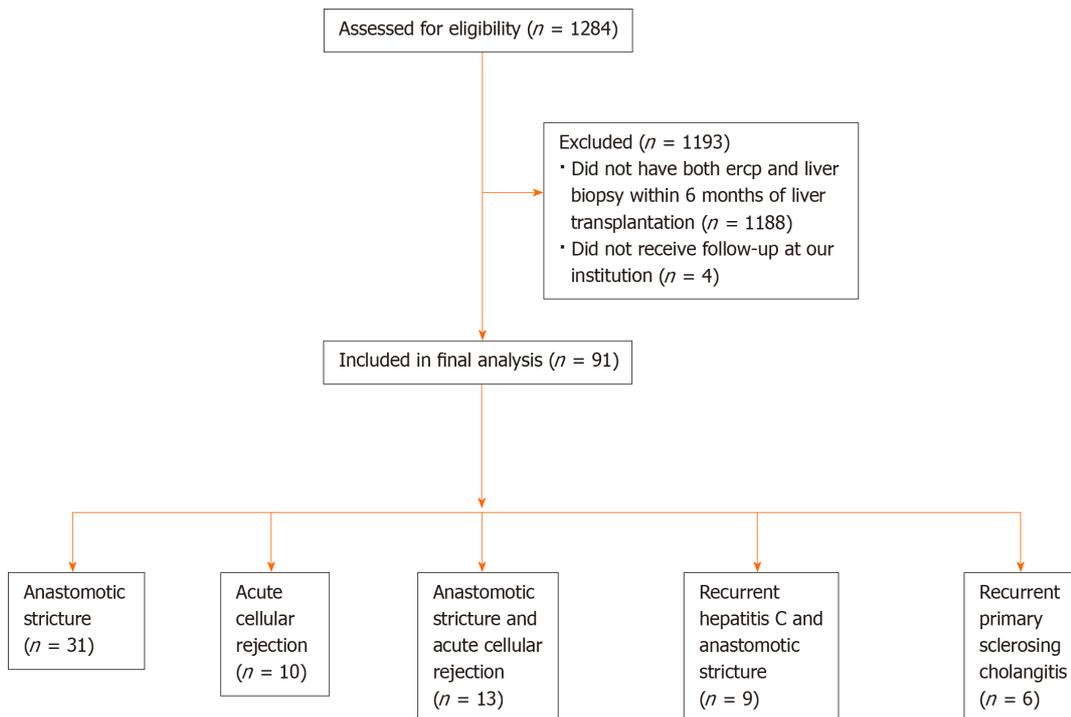


Figure 3 Flow diagram of patients. ERCP: Endoscopic retrograde cholangiopancreatography.

factor of 1.06 (0.7).

Adverse events

A total of 3 adverse events occurred after 96 ERCPs (3.1%): 1 case of mild post-ERCP pancreatitis treated conservatively, and 2 cases of post-procedure abdominal pain requiring overnight hospitalization and supportive care. One adverse event occurred after LB, a hepatoportal fistula that required hospitalization and angiography with embolization by Interventional Radiology. There was no significant difference in the adverse event rates due to ERCP or LB (3.1% vs 1.1%, $P = 0.31$).

DISCUSSION

It is common to encounter asymptomatic patients with abnormal LFTs in the post-LT setting, as well as symptomatic patients with normal LFTs. It is also common for patients to undergo multiple invasive diagnostic tests as part of the work-up. Abnormal LFTs post-LT are a major cause of unplanned hospital readmissions, and the ensuing work-up may consume significant resources[7]. ERCP is the accepted diagnostic and therapeutic test for suspected biliary pathology and LB is the accepted test for suspected hepatocellular pathology. But in reality, because of the poor specificity of LFT patterns and the limitations of cross-sectional imaging, patients with post-LT LFT elevations will too often undergo both procedures. The timing and order of these procedures is left to the discretion of the transplant surgeon, hepatologist and advanced endoscopist, with little evidence to guide them. Despite the high incidence of immune-mediated and biliary complications following LT, the usual clinical tools (*e.g.*, clinical history, LFT patterns, bile duct diameter on imaging) are poorly specific for any single diagnosis. Besides the main finding of our study, this study demonstrated that patients with AS had no significant difference from patients with ACR in terms of R factor, alkaline phosphatase level, total bilirubin level, AST level, ALT level, or bile duct diameter. Hence, additional testing with LB and ERCP was justified.

Ultrasound and MRCP have variable accuracy in diagnosing biliary pathology post-LT, since obstructive ductal dilation in the transplanted liver is variable. Several studies have demonstrated poor sensitivity and specificity of bile duct diameter post-LT[8-11]. While both modalities can detect biliary dilatation, MRCP offers an advantage over ultrasound in being able to detect biliary strictures with a sensitivity ranging from 64%-79%[9,12]. While both of these modalities are first-line options for imaging in the diagnostic work-up of elevated LFTs after LT, we have found that MRCP both under-estimates and over-estimates stenosis size and severity. Additionally, ERCP permits a real-time accurate assessment of strictures, based on contrast drainage and balloon passage, and the ability to perform stricture therapy. For these reasons, we generally go straight to ERCP and bypass MRCP when there is significant ductal dilation, a cholestatic pattern of LFTs, or a negative LB.

To our knowledge, this is the largest study evaluating the diagnostic performance of combined LB and LT in patients with abnormal LFTs after LT. Our novel finding in this study is the high diagnostic accuracy for ERCP and LB, in contrast to standard laboratory tests or cross-sectional imaging. Diagnostic accuracy was 79.1% overall for ERCP and 93.4% overall for LB. Combined, the 2 tests study had an overall diagnostic accuracy of 100%.

ACR and AS were the most frequent final diagnoses in our patients. These are commonly encountered diseases in the LT population, but the differential diagnosis remains broad (Figure 4) and includes de novo autoimmune hepatitis, recurrent liver disease (HCV, PSC, others), drug toxicity, de novo infection, biliary stones or casts, hepatic artery thrombosis, and more[2]. We recognize that a previously common clinical dilemma—differentiating recurrent HCV from ACR or other etiologies—is less common in the current direct-acting antiviral (DAA) era, and our study included patients in the current and pre-DAA eras.

In the early days of LT, ACR was a near-universal complication resulting in long-term graft failure [13,14]. Advances in immunosuppression have subsequently led to reduced rates of allograft rejection, though the incidence still ranges from 20% to 40% after LT, with most occurring within the first month [15-17]. In addition, ACR remains clinically significant, impacting long-term graft survival and mortality [18]. The incidence of biliary complications after LT is highly variable but still relatively common. The estimated incidence of AS post-LT is up to 20% for patients following deceased donor LT and 19%-40% after living donor liver transplantation. Risk factors include graft ischemia, DD anastomosis, reperfusion injury, deceased donor, and hepatic artery thrombosis. The incidence of non-anastomotic stricture is 0.5% to 10%, while stones/sludge are seen post-LT in approximately 5% of patients. Biliary cast syndrome is less common (2.5%-3%)[19-22].

It is critical to make a prompt and diagnosis when a transplanted patient presents with abnormal LFTs, since graft survival depends on timely and appropriate treatment. While ACR is successfully treated with various combinations of immunosuppressive medication, the management of biliary complications is procedural. AS may be treated successfully with endoscopic placement of multiple plastic stents or a covered metal stent. Recent data suggests that metal stents incur fewer procedures and costs while leading to stricture resolution similarly to plastic stents[23].

Our study sheds light on the frequency of dual diagnoses in patients with abnormal LFTs post-LT, which is an under-studied phenomenon. In this study, 34 (37.4%) patients had multiple diagnoses, of which the most common combination was AS plus ACR (14.3%). Four patients (4.4%) ultimately received 3 final diagnoses. In practice, patients receive therapy for multiple diseases concurrently (*e.g.* stenting for AS plus corticosteroid bursts for AS), so knowing which diagnosis is dominant can be challenging. Previous studies assessing abnormal LFTs in the post-LT population mostly included patients undergoing LB or ERCP but not both, so our study may represent more complex, sicker patients[7]. Alternatively, some of the various diagnoses in our patients may be clinically silent. AS, for example, is quite subjective and may be diagnosed or treated by endoscopists even though the stricture may not be high-grade or impede bile flow.

