



Review

Diagnosis and Therapeutic Management of Liver Fibrosis by MicroRNA

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Abstract: Remarkable progress has been made in the treatment and control of hepatitis B and C viral infections. However, fundamental treatments for diseases in which liver fibrosis is a key factor, such as cirrhosis, alcoholic/nonalcoholic steatohepatitis, autoimmune hepatitis, primary biliary cholangitis, and primary sclerosing cholangitis, are still under development and remain an unmet medical need. To solve this problem, it is essential to elucidate the pathogenesis of liver fibrosis in detail from a molecular and cellular perspective and to develop targeted therapeutic agents based on this information. Recently, microRNAs (miRNAs), functional RNAs of 22 nucleotides, have been shown to be involved in the pathogenesis of liver fibrosis. In addition, extracellular vesicles called “exosomes” have been attracting attention, and research is being conducted to establish noninvasive and extremely sensitive biomarkers using miRNAs in exosomes. In this review, we summarize miRNAs directly involved in liver fibrosis, miRNAs associated with diseases leading to liver fibrosis, and miRNAs related to complications of cirrhosis. We will also discuss the efficacy of each miRNA as a biomarker of liver fibrosis and pathology, and its potential application as a therapeutic agent.

Keywords: liver fibrosis; liver cirrhosis; microRNA; exosomal miRNA



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1. Introduction

The liver can be damaged by viral and parasitic infections, nonalcoholic steatohepatitis (NASH), heavy alcohol consumption, or autoimmune mechanisms, and chronic damage leads to fibrosis and cirrhosis [1]. Cirrhosis is the most common endpoint of chronic liver disease, and like hepatocellular carcinoma (HCC), is associated with a high mortality rate. Complications of cirrhosis, such as gastrointestinal bleeding, ascites, portal vein thrombosis, and hepatic encephalopathy (HE) due to portal hypertension, can significantly impair a patient's quality of life and ultimately lead to fatal outcomes. In uncompensated cirrhosis with complications, symptomatic treatment is generally the only option. Notably, liver failure and gastrointestinal bleeding are the leading causes of death in patients with cirrhosis. In recent years, it has become possible to control hepatitis virus infections and clinically reverse fibrosis, which is generally irreversible in advanced cases. Therefore, early diagnosis and further elucidation of the molecular mechanisms of liver fibrosis are necessary to develop specific therapies. Liver biopsy, the gold standard for the diagnosis of liver fibrosis, poses several challenges, including invasiveness and the risk of serious complications such as bleeding, sampling errors, variability in histopathological interpretation, and economic costs. It is also not suitable for diagnosing the early stages of cirrhosis. Hence, there is a need for alternative non-invasive diagnostic tests. The search for these tests has led to the development of alternative methods, such as image inspection (e.g., elastography), biochemical scoring (e.g., aspartate aminotransferase-to-platelet ratio index (APRI) and Fib-4 index), and the use of direct markers, such as hyaluronic acid, type IV collagen, Mac-2-binding protein glycosylation isomer, (M2BPGi), and autotaxin [2–4]. However, the efficacy of these biomarkers depends on the disease state, and in some instances, diagnostic performance is only moderate [2].

Activation of hepatic stellate cells (HSCs) is a pivotal event in liver fibrosis [5], and various inflammatory and fibrotic pathways are involved [6]. Activated HSCs are precursors of myofibroblasts that produce extracellular matrix (ECM) in the liver. Therefore, the treatment of hepatic fibrosis requires the prevention of hepatocellular damage and control of activated HSCs [7]. If HSC inactivation can be induced by cell- or target-specific pharmacological interventions, then, more effective, less toxic, and more accurate anti-fibrotic treatments than the currently available ones can be developed.

In recent years, research on organ fibrosis has rapidly evolved from classical pathological observations to molecular and cell biological approaches. The molecular mechanism underlying liver fibrosis is associated with non-coding RNAs (ncRNAs). MicroRNAs (miRNAs) are short ncRNAs that are involved in the epigenetic regulation of intracellular and extracellular signaling pathways and the post-transcriptional regulation of genes [8,9]. Furthermore, the effects of miRNA-mediated intercellular signaling mechanisms on liver fibrosis are gradually becoming clearer. Therefore, miRNAs are currently being studied for the diagnosis and monitoring of liver fibrosis and combining them with existing fibrosis scores may further improve diagnostic accuracy [10]. Additionally, extracellular vesicles (EVs), including exosomes, have been attracting attention as intercellular communication media for functional RNAs [11,12]. We will review the use of miRNAs in the pathology and diagnosis of hepatic fibrosis and the development of new therapeutics.

1.1. Liver Fibrosis and Cirrhosis

Cirrhosis is the end stage of a variety of chronic liver diseases. It affects 1%–2% of the world's population and kills more than one million people per year worldwide [13,14]. Many types of cells, cytokines, and miRNAs have been implicated in the initiation and progression of cirrhosis. In particular, the activation of HSCs is a pivotal event in fibrosis [15]. Moreover, Kupffer cells activated by viral infections and other factors attack hepatocytes and promote HSC activation. Repeated apoptosis and regeneration of hepatocytes, mainly HSCs, is the cause of liver cirrhosis.

HSCs, also known as Ito cells, are fat-storing cells containing vitamin A which are found in the space of Disse and account for approximately 10% of the total number of liver cells. HSCs correspond to pericytes that surround the sinusoidal endothelial cells with branch-like projections and contact hepatocytes [16]. HSCs have also been suggested to serve as antigen-presenting cells in the liver, presenting lipid antigens to CD1-restricted T lymphocytes such as natural killer T (NKT) cells and promoting NKT cell proliferation by presenting hepatic NKT cell lipid antigens via interleukin (IL)-15 [17].

HSCs and periportal fibroblasts are the main producers of ECM [5]. ECM deposition is a wound-healing response that protects residual tissue from epithelial cell death, inflammatory cell infiltration, and local proteolytic enzymes. It is reversible when the reaction is mild and terminated, but if the inflammation becomes chronic, the activated cells become myofibroblasts which amplify fibrosis and play a major role in the regulation of inflammation, immune responses, and the HCC microenvironment. At the molecular level, many cytokines are involved in mediating the signaling pathways that regulate HSC activation and fibrogenesis. Pro-inflammatory cytokines, such as platelet-derived growth factor (PDGF), transforming growth factor (TGF)- β , tumor necrosis factor (TNF)- α , and IL-1, shift HSCs from a quiescent state to an activated state [15]. Two types of PDGF, PDGF-BB and PDGF-AB, are important cytokines that promote the proliferation of activated HSCs in liver fibrosis. Notably, the dimeric cellular receptor, PDGF receptor β , is strongly upregulated in activated HSCs [18]. HSCs are activated and transformed into myofibroblast-like cells during liver injury [19], and they proliferate and contribute to inflammatory reactions and overproduce ECM while producing their own fibrosis-inducing factors, such as TGF- β [20].

