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## The Long and the Small Collide: LncRNAs and Small Heterodimer Partner (SHP) in Liver Disease

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### Abstract

Long non-coding RNAs (lncRNAs) are a large and diverse class of RNA molecules that are transcribed but not translated into proteins, with a length of more than 200 nucleotides. LncRNAs are involved in gene expression and regulation. The abnormal expression of lncRNAs is associated with disease pathogenesis. Small heterodimer partner (SHP, NROB2) is a unique orphan nuclear receptor that plays a pivotal role in many biological processes by acting as a transcriptional repressor. In this review, we present the critical roles of SHP and summarize recent findings demonstrating the regulation between lncRNAs and SHP in liver disease.

### Keywords

Non-coding RNAs; lncRNAs; Nuclear receptor; SHP

### 1. Introduction

Non-protein coding transcripts or non-coding RNAs (ncRNAs) account for 98% or so of the human transcriptome and play crucial roles in development, physiology, and disease (Esteller, 2011; Palazzo and Lee, 2015). Long non-coding RNAs (lncRNAs) are defined as those ncRNAs longer than 200 nucleotides, which are largely tissue-specifically expressed

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Author contributions

J.W. wrote the manuscript. L.E.N. and L.W. reviewed and finalized the manuscript.

Declaration of competing interest

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(Statello et al., 2021). LncRNAs participate in gene transcriptional, post-transcriptional, and epigenetic regulation and are essential in many physiological processes, such as X-chromosome inactivation in mammals (Cabili et al., 2011; Gomes et al., 2013; Zhao et al., 2017). Mechanistically, lncRNAs participate in histone modifications to remodel chromatin, direct the recruitment of RNA polymerase and cofactors, serve as scaffolds for the association of transcription factors (TFs) with other cofactors to mediate transactivation, act as decoys to prevent TFs from binding to their DNA elements, silence gene expression via modulation of translation and mRNA stability, or are involved in RNA alternative splicing (Fernandes et al., 2019; Wu et al., 2021; X. Zhang et al., 2019). About 20% of lncRNAs are derived from enhancer regions (termed eRNAs), participating in chromosomal enhancer-promoter looping (Bonasio and Shiekhattar, 2014). LncRNAs also cooperate with microRNAs (miRNAs) to regulate gene expression through competition of binding or acting as miRNA sponges (Lopez-Urrutia et al., 2019). LncRNAs can also be the precursors of miRNAs and serve as signals for the activation of specific biological events (P. Zhang et al., 2019).

Small heterodimer partner (SHP, NROB2) belongs to the nuclear receptor (NR) superfamily. Generally, it acts as a transcriptional repressor through interaction with a variety of other NRs, including androgen receptor (AR), estrogen receptor alpha (ER $\alpha$ ), hepatocyte nuclear factor 4 alpha (HNF4 $\alpha$ ), liver receptor homolog-1 (LRH-1), liver X receptor alpha (LXR $\alpha$ ), peroxisome proliferator-activated receptor gamma (PPAR $\gamma$ ), retinoic acid receptor alpha (RAR $\alpha$ ), and retinoid X receptor alpha (RXR $\alpha$ ), to regulate diverse biological processes, such as bile acid synthesis, glucose/lipid metabolism, and drug metabolism (Zhang et al., 2011). As an orphan NR, SHP contains dimerization and ligand-binding domains but lacks a DNA-binding domain. SHP may also interact with other non-NR TFs to inhibit gene transcription and regulate diverse signaling pathways involved in metabolism, inflammation, and cell proliferation (Song et al., 2017b).

There is increasing recognition of the role of ncRNAs in diseases. The most well-studied ncRNAs are miRNAs, but lncRNAs also play critical roles in cellular homeostasis and are inherent to diseases. In addition to recapitulating the essential functions of SHP, this review summarizes the up-to-date findings on the crosstalk between lncRNAs and SHP and reveals their pathophysiological relevance to liver disease.

## 2. The primary function of SHP

### 2.1. SHP in cholesterol and bile acid homeostasis

Cholesterol homeostasis in mammals is maintained through biosynthesis, cellular uptake, and hepatic conversion to bile acids.