Our findings suggest that physicians managing post-LT patients can have a lower threshold to perform both LB and ERCP when evaluating abnormal LFTs within the context of the patient's clinical presentation. While one modality alone has high diagnostic accuracy over lab tests and imaging, LB and ERCP combined have a very high diagnostic accuracy. Ultimately the decision to perform one test over the other depends on clinician experience, but both tests improve the diagnostic accuracy over one test alone. However, despite the high prevalence of multiple final diagnoses (37.4%), only 96 of 1284 transplanted patients at our center underwent both ERCP and LB during the study period, suggesting they are used sparingly overall. Finally, the adverse event rates of ERCP and LB are low, and we demonstrated no significant difference between the two.

This study was limited by its size and design. It was performed at a single, United States tertiary care hospital with experienced endoscopists and transplant hepatologists, so the results may not be generalizable to other centers. The final diagnosis was determined by review of the medical record and hence may be affected by bias or subjectivity amongst the various treating physicians. Moreover, a reproducible, objective grading score for AS has not been established. The study was also limited by its retrospective nature and by limiting the analysis to patients undergoing ERCP and LB early after LT during the 17-year study period. An additional limitation is the variable time gap between ERCP and LB, although across the entire study population the mean time interval between both procedures was relatively short (9.1 d) suggesting that the diagnostic evaluation typically occurred during a single clinical episode. Despite these limitations, our cohort represents the modern-day practice of ERCP and LB after LT, and the study permits a comparison between the 2 key diagnostic tests in the most common clinical scenarios. Future studies may include a prospective evaluation of abnormal LFTs post-LT or outcomes of post-LT patients who undergo empiric treatment without LB or ERCP.

CONCLUSION

In summary, these results offer insight into the diagnostic and etiology of abnormal LFTs after LT, in

ALLOGRAFT PARENCHYMAL DAMAGE
Immune-mediated disease (rejection and de novo AIH) Recurrent disease (HCV, HBV, PBC, PSC, AIH, and others) Drug toxicity (including immunosuppressive drugs) Alcohol and other toxins De novo infection (including de novo HBV and HCV) Space-occupying lesion (recurrent cancer) De novo or recurrent NAFLD
BILIARY DAMAGE
Biliary strictures (anastomotic strictures, hepatic artery thrombosis or stenosis, and others) Biliary stones/cast syndrome Recurrent PSC
VASCULAR DISEASE
Hepatic artery thrombosis Portal or hepatic vein thrombosis
METABOLIC DISEASE IN THE ALLOGRAFT
Gilbert's syndrome
NONHEPATIC DISEASE MIMICKING LIVER DISEASE
Hemolysis causing raised indirect bilirubin levels Bone disease causing raised alkaline phosphatase levels
NONHEPATIC DISEASE CAUSING LIVER ABNORMALITIES
Celiac disease Diabetes

Figure 4 Causes of liver test abnormalities after liver transplantation. Legend: Used with permission from Lucey *et al*[2], 2013. HBV: Hepatitis B virus; HCV: Hepatitis C virus; PBC: Primary biliary cholangitis; PSC: Pulmonary scar cancer.

which standard lab and imaging studies have poor specificity. Our study shows that LB and ERCP improve diagnostic accuracy over either test alone and carry low risk. Dual diagnoses are relatively common in this population. In the future, prospective and multicenter studies should include patients undergoing LB and ERCP beyond the early post-LT period and establish reproducible, objective criteria for the ultimate diagnosis.

ARTICLE HIGHLIGHTS

Research background

Elevated liver function tests (LFTs) are commonly encountered in the post-liver transplant (LT) setting. When a diagnosis is not made by history, labs, and cross-sectional imaging, endoscopic retrograde cholangiopancreatography (ERCP) and liver biopsy (LB) are commonly performed. However, the diagnostic performance of each of these tests individually and in combination remains unknown.

Research motivation

We first hoped to determine what are the most common diagnoses in the population of patients with elevated LFTs after LT. At the same time, we want to assess the diagnostic performance of both ERCP and LB in these patients so that we can decide which of these tests is safer and more effective at clinching the diagnosis.

Research objectives

We aimed to assess the diagnostic accuracy and safety of ERCP and LB together and in isolation for a final diagnosis in patients with unexplained LFT elevations after LT.

Research methods

In this single-center, retrospective study we evaluated patients undergoing both ERCP and LB for the evaluation of elevated LFTs within 6 mo of LT based on review of existing medical records. Diagnostic accuracy, sensitivity and specificity for the various final diagnoses were calculated for each test.

Research results

Anastomotic strictures (AS), acute cellular rejection (ACR) and concurrent AS and ACR were the most common diagnoses. ERCP carried an accuracy of 79.1%, LB had an accuracy of 93.4%, and the combination of the 2 had an accuracy of 100% (95%CI: 96-100). The pattern of liver chemistries (R Factor) did not diagnostic accuracy of either test. Adverse event rates did not differ between the 2 tests.

Research conclusions

While LB had a higher accuracy than ERCP, the combination of the 2 tests had an accuracy of 100% and a low adverse event rate, suggesting that physicians can have a low threshold in utilizing both modalities for the evaluation of elevated LFTs.

Research perspectives

In patients with elevated LFTs after LT without a diagnosis, neither LB nor ERCP is clearly superior. Both tests can be used and the decision to use one over the other will depend on the clinical context and physician preference. However, when necessary both tests can be used safely together to reach a final diagnosis in nearly all patients.

FOOTNOTES

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Country/Territory of origin: United States

ORCID number: Augustin Attwell 0000-0001-7122-8684; Samuel Han 0000-0001-7373-7984; Michael Kriss 0000-0002-4229-4858.

Corresponding Author's Membership in Professional Societies: American Society for Gastrointestinal Endoscopy; American College of Gastroenterology; and American Gastroenterological Association.

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Effectiveness of entecavir in preventing hepatocellular carcinoma development is genotype-dependent in hepatitis B virus-associated liver cirrhosis

Kazuo Tarao, Akito Nozaki, Makoto Chuma, Masataka Taguri, Shin Maeda

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Kazuo Tarao, Department of Gastroenterology, Tarao's Gastroenterological Clinic, Yokohama City 241-0821, Japan

Akito Nozaki, Makoto Chuma, Gastroenterological Center, Yokohama City University Medical Center, Yokohama 232-0024, Japan

Masataka Taguri, Department of Data Science, Yokohama City University School of Data Science, Yokohama 236-0004, Japan

Shin Maeda, Division of Gastroenterology, Yokohama City University Graduate School of Medicine, Yokohama 236-0004, Japan

Corresponding author: Kazuo Tarao, MD, PhD, Director, Department of Gastroenterology, Tarao's Gastroenterological Clinic, 2-58-6, Taiyo Building Futamatagawa, Asahi-ku, Yokohama 241-0821, Japan. duoluoweih7@gmail.com

Abstract

BACKGROUND

The oral nucleos(t)ide analogue, entecavir (ETV) was demonstrated to reduce the rate of hepatocellular carcinoma (HCC) in patients with hepatitis B virus (HBV)-associated liver cirrhosis. However, the reduction of HCC differs in various regions of the world.

AIM

To investigate the reduction of HCC development due to ETV therapy by meta-analysis.

METHODS

We surveyed the differences in HCC development following ETV treatment based on published articles using PubMed (2004-2019).