1.2. MicroRNA and Exosomal miRNA

The protein-coding DNA region is estimated to account for less than 2% of the entire human genome, yet approximately 80% of the human genome has some functional activity.

Although most of the human genome consists of DNA regions that do not encode proteins, some of these regions produce functional RNAs with a variety of functional activities. These functional RNAs can be divided into two groups: (i) small ncRNAs with less than 200 bases, including miRNAs, and (ii) long ncRNAs with more than 200 bases [21,22]. Small ncRNAs (miRNAs) are small molecules of approximately 22 nucleotides that play an important role in the regulation of gene expression. miRNAs bind complementarily to the 3' untranslated regions of the target gene and inhibit protein production by cleaving or inhibiting the function of messenger RNA (mRNA). On the other hand, miRNAs have also been reported to interact with other regions, such as the 5' untranslated regions, and under certain conditions, miRNAs can also activate translation [23]. miRNAs exert their function by binding to Argonaute proteins to form silencing complexes [24]. They regulate a variety of signal transduction processes, including cell proliferation and apoptosis, and inflammatory and fibrotic processes, and are involved in the pathogenesis of many diseases, including cancer [25–32]. For liver diseases which require early diagnosis for determining treatment guidelines but do not have established diagnostic methods or appropriate biomarkers as yet, there is a need for solutions to these challenges. The fact that miRNAs are stably present in body fluids such as blood, urine, and saliva, which are easily collected from living organisms, makes miRNAs suitable as biomarkers.

EVs have attracted attention as delivery media for functional RNAs, including miRNAs. Exosomes are a subset of EVs which are secreted from the endoplasmic reticulum in cells with a lipid bilayer membrane with an average diameter of 30–100 nm [33,34]. They contain mRNAs and miRNAs which they transmit between cells [33]. The endoplasmic reticulum-derived EVs, including exosomes, contain RNA, proteins, and other information from the donor (EV-secreting) cell, and transmit this information to the recipient cell. miRNAs are mostly contained in EVs and are transported to recipient cells by intercellular transport, affecting signal transduction in recipient cells and cell phenotype. miRNAs in EVs extracted from patients are useful as disease biomarkers for various diseases [33]. In addition, a new drug delivery system that hijacks exosomes to deliver anti-miR oligonucleotides into the cells that receive them has been developed and is expected to have therapeutic applications [35].

Furthermore, it is expected to be applied to the diagnosis of liver fibrosis and to the development of novel therapeutic agents using miRNAs.

2. Epigenetic Changes in Liver Fibrosis/Cirrhosis

2.1. Liver Fibrosis and miRNAs

2.1.1. miRNAs as Biomarkers of Liver Fibrosis

Several miRNAs are associated with organ-specific and systemic fibrosis in the liver [36]. Individual expression of miRNAs in plasma or serum is useful for liver fibrosis detection [3,37]. In addition, some miRNAs can distinguish between early and late fibrosis with high sensitivity and specificity equal to or greater than the APRI and Fib-4 index [38,39]. For example, patients with advanced cirrhosis showed significantly lower levels of miR-29a in their serum compared to healthy controls and patients with early fibrosis [40]. Additionally, serum levels of miR-138 and miR-143 are characteristic of the later stages of liver fibrosis and thus, miR-138 may be useful for detecting fibrosis in its early stages [41]. Furthermore, serum levels of miR-34a and miR-122 correlate with the progression of fibrosis, especially in patients with chronic hepatitis C or nonalcoholic fatty liver disease (NAFLD) [42]. In addition, miR-221 is upregulated in patients with liver cirrhosis [43]. Elucidation of the relationship between miRNAs and liver fibrosis may be useful for detection of fibrosis without invasive liver biopsy, early therapeutic intervention, and identification of high-risk patients. There are various microRNAs that are expected to be biomarkers for liver diseases (Table 1).

Table 1. miRNA as biomarker of liver fibrosis.

	miRNA	Expression Level	References
Liver fibrosis	miR-29a	Down	[40]
Liver fibrosis	miR-138	Up	[41]
Liver fibrosis	miR-143	Up	[41]
Liver fibrosis	miR-34a	Up	[42]
Liver fibrosis	miR-122	Up	[42]
Liver fibrosis	miR-221	Up	[43]
Portal vein thrombus	miR-19a	Up	[44]
Portal vein thrombus	miR-34a	Up	[44]
Portal vein thrombus	miR-21	Up	[45]
SBP	miR-122	Down	[46]
SBP	miR-155	Up	[47,48]
SBP	miR-223	Up	[49]
HBV	miR-21-5p	Up	[50]
HBV	miR-125a-5p	Up	[51]
HBV	miR-27a	Up	[52]
HBV	miR-181b	Up	[53]
HCV	miR-222	Up	[54]
HCV	miR-221	Up	[54,55]
HCV	miR-21	Up	[56]
HCV	miR-99a	Down	[57]
HCV	miR-215-5p	Up	[58]
HCV	miR-483-5p	Up	[58]
HCV	miR-193b-3p	Up	[58]
HCV	miR-34a	Up	[55,58]
HCV	miR-885-5p	Up	[58]
HCV	miR-26b-5p	Down	[58]
HCV	miR-197-3p	Down	[58]
HCV	miR-122	Down	[59]
HCV	miR-16	Up	[55]
HCV	miR-200c	Up	[60]
HCV	miR-20a	Up	[61]
NASH/NAFLD	miR-34a	Up	[62,63]
NASH/NAFLD	miR-372-3p	Down	[64]
NASH/NAFLD	miR-373-3p	Down	[64]
AIH	miR-133a	Up	[65,66]
AIH	miR-122	Down	[67]
AIH	miR-21	Down	[67]
PBC	miR-21	Up	[68]
PBC	miR-210	Up	[69]
PBC	let-7b	Up	[70]
PBC	miR-520a-5p	Up	[70]
PBC	miR-125b	Down	[70]
PBC	miR-92a	Down	[71]
PBC	miR-223-3p	Down	[72]
PBC	miR-21-5p	Down	[72]
PBC	miR-139-5p	Down	[73]
PSC	miR-150-5p	Down	[74]
PSC	miR-122	Down	[75]
PSC	miR-200c	Down	[76]

2.1.2. miRNAs as Regulators of Liver Fibrosis

Recently, the relationship between liver diseases and various miRNAs has been confirmed (Table 2). Some miRNAs such as miR-21, miR-221/222, and miR-181b, promote liver fibrosis through the TGF- β and NF- κ B pathways [77]. In addition, miR-221 regulates multiple targets, including cyclin-dependent kinase inhibitors (CDKN1C or CDKN1B), cytokine signaling 1, E-cadherin, phosphatase and tensin homolog (PTEN), and Bcl-2 modifying factor, which are involved in liver fibrosis [43]. miR-214 also plays an important

role in liver fibrosis by regulating the expression of suppressor of fused homolog protein, and knocking down its expression alleviates liver fibrosis in carbon tetrachloride (CCL4)-treated mice [78]. Moreover, the knockdown of the miR-23b miRNA cluster promotes bile duct differentiation and suppresses or restores TGF- β -induced liver fibrosis depending on stellate cell activation [79].