The well-established function of SHP is to suppress bile acid biosynthesis. Farnesoid X receptor (FXR) binds and activates the SHP promoter and SHP represses LRH-1-dependent activation of the cholesterol 7 $\alpha$ -hydroxylase (CYP7A1) promoter (Goodwin et al., 2000; Lu et al., 2000). CYP7A1 catalyzes the rate-limiting step in bile acid biosynthesis. FXR-mediated regulation of bile acid-related genes, including SHP and CYP7A1, depends on bromodomain-containing protein 4 (BRD4) that is required for the anti-inflammatory and

anti-fibrotic actions of obeticholic acid (OCA), a potent and selective FXR agonist (Jung et al., 2020). SHP also interacts with HNF4 $\alpha$  to repress the transcription of CYP8B1 that catalyzes the synthesis of cholic acid and determines the hydrophobicity of the bile acid pool (Zhang and Chiang, 2001). The role of SHP in hepatic bile acid biosynthesis is further elucidated in *Shp* knockout mice that exhibit mild defects in bile acid homeostasis, suggesting the existence of compensatory pathways of bile acid signaling (Wang et al., 2002). CYP8B1 is strongly induced in *Shp* knockout mice, which may increase the hydrophilicity of the bile acid pool and reduce the hepatotoxicity of bile acids (Wang et al., 2003). Besides, SHP maintains cholesterol homeostasis through repressing the expression of cholesterol biosynthesis enzyme, 3-hydroxy-3-methylglutaryl-coenzyme A reductase (HMGCR), the rate-limiting enzyme of the mevalonate pathway in producing cholesterol and other isoprenoids; mechanistically, SHP inhibits LRH-1 and sterol regulatory element binding transcription factor 2 (SREBF2) from binding to the HMGCR promoter (Datta et al., 2006; Kim et al., 2015). The double knockout mice of SHP and FXR develop intrahepatic cholestasis, which recapitulates human progressive familial intrahepatic cholestasis (PFIC) and can be used to investigate the molecular pathogenesis of PFIC (K. H. Kim et al., 2018).

Hepatic miR-210 levels are elevated in cholestatic mouse models and patients with primary biliary cholangitis. MiR-210 promotes bile acid-induced liver injury in part by targeting the mixed-lineage leukemia-4 (MLL4) methyltransferase. SHP inhibits miR-210 expression by repressing a transcriptional activator, Kruppel-like factor-4 (KLF4), and nuclear levels of SHP are reduced in cholestatic livers (Kim et al., 2020a).

SHP is also highly expressed in the intestine. Postprandial fibroblast growth factor (FGF) 19 (human FGF19, mouse FGF15) induces SHP phosphorylation that inhibits the transcriptional activity of SREBF2, leading to the repression of intestinal NPC1-like intracellular cholesterol transporter 1 (NPC1L1) expression and cholesterol absorption (Kim et al., 2015; Y. C. Kim et al., 2019).

## 2.2. SHP in glucose and lipid metabolism

SHP has a major function in regulating glucose metabolism by inhibiting gluconeogenic gene expression. Glucose 6-phosphatase (G6Pase) and phosphoenolpyruvate carboxykinase (PEPCK) are the rate-limiting enzymes in hepatic gluconeogenesis. SHP represses G6Pase and PEPCK gene expression via inhibition of the forkhead transcription factors HNF3 and HNF6 (Kim et al., 2004; Lee et al., 2008). SHP antagonizes peroxisome proliferator-activated receptor gamma coactivator 1-alpha (PGC-1 $\alpha$ ) coactivation of glucocorticoid receptor (GR), leading to the inhibition of PEPCK expression (Borgius et al., 2002). SHP represses CCAAT/enhancer-binding protein alpha (C/EBP $\alpha$ )-driven transcription of PEPCK and FOXO1-mediated transcription of G6Pase (Park et al., 2007; Yamagata et al., 2004). SHP also inhibits the transcriptional activity of LXR $\alpha$  and PPAR $\gamma$  by competing for binding to their common heterodimer partner RXR $\alpha$  to decrease hepatic glucokinase expression (Kim et al., 2009).

