MicroRNAs as Important Players in Host-hepatitis B Virus Interactions

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Abstract

Hepatitis B virus (HBV) infection, a major public health problem, causes acute and chronic hepatitis that is often complicated by liver cirrhosis and hepatocellular carcinoma. The pathogenic mechanisms of HBV-related liver disease are not well understood, and the current licensed therapies are not effective in permanently clearing virus from the circulation. In recent years, the role of micro-ribonucleic acids (miRNAs) in HBV infection has attracted great interest. Cellular miRNAs can influence HBV replication directly by binding to HBV transcripts and indirectly by targeting cellular factors relevant to the HBV life cycle. They are also involved in the regulation of cellular genes and signaling pathways that have critical roles in HBV pathogenesis. HBV infection, in turn, can trigger changes in cellular miRNA expression that are associated with distinctive miRNA expression profiles depending on the phase of liver disease. These alterations in miRNA expression have been linked to disease progression and hepatocarcinogenesis. We provide here an up to date review regarding the field of miRNAs and HBV interplay and highlight the potential utility of miRNAs as diagnostic biomarkers and therapeutic targets for the management of HBV-related liver disease.

Introduction

Hepatitis B virus (HBV) is a prototype member of the Hepadnaviridae family and one of most common human pathogens worldwide. Despite the availability of an effective prophylactic vaccine for nearly three decades, HBV remains the cause of a number of important public health problems.1 HBV is transmitted among humans by contact with the blood or other bodily fluids of an infected person and is commonly acquired through perinatal, horizontal, sexual, and parenteral/percutaneous transmission. The clinical manifestations of HBV infection range from acute to fulminant chronic hepatitis to various forms of chronic infection, which may evolve to liver cirrhosis and hepatocellular carcinoma (HCC).2 According to World Health Organization estimates, more than 240 million people worldwide have chronic hepatitis B, and more than 780,000 people die annually due to the acute or chronic complications of hepatitis B.3 At present, two types of antiviral drugs are approved for the treatment of chronic hepatitis B, including conventional or pegylated interferon alpha (IFN-α or PEG-IFN-α) and nucleos(t)ide analogs.4 IFN-α or PEG-IFN-α have significant toxicity. Nucleos(t)ide analogs have limited success in achieving sustained virological response and are susceptible to drug resistance.4,5 Growing evidence has highlighted the importance of investigating the interactions between HBV and the host in order to understand better the mechanisms of HBV pathogenesis and to develop novel and improved anti-HBV therapeutic strategies.6,7

Recent findings about the role of micro-ribonucleic acids (miRNAs/miRs) in various aspects of HBV-host interactions have added another dimension to our understanding of HBV pathogenesis. MiRNAs represent a large class of highly conserved noncoding RNAs of ~22 nucleotides (nt) in length, which modulate gene expression at the post-transcriptional level. They bind to the 3′-untranslated region (3′-UTR) of target messenger RNAs (mRNAs), resulting in gene silencing through translational repression or mRNA degradation.8 First discovered in the nematode Caenorhabditis elegans, miRNAs have been identified in all multicellular eukaryotes and some viruses.9-11 MiRNAs modulate HBV replication and host responses. Therefore, exploring the function of miRNAs and...
their application in therapeutics and diagnostics has become an emerging area of interest in the field of HBV research. In the current review, we will describe the current knowledge regarding the biological relevance of miRNAs in the context of HBV infection. We will also discuss the potential value of miRNAs as diagnostic biomarkers and therapeutic targets for HBV-related liver disease.