Table 2. Fibrosis-associated miRNAs.

	miRNA	Predicted Target	Involvement in Disease Progression	References
Liver fibrosis	miR-21	TGF- β pathway, NF- κ B pathway	promote	[77]
Liver fibrosis	miR-221/222	TGF- β pathway, NF- κ B pathway	promote	[77]
Liver fibrosis	miR-181b	TGF- β pathway, NF- κ B pathway	promote	[77]
Liver fibrosis	miR-221	CDKN1C, CDKN1B, Socs1, E-cadherin, PTEN, BMF	promote	[43]
Liver fibrosis	miR-214	Sufu	promote	[78]
Liver fibrosis	miR-23b	TGF- β pathway	inhibit	[79]
Liver fibrosis	miR-30a	Beclin1, α -SMA, TIMP-1, Collagen I	inhibit	[80]
Liver fibrosis	miR-29b	TGF- β pathway	inhibit	[77]
Liver fibrosis	miR-101	TGF- β pathway	inhibit	[77]
Liver fibrosis	miR-122	TGF- β pathway	inhibit	[77]
Liver fibrosis	miR-214-3p	TGF- β pathway	inhibit	[77]
Liver fibrosis	miR-29a	BRD4, CD36	inhibit	[81–83]
Liver fibrosis	miR-34	TGF- β 1/Smad3 pathway	inhibit	[84]
Liver fibrosis	miR-223	NLRP3	inhibit	[85]
Liver fibrosis	miR-455-3p	HSF1	inhibit	[86]
Liver fibrosis	miR-125b	Gli3	inhibit	[87]
Liver fibrosis	miR-378	Gli3	inhibit	[88]
Liver fibrosis	miR-152	Gli3	inhibit	[89]
Portal hypertension	miR-29	VEGF	inhibit	[90]
Portal hypertension	miR-126 family	SPRED1, PIK3R2/p85-beta	inhibit	[91]
HBV	miR-21-5p	TGF- β 1	promote	[50]
HBV	miR-27a	PPAR γ , FOXO1, APC, P53, RXR α	promote	[52]
HBV	miR-181b	PTEN/Akt pathway	promote	[53]
HCV	miR-21	Smad7	promote	[56]
HCV	miR-99a	mTOR	inhibit	[57]
HCV	miR-200c	FAP-1	promote	[60]
ALD	miR-122	HIF1 α	inhibit	[92]
ALD	miR-223	IL-6-p47phox pathway	inhibit	[93]
ALD	miR-155	PPAR γ , PPRE	promote	[94]
ALD	miR181b-3p	importin α 5	inhibit	[95]
ALD	miR-217	SIRT1	promote	[96]
NASH/NAFLD	miR-21	STAT3 signaling pathway, TGF- β /Smad3/Smad7 signaling pathway	promote	[97]
NASH/NAFLD	miR-29a	CD36	inhibit	[98]

Table 2. Cont.

	miRNA	Predicted Target	Involvement in Disease Progression	References
NASH/NAFLD	miR-122	AGPAT1, DGAT1	inhibit	[99]
NASH/NAFLD	miR-34a	PPAR α signaling pathway	promote	[62,63]
NASH/NAFLD	miR-129-5p	PEG3	inhibit	[100]
NASH/NAFLD	miR-188-5p	PTEN/PI3K/AKT pathway	promote	[101]
NASH/NAFLD	miR-223	Cxcl10, Nlrp3, Taz	inhibit	[102]
NASH/NAFLD	miR-27	insulin signaling pathway	promote	[103]
NASH/NAFLD	miR-372-3p	AEBP1	inhibit	[64]
NASH/NAFLD	miR-373-3p	AEBP1	inhibit	[64]
AIH	miR-375	AEG-1	promote	[104]
AIH	miR-138	p53	promote	[105]
AIH	miR-15a/miR-16-1	aryl hydrocarbon receptor-IL-22 regulatory axis	promote	[106]
AIH	miR-674-5p	5-LO	inhibit	[107]
AIH	miRNA-143	phosphorylation of TAK1	inhibit	[108]
AIH	miR-223	AIM2	inhibit	[109]
PBC	miR-21	CDK2AP1	promote	[68]
PBC	miR-210	MLL4	promote	[69]
PBC	miR-506	AE 2, InsP3R3	promote	[67]
PBC	miR-92a	IL-17A	inhibit	[71]
PBC	miR-223-3p	TGFBR2,MEF2C,FOXP1,RBPJ	promote	[72]
PBC	miR-21-5p	TGFBR2,MEF2C,FOXP2,RBPJ	promote	[50]
PBC	miR-139-5p	c-FOS	promote	[73]
PSC	miR-7a	Ngn-3	promote	[110]
PSC	miR-873-5p	GNMT	promote	[111]
PSC	miR-24	menin	inhibit	[112]

In one study, miR-30a inhibited HSC autophagy, increased lipid accumulation, and improved fibrosis in the livers of mice [80]. miR-29b, miR-101, miR-122, and miR-214-3p prevent fibrosis by inhibiting collagen synthesis and suppressing TGF- β pathway activation [77]. Supplementation with miR-29a improved liver fibrosis in vivo and when administered in advance, it suppressed HSC activation by TGF- β in vitro [81]. miR-29a also plays an important role in the improvement of fibrosis by inhibiting bromodomain-4 protein (BRD4) and the fatty acid translocase protein CD36 [82,83]. Furthermore, overexpression of miR-34 ameliorates the onset and progression of liver fibrosis by regulating the TGF- β 1/mothers against decapentaplegic homolog 3 (Smad3) pathway in HSCs [84]. Neutrophils in the liver inhibit liver inflammation and fibrosis by inducing inflammatory macrophages into a reparative phenotype via miR-223 [85]. In addition, miR-455-3p suppresses the expression of heat shock factor 1 and inhibits HSC activation by suppressing the heat shock protein (HSP)-47/TGF- β /Smad4 signaling pathway [86]. Moreover, miR-125b [87], miR-378 [88], and miR-152 [89] can prevent liver fibrosis by regulating the expression of GLI family zinc finger 3 (Gli3).