SHP is essential to maintain hepatic lipid homeostasis (Watanabe et al., 2004). SHP-deficient mice are protected against fatty liver in part by increasing very-low-density lipoprotein (VLDL) secretion. VLDL secretion is controlled by microsomal triglyceride

transfer protein (MTTP), and SHP represses LRH-1-mediated transactivation of the MTTP promoter in hepatocytes (Huang et al., 2007; Lee et al., 2015; Wang et al., 2005). Mice with hepatocyte-specific deletion of SHP are protected against dyslipidemia induced by either a cholesterol/cholic acid diet or hypothyroidism (Hartman et al., 2009), and against fatty liver development by suppressing the expression of PPAR $\gamma$  and lipid-droplet protein fat-specific protein 27 (FSP27) (Akinrotimi et al., 2017). A recent study shows that hepatocyte-specific deletion of SHP reduces high-fat, -cholesterol, and -fructose (HFCF) diet-induced hepatic steatosis but aggravates the development of liver inflammation and fibrosis; interestingly, if the mice already present hepatic steatosis induced by HFCF diet, the adeno-associated virus-mediated hepatic depletion of SHP is no longer effective in reducing steatosis but still exacerbates liver inflammation and fibrosis (Magee et al., 2020). Indeed, SHP-deficient hepatocytes have an enhanced ability to recruit neutrophils to the injured liver, and SHP is a negative regulator of c-Jun-mediated transcription of chemokine (C-X-C motif) ligand 2 (CXCL2) and NF- $\kappa$ B p65-mediated induction of chemokine (C-C motif) ligand 2 (CCL2) (Noh et al., 2018; Zou et al., 2018).

As an integral component of the liver circadian network, SHP inhibits neuronal PAS domain-containing protein 2 (NPAS2) expression; they form a negative feedback loop to regulate the cyclic expression patterns of liver metabolic genes and maintain triglyceride and lipoprotein homeostasis (Lee et al., 2015). Constitutive SHP expression in transgenic mice can deplete the hepatic bile acid pool and induce triglyceride accumulation in the liver (Watanabe et al., 2004). This phenotype is attributable to SHP-mediated direct repression of downstream target genes including the bile acid sensor FXR $\alpha$ , and the indirect activation of the lipogenic PPAR $\gamma$  and SREBF1 gene expression (Boulias et al., 2005).

In contrast to the former findings that SHP contributes to or plays a promoting role in hepatic steatosis, a recent study focusing on the effect of FGF15/19 on hepatic lipogenesis reveals that FGF19 induces SHP phosphorylation to epigenetically silence the expression of lipogenic genes, such as SREBF1 and FASN, in a DNA methyltransferase-3a (DNMT3A)-dependent manner; further, the virus-mediated overexpression of SHP in obese mice substantially reduces liver triglyceride levels and inhibits lipogenesis in part by regulating phosphatidylcholine levels (Kim et al., 2020b; Y. C. Kim et al., 2018). In line with this, a decrease of FXR and SHP expression is found in beta-carotene oxygenase 1 and beta-carotene oxygenase 2 double knockout mice which develop hepatic steatosis (Lim et al., 2018). The phenotypic discrepancy between germline loss and adult manipulation of SHP expression in lipid metabolism is currently unclear. Possible compensatory changes in metabolic pathways in transgenic/knockout mice need to be taken into consideration.

Obesity-induced overexpression of miR-802 impairs hepatic insulin sensitivity and glucose metabolism (Kornfeld et al., 2013). SHP inhibits the transactivation of miR-802 by aromatic hydrocarbon receptor (AHR), which is attenuated in non-alcoholic fatty liver disease (NAFLD) patients and obese mice; activation of FXR by OCA reduces miR-802 expression and improves insulin resistance and hepatic steatosis (Seok et al., 2020). In accordance with this, as a repressor of AHR, SHP mitigates the AHR overexpression-induced hepatic increase of phosphatidylcholines and steatosis in obese mice (Y. C. Kim et al., 2018). These

findings suggest that the FXR-SHP-miR-802 pathway may be targeted for the treatment of type 2 diabetes and NAFLD.