RESULTS

The regions with the most marked reduction in HCC development due to ETV therapy were Spain (1.0%/year) and Canada (Southern part, 1.3%/year), and the most ineffective areas were South Korea (3.6%-3.8%/year), China (3.3%/year), Taiwan (2.4%-3.1%/year), and Hong Kong (2.8%/year). Following ETV administration, the incidence of HCC in genotype D regions ($1.89\% \pm 0.28\%$ /year, mean \pm

SE) was significantly lower than that in genotype C regions ($2.91\% \pm 0.24\%/year$, $P < 0.01$). With regard to the initial HBV-DNA level, in genotype C patients (average: $5.61 \text{ Log}_{10} \text{ IU/mL}$) this was almost the same as that in genotype D patients (average: $5.46 \text{ Log}_{10} \text{ IU/mL}$). Moreover, there was no association between the prevalence ratio of HBV and the incidence of HCC on ETV treatment.

CONCLUSION

The effectiveness of ETV in preventing HCC development in HBV-associated liver cirrhosis is genotype-dependent.

Key Words: Hepatocellular carcinoma; Entecavir; Genotype of hepatitis B virus; Oral nucleos(t)ide analogue

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Core Tip: Entecavir was demonstrated to reduce the rate of hepatocellular carcinoma (HCC) in patients with hepatitis B virus (HBV)-associated liver cirrhosis. The reduction of HCC differs in various regions of the world. We surveyed these differences based on published articles using PubMed (2004-2019). Following entecavir administration, the incidence of HCC in genotype D regions ($1.89\% \pm 0.28\%/year$, mean \pm SE) was significantly lower than that in genotype C regions ($2.91\% \pm 0.24\%/year$, $P < 0.01$). The initial HBV-DNA level in genotype C patients was almost the same as that in genotype D patients. The effectiveness of entecavir in preventing HCC development in patients with HBV-associated liver cirrhosis is genotype-dependent.

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INTRODUCTION

The third-generation nucleos(t)ide analogue, entecavir (ETV) is currently recommended as one of the first-line antiviral therapies for chronic hepatitis B virus (HBV) infection. Moreover, it is generally accepted that long-term ETV treatment may reduce the incidence of hepatocellular carcinoma (HCC) in HBV-infected patients. Wong *et al*[1] demonstrated that the 5-year cumulative incidence of HCC was 13.8% in an ETV cohort *vs* 26.4% in a control cohort.

However, on surveying published reports, the effect of ETV in preventing HCC differed in various regions of the world. In this study, we examined the reduction of HCC development in various regions of the world, and the possible reasons for these differences.

MATERIALS AND METHODS

The PubMed database was searched (2004-2019) for studies published in English regarding the follow-up results of the development of HCC in patients with HBV-associated liver cirrhosis after treatment with ETV for more than 2 years. Studies with follow-up periods shorter than 3 years after ETV treatment were excluded.

In this study, we included only HBV cirrhotic cases. Furthermore, we surveyed the possible reasons for the differences in HCC reduction. We examined the association between the reduction in HCC development and initial HBV-DNA levels, which is a strong accelerating factor for HCC development [2], the prevalence of HBV in these regions, and HBV genotypes.

To compare the incidence of HCC between the main genotypes C and D, we calculated the weighted mean of the HCC incidence rate for each genotype using the random effect model (ref: Dersimonian R, Laird N. Meta-analysis in clinical trials. *Controlled Clinical Trials* 1986; 7: 177-188). To assess whether the incidence rate among genotype D patients was lower than that among genotype C patients, we calculated the *P* value using a *Z* test. All reported *P* values correspond to two-sided tests, and those with $P < 0.05$ were considered significant. All analyses were performed with JMP version 12 (SAS Institute, Cary, NC, United States).

RESULTS

The results of HBV-associated cirrhotic patients administered ETV are presented in [Table 1](#).

The regions where HCC development was markedly reduced by ETV therapy were Spain (1.0%/year)[3] and Canada (Southern part) (1.3%/year)[4]. The most ineffective regions were South Korea (3.6%-3.8%/year)[5,6], China (3.3%/year)[7], Taiwan (2.4%-3.1%/year)[8,9], Japan (Ehime, southern part of Japan 2.9%/year)[10], and Hong Kong (2.8%/year)[1]. The regions with a moderate reduction were Turkey (2.2%-2.7%/year)[11,12], the Caucasus (2.2%/year)[13], and Greece (1.8%/year)[14].

With regard to the genotype of HBV, the incidence of HCC in regions where the main prevalent type is D ($1.89\% \pm 0.28\%$ /year, mean \pm SE) was significantly lower than that in regions where the main prevalent genotype is C ($2.91\% \pm 0.24\%$ /year, $P < 0.01$) ([Table 2](#)).

Moreover, the incidence of HCC in regions where the main prevalent genotype is C was significantly higher than that in regions where the main prevalent genotype was other than C (D + A, $1.61\% \pm 0.21\%$ /year, $P < 0.0001$).

The initial HBV-DNA levels in genotype C patients (average 5.61 Log₁₀IU/mL) was almost the same as that in genotype D patients (average 5.46 Log₁₀IU/mL) ([Table 3](#)).

The association between the prevalence ratio of HBV in various countries and the incidence of HCC with ETV treatment was as follows ([Table 1](#)): The incidence of HCC with ETV treatment with a prevalence ratio of HBV of more than 8% was $2.64\% \pm 0.16\%$ /year (mean \pm SE), as compared with $2.39\% \pm 0.14\%$ /year in regions where the prevalence ratio of HBV was 2%-7% (not significant, $P = 0.576$).

DISCUSSION

We demonstrated that there were marked differences in the impact of ETV treatment on reducing the risk of HCC in patients with HBV-associated cirrhosis in many countries of the world. We must consider why such differences exist.

Firstly, the genotypes of HBV should be considered. Genotype C is seen mostly in Asia, and genotype A in Northwest Europe, North America, India, and Africa. Genotype D is seen in Southern Europe, Middle Eastern Europe, and India. Various cross-sectional studies have found that patients with genotype C have more severe liver disease including cirrhosis or HCC than those with other genotypes [15,16].

In cohort studies of 426 chronic hepatitis B patients from Hong Kong[17] and of 4841 HBsAg-positive men from Taiwan[18], genotype C was associated with a 3-to 5-fold increased risk of HCC, respectively, compared with other HBV genotypes. Moreover, it was reported that the estimated 5-year cumulative incidence of HCC was 17% in East Asia where HBV genotype C is predominant and 10% in Western regions where HBV genotype D or A is predominant[19].

It is considered that the same tendency exists even on long-term treatment with ETV, and the incidence of HCC is higher in genotype C regions than in regions with other genotypes (especially genotype D).

In our studies, we demonstrated that ETV treatment of HBV cirrhotic patients with genotype C was less effective at preventing the occurrence of HCC than in those with other genotypes (chiefly genotype D).

In support of our findings, Kao *et al*[20] demonstrated differences in the response to lamivudine between HBV genotypes. They reported that genotype B showed a better virological response to lamivudine than genotype C in Taiwan.

Another factor that must be taken into account is the association between the prevalence ratio of HBV in various places and the incidence of HCC under ETV treatment. The incidence of HCC under ETV treatment where the prevalence ratio of HBV is more than 8% was $2.64\% \pm 0.16\%$ /year, as compared with $2.39\% \pm 0.14\%$ /year in regions where the prevalence ratio of HBV was 2%-7% (not significant, $P = 0.576$).

Another important factor that must be taken into consideration is the initial HBV-DNA level. However, we demonstrated that the initial HBV-DNA level in genotype C patients was almost the same as that in genotype D patients.

CONCLUSION

The impact of long-term ETV treatment on reducing the risk of HCC in patients with HBV cirrhosis differs in many countries of the world[1-13,21]. Moreover, it was demonstrated that effectiveness of ETV in preventing HCC development is genotype-dependent in HBV-associated liver cirrhosis.