**miRNAs biogenesis and functions**

The biogenesis of miRNAs involves numerous critical steps that occur in both the nucleus and cytoplasm. The genes encoding miRNAs can be mono- or polycistrionic and are frequently located in intergenic regions of genomes and introns of protein-coding or noncoding genes.12,13 Generally, miRNA genes are transcribed by RNA polymerase II (Pol II) as large primary transcripts (pri-miRNAs) that contain a stem-loop structure of ~80 nt.14 Pri-miRNAs are subsequently cleaved by the RNaseIII-like enzyme Drosha together with its binding partner DiGeorge syndrome critical region 8 (DGCR8), to produce the ~60-70 nt precursor miRNAs (pre-miRNAs).15 These are transported into the cytoplasm by Exportin-5 via a Ran-GTP-dependent mechanism.15,16 Once in the cytoplasm, pre-miRNAs are processed by Dicer, another RNaseIII-like enzyme, and transactiivation-response RNA-binding protein (TRBP) to generate the ~22 nt duplexes comprising the mature miRNAs and the complementary fragments miRNA*.17 Mature miRNAs are connected to the RNA-induced silencing complex (RISC), whereas miRNA* are rapidly degraded.18 TRBP, Argonauta 2 protein (AGO2), and Dicer are involved in the formation of the RISC loading complex (RLC), which can facilitate the binding of the mature miRNAs to RISC.19,20 Finally, mature miRNAs guide RISC to complementary sites within the target mRNAs to execute the post-transcriptional regulatory activity. In the case of perfect sequence complementarity between target mRNAs and miRNAs, mRNAs are degraded by RISC, whereas in the case of partial sequence complementarity, a repression of mRNA translation occurs.21,22 Evidence also indicates that miRNA-bound transcripts are sequestered into processing bodies (P-bodies), where they are maintained in a silenced state.23 Thus, P-bodies serve as a site of temporary storage before mRNA degradation or translational inhibition.23

The human genome encodes 2,565 miRNAs (miRBase ver. 21; http://www.mirbase.org/, released in June 2014). Each miRNA can regulate hundreds of different mRNAs, and conversely, a single miRNA can be targeted by several miRNAs. Bioinformatic analyses have indicated that more than 30% of human genes are under miRNA-mediated regulation.24 Accordingly, cellular miRNAs play an important role in several biological and physiological processes, such as cell differentiation, proliferation, metabolism, apoptosis, developmental timing, and immune responses.25 Deregulation of their expression and function is also involved in various diseases, especially cancers.26,27 In viral infections, cellular miRNAs can positively or negatively influence virus replication by regulating the expression of viral genes and/or cellular factors relevant to the course of virus-induced disease.28 At the same time, viruses can alter cellular miRNA expression. In fact, viruses are equipped with complex machinery to exploit and manipulate the host pathways to establish an environment favorable for their persistence.29 It is not surprising, therefore, that the miRNA pathway can be used to do this, either by encoding their own miRNAs or encoding molecules that inhibit or stimulate cellular miRNA expression.30

**miRNAs in HBV replication**

HBV has a relaxed circular, partially double-stranded (RC-DNA) genome containing four overlapping open reading frames (ORF).31 The preS/S ORF encodes three viral surface proteins [large hepatitis B surface antigen (LHBsAg), middle HBsAg (mHBsAg), and small HBsAg (sHBsAg)], the preC/C ORF encodes the core protein (hepatitis B core antigen (HBCAg)) and the soluble e protein (hepatitis B early antigen (HBeAg)), the X ORF encodes the hepatitis B X protein (HBx), and the Pol ORF encodes the viral polymerase that possesses DNA polymerase and reverse transcriptase activities.31 After infecting hepatocytes, the HBV genome is released into the nucleus and converted to covalently closed circular DNA (cccDNA), which serves as a template for the transcription of all viral transcripts, including pregenomic RNA (pgRNA) and subgenomic RNAs (pre-S, S and X mRNAs).32 The transcription of viral transcripts is regulated by four distinct viral promoters that are under the control of two regulators, designated enhancers I and II.33 In addition, a variety of liver-enriched transcription factors and nuclear receptors have been shown to bind to HBV promoter/enhancer elements and to be critical for the regulation of HBV transcription.33,34 Viral miRNAs encoded by HBV have not been identified, but one putative HBV-encoded pre-miRNA was predicted using computational approaches.35 Nevertheless, numerous cellular miRNAs have emerged that either repress or promote HBV replication by direct interaction with HBV transcripts or indirectly by targeting crucial cellular factors relevant to HBV life cycle (Fig. 1).