### 2.3. SHP in cell proliferation

SHP is identified as a tumor suppressor (He et al., 2008; Suresh et al., 2017). SHP expression is down-regulated in hepatocellular carcinoma (HCC). SHP inhibits hepatocyte proliferation and activates apoptosis to suppress tumor growth in HCC (He et al., 2008; Zhang et al., 2010, 2008). A small molecule activator of SHP, 5-(diethylsulfamoyl)-3-hydroxynaphthalene-2-carboxylic acid, has a strong inhibitory effect on HCC cell migration by suppressing CCL2 expression (Z. Yang et al., 2016). Interestingly, thymine DNA glycosylase (TDG) is essential for SHP expression in the liver in response to FXR agonists, and conditional deletion of TDG in adult mice results in a male-predominant onset of HCC (Hassan et al., 2020).

### 2.4. Other roles of SHP

**2.4.1. SHP in mitosis**—SHP displaces a major fraction of pregnane X receptor (PXR) and ER $\alpha$  from the mitotic chromatin via intermolecular interactions, resulting in attenuation of transcriptional activities during mitosis and implying the potential function of SHP in the regulation of “gene-bookmarking” events in cellular development (Kumar et al., 2021).

**2.4.2. SHP in immunity**—Specific roles of SHP in liver non-parenchymal cells have been described recently. FXR activation protects livers from ischemia/reperfusion injury (IRI) by up-regulating SHP in Kupffer cells (KCs) to inhibit the pro-inflammatory responses (Jin et al., 2020). SHP knockdown increases hepatic IRI in myeloid glycogen synthase kinase 3 $\beta$  (*Gsk3 $\beta$* ) knockout mice, suggesting a negative role of SHP in regulating innate immunity (Zhou et al., 2018). SHP overexpression can attenuate platelet-derived growth factor-BB (PDGF-BB)-stimulated activation of hepatic stellate cells (HSCs) *in vitro* (Ma et al., 2020), and a SHP agonist, ISO-COOH, attenuates HSCs trans-differentiation and ECM deposition *in vitro* and shows anti-fibrotic activity in carbon tetrachloride (CCl<sub>4</sub>)- or  $\alpha$ -naphthyl-isothiocyanate (ANIT)-induced liver fibrosis in mice (Cipriani et al., 2017).

Other findings also support the emerging roles of SHP in immunity. For instance, the expression and activity of SHP within macrophages can alter T cell fate (Cipriani et al., 2017). SHP blocks the transcription of type I interferon (IFN) and serves as a potent negative regulator of the virus-mediated type I IFN signaling (J. H. Kim et al., 2019). SHP is a transcriptional target and repressor of LRH-1; the latter is the transcriptional regulator of intestinal glucocorticoid (GC) synthesis; the SHP/LRH-1 axis regulates virus-induced intestinal GC synthesis to maintain intestinal immune homeostasis (Huang et al., 2018).

**2.4.3. SHP in autophagy**—SHP regulates autophagy. FXR acts early, but SHP acts relatively late after feeding to epigenetically sustain postprandial inhibition of autophagy via a FGF19-SHP-LSD1 axis (Byun et al., 2017). Both global and hepatocyte-specific double knockout of FXR and SHP have a beneficial impact on glucose and fatty acid metabolism in aged mice, as shown by lower hepatic triglyceride accumulation, improved glucose/insulin

tolerance, and accelerated fatty acid use, which are associated with enhanced expression of fatty acid metabolism and autophagy-machinery genes (Kim et al., 2017).

**2.4.4. SHP in hepatotoxicity and endoplasmic reticulum (ER) stress**—SHP participates in the circadian regulation of cytochrome P450 (CYP) enzymes, thereby impacting xenobiotic metabolism and drug-induced hepatotoxicity (T. Zhang et al., 2018). Indeed, hepatocyte SHP deficiency protects mice from acetaminophen APAP-induced liver injury (Y. H. Kim et al., 2018).