Table 1 Difference in the impact of entecavir treatment on the risk of hepatocellular carcinoma in patients with hepatitis B virus-associated cirrhosis in various regions of the world

Ref.	Region	Main genotype	Prevalence ratio	Entecavir administered to HBV cirrhotics patients	Observation period (yr)	Incidence of HCC (%/yr)
Riveiro-Barciela <i>et al</i> [3]	Spain (Caucasian)	D	2%-7%	64	4.6	1.0
Coffin <i>et al</i> [4]	Canada (South)	D	< 2%	25	3.2	1.3
Hosaka <i>et al</i> [21]	Japan (Tokyo)	C	< 2%	79	5.0	1.4
Papatheodoridis <i>et al</i> [14]	Greece	A	2%-7%	69	3.3	1.8
Idilman <i>et al</i> [11]	Turkey	D	2%-7%	72	4.0	2.2
Arends <i>et al</i> [13]	Caucasus	D	> 8%	155	3.5	2.2
Su <i>et al</i> [8]	Taiwan	C	> 8%	1315	4.0	2.4
Köklü <i>et al</i> [12]	Turkey	D	2%-7%	73	3.0	2.7
Wong <i>et al</i> [1]	Hong Kong	C	> 8%	482	5.0	2.8
Watanabe <i>et al</i> [10]	Japan (Ehime)	C	2%-7%	86	5.0	2.9
Chen <i>et al</i> [9]	Taiwan	C	> 8%	586	4.9	3.1
Chen <i>et al</i> [2]	China (Chinese)	C	> 8%	61	4.0	3.3
Kim <i>et al</i> [5]	Korea	C	2%-7%	367	5.0	3.6
Choi <i>et al</i> [6]	Korea	C	2%-7%	510	4.0	3.8

HCC: Hepatocellular carcinoma; HBV: Hepatitis B virus.

Table 2 Difference in the incidence of hepatocellular carcinoma under long-term treatment with entecavir between genotype C and genotype D cirrhotic patients

	Incidence of HCC (%/yr)	P value
Genotype C group (n = 8)	2.91 ± 0.24 (SE)	P < 0.01
Genotype D group (n = 5)	1.89 ± 0.28 (SE)	P < 0.01

HCC: Hepatocellular carcinoma.

Table 3 Comparison of initial hepatitis B virus deoxyribonucleic acid levels (log₁₀ IU/mL) between genotype C and D cirrhotic patients treated with entecavir

Main genotype	Ref.	Entecavir administered to HBV cirrhotic patients	Initial HBV DNA	Average
C	Su <i>et al</i> [8]	1315	5.5	5.61
C	Wong <i>et al</i> [1]	482	5.0	
C	Watanabe <i>et al</i> [10]	86	6.4	
C	Chen <i>et al</i> [9]	586	5.9	
C	Chen <i>et al</i> [2]	61	5.8	
C	Kim <i>et al</i> [5]	367	4.6	
C	Choi <i>et al</i> [6]	510	6.7	
D	Riveiro-Barciela <i>et al</i> [3]	64	4.9	
D	Coffin <i>et al</i> [4]	25	6.5	
D	Idilman <i>et al</i> [11]	72	5.5	
D	Arends <i>et al</i> [13]	155	5.4	
D	Köklü <i>et al</i> [12]	73	5.7	

HBV DNA: Hepatitis B virus deoxyribonucleic acid.

ARTICLE HIGHLIGHTS

Research background

The oral nucleos(t)ide analogue, entecavir (ETV) was demonstrated to reduce the rate of hepatocellular carcinoma (HCC) in patients with hepatitis B virus (HBV)-associated liver cirrhosis. However, the reduction in HCC is different in various countries of the world.

Research motivation

The relationship between the reduction of HCC and HBV genotypes is interesting.

Research objectives

We surveyed the differences in the reduction of HCC development following ETV administration in many countries.

Research methods

We surveyed the differences in the reduction of HCC development following long-term administration of ETV based on already published articles using PubMed (2004-2019).

Research results

The countries which showed the greatest reduction in HCC development following ETV administration were Spain, Canada, and most ineffective countries or regions were South Korea, China, Taiwan, and Hong Kong. With ETV administration, the incidence of HCC in genotype D regions was significantly lower than that in genotype C regions. The initial HBV-DNA levels in genotype C patients was almost the same as that in genotype D patients. No relationship was observed between the prevalence ratio of HBV and the incidence of HCC following ETV treatment.

Research conclusions

The effectiveness of ETV in preventing HCC development in HBV-associated liver cirrhosis is genotype-dependent.

Research perspectives

In countries with low effectiveness of ETV in the prevention of HCC development, frequent surveillance using imaging modalities will be necessary.

FOOTNOTES

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Country/Territory of origin: Japan

ORCID number: Kazuo Tarao 0000-0002-7161-6748; Akito Nozaki 0000-0002-3310-6632; Makoto Chuma 0000-0002-0963-9172; Masataka Taguri 0000-0001-8902-0056; Shin Maeda 0000-0002-0246-1594.

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Living-donor liver transplantation in Budd-Chiari syndrome with inferior vena cava complete thrombosis: A case report and review of the literature

Vinicius Rocha-Santos, Daniel Reis Waisberg, Rafael Soares Pinheiro, Lucas Souto Nacif, Rubens Macedo Arantes, Liliana Ducatti, Rodrigo Bronze Martino, Luciana Bertocco Haddad, Flavio Henrique Galvao, Wellington Andraus, Luiz Augusto Carneiro-D'Albuquerque

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Vinicius Rocha-Santos, Daniel Reis Waisberg, Rafael Soares Pinheiro, Lucas Souto Nacif, Rubens Macedo Arantes, Liliana Ducatti, Rodrigo Bronze Martino, Luciana Bertocco Haddad, Flavio Henrique Galvao, Wellington Andraus, Luiz Augusto Carneiro-D'Albuquerque, Department of Gastroenterology, Abdominal Organs Transplantation Division, Hospital das Clinicas da Faculdade de Medicina da Universidade de Sao Paulo (HC-FMUSP), Sao Paulo 05403900, SP, Brazil

Flavio Henrique Galvao, Wellington Andraus, Luiz Augusto Carneiro-D'Albuquerque, Department of Gastroenterology, Laboratory of Medical Investigation 37 (LIM-37), Faculdade de Medicina da Universidade de Sao Paulo (FMUSP), Sao Paulo 01246903, Brazil

Corresponding author: Vinicius Rocha-Santos, MD, PhD, Adjunct Professor, Attending Doctor, Department of Gastroenterology, Abdominal Organs Transplantation Division, Hospital das Clinicas da Faculdade de Medicina da Universidade de Sao Paulo (HC-FMUSP), Av. Dr Eneas de Carvalho Aguiar, nº255, 9th Floor, Room 9114, Sao Paulo 05403900, SP, Brazil.

dr_vinicius@uol.com.br

Abstract

BACKGROUND

Budd-Chiari syndrome (BCS) is a challenging indication for liver transplantation (LT) due to a combination of massive liver, increased bleeding, retroperitoneal fibrosis and frequently presents with stenosis of the inferior vena cava (IVC). Occasionally, it may be totally thrombosed, increasing the complexity of the procedure, as it should also be resected. The challenge is even greater when performing living-donor LT as the graft does not contain the retrohepatic IVC; thus, it may be necessary to reconstruct it.

CASE SUMMARY

A 35-year-old male patient with liver cirrhosis due to BCS and hepatocellular carcinoma beyond the Milan criteria underwent living-donor LT with IVC reconstruction. It was necessary to remove the IVC as its retrohepatic portion was completely thrombosed, up to almost the right atrium. A right-lobe graft was retrieved from his sister, with outflow reconstruction including the right hepatic vein and the branches of segment V and VIII to the middle hepatic vein. Owing to

massive subcutaneous collaterals in the abdominal wall, venovenous bypass was implemented before incising the skin. The right atrium was reached *via* a transdiaphragmatic approach. Hepatectomy was performed *en bloc* with the retrohepatic vena cava. It was reconstructed with an infra-hepatic vena cava graft obtained from a deceased donor. The patient remains well on outpatient clinic follow-up 25 mo after the procedure, under an anticoagulation protocol with warfarin.

CONCLUSION

Living-donor LT in BCS with IVC thrombosis is feasible using a meticulous surgical technique and tailored strategies.