**miRNAs suppressing HBV replication**

The first attempt to search for miRNAs that directly target HBV transcripts was made by Zhang et al., using a miRNA-loss-of-function approach.36 A total of 328 human miRNAs were individually knocked-down in HepG2.2.15 cells that are designed to support the HBV life cycle.37 Among these, miR-199a-3p and miR-210 efficiently reduced HBsAg expression and HBV replication. Bioinformatics analysis revealed that miR-199a-3p and miR-210 inhibited HBV by directly targeting the HBsAg encoded region and the pre-S1 region of the HBV genome, respectively.38 The ability to affect HBsAg expression was also demonstrated for miR-125a-5p, which binds to HBsAg mRNA and inhibits its translation.39 Another study revealed a self-inhibitory feedback loop where HBV, through HBx, increased the expression of miR-125a-5p and subsequently interfered with HBsAg expression.40 Furthermore, extensive studies reported a remarkable decrease in HBV replication when the expression of miR-122, the most abundant liver-specific miRNA, was upregulated in both cell lines and liver tissues.39,41 These studies proposed several mechanisms underlying miR-122-mediated suppression of HBV replication. Chen et al. found that miR-122 binds to a highly conserved sequence of HBV pgRNA, which is a bicistronic mRNA encoding the viral polymerase and core protein, resulting in a decrease in HBV core-associated DNA level.35 Qiu et al. suggested that miR-122 inhibited HBV replication through increasing expression of cellular heme oxygenase-1 (HO-1), a cytoprotective enzyme that decreases HBV cccDNA levels both in vitro and in vivo.42 Another regulatory mechanism of
miR-122 involved cyclin G1-modulated p53 activity. Cyclin G1 specifically interacted with p53, and this interaction blocks the binding of p53 to HBV enhancers, subsequently abrogating p53-mediated inhibition of HBV transcription. However, cyclin G1 was targeted by miR-122, thereby promoting the anti-HBV activity of p53. Reduced HBV replication has been also observed in presence of high miR-1231 levels in HBV-transfected HepG2 cells. Extensive analysis revealed that miR-1231 targeted HBV core and HBx sequences, resulting in decreased expression of HBV core protein with no reduction in HBx protein. Other viral sequences critical for HBV replication, including the coding region for HBV polymerase and the overlapping region between HBV polymerase and HBx, were shown as potential targets for miR-15a/miR-16-1 cluster. The antiviral effect of miR-15a/miR-16-1 was validated in vitro, showing a negative correlation between the expression of this cluster and HBV replication in HBV-transfected HepG2 cells.

Besides miRNAs targeting HBV transcripts, other miRNAs elicit their antiviral activity by targeting a positive regulator of HBV. The peroxisome proliferator-activated receptor-α (PPARα), which binds and transactivates HBV promoters, was described as a target of miR-141. Tranfection of synthetic miR-141 in HBV-transfected HepG2 cells suppressed PPARα expression, leading to reduced HBV transcription. The role of the CCAAT enhancer-binding protein (C/EBP) in transactivation of HBV enhancer II, core, and S promoters was abolished by miR-155, which targets and downregulates C/EBP, thereby repressing HBV replication. Recently, it was reported that elevated miR-26a levels in hepatoma cells resulted in a marked decrease in HBV-DNA and protein expression. Subsequent analysis demonstrated that miR-26b inhibited the expression of cysteine- and histidine-rich domain containing 1 (CHORDC1), which functions as a positive regulator of HBV enhancer/promoter activities. Targeted inhibition by miR-125b of another cellular factor, the sodium channel nonvoltage-gated 1 alpha (SCNN1A), repressed HBV protein expression. However, the mechanism by which SCNN1A affects HBV replication is not well-known and needs further investigation.