SHP interacts with and regulates the protein stability of the spliced form of X-box-binding protein 1 (XBP1s) to govern ER homeostasis (Sun et al., 2019). It has been demonstrated that FXR/SHP signaling activates XBP1s expression, and hepatic XBP1s expression is reduced in FXR- and SHP-null mice (X. Liu et al., 2018).

### 3. LncRNAs and SHP

It is well-established that SHP is a downstream target gene of FXR that activates SHP transcription to restrain bile acid synthesis and maintain the homeostasis of bile acid metabolism (Kim et al., 2017). SHP expression is rhythmically controlled by NPAS2, CLOCK-BMAL1, and LRH-1 (Lee et al., 2015; Oiwa et al., 2007). The reciprocal regulation between NRs and ncRNAs has emerged as essential mechanisms influencing diverse biological processes (Mahpour and Mullen, 2021; Wu et al., 2021). SHP inhibits the expression of several miRNAs, including miR-433, miR-127, miR-34a, and miR-200c, conforming to its general function of performing transcriptional repression (Song et al., 2017b). Intriguingly, it is notable that miR-433 plays an inhibitory role in liver cancer cell migration (Mansini et al., 2018; Yang et al., 2013), opposing SHP's tumor suppression function. On the other hand, SHP is targeted by miR-142-3p in the regulation of cholestasis (Pan et al., 2017). Despite these findings, little is known about the crosstalk between lncRNAs and SHP. Several studies shed light on this in recent years.

#### 3.1. MEG3 and SHP

Maternally expressed gene 3 (MEG3) is an imprinted gene encoding a lncRNA expressed in many normal tissues, and functions as a tumor suppressor (Al-Rugeebah et al., 2019; Zhou et al., 2012). MEG3 is required for embryonic development, as *Meg3* knockout mice die prematurely. MEG3 expression is frequently lost in human cancers, possibly due to gene deletion and promoter methylation. Re-expression of MEG3 inhibits proliferation, induces apoptosis, and suppresses anchorage-independent growth of human tumor cells. MEG3 expression is frequently down-regulated in human HCC due to the methylation of *DLK1-MEG3* locus on human chromosome 14q32 which encodes a cluster of metastasis-suppressive miRNAs predominantly regulated by DNA methylation (Anwar et al., 2012; Oshima et al., 2019). MEG3 also inhibits the growth of human liver cancer stem cells by reducing the activity of telomerase (Jiang et al., 2020).

MEG3 expression is down-regulated in murine and human fibrotic livers, which might be ascribed to the hypermethylation of gene promoter. Indeed, lncRNA HOX antisense intergenic RNA (HOTAIR) promotes the accumulation of polycomb repressive complex 2



(PRC2) and H3K27 trimethylation at the MEG3 promoter in LX-2 cells (a human HSC cell line) (Bian et al., 2017). MEG3 is a target gene of miR-212 and inhibits hedgehog-mediated epithelial-mesenchymal transition (EMT) in liver fibrosis (Yu et al., 2018). MEG3 overexpression inhibits HSC proliferation by activating the p53/caspase-3 signaling pathway (He et al., 2014). These findings suggest that MEG3 plays an inhibitory function in liver fibrosis.

Knockdown of MEG3 expression causes senescence in hepatic endothelial cells in diet-induced obese mice, potentiating obesity-induced insulin resistance and impairing glucose homeostasis (Cheng et al., 2021). However, hepatic expression of MEG3 is increased (about 2-fold) in patients with NAFD or nonalcoholic steatohepatitis (NASH), and obese mice, likely due to a compensatory regulation and suggesting a protective role of MEG3 in metabolic disorders (Cheng et al., 2021). Interestingly, another study shows that hepatic MEG3 is downregulated in murine NAFLD models and can bind to and antagonize the function of miR-21 to increase the expression of low-density lipoprotein receptor-related protein 6 (LRP6), a gene target of miR-21; this study also demonstrates a protective role of MEG3 in the pathogenesis of NAFLD (Huang et al., 2019). Nevertheless, MEG3 expression is up-regulated in the livers of ethanol-fed mice and induced by ethanol in AML-12 cells (a hepatocyte cell line) (Wang et al., 2018). The knockdown of MEG3 expression inhibits ethanol-induced steatosis and apoptosis and impairs the expression of NOD-like receptor family CARD domain containing 5 (NLRC5), a critical regulator of immune responses, in AML-12 cells; moreover, MEG3 is proposed as an endogenous competing lncRNA for miR-let-7c-5p that targets NLRC5. The MEG3/miR-let-7c-5p/NLRC5 axis might contribute to ethanol-induced liver injury but needs further investigation.