Key Words: Liver transplantation; Living donors; Budd-Chiari syndrome; Hepatic veno-occlusive disease; Inferior vena cava; Case report

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Core Tip: A right-lobe living-donor liver transplantation (LT) with inferior vena cava (IVC) resection and reconstruction was performed in a patient with liver cirrhosis due to Budd-Chiari syndrome and hepatocellular carcinoma beyond the Milan criteria. It was necessary to remove the IVC because its retrohepatic portion was completely thrombosed, up to almost the right atrium. It was reconstructed with an infra-hepatic vena cava graft obtained from a deceased donor. The patient remains well 25 mo after the procedure. This case highlights the meticulous surgical technique and tailored strategies required for dealing with these challenging procedures in living-donor LT.

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INTRODUCTION

Budd-Chiari Syndrome (BCS) is characterized by the obstruction of hepatic venous drainage that leads to progressive hepatic congestion and, ultimately, portal hypertension and liver cirrhosis[1]. This blockage may be present in the hepatic venules, main hepatic veins, inferior vena cava (IVC) or right atrium[2]. Several nonsurgical therapeutics have been described, such as anticoagulation therapy, percutaneous transluminal angioplasty and interventional radiologic placement of a transjugular intrahepatic portosystemic shunt (TIPS) or direct intrahepatic portocaval shunt[1-3]. Liver transplantation (LT) is indicated in acute cases of fulminant hepatic failure or chronic cases with cirrhosis, which commonly evolve with gastrointestinal bleeding, untreatable ascites, sarcopenia, encephalopathy and hepatocellular carcinoma (HCC)[4]. In such scenarios, TIPS is often unfeasible due to extensive venous thrombosis or advanced liver disease[5].

Venous thrombosis can affect not only the hepatic veins but also a prolonged segment of the retrohepatic IVC, occasionally very close to the right atrium. The association between the severity of the disease, the extension of the venous thrombosis and the massive liver that is frequently present in BCS makes LT a particularly difficult procedure in these cases[1]. The hypercoagulative nature of the syndrome further increases the challenge, owing to vascular complications[6].

The challenge is even greater when considering living donor liver transplantation (LDLT) since the graft does not contain the retrohepatic IVC, as in deceased-donor liver transplantation (DDLT). Therefore, hepatic venous reconstruction is more complex, especially if the IVC is also obliterated[7]. That is the reason why only approximately 70 patients with BCS underwent LDLT worldwide between 1989 and 2015[1,8]. When LDLT is performed and HCC is also present, DDLT may not be possible in case of postoperative complications if the patient is beyond the Milan criteria[9], depending on local legislation in some countries, such as Brazil. Thus, performing LDLT for BCS in such a scenario is even more risky.

We report a case of a complex retrohepatic IVC thrombosis due to BCS in a patient with HCC beyond the Milan criteria. As the patient had a good response to transarterial chemoembolization (TACE) and his alpha fetoprotein levels decreased, we decided to perform LDLT.

CASE PRESENTATION

Chief complaints

A 35-year-old cirrhotic male patient was referred for LT evaluation due to BCS and HCC.

History of present illness

The patient had been diagnosed with cirrhosis and BCS four years previously, after presenting with ascites and hematemesis due to esophageal varices. Abdominal computed tomography (CT) scan on this occasion showed hepatic veins thrombosis and signs of chronic hepatopathy with paraumbilical vein recanalization and extensive collateral circulation in the splenic hilum, around the stomach, and in the anterior and lateral abdominal walls. The liver also showed multiple hepatic nodules of up to 1.5 cm in diameter, some them hypervascularized, which in the context of BCS, were compatible with regenerative hepatic nodules. Hepatic biopsy revealed chronic hepatic outflow obstruction. Laboratory testing for autoimmune hepatitis was negative, as were serological markers for hepatitis C and B viruses. The patient also denied previous alcohol abuse. No thrombophilia was diagnosed, despite extensive hematological investigation. The patient was then maintained on oral anticoagulation with warfarin.

History of past illness

The patient had no previous medical history.

Personal and family history

The patient was a smoker (10 cigarettes/day for 20 years). There was no relevant family history concerning this case.

Physical examination

The patient exhibited mild jaundice and extensive subcutaneous collateral veins in the anterior abdominal wall (Figure 1). Further physical examination was unremarkable.

Laboratory examinations

Blood analysis revealed normal hemoglobin, mild leukopenia and mild thrombocytopenia with mildly elevated total bilirubin, direct bilirubin and gamma-glutamyl-transferase (Table 1). Kidney function and electrolytes were normal as well as serum albumin, alanine aminotransferase, aspartate aminotransferase and alkaline phosphatase. The patient's prothrombin time was elevated even without warfarin (Table 1). Considering that the patient did not present encephalopathy or ascites, his Child-Pugh score was A6, and his Model of End-Stage Liver Disease (MELD) score was 15. His alpha-fetoprotein level was 58.7 ng/mL (normal range < 10 ng/mL), although 6 mo earlier, it was 9.4 ng/mL.

Imaging examinations

During outpatient follow-up, an abdominal CT scan showed a heterogeneously vascularized nodule in segment V, which increased from 2 cm to 4 cm in three years (Figure 2A and B). He also showed complete thrombosis of the retrohepatic IVC, up to almost the right atrium, with large subcutaneous veins in his abdominal wall (Figure 2C). Further evaluation with abdominal liver magnetic resonance imaging with hepatobiliary contrast showed two hypervascularized nodules with hypocaptation in the biliary phase in segments V and II, 4 and 2.3 cm in size, respectively (Figure 3). Considering the previous CT scans with multiple regenerative nodules, these 2 specific nodules were classified as indeterminate lesions. Given their growth, the atypical pattern of contrast uptake and the rise in alpha-fetoprotein serum levels, further investigation with biopsy of these nodules was indicated due to the suspicion of HCC.

FINAL DIAGNOSIS

Percutaneous ultrasound-guided biopsy of the largest nodule confirmed a moderately differentiated HCC (grade 3 Edmondson-Steiner grading system). Therefore, the patient presented liver cirrhosis due to BCS with retrohepatic vena cava thrombosis and multicentric HCC beyond the Milan criteria.

TREATMENT

According to Brazilian legislation, the patient could not be listed for DDLT due to being beyond the Milan criteria. He underwent 2 TACE procedures in order to downstage the lesions to within the Milan criteria so that he could be listed. Even though the serum alfa-fetoprotein level decreased from 58.7 to 18

Table 1 Laboratory tests results and normal range

Laboratory test	Result	Normal range
Hemoglobin	12.6 g/dL	12.5-17.5 g/dL
Leukocytes	$3.5 \times 10^9/L$	$4-11 \times 10^9/L$
Platelets	$80 \times 10^3/mm^3$	$150-400 \times 10^3/mm^3$
Total bilirubin	1.73 mg/dL	0.2-1 mg/dL
Direct bilirubin	0.85 mg/dL	< 0.3 mg/dL
Alanine aminotransferase	20 U/L	< 41 U/L
Aspartate aminotransferase	35 U/L	< 37 U/L
Alkaline phosphatase	78 U/L	40-129 U/L
Gamma-glutamyl-transferase	115 U/L	8-91 U/L
Creatinine	0.79 mg/dL	0.7-1.2 mg/dL
Blood urea nitrogen	31 mg/dL	10-50 mg/dL
Sodium	143 mEq/L	135-145 mEq/L
Potassium	3.9 mEq/L	3.5-4.5 mEq/L
Albumin	4.4 g/dL	3.4-4.8 g/dL
Prothrombin time	21.8 s	9.4-12.5 s
International normalized ratio	1.75	0.95-1.2

