Review Article Non-alcoholic fatty liver disease associated molecular mechanisms of hepatocarcinogenesis

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Received August 26, 2020; Accepted January 24, 2021; Epub April 15, 2021; Published April 30, 2021

Abstract: With the prevalence of obesity and insulin resistance, nonalcoholic fatty liver disease (NAFLD) has become one of the most common chronic liver diseases worldwide. As NAFLD can progress to non-alcoholic steatohepatitis (NASH), liver fibrosis and cirrhosis with higher frequency of hepatocellular carcinoma (HCC). Meanwhile, some studies have demonstrated that HCC may also develop in the context of NAFLD without association with advanced fibrosis and cirrhosis, just from simple steatosis. Growing evidence supports that NAFLD is associated with HCC. The mechanism of NAFLD-related HCC involves genetics, metabolic, immunologic, intestinal microbiota and so on. A better understanding of the pathogenesis is conducive to the prevention and individualized treatment of disease. This review summarizes the molecular mechanism of NAFLD-related HCC in recent couple of years.

Keywords: Non-alcoholic fatty liver disease, hepatocellular carcinoma, molecular mechanism

Introduction

Hepatocellular carcinoma (HCC) is the fifth most common cancer and the second leading cause of cancer-related death all over the world [1, 2]. HCC is identified as a typical inflammation-associated neoplasm, usually occurs in patients with potential chronic liver disease, including infection of hepatitis B virus (HBV) [3], hepatitis C virus (HCV) [4], and alcoholic liver disease [5]. In recent years, nonalcoholic fatty liver disease (NAFLD) becomes the most common chronic liver disease in developed countries and increases exponentially in developing countries, and has become one of the leading causes of HCC [6, 7]. NAFLD comprises a wide histological spectrum, ranging from simple steatosis to liver injury and inflammationnon-alcoholic steatohepatitis (NASH) [8]. NASH is more serious phase of NAFLD which is defined by the presence of lobular inflammation and hepatocyte ballooning histologically [9]. Several studies have demonstrated that NASH patients are more likely to develop advanced fibrosis and cirrhosis, and therefor at a higher risk of HCC [10-12]. However, in the absence of cirrhosis, NAFLD can also progress

to HCC [13, 14]. The mechanism of NAFLDrelated HCC is still unclear. It may involve genetic, immunologic, metabolic and gut microbiota pathways. This review attempts to summarize the pathogenesis of NAFLD-related HCC in recent couple of years (**Figure 1**).

Epidemiology

NAFLD is associated with obesity, insulin resistance, diabetes, known as metabolic syndrome [15-17]. It is reported that NAFLD affects up to 25% adult population in the worldwide [18], about 20% individuals with NAFLD develop NASH [19]. With the prevalence of obesity, NAFLD population will rapidly increase. A metaanalysis shown that the prevalence of NAFLD is estimated at 33.5% in adult population by 2030 [20]. Meanwhile, several studies have shown that the morbidity of NAFLD-related HCC is increasing exponentially [21-23]. In the first large population-based study on NAFLD-related liver cancer registered with the United States Surveillance, Epidemiology and Results (SEER), the proportion of NAFLD-related HCC increased by 9% annually between 2004 and 2009 [24]. Another study used data from the United States



Figure 1. Interaction influence diagrams of NASH associated HCC molecular mechanisms.

Organ Sharing Network (UNO), the researchers noted that the number of NASH-related HCC increased nearly 4-fold from 2002 to 2012 [25]. In the British, the proportion of NAFLDrelated HCC increased tenfold from 2000 to 2010 [26]. In Japan, a multi-center retrospective study found that the proportion of patients with non-viral HCC increased from 10.0% to 24.1% in 1991-2010 [27]. They attributed the findings to the growing obesity population and the rising morbidity of diabetes caused by dietary changes [27]. Accordingly, the number of NASH-related HCC patients receiving liver transplantation is also increasing [25].