Thus, various miRNAs are involved in the regulation of liver fibrosis (Figure 1). The identification of miRNAs involved in the pathogenesis of liver fibrosis will enable miRNA-based therapies, and even if this is difficult, miRNA-associated mechanisms can be targeted for therapy.

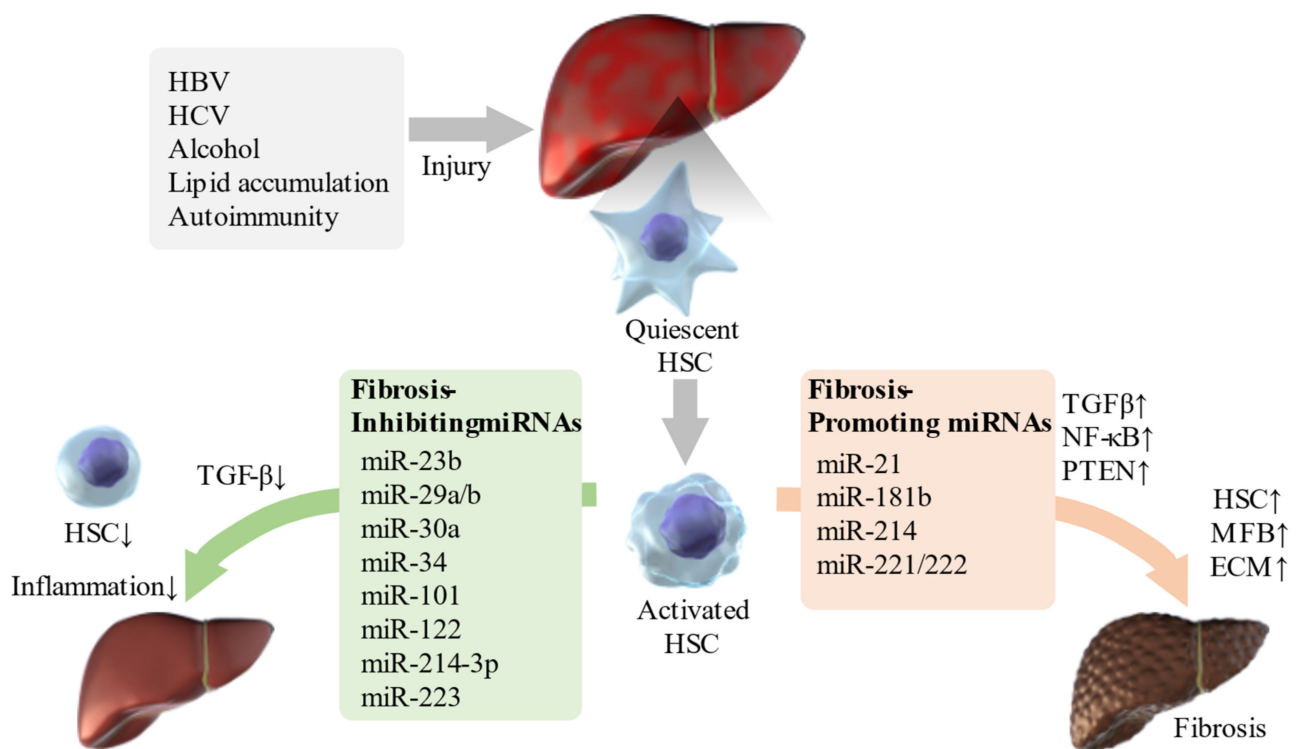


Figure 1. Schematic diagram of the relationship between miRNAs and liver fibrosis. HSCs are activated in livers damaged by viruses, alcohol, lipid accumulation, and autoimmunity. Various miRNAs are involved in this process and affect molecules such as TGF- β , NF- κ B, and PTEN, which are involved in different pathways. This can improve inflammation or, conversely, result in ECM accumulation and cirrhosis. HSC: hepatic stellate cell; TGF- β : transforming growth factor- β ; NF- κ B: nuclear factor-kappa B; PTEN: phosphatase and tensin homolog; MFB: myofibroblast; ECM: extracellular matrix; miRNA: micro ribonucleic acid; HBV: hepatitis B virus; HCV: hepatitis C virus.

2.2. Liver Fibrosis and Exosomal miRNAs

HSCs suppress the expression and function of connective tissue growth factor (CTGF also known as CCN2). Of note, miR-214 is upregulated by the transcription factor Twist1; both are highly expressed in quiescent HSCs and in exosomes secreted by HSCs. Moreover, exosome-mediated delivery of miR-214 to HSCs inhibits recipient cell activation via the repression of CCN2 expression. In contrast, Twist and miR-214 are under-expressed in exosomes secreted from activated HSCs. Thus, the Twist-miR-214-CCN2 pathway is one of the mechanisms that regulate HSC activation [113]. Likewise, miR-199a-5p is highly expressed in exosomes secreted from quiescent HSCs and inhibits HSC activation by inhibiting CCN2 activity in the destination HSCs [114].

When hepatocytes are exposed to lipotoxicity, such as excessive fat deposition in the liver tissue, EVs containing miR-128-3p are released. miR-128-3p reaches and is taken up by HSCs, then suppresses peroxisome proliferator-activated receptor (PPAR)- γ function and activates HSCs [115]. In addition, the miR17-92 cluster is highly expressed in the serum exosomes of patients with alcoholic liver disease (ALD), and these miRNAs promote liver fibrosis [116].

Exosomes secreted by fibroblasts contain multiple miRNAs (miR-21, miR-124a, miR-125b, miR-126, miR-130a, and miR-132), HSP-90a, and signal transducer and activator of transcription 3 (STAT3). Fibroblast-derived exosomes enhance the expression of collagen alpha 1 and alpha-smooth muscle actin (alpha-SMA) in tissues and promote fibrosis through the accumulation of ECM. These miRNAs encapsulated in exosomes can promote wound healing and may contribute to tissue fibrosis [117].

Exosomes secreted by mesenchymal stem cells derived from adipose tissue express high levels of miR-122 which is known to have growth- and hepatic fibrosis inhibitory

effects on HCC. When these exosomes were administered to CCL4-induced liver injury mice, miR-122 in the exosomes suppressed liver tissue damage and fibrosis via suppression of HSC activation in mice [118].