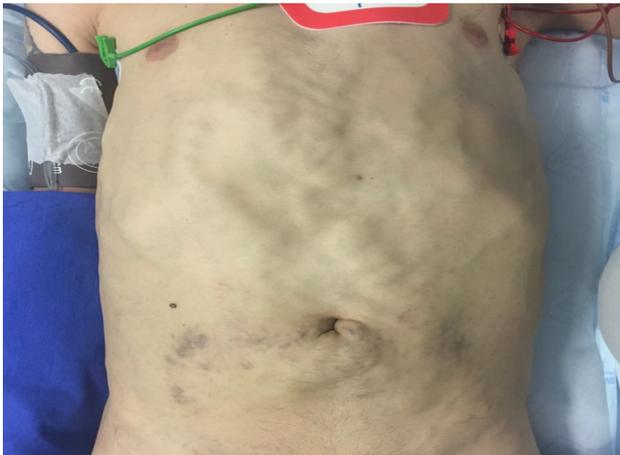


Figure 1 Massive blood return by subcutaneous veins in the anterior abdominal wall, which required the use of venovenous bypass prior to the abdominal incision.

ng/mL, the nodules did not decrease in size and the patient remained beyond the Milan criteria. His sister then volunteered for liver donation and the patient was selected for LDLT. She was a healthy 51-year-old female with a body mass index of 22.6 kg/m². Liver volumetry revealed a right lobe of 724 cm³ (66% of the entire organ), and usual biliary tree anatomy was found on magnetic resonance cholangiopancreatography. Liver parenchyma also showed simple cysts.

The patient weighed 71 kg, resulting in a predicted graft-to-recipient weight ratio (GRWR) of 0.81%. Donor operation consisted of a right hepatectomy with middle hepatic vein preservation. The procedure was uneventful, resulting in a 560 g right lobe graft with usual anatomy (GRWR of 0.79%). In the backtable operation, the right hepatic vein and the V5 and V8 branches of the middle hepatic vein were reconstructed to avoid outflow blockage.

For the recipient, the surgical strategy included the use of a venovenous bypass prior to incising the abdomen due to very large subcutaneous collaterals in the abdominal and thoracic walls. The left femoral and left axillary veins were used to implement the venovenous bypass. Hepatectomy was performed with the retrohepatic vena cava, close to the right atrium. The explanted liver weighed 1880 g. The portal vein was then cannulated and added to the venovenous bypass. As the right lobe graft did not include the retrohepatic vena cava, it was reconstructed using an infra-hepatic IVC from a deceased

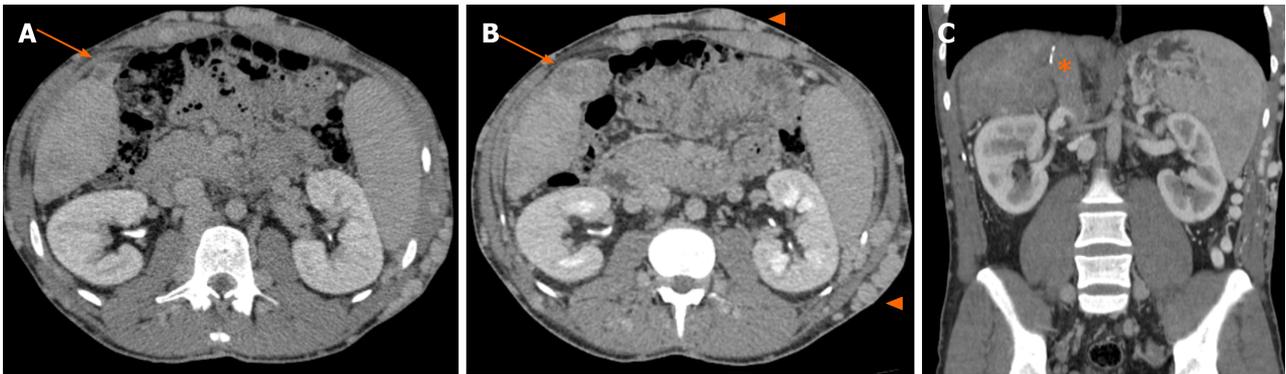


Figure 2 Abdominal computed tomography scans, with a 3-year interval. A: Heterogeneously vascularized nodule in segment V, of 2 cm, more visible in delayed phase due to hypocaptation (arrow); B: Same nodule in segment V in an exam scan performed 3 years later, with 4 cm (arrow). Massive subcutaneous veins in the abdominal wall are noted (arrowhead); C: The retrohepatic vena cava is completely thrombosed, up to almost the right atrium (asterisk).

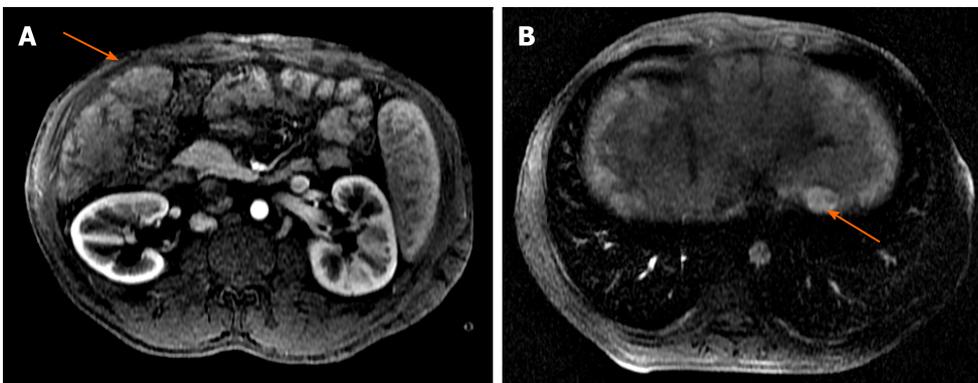


Figure 3 Liver magnetic resonance imaging with hepatobiliary contrast (arterial phase). A: Hypervascularized nodule in segment V of 4 cm (arrow); B: Hypervascularized nodule in segment II of 2.3 cm (arrow).

donor (Figure 4A). The graft was then implanted using this newly formed IVC to be anastomosed with the graft venous conduit for the outflow reconstruction. The right portal vein, right hepatic artery and right hepatic duct of the graft were then respectively anastomosed to their counterparts in the recipient (Figure 4B and C). Total and warm ischemia times were 370 and 30 min, respectively.

OUTCOME AND FOLLOW-UP

The donor's postoperative course was uneventful, and she was discharged home on postoperative day (POD) 5. The recipient was extubated on POD 2, and anticoagulation with enoxaparin was restarted, as well as low-dose aspirin. Liver Doppler ultrasound on POD 1 and 15 showed preserved graft vascularization. Renal function remained preserved, and the patient's condition progressively improved. The patient's immunosuppression regimen included intraoperative corticoid bolus and tapering associated with tacrolimus. The patient was discharged home on POD 19. Everolimus was added to the tacrolimus regimen 3 mo after the transplantation. Low-dose corticoid was maintained for 6 mo.

On histopathological analysis, the explanted liver confirmed hepatic cirrhosis related to chronic BCS and two moderately differentiated HCCs in segment V (4.5 cm) and segment II (2.5 cm).

Routine abdominal CT scan performed 23 mo after transplant showed a patent retrohepatic vena cava and adequate right lobe vascularization (Figure 5). The patient remains well on outpatient clinic follow-up 25 mo after the procedure, under an anticoagulation protocol with warfarin and without signs of HCC recurrence (alpha-fetoprotein 6.5 ng/mL).