miRNAs promoting HBV replication

For miRNAs that promote HBV replication, it appears they share a common pattern of targeting negative cellular regulators of HBV replication. HBx-interacting protein (HBXIP) was originally isolated as a human protein that binds to HBx protein and may reduce HBV replication by interacting with a domain necessary for HBx transactivation. However, HBXIP was identified as a putative target of miR-501, and its expression was inversely correlated with miR-501 expression in HepG2.2.15 cells. Moreover, downregulation of miR-501 significantly inhibited HBV-DNA replication, and HBXIP knockdown rescued the inhibition of HBV with miR-501 loss in HepG2.2.15 cells, suggesting that miR-501 enhanced HBV replication by targeting HBXIP.
also identified between miR-372/373 and nuclear factor I/B (NFIB), a transcription factor that downregulates HBV enhancer I and core promoter activities. High expression of miRs-372/373 reduced endogenous NFIB levels in HepG2 cells. Further analysis of the 3' UTR of NFIB mRNA revealed two predicted sites for miR-372/373. In addition, knockdown of NFIB in HepG2 cells resulted in increased HBV gene expression, whereas enhanced expression of miR-372/373 stimulated the production of HBV proteins. Taken together, these findings indicated that miR-372/373 can promote HBV expression through a pathway involving NFIB. Another negative regulator of HBV enhancer I activity, the hepatocyte nuclear factor 1α (HNF1α), was recently described as a mediator in miRNA promotion of HBV replication. HNF1α-mRNA was directly downregulated by miR-15b, resulting in transcriptional activation of HBV Enhancer I. However, it has been shown that increased expression of HBV proteins, especially HBx, resulted in downregulation of miR-15b expression in both HBV-producing cells and an HBV transgenic mouse model. This reciprocal regulation between miR-15b and HBV may help to control the level of HBV replication. Moreover, dysregulation of the estrogen pathway by miRNAs may be an important mechanism underlying the regulation of HBV replication. The estrogen pathway can reduce HBV replication by enhancing the expression of estrogen receptor alpha (ERα), which interacts with hepatocyte nuclear factor 4 alpha (HNF4α), and preventing HNF4α binding to the HBV enhancer I and activation of HBV transcription. For instance, miR-18a has been shown to repress ERα translation by binding to its mRNA, thus promoting HBV transcription.

Epigenetic modifications of HBV cccDNA, such as DNA methylation and deacetylation, play a pivotal role in the control of HBV replication by suppressing cccDNA transcription to viral mRNAs. Epi-miRNAs, including miR-1 and miR-152, have been recently implicated in the regulation of epigenetic modifications of HBV cccDNA. In a study by Zhang et al., miR-1 was shown to directly target histone deacetylases-4 (HDAC4), and transfection of miR-1 in HepG2 cells led to marked repression of histone deacetylases-4 (HDAC4) and enhanced HBV transcription. Furthermore, cotransfection of an HDAC4 expression vector with miR-1 attenuated HBV mRNAs levels. These findings indicated that HDAC4 plays a significant role in the action of miR-1 on HBV replication. The modulation of HDAC4 expression by miR-1 may lead also to enhanced expression of farnesoid X receptor alpha (FXRα), resulting in a marked increase in HBV-DNA and proteins levels by enhancing transcriptional activity of the HBV core promoter. Regarding miR-152, its expression was shown to be inversely correlated with DNA methyltransferase (DNMT1) expression in liver cell lines. In silico predictions defined DNMT1 as a potential inhibitory target of miR-152. Consequently, the downregulation of DNMT1 resulted in a decrease of cccDNA methylation, subsequently enhancing HBV replication.

miRNAs in HBV-related liver disease

The clinical course of hepatitis B is dynamic and varies widely between patients from self-limited infection to acute hepatitis to chronic infection with a clinical presentation ranging from asymptomatic carrier state to severe expressions of disease, including active chronic hepatitis, liver cirrhosis, and HCC. Approximately 90–95% of immunocompetent individuals who acquire HBV infection in adulthood will clear the virus spontaneously, whereas the remaining (5–10%) develop chronic hepatitis. The rate of chronicity is higher in perinatal and early childhood infections (over 90% and 30%, respectively). Approximately 15–40% of HBV chronic carriers develop liver cirrhosis and HCC. Several host and viral mechanisms have been described to explain these diverse liver disease outcomes. There is accumulating evidence detailing the functions of miRNAs in HBV pathogenesis and identifying differentially expressed miRNAs and target genes in the different phases of liver disease. Some miRNAs have been shown to be altered by HBV, especially liver-specific miRNAs, contributing to liver damage and HCC development.