In contrast to EVs in serum extracted from mice with induced liver fibrosis, miR-34c, miR-151-3p, miR-483-5p, miR-532-5p, and miR-687 were upregulated in serum EVs from mice without fibrosis. When these EVs were administered to mice with CCL4-induced liver injury, hepatocellular damage and liver fibrosis were suppressed in the healthy mouse-derived EV group, and inflammatory cytokines and transaminases in the blood were reduced. Furthermore, in serum EVs from patients with F3/4 hepatic fibrosis and healthy subjects, levels of miR-34c, miR-151-3p, miR-483-5p, and miR-532-5p were upregulated in healthy subjects compared to levels in patients with F3/4 hepatic fibrosis. When EVs from healthy subjects were administered to human-derived HSCs, HSC activation was suppressed. These EV miRNAs suppress HSC activation and contribute to the suppression of liver fibrosis [119].

As described above, there are increasing reports of exosomal miRNAs involved in liver fibrosis, and their clinical application is expected. However, improvement of the quality and accuracy of exosomes and standardization of extraction methods are necessary.

3. miRNAs Associated with Complications of Liver Cirrhosis

In addition to HCC, gastrointestinal bleeding due to portal hypertension, ascites, portal vein thrombosis, and HE are some of the most common complications of cirrhosis.

Portal hypertension is caused by an increase in portal venous inflow and intrahepatic vascular resistance, leading to esophageal varices, ascites, HE, and hypersplenism, and it is a major cause of death in patients with cirrhosis [120]. TGF- β -mediated HSC activation is involved in ECM production and is a mechanistic factor in regulating vascular resistance and pressure in the liver [121]. Animal studies have shown that inhibition of TGF- β 1 synthesis and blockade of TGF- β receptors can significantly reduce portal hypertensive pressure [122]. Intrahepatic angiogenesis by vascular endothelial growth factor (VEGF), an angiogenic growth factor, is also a cause of sinusoidal systemic circulation and portal hypertension [123]. miR-29 acts as an anti-fibrotic mediator by inhibiting angiogenic factors such as VEGF [90]. The miR-126 family is associated with angiogenesis and directly inhibits negative regulators of the VEGF pathway, such as the Sprouty-related, equine herpesvirus-1 domain-containing protein 1 (SPRED1) and phosphoinositol-3 kinase regulatory subunit 2 (PIK3R2) [91]. Thus, these miRNAs, which affect TGF- β and VEGF, may be key to the treatment of portal hypertension.

A portal vein thrombus in cirrhosis causes worsening of the liver reserve, gastroesophageal varices, and ascites. The pathophysiology of portal vein thrombosis encompasses one or more of the following features: decreased portal blood flow, hypercoagulable state, and damage to the vascular endothelium. As liver function declines, platelets and hepatic-derived coagulation factors are reduced, while hepatic-derived anticoagulation factors are also reduced, and when this balance is disrupted, portal vein thrombi form [124]. Notably, miR-19a and miR-34a levels are correlated with portal vein thrombosis [44], and miR-21 is considered an independent predictor of portal vein thrombosis in patients with HCC [45].

Patients with ascites, spontaneous bacterial peritonitis (SBP), and hepatorenal syndrome had significantly lower levels of miR-122 than those without these complications. In addition, serum miR-122 levels were associated with survival of patients with cirrhosis, independent of the Model for End-Stage Liver Disease (MELD) score or patient's age [46]. One study indicated that miR-155 is an outstanding diagnostic marker for SBP, and detection of both serum CD64 and calprotectin levels also provide a more useful diagnosis when using blood samples from patients with cirrhosis and ascites [47]. Furthermore, miR-155 [48] and miR-223 [49] were elevated in ascites from patients with cirrhosis and SBP, indicating that these miRNAs may be involved in the immune response in ascites upon SBP. Animal models of HE also show changes in miRNAs in the blood

and cerebral cortex [125,126]. In the HE model, ammonia-induced changes in miRNA expression regulate the expression of heme oxygenase 1 (HO-1) and induce astrocyte senescence [127].

Complications of cirrhosis often occur in the non-compensated phase, so there is little time to wait for the improvement of liver fibrosis, and a direct approach is needed for diagnosis and treatment. Therefore, miRNA-based diagnostic and therapeutic approaches should be developed.

4. Association of the Causes of Liver Cirrhosis and miRNAs

4.1. Chronic Hepatitis B Virus (HBV) Infection and miRNAs

An HBV infection causes acute and chronic hepatitis, cirrhosis, and HCC. The annual incidence of cirrhosis from a chronic HBV infection was 2.1~6.0% [128,129]. Although antiviral treatment with peginterferon-alpha or nucleic acid analogs inhibits fibrosis progression [130,131], there is still no treatment to improve HBV-related cirrhosis once treatment is completed.

Toll-like receptors (TLRs) and several miRNAs involved in the TLR signaling pathway play important roles in innate immunity against HBV infection [132]. miR-21 [50], miR-22 [133,134], miR-122 [133–137], miR-194 [137], and miR-219-1 [138] are associated with chronic persistent HBV infections. During the progression from chronic hepatitis to cirrhosis and HCC, miR-21, miR-199b, miR-145, and miR-602 were aberrantly expressed from the initial stage to the end stage [50]. In HBV infections, miR-22 is involved in the regulation of cell fate and development of HCC [133,134]. Overexpression of miR-122 downregulates HO-1 and inhibits HBV expression [139]. miR-122 and miR-22 are downregulated in patients with HBV-associated HCC, are associated with HCC development and progression, and correlate with clinical and pathological indicators [140]. Additionally, miR-219-1 is associated with the clearance of HBV infections and may influence the outcome of persistent HBV infections [138].

Liver biopsies of HBV-infected patients indicate a correlation between miRNAs and liver fibrosis [141,142]. In early liver fibrosis, miR-34b-3p, miR-1224-3p, and miR-1227-3p expression is increased, and miR-499a-5p expression is decreased. Contrastingly, in advanced hepatic fibrosis, miR-1, miR-10b-5p, miR-96-5p, miR-133b, and miR-671-5p are upregulated, while miR-20b-5p and miR-455-3p are downregulated [141,142]. Moreover, miR-21-5p expression is strongly positively correlated with hepatic fibrosis and causes HBV-induced hepatic fibrosis via TGF- β 1 signaling [50]. miR-125a-5p levels are significantly increased in patients with cirrhosis, and miR-125a-5p may be a novel biomarker for liver injury [51]. miR-27a is elevated in HBV-associated cirrhosis and is a predictor of HSC activation, differentiation, and proliferation [52]. miR-181b activates HSCs through the PTEN/protein kinase B (Akt) pathway and has been identified as an independent predictor of disease progression in HBV [53].