DISCUSSION

Despite the numerous treatment modalities available for BCS, LT is performed in 10% to 20% of patients [1,2]. Nevertheless, it is a rare cause for LT, accounting for approximately 1% [10,11]. This a challenging

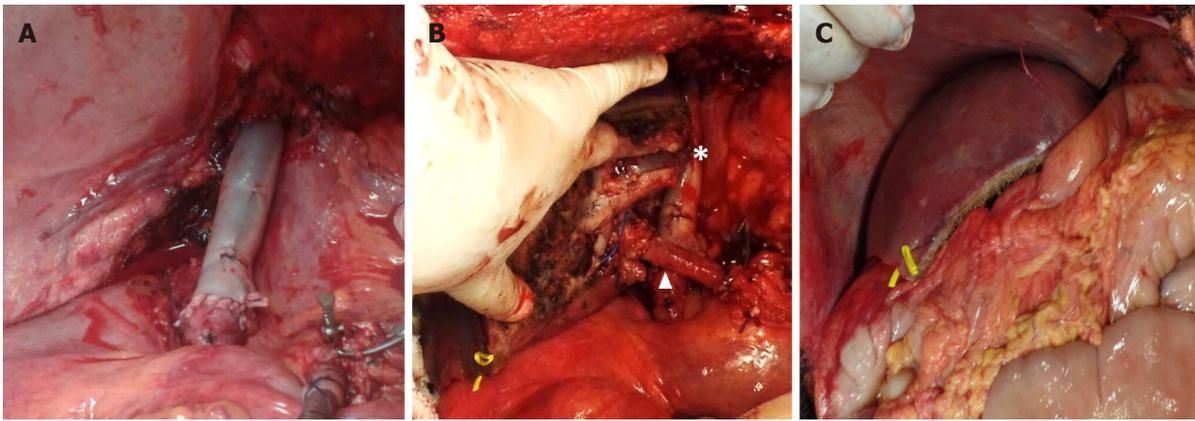


Figure 4 Intraoperative images. A: Reconstructed retrohepatic vena cava using an infrahepatic vena cava graft of a deceased donor; B: Revascularized graft showing the venous conduit anastomosed to the newly formed vena cava (asterisk) and the portal vein anastomosis (arrowhead); C: Graft final aspect after arterialization at the end of transplantation.

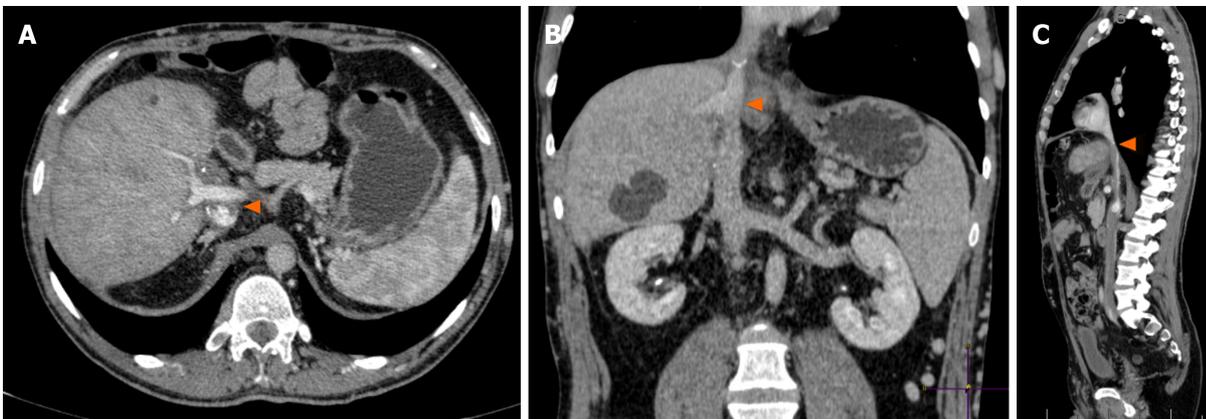


Figure 5 Late postoperative abdominal computed tomography scan, portal phase. A: Graft with adequate aspect and preserved portal inflow (arrowhead); B: Coronal view showing patent retrohepatic vena cava (arrowhead) and preserved graft outflow; C: Sagittal view of patent retrohepatic vena cava (arrowhead).

indication for LT due to a combination of massive liver and increased bleeding, caudate lobe enlargement, retroperitoneal diffuse fibrosis, firm retrohepatic IVC adhesions and frequently presents with stenosis and/or thrombosis of the IVC[3]. Especially in LDLT, in which the donor's IVC cannot be used, the retrohepatic IVC dissection performed during the piggyback technique and the venous outflow reconstruction are particularly problematic. Novel alternative techniques, aimed at eliminating stenosis or obstruction in the recipient IVC, are thus needed for LDLT in the context of BCS[6]. Some of them include cross-clamping the supra- and infrahepatic IVC and excising its thickened wall to create a wide orifice for graft implantation[7] or the V-Y plasty technique[12].

Nevertheless, when the IVC is completely occluded, which is known as obliterative hepatocavopathy (OHC), it is advisable to remove the IVC *en bloc* with the native liver[13], as the piggyback dissection becomes technically unfeasible due to dense inflammatory adhesions, enlarged collaterals and hypertrophied caudate lobe. If an LDLT is performed in this situation, it may be necessary to reconstruct the retrohepatic IVC. In 2006, Yan *et al*[14] reported the first LDLT for BCS with IVC reconstruction using an interposed cryopreserved cadaveric IVC graft[14]. Since then, many other studies have addressed IVC reconstruction with interposing autologous veins[15], cadaveric venous allografts[3,7,16-18], cadaveric aortic allografts[7,17-20], synthetic material[12,13,18] or a combination of synthetic material and autologous vein[21,22] or venous allografts[18,23]. Table 2 provides a review of all cases found in the literature of LDLT for BCS with IVC resection.

In the present report, we faced three ordeals in the preoperative period. First, the massive liver was associated with extensive IVC thrombosis starting close to the renal veins and progressing up to the transition between the IVC and the right atrium. Second, it was necessary to use a living donor right lobe with the potential risk of postoperative small-for-size syndrome, given the association of extensive thrombosis, portal hypertension and partial graft[12]. Finally, the LDLT was performed in a patient with HCC beyond the Milan criteria, which, according to Brazilian law, prevented the use of a deceased-donor graft in case of postoperative graft dysfunction.

Table 2 Summary of all reported cases of living-donor liver transplantation for Budd-Chiari syndrome with inferior vena cava resection

Ref.	Number of cases	Technique	Venovenous bypass use	Outcomes
Yan <i>et al</i> [14], 2006	<i>n</i> = 1	IVC replacement with cadaveric IVC allograft	Yes	Alive after 3 mo
Yamada <i>et al</i> [2], 2006	<i>n</i> = 1	IVC resection without replacement	No	Alive after 10 mo
Shimoda <i>et al</i> [15], 2007	<i>n</i> = 1	IVC replacement with autologous internal jugular vein, external iliac vein and suprarenal IVC	No	Alive after 17 mo
Sasaki <i>et al</i> [16], 2009	<i>n</i> = 1	IVC replacement with cadaveric IVC allograft	No	N/A
Kazimi <i>et al</i> [32], 2009	<i>n</i> = 1	IVC resection without replacement	No	Alive after 3 mo
Choi <i>et al</i> [3], 2010	<i>n</i> = 2	IVC replacement with cadaveric IVC allograft (<i>n</i> = 1) and RHV-atrial shunt using preexisting mesoatrial shunt (<i>n</i> = 1)	No	Both alive after a median follow-up of 18 mo
Ogura <i>et al</i> [21], 2011	<i>n</i> = 1	IVC replacement with an inverted composite graft (Gore-Tex stretch vascular graft and transposed IVC)	Yes	Alive after 24 mo
Sakçak <i>et al</i> [19], 2012	<i>n</i> = 1	IVC replacement with cadaveric aortic allografts	No	Alive after 4 mo
Fukuda <i>et al</i> [24], 2013	<i>n</i> = 1	IVC resection without replacement	No	Alive after 60 mo
Yagci <i>et al</i> [17], 2015	<i>n</i> = 4	IVC replacement with cadaveric IVC (<i>n</i> = 1), iliac vein (<i>n</i> = 1) and aorta allografts (<i>n</i> = 2)	No	2 patients died due to biliary complications after 5 mo of follow-up
Cetinkunar <i>et al</i> [20], 2015	<i>n</i> = 1	IVC replacement by cadaveric aortic allograft	No	Alive after 4 mo
Ara <i>et al</i> [7], 2016	<i>n</i> = 7	IVC replacement with cadaveric IVC (<i>n</i> = 4) and cadaveric aorta allografts (<i>n</i> = 2). No replacement in one case	No	2 patients died due to recent HAT after LT, and 2 patients died of sepsis during follow-up
Pahari <i>et al</i> [12], 2016	<i>n</i> = 2	IVC replacement with e-PTFE graft	No	Both alive after a median follow-up of 18 mo
Karaca <i>et al</i> [6], 2017	<i>n</i> = 3	IVC resection without replacement	No	N/A
Sabra <i>et al</i> [25], 2018	<i>n</i> = 1	IVC resection without replacement	No	Alive after 3 mo
Yagi <i>et al</i> [22], 2018	<i>n</i> = 1	IVC replacement with an inverted composite graft (e-PTFE graft and transposed IVC)	Yes	Alive after 36 mo
Ionescu <i>et al</i> [23], 2018	<i>n</i> = 2	IVC replacement with caval-dacron composite graft	No	Both alive (follow-up not available)
Yoon <i>et al</i> [13], 2019	<i>n</i> = 5	IVC replacement with synthetic material (ringed polyester)	Yes (<i>n</i> =3)	All alive after a median follow-up of 10.5 years
Gonultas <i>et al</i> [18], 2020	<i>n</i> = 12	IVC replacement with cadaveric IVC allograft (<i>n</i> = 6), cadaveric aorta allograft (<i>n</i> = 1), synthetic material (<i>n</i> = 3, Dacron) and caval-dacron composite graft (<i>n</i> = 2)	No	All alive after median follow-up of 15 mo
Present study	<i>n</i> = 1	IVC replacement with cadaveric IVC allograft	Yes	Alive after 25 mo