Molecular mechanism of NAFLD-induced HCC

Genetic mechanism

With the development of genetic technology, researchers are allowed to obtain comprehensive data on genetic changes associated with NAFLD-related HCC. The differential expression of some genes caused by gene mutation and epigenetic changes is closely related to NAFLD-related HCC.

Hundreds of NAFLD-HCC candidate oncogenes were identified by mutation of "Sleeping Beauty" transposon in NAFLD-HCC mice model (PTEN-KO mice and HFD-fed mice) [28, 29]. Among them, 10 genes were identified as trunk drivers and Sav1 is the only gene identified as specific to NAFLD-HCC [30]. SAV1 is a vital component of hippo signal pathway and is involved in the regulation of organ size, Cell Fate, and Carcinogenesis [31-33]. In mammals, the Hippo signaling pathway consists of macrophage stimulating protein (MST), SAV, large tumor suppressor kinase (LATS) MOB1A and MOB1B, yes-associated protein (YAP), transcription regulator (TAZ), and TEAD [34]. MST negatively regulate transcriptional co-activators YAP and TAZ, which co-regulate gene expression that controls proliferation and differentiation [35]. Activation of YAP and TAZ is associated with liver development, regeneration and tumorigenesis [36]. Kodama T et al. [30] reported that SAV1 attenuates liver injury and apoptosis by reducing hepatic lipid accumulation. Furthermore, SAV1 can inhibit the activation of M1 macrophages and alleviate liver inflammation and fibrosis. Such pathological injuries are important factors in NAFLD-HCC transformation.

The mechanism is that SAV may affect the differentiation of hepatic progenitor cells by inhibiting YAP activity [37]. Akashi M et al. found that junctional protein associated with coronary artery disease (JCAD), coronary artery diseaseassociated gene product, was located at the cell-cell junction of endothelial cells [38]. Continuous studies have found that JCAD is closely related to apoptosis and proliferation, monocyte adhesion, migration and angiogenesis [39, 40]. Recent studies have found that JCAD mRNA is significantly increased in human and mouse NASH-HCC specimens. Overexpression of JCAD in HCC cell lines induced hepatoma cell free fatty acid overload. Moreover. overexpression of JCAD not only promotes the proliferation of HCC cell lines in vitro, but also promotes the growth of subcutaneous xenotransplanted tumor in vivo [41]. The main reason is that JCAD can bind to the kinase domain of LATS2 and inhibit the kinase activity of LATS2, which induces dephosphorylation and nuclear localization of YAP in the Hippo signaling pathway that plays a key role in tumor growth [42, 43]. Endoplasmic reticulum (ER) stress can activate unfolded protein response (UPR) and has been involved in the development of HCC [44]. Inositol-requiring enzyme 1 (IRE1), PKR-like endoplasmic reticulum kinase (PERK), and activating transcription factor 6 (ATF6) are three transmembrane signal transducers mediating UPR on endoplasmic reticulum [45]. Continuous activation of these transducers is associated with increased tumorigenicity [46, 47]. Previous studies have confirmed that IRE1 α is hyperactivated in obesity mice model and is closely associated with liver repair and regeneration [48]. Wu et al. found that the ablation of hepatocyte IRE1 α not only significantly reduced the incidence of diethylnitrosamine-induced HCC in IRE1α-KO mice fed a normal diet, but also prevented the HCC progression during high-fat diet [49]. IRE1α induces the phosphorylation of STAT3 and promote the HCC development by interacting with STAT3 in a positive feedback loop [50]. Pogribny IP et al. investigated hepatic transcriptomic and histone modification profiles using Stelic Animal Model (STAM) mice, an animal model of NASHrelated liver carcinogenesis resembling disease development in humans [51]. Gene enrichment analysis shows that many pathways have changed significantly in STAM model [52]. The most significant changes in NASH-fibrotic and HCC stages are inhibition of apoptosis and activation of hepatic stellate cells [51]. Further mechanism studies showed that these changes were caused by gene-specific deacetylation of histone H4 lysine 16 (H4K16) [53]. Fraga MF et al. found that the loss of histone H4K16 is a common epigenetic feature of human cancer [54]. In NASH-HCC, NUPR1 promotes the continuous deacetylation of H4K16 by inhibiting the activity of lysine acetyltransferase KAT8, which eventually leads to HCC [51]. Aberrant activation of the Hedgehog (Hh) pathway is associated with malignant tumors, such as medulloblastoma and basal cell carcinoma, and can mediate fibrotic response to chronic liver injury [55-57]. Indian Hedgehog (Ihh) was up-regulated in NAFLD-HCC and correlated with the volume and number of tumors [58]. Ihh regulates the transdifferentiation of quiescent hepatic stellate cells into proliferative myofibroblasts and the proliferation of EpCAM+ ductal cells to promote fibrosis [59, 60]. More importantly, lhh can up-regulate the expression of Wnt protein in HSCs and promote the progression of poorly differentiated HCC [61].