miRNAs in the chronicity of HBV infection

It is widely believed that ineffective immune responses play an important role in HBV persistence and disease chronicity. MiRNAs have been found to function as regulators of the immune responses against HBV (Table 1). Su et al. demonstrated that miR-155 enhances the expression of several IFN-inducible antiviral genes against HBV through direct suppression of the expression of suppressor of cytokine signaling 1 (SOCS1), and subsequently enhancing the Janus kinase/signal transducer and activator of transcription (JAK/STAT) signaling pathway. In contrast, miR-548 downregulates host antiviral responses by direct targeting IFN-α/IFN-β receptors. Interestingly, endogenous miR-548 levels are reduced during HBV infection, which may be a host mechanism to defend against HBV. In turn, HBV infection may modulate the expression of many miRNAs involved in immune responses. By comparing the expression of 1,008 miRNAs between HepG2.2.15 cells and parenteral hepatoma cells HepG2, Jiang et al. observed a differential expression of miRNAs related to toll-like receptor (TLR) pathways. The expression of seven miRNAs (miR-200b-3p, miR-148a-3p, miR-145-5p, miR-146b-5p, miR-200c-3p, miR-455-3p and miR-455-5p) was upregulated by 5-fold or greater in HepG2.2.15 cells compared to HepG2 cells, whereas the expression of eight miRNAs (from let-7 family) was downregulated by 5-fold or greater in HepG2.2.15 cells compared to HepG2 cells. Most upregulated miRNAs have been demonstrated to modify the efficiency of TLR signaling. In addition, repression of the let-7 family of miRNAs relieved interferon (IL)-6 and IL-10 mRNAs from negative posttranscriptional control in the TLR4 signaling pathway. This induced an inhibition of immune responses directed against HBV. These findings indicated that alteration of miRNAs related to the TLR pathway during HBV infection could play an important role in the prevention of HBV elimination by host innate immunity. Furthermore, it has been reported that HBV infection promoted the transcriptional activity of miR-146a in HepG2.2.15 cells, which represses the production of type I interferon-induced antiviral factors, particularly STAT1, and results in interferon resistance. These observations revealed an important role for miR-146a in HBV immunopathogenesis. Another study analyzing the modified expression profiles of miRNAs in a stable HBV-expressing cell line revealed that upregulation of miR-181a might participate in HBV persistence through inhibition of the human leukocyte antigen A (HLA-A)-dependent HBV antigen presentation. Recently, Momeni et al. showed that expression of miR-1, miR-21, and miR-125a in peripheral blood immune cells was significantly increased in patients with chronic HBV infection compared to healthy controls and that ectopic expression of these miRNAs was responsible for it...
impaired immune responses in chronic HBV carriers. However, the role of these miRNAs in persistent HBV infection remains elusive and still awaits further investigation.

**miRNAs in HBV-related liver fibrosis and cirrhosis**

Long term persistence of HBV infection can result in the development of liver inflammation and injury. HBV itself is considered to be a noncytopathic virus, and it is usually accepted that the process of destruction of HBV-infected cells is due to cell-mediated immune responses. Persistent inflammation has been shown to be the driving force leading to liver fibrosis, generated by an imbalance between production of extracellular matrix (ECM) by hepatic stellate cells (HSCs). This imbalance results in an excessive accumulation of ECM and fibrogenesis. A number of studies have focused on the role of miRNAs in HBV-associated liver fibrosis/cirrhosis and unveiled the miRNA expression profiles during this phase (Table 1). Guo et al. identified several miRNAs that were differentially expressed during HSCs activation and showed that different signaling pathways, already reported to take part in HSCs activation, were modulated by miRNAs. Lakner et al. reported that miR-19b inhibited HSC-mediated fibrogenesis by regulating transforming growth factor-β (TGF-β) signaling in activated HSCs. In addition, Venugopal et al. showed that liver fibrosis may cause downregulation of miR-150 and miR-194 in HSCs and that their overexpression could repress HSCs activation. These miRNAs were observed to be downregulated in a feedback mechanism that occurs during the early phases of liver regeneration. Roderburg et al. applied a systematic approach to identify miRNAs involved in liver fibrosis using the well-established model of carbon tetrachloride (CCL4) treatment for hepatic...
fibrogenesis in mice. They identified a panel of miRNAs that were specifically regulated in fibrotic-livers from mice treated with CCI\textsubscript{4} compared to livers from control mice. Within those, the miR-29-family members (miR-29a/b/c) were significantly downregulated in CCI\textsubscript{4}-treated mice. Interestingly, decreased expression of miR-29 in these animals was significantly correlated with the degree of liver fibrosis. The same study showed that miR-29b was downregulated during the activation of HSCs in a TGF-\(\beta\)- and lipopolysaccharide/nuclear factor kappa B (NF-\(\kappa\)B)-dependent manner, whereas overexpression of miR-29b in murine HSCs resulted in downregulation of collagen expression. Another study reported that miR-33a levels in liver tissue from chronic HBV-infected patients increased significantly in a fibrosis progression manner. Interestingly, stimulation of HSCs with TGF-\(\beta\) led to a critical increase of miR-33a.