Although hepatitis B viral load can be controlled by nucleic acid analogs and interferons, carcinogenesis cannot be completely prevented. Elucidating the relationship between HBV and miRNAs is expected to lead to breakthroughs in the treatment of HBV.

4.2. Chronic Hepatitis C Virus (HCV) Infection and miRNAs

HCV infections are one of the most serious health problems worldwide. More than 170 million people are chronically infected with HCV and are at a high risk of developing liver cirrhosis and HCC. HCV infections cause acute and chronic hepatitis, cirrhosis, and HCC. The annual incidence of cirrhosis due to hepatitis C is 1.1% [129]. Although the development of treatment for hepatitis C has made it possible to eradicate the disease, it is unclear to what extent fibrosis will improve in patients who would have already progressed to cirrhosis. In addition, there is no 100% inhibition of carcinogenesis. Several miRNAs are associated with liver fibrosis in HCV infections.

Serum miRNAs are considered important non-invasive biomarkers of advanced stages of HCV-related liver fibrosis [143]. miR-16, miR-146a, miR-221, and miR-222 are upreg-

ulated in early and late fibrosis, and miR-222 and miR-221 exhibit high sensitivity and specificity in late fibrosis [54]. Liver biopsies of HCV-related liver fibrosis samples indicate upregulation of miR-21 [56], and this miRNA enhances TGF- β signaling by targeting SMAD7, a negative regulator of TGF- β , and consequently induces fibrogenesis [56]. miR-16, miR-34a, and miR-221 are elevated in liver damage caused by HCV and can be used to detect fibrosis and cirrhosis [55]. Compared with patients with mild fibrosis, five circulating miRNAs (miR-215-5p, miR-483-5p, miR-193b-3p, miR-34a-5p, and miR-885-5p) showed increased expression, and two miRNAs (miR-26b-5p and miR-197-3p) showed decreased expression in patients with HCV cirrhosis [58]. miR-122 and miR-130a play important roles in chronic hepatitis C [132]. miR-122 stimulates HCV translation, stabilizes the genome, and induces viral genomic RNA replication [144]. Additionally, miR-122 is negatively correlated with fibrosis in HCV-infected patients [59]. The expression of miR-20a is significantly upregulated in the sera of patients with HCV-associated liver fibrosis and gradually increased from the early to late stages of fibrosis [61].

The expression of miR-99a was significantly lower in patients with chronic HCV infection than in healthy subjects. miR-99a modulates the expression of the mammalian target of rapamycin protein (mTOR) to improve intracellular lipid accumulation and limit HCV replication [57]. miR-200c, which is increased in HCV-infected patients, regulates the Src kinase signaling pathway and promotes liver fibrosis by directly targeting Fas-associated phosphatase 1 (FAP-1), a negative regulator of Src signaling [60].

Direct-acting antivirals are highly effective, but HCV elimination is not a cure for liver disease, especially in patients with advanced fibrosis or cirrhosis. However, miRNAs show promise as a treatment for residual liver fibrosis after antiviral treatment.

4.3. ALD and miRNAs

ALD is the leading cause of chronic liver disease, liver fibrosis, and cirrhosis worldwide [145], and Kupffer cells play an important role in the development of ALD. The human intestinal tract contains many bacteria which produce endotoxins. The gut-derived endotoxins are transported to the liver, where they are removed by Kupffer cells. Studies have shown that these endotoxins activate Kupffer cells. Two mechanisms have been suggested to explain the relationship between endotoxin levels and alcohol intake: (i) chronic alcohol consumption increases endotoxin levels in the circulating blood because Kupffer cells are unable to effectively remove endotoxins from the blood, and (ii) alcohol consumption increases intestinal permeability, leading to increased intestinal endotoxin absorption [145].

Serum miR-122, miR-223, miR-155, and miR-146a levels are increased in ALD [146,147]. miR-122 protects the liver from inflammation by decreasing the expression of hypoxia-inducible factor 1 α (HIF-1 α) in the liver [92]. Previous studies show that the levels of neutrophil-specific miR-233 in the serum and liver were elevated in both patients with ALD and animal models. This miRNA plays an important role in inhibiting neutrophil hyperactivation by targeting the IL-6-p47phox pathway in neutrophils [93]. miR-155, a major regulator of inflammation and immunity, promotes inflammation in alcoholic steatohepatitis (ASH). Alcohol induces miR-155 expression in the liver via the TLR4 pathway, and miR-155 promotes liver fibrosis by targeting peroxisome proliferator response elements (PPREs) and PPAR- α [94]. Ethanol regulates innate immune activity and causes ethanol-induced liver injury. Of note, miR-181b-3p suppresses inflammation via targeting importin α 5 and normalizes lipopolysaccharide-stimulated TNF α expression in Kupffer cells [95]. miR-217 promotes fat accumulation in hepatocytes in ALD by suppressing sirtuin 1. In addition, it reduces the function of lipin-1, an important regulator of lipids in hepatocytes [96].

Although ALD is a global problem, there is limited progress its treatment. The lack of therapeutic progress in the field of ALD is partly due to the lack of experimental models of advanced ALD and the difficulty of conducting clinical trials in active addicts. However, miRNA research may lead to a breakthrough in ALD treatment.

4.4. NASH/NAFLD and miRNAs

NAFLD is one of the most common causes of chronic liver disease and is a serious medical problem in developed countries [148]. In patients with NAFLD, the degree of liver damage varies from NAFL to NASH and may progress to HCC in the early stages of liver fibrosis [149]. NASH is mediated by inflammatory cytokines, mitochondrial dysfunction secondary to nutrient excess, and oxidative stress, resulting in hepatocyte inflammation, ballooning, apoptosis, and activation of HSCs [150,151]. Numerous factors have been implicated in the pathogenesis and progression of NAFLD, including insulin resistance, adipose tissue dysfunction, mitochondrial dysfunction, endoplasmic reticulum stress, dietary factors, fatty acids, iron loading, inflammatory activation, lipopolysaccharide produced by the gut microbiota, chronic inflammatory conditions, and the involvement of genetic and epigenetic factors [152,153]. However, the detailed mechanisms of NAFLD/NASH remain unknown, and there is no breakthrough treatment.