Metabolic pathways

Abnormal energy metabolism is considered to be a key factor in the natural course of NAFLD/ NASH-induced HCC. Like other cancers, changes in cell metabolism promote malignant transformation of hepatocytes. O-GlcNAc transferase (OGT) is a glycosyltransferase that catalyzes the post-translational modification of a single N-acetylglucosamine from UDP-GlcNAc to a serine or threonine residue in nuclear, mitochondrial and cytoplasmic proteins via a betalinked N-acetylglucosamine (O-GlcNAc) [62]. It was also found that OGT was overexpressed in several cancers and involved in the metabolic changes of cancer cells [63, 64]. Recent studies have found that OGT is up-regulated in human NAFLD-HCC patients and HCC cell lines and promotes invasion and migration of NAFLD-HCC cell lines [65]. Further studies showed that OGT could induce elevation of palmitic acid in NAFLD-HCC cell lines, and palmitic acid could facilitate the proliferation of NAFLD-HCC cell lines [65]. The specific mechanism is that OGT can activate endoplasmic reticulum (ER) stress

and trigger the progress of NAFLD-HCC by phosphorylating JNK and NF-kB subunits [66, 67]. Squalene epoxidase (SQLE) is the second key regulatory enzyme in cholesterol biosynthesis [68], and involved in NAFLD-HCC progression [69]. SQLE implements its carcinogenic role through its metabolites-cholesterol ester and nicotinamide adenine dinucleotide phosphate (NADP⁺) [70]. SQLE overexpressed promotes accumulation of liver free cholesterol and cholesteryl ester, which is lipotoxic and can lead to NASH [71], which is highly susceptible to HCC [11]. Increased NADP+/NADPH ratios triggered a series of events, including oxidative stress-induced DNA methyltransferase 3a (DNMT3A) expression [72], DNMT3A-mediated epigenetic silencing of phosphatase and tensin homolog (PTEN) and activation of AktmTOR (rapamycin mammalian target) [73, 74]. Acylcarnitines is a compound of acyl-coenzyme A and carnitine catalyzed by carnitine palmitoyltransferase (CPT) located on mitochondrial membrane. Acylcarnitine metabolism is a key factor in regulating the balance of intracellular glucose and lipid metabolism and involved in many metabolic diseases [75]. Fujiwara N et al. reported that acylcarnitine species accumulated in NASH-driven HCC due to the downregulation of CPT2 and its transcriptional regulators peroxisome proliferator-activated receptor α (PPAR α) [76]. On the one hand, decreased expression of CPT2 alleviates lipotoxicity by restraining Src-mediated JNK activation, on the other hand, oleoylcarnitine accumulation induced by CPT2 down-regulation can activate STAT3 and its downstream signaling molecules and induce self-renewal of HCC cells [76]. Sun H et al. demonstrated that androgen receptor (AR)-driven oncogene, cell cycle-related kinase (CCRK), cooperates with obesity-induced proinflammatory signaling to promote NASH-related hepatocarcinogenesis [77]. CCRK, as a member of cell cycle-dependent kinase, has been confirmed as a direct AR-regulated oncogene in hepatocellular carcinogenesis by activating GSK3β/β-catenin and AKT/EZH2 signaling pathways [78, 79]. In mice, CCRK liver specific ablation not only eliminates obesity-related lipid accumulation, glucose intolerance and insulin resistance, but also eliminates the development of HCC. Mechanistically, CCRK accelerates feedforward loop by inducing cooccupancy and transcriptional up-regulation of STAT3-AR promoter, which activates mTORC1/