N/A: Not available; e-PTFE: Polytetrafluoroethylene; HAT: Hepatic artery thrombosis; IVC: Inferior vena cava; RHV: Right hepatic vein; LT: Liver transplantation.

Most authors describe a transdiaphragmatic access to the supradiaphragmatic IVC or even the right atrium, although a rarely performed lower median sternotomy may be helpful in some cases[13,24]. In the present report, through a standard *Makuuchi* incision, the recipient's liver was removed *en bloc* with the retrohepatic vena cava, from just above the renal veins to the beginning of the right atrium. This surgical approach, without thoracic access, was very useful as the patient had no major bleeding or hemodynamic instability. The interposition of a conduit replacing the retrohepatic IVC was necessary because we could observe considerable venous flow from the suprarenal vena cava. There is no consensus in the literature regarding the best material for IVC reconstruction[18]. The use of synthetic material raises concerns regarding the long-term patency of the anastomosis between the hepatic vein from the liver graft and the prosthesis, due to the possibility of thrombosis, deformity of the synthetic

orifice and anastomosis kinking consequent to growth of the liver graft[25]. Infection of prosthetic material is also an issue[26]. Many centers, including ours, therefore prefer autologous or allogeneic grafts, which present less thrombosis and infection risk[18,27]. Even cadaveric IVC recovered 25 h after the donor's circulatory death has been successfully used[28]. As a high-volume center of DDLT, there is great availability of allografts in our institution biobank. Storage of such grafts is feasible and inexpensive, only requiring sterile Ringer Lactate solution and a laboratory freezer[29]. However, in countries with scarce deceased donor organ donation and in centers with a high volume of LDLT, access to these grafts may be difficult[18].

Given the complexity of such procedures, it is paramount to obtain a suitable amount of liver parenchyma[30]. Therefore, we used the right lobe, as in most reported cases; however, some authors have also used the right posterior segment[15], the left lateral segment (pediatric recipients)[7,17,19], the left lobe[2,22,24,25] and dual grafts[13]. Another concern is the possibly elevated portal inflow to the graft[31]. That is the reason why we routinely measure the portal venous pressure by a catheter inserted *via* a jejunal branch. As the portal pressure was below 14 mmHg in this case after graft implantation, we did not implement further strategies to decrease the portal inflow.

In most cases reported, venovenous bypass was not used (Table 2). Due to the chronicity of IVC obstruction, venous return is expected to occur *via* collaterals involving the azygos, hemiazygos, accessory hemiazygos and thoracolumbar veins[24]. In a large series addressing LDLT with IVC resection for various reasons in 29 patients by Gonultas *et al*[18], venovenous bypass was not used in any case, as there was no hemodynamic instability during IVC clamping. In our case, the patient presented a well-developed collateral circulation; however, we observed that it was mainly composed of a massive subcutaneous plexus in the abdominal and thoracic wall (Figures 1 and 2). Thus, we decided to use the extracorporeal venovenous bypass before the abdominal skin was incised. We feared that an abdominal incision could lead to hemodynamic instability, since it was necessary to ligate the collaterals forming this enormous subcutaneous plexus. Therefore, when we accessed the abdominal cavity and clamped the IVC, the patient was already on venovenous bypass.

Retrohepatic IVC resection without replacement in LDLT for BCS has also been reported[2,6,7,24,25,32], in which the liver graft is anastomosed directly to the right atrium[6,32], to the intrapericardial IVC [24,25] or to the rarely preserved supra-hepatic IVC[2,6,7]. In one patient, the graft was directly anastomosed to a previous mesoatrial shunt[3]. This raises the question of whether or not it necessary to reconstruct the IVC. As addressed by Gonultas *et al*[18], the venous continuity should be maintained in patients without a venous collateral circulation system or in those with insufficient venous drainage. For patients that have a well-developed venous collateral, on the other hand, the liver graft may be, in theory, anastomosed directly to the suprahepatic IVC without the need for reconstruction. In our case, as the collaterals forming the subcutaneous plexus were ligated during the skin incision, the IVC reconstruction was required. We also observed a significant blood flow in the infra-hepatic IVC after the native liver was removed, suggesting the necessity of venous continuity restoration with an IVC interposition graft.

Despite the complexity of cases, most studies describe successful outcomes after LDLT (Table 2). The literature review identified 2 deaths due to early hepatic arterial thrombosis and another 4 patients died during follow-up due to infectious and biliary complications occurring months after transplant. In the series by Gonultas *et al*[18], 4 patients experienced late thrombosis of the replaced IVC during follow-up that were successfully treated with percutaneous balloon dilatation and/or stenting. The early use of low-dose aspirin and low molecular weight heparin a few days after LDLT is important to prevent the recurrence of thrombosis[12,13,18,32].

CONCLUSION

We describe a novel surgical approach for LDLT in BCS with OHC and HCC beyond the Milan criteria that can be used in highly selected patients. Due to its complexity and rarity, LDLT in such situations is feasible using a meticulous surgical technique and tailored strategies.

FOOTNOTES

Author contributions: Rocha-Santos V, Carneiro-D'Albuquerque LA, Nacif LS and Waisberg DR were the patient's surgeons; Andraus W, Pinheiro RS and Ducatti L performed the donor operation; Rocha-Santos V, Waisberg DR, Pinheiro RS and Nacif LS drafted the manuscript; Arantes RM, Ducatti L, Martino RB and Haddad LB performed the literature review and contributed to manuscript drafting; Galvao FH, Andraus W and Carneiro-D'Albuquerque LA were responsible for revision of the manuscript and for important intellectual content; all authors issued final approval for the version to be submitted.

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Country/Territory of origin: Brazil

ORCID number: Vinicius Rocha-Santos 0000-0002-2643-6094; Daniel Reis Waisberg 0000-0003-4284-0633; Rafael Soares Pinheiro 0000-0001-8632-3529; Lucas Souto Nacif 0000-0002-7059-3978; Rubens Macedo Arantes 0000-0001-5505-6480; Liliana Ducatti 0000-0001-9099-4974; Rodrigo Bronze Martino 0000-0001-5343-5057; Luciana Bertocco Haddad 0000-0003-0202-9037; Flavio Henrique Galvao 0000-0003-1924-3208; Wellington Andraus 0000-0002-5162-138X; Luiz Augusto Carneiro-D'Albuquerque 0000-0001-7607-7168.

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