There have been many studies on the relationship between pathogenesis and miRNAs in NASH/NAFLD [154]. Serum miRNA-34a is effective in diagnosing NAFLD. In lipid metabolism, it may downregulate the PPAR α signaling pathway and induce lipid accumulation in hepatocytes [63]. Neutrophil-specific miR-223 is upregulated in hepatocytes and inhibits the progression of NASH in obese mice. Some of the target genes of miR-223 (such as *CXCL10*, *NLRP3*, and *TAZ*) induce inflammation and fibrosis in the liver and promote the progression of NAFLD. EV-derived miR-223, when taken up by hepatocytes, suppresses hepatic inflammatory and fibrogenic gene expression [102]. miR-372-3p and miR-373-3p, which downregulate adipocyte enhancer binding protein 1 (AEBP1), are reduced in patients with NASH and advanced fibrosis [64].

miR-21 induces NASH via the STAT3 signaling pathway and induces liver fibrosis via HSC activation and collagen deposition via the TGF- β /Smad3/Smad7 signaling pathway [97]. Overexpression of hepatic miR-27 promotes the expression of hepatic insulin receptors, while inhibition decreases insulin sensitivity, suggesting that miR-27 may contribute to the early development of hepatic insulin resistance [103]. In one study, the overexpression of miR-29a ameliorated NASH and NAFLD by suppressing CD36 in a mouse model [98]. Another study demonstrated that decreasing miR-122 increased fat deposition and total triglyceride content in the liver and decreased beta-oxidation and energy expenditure, resulting in increased weight gain in mice [99]. miR-34a downregulates the PPAR α signaling pathway, which is a key transcription factor for fatty acid oxidation and facilitates the transfer of fatty acids to mitochondria for oxidation. Conversely, blocking the PPAR α signaling pathway may induce lipid accumulation in the liver [62]. miR-129-5p negatively regulates HSC activation induced by paternally expressed gene 3 (PEG3) [100]. Inhibition of miR-188-5p alleviates liver fibrosis by suppressing HSC activation through the PTEN/PI3K/Akt pathway [101].

Since the incidence of NAFLD/NASH is expected to continue to increase, there is an urgent need to develop early diagnosis and treatment methods using miRNAs.

4.5. Autoimmune Liver Diseases and miRNAs

Autoimmune liver diseases include autoimmune hepatitis (AIH), primary biliary cholangitis (PBC), and primary sclerosing cholangitis (PSC), which are characterized by chronic liver and biliary inflammation. These diseases require persistent treatment, but the underlying causes of these diseases are still unknown. To date, numerous susceptible loci for autoimmune liver diseases in the human leukocyte antigen (HLA) and non-HLA regions have been identified by a genome-wide association studies (GWAS) [155,156]. However, genetic analysis alone is inadequate to identify the cause of autoimmune liver diseases, and environmental factors may be involved in the development of these diseases.

In recent years, the pathological and diagnostic relevance of miRNAs in autoimmune liver diseases have been reported.

4.5.1. AIH and miRNAs

AIH is a chronic, progressive liver disease that usually occurs in middle-aged and older women, and autoimmune mechanisms have been implicated in the development of this hepatocellular damage [157,158]. In patients with untreated AIH, serum levels of miR-122 and miR-21 are significantly elevated but decrease during remission with glucocorticoid treatment [67]. In addition, miR-122 and miR-21 levels are negatively correlated with liver fibrosis [67].

Using a concanavalin A (Con A)-induced AIH mouse model, miRNA expression was altered in the mice compared to a control group. Moreover, expression of miR-133a was increased in the AIH mouse model [65,66]. After Con A treatment, the levels of miR-375, IL-6, IL-1 β , and TNF- α were increased in Kupffer cells. Furthermore, a miR-375 inhibitor decreased apoptosis in Kupffer cells by targeting astrocyte elevated gene 1 (AEG1) and restoring immune abnormalities in the liver [104]. Downregulation of miR-138 affected liver macrophage function and improved immune status by targeting p53 in an AIH mouse model [105]. Reduction of miR-15a/16-1 in damaged hepatocytes contributes to IL-22-mediated tissue repair by decreasing cell apoptosis and promoting cell proliferation [106]. In Con A-induced murine immune hepatotoxicity, 5-lipoxygenase (5-LO) is involved in the production of cysteinyl-leukotrienes which exacerbate hepatotoxicity. miR-674-5p may ameliorate liver injury by negatively regulating the expression of 5-LO [107]. miRNA-143 regulates inflammation and fibrosis by regulating the phosphorylation of TGF- β -activated kinase 1 (TAK1) [108]. miRNAs modulate apoptosis and inflammatory reactions by affecting macrophages, regulatory T cells, Th17 cells, CD4⁺ T cells, and hepatocytes [67]. For example, miR-223 suppressed Kupffer cell activation in a mouse model of AIH by decreasing IL-1 β secretion via the absent in melanoma 2 (AIM2) pathway [109].

Since AIH is a disease with an unknown cause, this delays diagnosis, which can be fatal, and there is an urgent need to develop new diagnostic and therapeutic methods using miRNAs and other technologies.

4.5.2. PBC and miRNAs

PBC is a progressive cholestatic liver disease that is caused by a combination of genetic predisposition and environmental triggers [157]. It is characterized by chronic non-suppurative inflammation and destruction of interlobular bile ducts, which in turn may lead to liver cirrhosis, liver failure, and death, unless liver transplantation is undertaken. miR-21 and miR-210 levels in the liver tissue of patients with PBC are increased compared to those in healthy individuals [68,69]. Elevation of a let-7 miRNA (let-7b) and miR-520a-5p, and a decrease in miR-125b, are biomarkers in refractory PBC [70]. The expression of miR-223-3p and miR-21-5p was suppressed in the peripheral blood B cells of patients with PBC as the PBC stage progressed [72]. miR-139-5p targets the proto-oncogene, c-FOS, and promotes the NF- κ B signaling pathway, leading to an increase in TNF- α levels [73]. It was significantly downregulated in clinically advanced PBC (portal hypertension type and hepatic failure type). Increased levels of immunomodulatory miR-451a and miR-642a-3p were observed in plasma-derived EVs of patients with PBC compared to the levels in healthy controls [159].

miRNAs regulate immune responses, hepatocyte apoptosis, bile acid metabolism, and biliary fibrosis by inhibiting various signaling pathways in PBC. miR-21 targets cyclin-dependent kinase 2-associated protein 1 (CDK2AP1), and inhibition of miR-21 ameliorates liver damage, necrosis, and fibrosis [68,69]. miR-506 plays an important role in the pathogenesis of PBC by regulating bicarbonate secretion [67]. In addition, miR-92a was downregulated in patients with PBC, suggesting that it directly regulates IL-17A and is involved in disease progression [71].

The diagnosis of PBC is relatively straightforward if the anti-mitochondrial antibody (AMA) test is positive. However, there are patients who may have negative AMA test results, and these patients require a liver biopsy for diagnosis. This can be problematic in the presence of ascites or an infection, and noninvasive biomarkers are needed. In addition,

PBC is gradually progressive, and some patients are refractory to treatment and may not recover. Consequently, miRNAs may be useful in the diagnosis and treatment of such cases.