Forced overexpression of MEG3 in mouse livers causes rapid SHP mRNA decay, resulting in increased *Cyp7a1* and *Cyp8b1* expression, the disruption of bile acid homeostasis, and cholestatic liver injury (Zhang et al., 2017). There are multiple predicted RNA-binding protein polypyrimidine tract-binding protein 1 (PTBP1)-binding sites within the coding sequence and 3'-UTR of SHP mRNA; MEG3 interacts with PTBP1 and facilitates PTPB1 binding to SHP mRNA, which promotes SHP mRNA decay (Zhang et al., 2017). Despite the intramolecular interaction, how PTPB1 links the RNA-degradation machinery to SHP mRNA is still elusive. In fact, there are reports showing that PTBP1 protects transcripts from nonsense-mediated mRNA decay (Fritz et al., 2020; Ge et al., 2016). On the other hand, MEG3 RNA is dramatically elevated in the livers of *Shp* knockout mice and that SHP inhibits MEG3 expression by repressing cAMP response element-binding protein (CREB)-mediated transactivation of *Meg3* gene promoter (Zhang et al., 2017). Thus, MEG3 and SHP constitute a feedback loop of reciprocal inhibition to maintain bile acid homeostasis, suggesting that MEG3 could be a therapeutic target to manage bile acid homeostasis and improve cholestatic liver injury.

### 3.2. H19 and SHP

H19 imprinted maternally expressed transcript (H19) is one of the earliest described lncRNAs (Mahpour and Mullen, 2021). The *H19* locus is located on chromosome 11p15.5 in humans and on chromosome 7 in mice. It plays a pivotal role in embryonic development

and growth control (Gabory et al., 2010; Monnier et al., 2013). The *H19* gene cluster contains the insulin-like growth factor 2 (*IGF2*) gene located 90 kb upstream of *H19*. There is an intergenic differentially methylated region (DMR) upstream of *IGF2*, an imprinting control region (ICR) between *IGF2* and *H19*, and an enhancer downstream of *H19* (Thorvaldsen et al., 1998). The methylation status and the alternative binding of the enhancer to DMR or ICR determine the expression of these two imprinting genes, *IGF2* and *H19*. *H19* is expressed from the maternal allele, and *IGF2* is expressed from the paternal allele (Kurukuti et al., 2006; Pope et al., 2017). *H19* is highly expressed in embryonic tissues and the placenta. Its expression is drastically attenuated after birth in most tissues except for the skeletal muscle, cardiac muscle, and cartilage (Zeira et al., 2015).

The role of *H19* is elucidated by its importance in diverse liver pathophysiology, including NAFLD (C. Liu et al., 2018; J. Liu et al., 2019; H. Wang et al., 2020; N. Zhang et al., 2018), cholestasis (Li et al., 2020, 2018, 2017; R. Liu et al., 2019; Song et al., 2017a; Xiao et al., 2019; L. Zhang et al., 2019; Zhang et al., 2016), fibrosis (Z. M. Wang et al., 2020; Xiao et al., 2019; J. J. Yang et al., 2016; Yang et al., 2018; Zhu et al., 2019), acute liver failure (Jin et al., 2018), hepatitis B viral (HBV) infection (Li et al., 2019; Y. Liu et al., 2019), and HCC (Matouk et al., 2007; Wei et al., 2019; Zhou et al., 2019). The level of specific lncRNAs in circulation can be useful biomarkers for the diagnosis and prognosis of liver disease. Indeed, high plasma *H19* is associated with poor disease-free survival in patients with HCC and after curative hepatectomy (Yang et al., 2015).