Hypersplenism is common in portal hypertension in patients with liver cirrhosis and results mostly from the increased phagocytosis and destruction of blood cells by splenic macrophages. To determine whether miRNA expression is altered in hypersplenism during HBV-related cirrhosis, Li et al. analyzed the entire miRNAome in macrophages from normal and portal hypertensive spleen samples. Compared to normal spleen samples, 99 miRNAs were found to be differentially expressed in spleenic macrophages associated to portal hypertension, with a remarkable overexpression of miR-615-3p. These findings suggest that miRNAs could be novel regulators in hypersplenism in patients with HBV-related cirrhosis.

### miRNAs in HBV-related HCC

Chronic HBV infection remains a major etiological factor of HCC worldwide, increasing the risk for HCC development by 100-fold compared to uninfected individuals. Many reports have shown that HCC develops through aberrant activation of various signaling pathways involved in cell proliferation, differentiation, and angiogenesis. However, the precise mechanisms underlying HBV-related HCC development remain unclear. It is now well-established that miRNAs play a critical role in HBV-associated hepatocarcinogenesis, as they can function as oncogenes or tumor suppressor genes depending on the cellular function of the target genes (Table 2). A study performed by Ura et al. showed that HBV infection induced specific sets of miRNAs during hepatocarcinogenesis, and their targets included genes involved in pathways related to cell proliferation, apoptosis, DNA damage, and signal transduction. Several research groups found that the liver-specific miR-122 was repressed in HBV-expressing HCC cell lines and in clinical tumor specimens. Suppression of miR-122 led to upregulation of its target N-myc downstream-regulated gene 3 (NDRG3), a tumor promoter, contributing to a malignant phenotype. In another study, low miR-122 levels promoted an overexpression of pituitary tumor-transforming gene 1 (PTTG1) binding factor (PBF), leading to increased transcriptional activity of PTTG and HCC cell growth and invasion. Furthermore, decreased miR-122 expression was linked to upregulation of cyclin G1, which promoted phosphorylation of Mdm-2, a repressor protein of p53, and led to HCC with unrestricted growth. A recent study showed that decreased miR-122 led to increased expression of its target UDP-N-acetylgalactosamine poly-N-acetylgalactosamyltransferase-10 (GALNT10), conferring a malignant phenotype to HCC cells by modifying EGFR O-glycosylation and activating the phosphatidylinositol 3-kinase (PI3K)/AKT signaling pathway. Given the functions of miR-122, investigators sought to explain its low expression in HBV-infected livers and found that miR-122 was downregulated by HBx. HBx is a multifunctional HBV-encoded protein that acts as a pleiotropic transactivator and modulates host gene expression by interacting with various cellular transcription factors and signaling pathways. Besides miR-122, several tumor suppressor-like miRNAs were shown to be suppressed by HBx. Decreased expression of miR-101 by HBx resulted in overexpression of DNA methyltransferase 3A (DNMT3A), promoting aberrant DNA hypermethylation of several tumor suppressor genes. In addition, under-expression of miR-101 contributed to increased levels of myeloid cell leukemia sequence 1 (Mcl-1), an antipototic member of the Bcl-2 family. Antitumorigenic function of miR-148a was repressed by HBx via inhibition of p53-mediated activation of miR-148a. This led to increased expression of hematopoietic pre-B cell leukemia transcription factor (HPLP) and subsequent activation of the mammalian target of rapamycin (mTOR) pathway, which plays a critical role in cancer cell growth. HBx also downregulated the let-7 family of miRNAs, widely viewed as potential growth suppressor miRNAs in many cancers. Particularly important is the ability of the HBx protein and its RNA to act synergistically to downregulate another tumor suppressor pathway involving the miR-15a/miR-16-1cluster, which contributes to the activation of the proto-oncogene c-Myc. Epigenetic modulation of miRNA expression could also be an important mechanism underlying HBV-mediated hepatocarcinogenesis. For example, HBx induces epigenetic repression of two tumor-suppressors, miR-132 and miR-205, through DNA methylation of its promoters. Chen et al. found in HBV-HCC tissues that increased miR-129-2 methylation was associated with subsequent miR-129-2 suppression. This suppression may be involved in HCC development through enhancing oncogenic SOX4 expression. Moreover, miR-152 was shown to be targeted and downregulated by HBx, causing an upregulation of DNMT1 activity and consequent DNA methylation of promoters of many tumor suppressor genes. Subsequent studies reported that miRNAs involved in the inhibition of cell proliferation (miR-15b, miR-22, miR-26a/b, miR-29c, miR-145, and mir199-a-3p) were downregulated in HBV-related HCC.