4E-BP1/S6K/SREBP1 cascade through GSK3β phosphorylation. In addition, CCRK induces mTORC1-dependent G-csf expression to enhance the recruitment and tumorigenicity of polymorphonuclear bone marrow-derived suppressor cells [77]. These findings reveal the dual role of inflammation-CCRK in promoting metabolism and immunosuppressive reprogramming through mTORC1 activation, thus establishing a tumorigenic microenvironment for the development of NASH-HCC.

Immunologic pathways

Shalapour S et al. reported that the accumulation of liver resident IgA+ cell in human and mice with NASH-induced HCC. These inflammation-induced IgA⁺ cells expressed programmed death ligand 1 (PD-L1) and interleukin-10 [80]. Further studies demonstrated that these IgA⁺ cells had immunosuppressive effect and could directly inhibit liver cytotoxic CD8+ T lymphocytes [81]. CD8⁺ T lymphocytes deficiency can accelerate HCC development [82]. Neutrophil extracellular traps (NETs) are large reticular structures consisting of decondensed chromatin, neutrophil-derived nuclear, cytoplasmatic and granular proteins, which can capture and kill pathogens [83]. NETs are considered to be a significant apparatus of innate immune system against pathogens, but also related to autoimmunity, chronic inflammation and cancer pathophysiology [84]. Tsung A et al. reported that NETs formation increases in NASHrelated HCC. Inhibiting the NETs formation through deoxyribonuclease (DNase), the subsequent inflammation pattern of the liver was changed, resulting in a decrease in the number and volume of tumors [85]. In viral hepatitis models, activated platelets contribute to hepatic injury mediated by cytotoxic T lymphocyte (CTL) [86]. In addition, blocking platelet activation and aggregation eliminates the influx of hepatic T cells and subsequent liver injury and tumorigenesis, without affecting the function of peripheral T cells in viral hepatitis [86]. Heikenwalder M et al. reported that the number of platelets and platelet aggregates in the liver of mice fed with high fat diet and NAFLD/NASH patients increased significantly [87]. Aspirinclopidogrel (Asp-Clo) therapy can inhibit the infiltration of immune cells in the liver and further inhibit NASH and NASH-induced HCC [88]. Kupffer cells, a special macrophage of the liver,

Authors	Model	Comments/Outcomes
Kodama T et al., 2018	Liver specific PTEN-KO	\uparrow Lipid accumulation, apoptosis, fibrogenesis and hepatocarcinogenesis vs WT mice
Wu Y et al., 2018	liver-specific IRE1a KO	\downarrow Hepatocyte proliferation, \uparrow Hepatic apoptosis, TNF and IL-6 vs WT mice
Chong YC et al., 2019	liver-specific IHH-KO	\downarrow Stellate cells activation, Epcam+ ductal cells proliferation and fibrosis vs WT mice
Sun H et al., 2018	liver-specific CCRK-KO	\uparrow Lipid accumulation, glucose intolerance and insulin resistance vs WT mice
Tsung A et al., 2018	Whole body PAD4 KO	\downarrow Neutrophil extracellular traps formation, liver inflammation, tumor growth vs WT mice
Weber A et al., 2019	Whole body GPIbα KO	\downarrow Platelet cargo, platelet adhesion and platelet activation vs WT mice
Tiganis T et al., 2018	liver-specific PTPN2-K0	↑ T cell recruitment, fibrosis and tumor formation vs WT mice
Loo TM et al., 2017	Whole body TLR2 KO	\downarrow Secretory phenotype of hepatic stellate cells and tumor formation vs WT mice