*H19* expression is reactivated and remarkably induced in adult human livers with cholestatic fibrosis and cirrhosis (Zhang et al., 2016). Bile duct ligation (BDL)-induced cholestasis activates hepatic *H19* expression, which enhances intrahepatic inflammation, HSC activation, ductular reaction, and cholestatic liver fibrosis in mice; (Song et al., 2017a). BDL-induced cholestasis also reduces SHP mRNA expression, which can be blunted by *H19* overexpression (Song et al., 2017a). Despite this, it seems that SHP and *H19* antagonize the expression of each other (Li et al., 2018; Zhang et al., 2016). In mouse livers, forced overexpression of the anti-apoptotic protein BCL2 induces SHP protein degradation, leading to the re-expression of *H19* due to the loss of SHP's transcriptional repression function (Zhang et al., 2016). On the other hand, via exosomal transportation, cholangiocyte-derived *H19* suppresses SHP expression in hepatocytes at both transcriptional and post-transcriptional levels (Li et al., 2018). Besides, cholangiocyte-derived *H19* promotes the activation and proliferation of HSCs, which results in cholestatic liver injury in BDL and *Mdr2*<sup>-/-</sup> mice modeling biliary fibrosis (R. Liu et al., 2019). The inhibitory function of SHP in HSC activation has been shown *in vitro* (Cipriani et al., 2017; Ma et al., 2020). It is possible that cholangiocytes- or other types of liver cells-derived *H19* also regulate SHP's function in HSCs. It is obvious that intercellular communications are required for *H19* and SHP to cooperatively control bile acid homeostasis and regulate the severity of cholestatic liver injury. It is noteworthy that a recent study using the RNAscope assay, a novel *in situ* RNA analysis platform, shows that *H19* RNA is localized in HNF4α<sup>+</sup> periportal hepatocytes, SOX9<sup>+</sup> ductal progenitor cells, and F4/80<sup>+</sup> KCs but not in CK19<sup>+</sup> cholangiocytes and desmin<sup>+</sup> HSCs in cholestatic livers (Jiang et al., 2018). In contrast, using immuno-purification or laser-capture microdissection, *H19* RNA is shown to be



predominantly expressed in cholangiocytes, about 100-fold higher than hepatocytes, HSCs, and KCs (R. Liu et al., 2019).

When expressed in the same cell type, how SHP and H19 mechanistically inhibit the expression of each other at the molecular level is still elusive. The upstream signaling pathways that activate H19 expression are still not fully understood (Chiang, 2017). It is known that H19 expression is regulated by multiple TFs, such as forkhead box A1 (FOXA1), hypoxia-inducible factor 1 subunit alpha (HIF1 $\alpha$ ), Paxillin (PXN), E2F transcription factor 1 (E2F1), SRY-sex determining region Y- box 2 (SOX2) (Yang et al., 2020). Defining the functional connections between these TFs and H19/SHP would help address the above question in various liver diseases. Interestingly, similar to MEG3, H19 likewise interacts with PTBP1 to modulate hepatic lipogenesis and glucose metabolism (C. Liu et al., 2018). However, H19 intriguingly decreases PTPB1 expression in cholestasis (L. Zhang et al., 2019). It is unknown whether this interaction can also accelerate SHP mRNA decay the same as MEG3 (Zhang et al., 2017).

#### 4. Conclusions and Perspectives

The above critical roles and molecular connections of SHP in liver physiology and pathophysiology are summarized (Figure 1). Recent studies have demonstrated the association of lncRNAs with SHP expression in liver disorders (Chiang, 2017). Only a few studies reveal SHP regulation of lncRNAs, and the regulatory mechanism is confined to SHP's canonical function as a transcriptional repressor (Zhang et al., 2017, 2016). Because SHP lacks a DNA-binding domain, it is reasonable to postulate that SHP interacts with other TFs to regulate lncRNA expression. Indeed, SHP physically interacts with CREB to inhibit CREB-dependent hepatic gluconeogenesis (Lee et al., 2010), which underlies the molecular basis of SHP inhibition of *Meg3*. Defining the genome landscape of DNA association regions for SHP and other TFs and distinguishing their colocalized genomic loci will be informative to reveal more SHP-regulated lncRNAs.