4.5.3. PSC and miRNAs

In PSC, T cell-related risk genes have a strong correlation with disease progression. Dysfunctional gene products can disrupt immune homeostasis by regulating cytokine production, immune tolerance, and immune responses [157]. Unfortunately, there are no effective drugs to slow down the natural progression of PSC, and liver transplantation is the only option for advanced PSC. Three miRNAs (miR-3178, miR-4484, and miR-150-5p) were abnormally altered in serum samples [74]. Low miRNA-122 levels in the serum may be associated with a poor prognosis [75]. The downregulation of miR-200c may be a new diagnostic biomarker for PSC detection [76].

miRNAs are involved in the pathogenesis of PSC through regulation of angiogenesis, apoptosis, cholangiocyte proliferation, and liver fibrosis. In isolated cholangiocytes from a model of sclerosing cholangitis created by treatment with 3,5-diethoxycarbonyl-1,4-dihydrocollidine (DDC), the expression of miR-7a and the transcription factor neurogenin-3 was increased, resulting in the proliferation of cholangiocytes [110]. miR-873-5p targets glycine N-methyltransferase (GNMT). A deficiency of GNMT exacerbates fibrogenesis caused by bile stasis causing high blood levels of miR-873-5p in patients with bile stasis and liver cirrhosis. In addition, administration of an anti-miR-873-5p antibody to a PSC mouse model restored GNMT levels and ameliorated inflammation and fibrosis [111]. Inhibition of miR-24 increases menin and TGF- β 1 expression and exacerbates liver fibrosis in a mouse model of PSC [112].

The only treatment for advanced PSC is liver transplantation, and early diagnosis and treatment using miRNAs might be established in the future.

5. Conclusions

Despite the excellent disease control by antiviral therapy for viral liver diseases, no treatment has yet been established to improve liver fibrosis once it has progressed. In addition, there is an urgent need to establish biomarkers for the diagnosis of liver fibrosis that do not require invasive liver biopsy.

Some liver miRNAs have been reported to be associated with hepatic fibrosis, and the establishment of these miRNAs may lead to early detection and better treatment for liver cirrhosis. In fact, accumulating evidence has revealed that miRNAs (including exosomal miRNAs) play important roles in many biological processes involved in liver fibrosis, including viral hepatitis, ALD, NASH, and autoimmune liver diseases. Several studies have demonstrated the relationship between various pathogens and miRNAs as biomarkers for liver fibrosis. Furthermore, elucidating the details of miRNAs involved in liver fibrosis and the mechanisms of their regulation will be beneficial for the development of anti-fibrosis therapies. A combination of conventional and miRNA-based therapies may be effective in the treatment of advanced liver cirrhosis. However, the regulation of miRNAs *in vivo* may not always be observed due to their inherent complexity, and further studies to elucidate their detailed mechanisms are required for the clinical application of miRNAs. Future studies of miRNAs in liver fibrosis will bring about the usefulness of miRNAs in clinical applications for the treatment of liver cirrhosis.

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Abbreviations

5-LO	5-lipoxygenase
AE 2	Anion exchanger 2
AEBP1	Adipocyte enhancer binding protein 1
AEG-1	Astrocyte elevated gene 1
AGPAT1	1-acylglycerol-3-phosphate O-acyltransferase 1
AIH	Autoimmune hepatitis
AIM2	Absent in melanoma 2
ALD	Alcoholic liver disease
alpha-SMA	Alpha-smooth muscle actin
AMA	Anti-mitochondrial antibody
APC	Adenomatous polyposis coli
ASH	Alcoholic steatohepatitis
BMF	Bcl-2 modifying factor
BRD4	Bromodomain-4 protein
CCL4	Carbon tetrachloride
CDK2AP1	Cyclin dependent kinase 2 associated protein 1
CDKN	Cyclin-dependent kinase inhibitor
ConA	Concanavalin A
CTGF	Connective tissue growth factor
CXCL10	C-X-C motif chemokine ligand 10
cys-LT	Cysteinyl-leukotrienes
DDC	3,5-diethoxycarbonyl-1,4-dihydrocollidine
DGAT1	Diacylglycerol O-acyltransferase 1
ECM	Extracellular matrix
EV	Extracellular vesicle
FAP-1	FAS-associated phosphatase 1
FOXO1	Forkhead box protein O1
FOXP1	Forkhead box P1
Gli3	GLI family zinc finger 3
GNMT	Glycine N-methyltransferase
GWAS	Genome-wide association study
HBV	Hepatitis B virus
HCC	Hepatocellular carcinoma
HCV	Hepatitis C virus
HE	Hepatic encephalopathy
HIF1 α	Hypoxia inducible factor α
HLA	Human leukocyte antigen
HO-1	Heme oxygenase 1
HSC	Hepatic stellate cell
HSF1	Heat shock factor 1
HSP	Heat shock protein
IL	Interleukin
InsP3R3	Type III inositol 1,4,5-trisphosphate receptor-3
LPS	Lipopolysaccharide
M2BPGi	Mac-2-binding protein glycosylation isomer
MEF2C	Myocyte enhancer factor 2C
MFB	Myofibroblast
miRNA	MicroRNA
MLL4	Histone methyltransferase mixed-lineage leukemia-4
mRNA	Messenger RNA
mTOR	Mammalian target of rapamycin protein

NAFLD	Nonalcoholic fatty liver disease
NASH	Nonalcoholic steatohepatitis
ncRNA	Non-coding RNA
NF- κ B	Nuclear factor-kappa B
NKT	Natural killer T
NLRP3	NLR family pyrin domain containing 3
PBC	Primary biliary cholangitis
PDGF	Platelet-derived growth factor
PEG3	Paternally expressed gene 3
PIK3R2	Phosphoinositol-3 kinase regulatory subunit 2
PPAR	Peroxisome proliferator-activated receptor
PSC	Primary sclerosing cholangitis
PTEN	Phosphatase and tensin homolog
RBPJ	Recombination signal binding protein for immunoglobulin kappa J region
RXR α	Retinoid X receptor alpha
SBP	Spontaneous bacterial peritonitis
SIRT1	Sirtuin 1
Smad	Mothers against decapentaplegic homolog
Socs1	Suppressor of cytokine signaling 1
SPRED1	Sprouty related EVH1 domain containing 1
STAT3	Signal transducer and activator of transcription 3
TAK1	TGF-beta activated kinase 1
TAZ	Tafazzin
TGF	Transforming growth factor
TGFBR2	Transforming growth factor beta receptor 2
TLR	Toll-like receptor
TNF	Tumor necrosis factor
VEGF	Vascular endothelial growth factor

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