Table 1. Application of gene knockout mouse model in NASH associated HCC

† Increased; ↓ decreased; KO knockout; PTEN phosphatase and tensin homolog; IRE1α inositol-requiring enzyme 1; IHH Indian hedgehog; CCRK cell cycle-related kinase; PAD4 peptidyl arginine deaminase type 4; GPIbα platelet membrane glycoprotein 1b-α; PTPN2 ; TLR2 toll-like receptor 2.

play a key role in platelet aggregation in the liver [89]. Kupffer cells can "dock" with GPIba, a glycoprotein on the surface of platelet membrane [90]. When GPIbα was blocked, liver inflammation was improved. It is inferred that blocking GPlbα can reduce NASH-reduced HCC [87]. Previous studies have confirmed that protein tyrosine phosphatase (PTP) is extensively oxidized and inactivated in obese mice with NAFLD [89]. T cell protein tyrosine phosphatase (TCPTP) plays a key role in the immune system and is considered as a negative regulator of inflammation [91]. TCPTP is a negative regulator of STAT family proteins, the oxidation of TCPTP promotes the phosphorylation of signal transducer and activator of transcription (STAT) family proteins, including STAT-1, STAT-3, and STAT-5 [92, 93]. Gurzov et al. found that TCPTP oxidized significantly in the liver of NAFLD patients and obese mice [89]. Further study demonstrated that TCPTP inactive results the recruitment of immune cells (especially CD4⁺ and CD8⁺ T cell) in the liver and promotes the expression of fibrosis genes (encoding a-smooth muscle actin (ACTA2) and transforming growth factor β (TGF β) [94]. These pathological changes contribute progression from NAFL to NASH and eventually lead to liver fibrosis and even cirrhosis. This fibrosis/cirrhosis liver may contain HCC progenitor cells, which can suffer malignant transformation and progress to HCC.

Gut microbiota

Intestinal barrier consists of intact epithelial lining, mucus layer, Paneth and goblet cells, mucosa-associated lymphoid tissue and a number of secreted factors, and is a highly dynamic system. It is well known that gut microbiota plays a critical role in health maintenance and disease progression [95]. Liver is directly exposed to intestinal microbial components and metabolites through portal vein (the gutliver axis), which are known closely related to HCC [96]. Analysis of the gut microbial profiles of DMBA-treated mice show that HFD-fed mice exhibited a prominent increase in Grampositive gut microbiota in their feces [97]. lipoteichoic acid (LTA), a major cell wall component in Gram-positive gut microbial component. translocates to the liver to form a carcinogenic microenvironment and promote obesity-induced HCC. LTA cooperates with the gut microbial metabolite deoxycholic acid (DCA) to enhance the senescence hepatic stellate cells (HSC) and increase the expression of senescence-associated secretory phenotype (SASP) and cyclooxygenase-2 (COX-2) through Toll-like receptor 2 (TLR2). COX-2 induces the elevation of prostaglandin E2 (PGE2), which binds to PTEP4 receptor to inhibit the anti-tumor immunity and promote the development of obesityassociated HCC [98].

Conclusion

NAFLD is common global epidemic and is associated with a variety of health-related complications, one of which is elevated frequency of cancer. Increasing evidence suggests that NAFLD, especially NASH, contributes to the HCC development in recent years (**Table 1**). Although the new cellular and molecular mechanisms leading to NAFLD-related HCC have been revealed in recent studies. No effective target has yet been found to control the transition from NAFLD to HCC. More importantly, we should pay more attention to whether there are "multiple types" of NAFLD, one or several of which are more likely to be converted to HCC and whether there are sensitive and specific biomarker to predict the transition. In addition, we also need to pay attention to the disease course and treatment response of "different types" of NAFLD-related HCC. Resolving these problems will not only reduce the incidence of NAFLD-related HCC, but also help clinicians to personalize the treatment of NAFLD-related HCC patient.

Acknowledgements

This study was supported by National Natural Science Foundation of China (Grant No. 81900516), Science and Technology Support Project of Sichuan Province (2020YSF0238) and China Postdoctoral Science Foundation (Grant No. 2019M653432).

Disclosure of conflict of interest

None.

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