SHP might indirectly regulate lncRNA expression through epigenetic mechanisms because it has been reported that SHP can impair estrogen-related receptor gamma (ERR $\gamma$ )-mediated transcription of DNA (cytosine-5)-methyltransferase 1 (DNMT1) that silences gene expression through CpG island methylation, pointing to the potential role of SHP in gene transactivation (Zhang and Wang, 2011).

The pathophysiological significance of lncRNAs has been increasingly recognized (Pielok and Marycz, 2020). For instance, lncRNAs AK054921 and AK128652 are potential biomarkers to predict the progression of alcohol-associated liver disease (ALD) in individuals with excessive alcohol consumption; they are predictors of survival in patients with cirrhosis (Yang et al., 2017). The serum level of MEG3 is decreased in patients with chronic hepatitis B and negatively correlates with the severity of liver fibrosis (Chen et al., 2019). Multiple approaches have been proposed to regulate lncRNA expression to manage liver diseases, including RNA interference to target lncRNA, induction of lncRNA expression with agonistic or antagonistic compounds, manipulation of extracellular vesicles (EVs) (Sato et al., 2020). Studies to deorphanize SHP and further dissect the ncRNA-SHP

network are warranted for developing lncRNA- or SHP-based novel diagnostics, therapeutics, and prevention strategies for liver disease.

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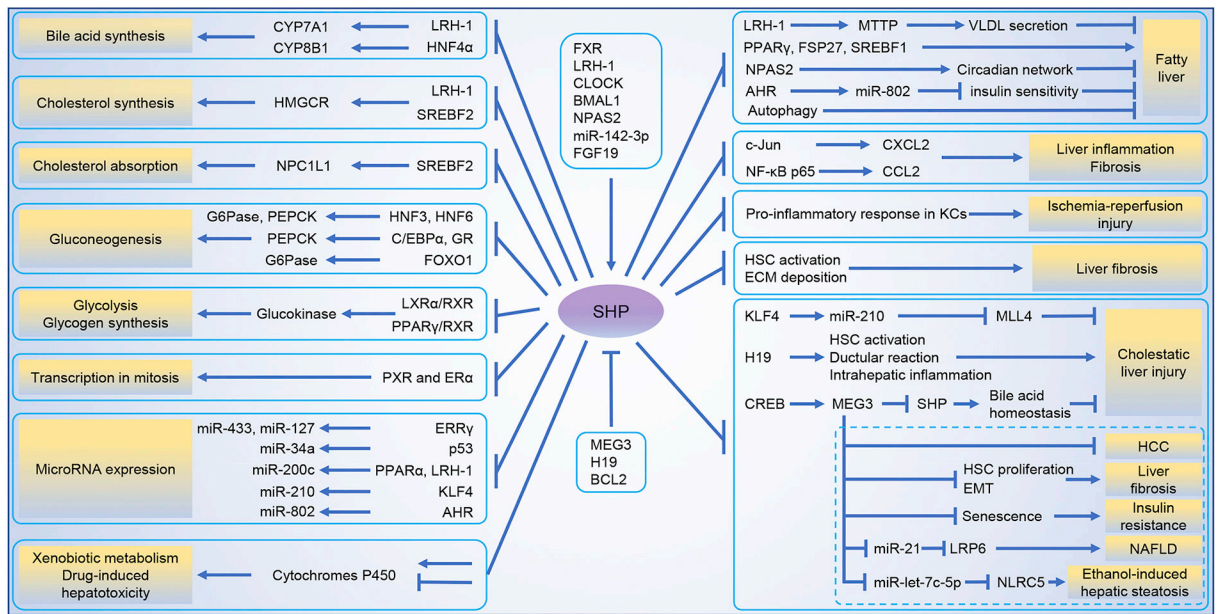
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**Figure 1.**  
The critical roles and molecular connections of SHP in liver physiology and pathophysiology presented in this review.