Several oncogene-like miRNAs have been found to be upregulated in HBV-related HCC. Connolly et al. found that miR-17-92 cluster and miR-21 were significantly increased in human HBV-positive HCC tissues and woodchuck hepatitis virus-positive HCCs. They also demonstrated that miR-17-92 and miR-21 contributed to a malignant phenotype by promoting cell proliferation and anchorage-independent growth. Oncogenic properties of the miR-17-92 cluster was shown to be related to a complex interaction network involving HBx protein and the transcription factors c-Myc and E2F1. Indeed, HBx transactivation of c-Myc led to induction of miR-17-92 expression by binding to its promoter. In turn, miR-17-92 inhibited E2F1 expression, causing defects in cell cycle control and HCC formation. Regarding miR-21, its expression was mediated by HBx-activation of the IL-6 pathway followed by activation of STAT3, a positive regulator of the miR-21 promoter. MIIR-21 enhanced cell proliferation by targeting tumor suppressor genes, including phosphatase and tensin homolog (PTEN) and programmed cell death protein-4 (PDCD4). Suppression of PTEN activity has been also...
attributed to miR-29a and miR-222, which are upregulated by HBx to promote HCC cell growth and migration. Another relevant miR-222 target is the p27 (kip1) protein, a cell cycle inhibitor and tumor suppressor. In addition, HBx can induce the expression of nuclear factor-kappa B (NF-κB), an activator of miR-143 expression in HBV-related HCC. Overexpression of miR-143 inhibited the expression of fibronectin type III domain containing 3B (FNDC3B), a regulator of cell motility, thus stimulating HCC metastasis. Another HBx-upregulated miRNA was miR-602, which was shown to inhibit the tumor suppressive function of Ras-associated domain family member 1A (RASSF1A). Notably, in chronic HBV hepatitis, liver cirrhosis to HCC, there is a progressive trend where an increase in miR-602 expression is correlated with a decrease in RASSF1A level, suggesting that miR-602 may promote HCC in HBV carriers at a very

Table 2. Summary of oncogene- and tumor suppressor-like miRNAs involved in HBV-related HCC

<table>
<thead>
<tr>
<th>miRNA</th>
<th>Expression</th>
<th>Target gene (s)</th>
<th>Functions</th>
</tr>
</thead>
<tbody>
<tr>
<td>Tumor suppressor-like miRNAs</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Let-7</td>
<td>Down</td>
<td>STAT3</td>
<td>Inhibits cell proliferation</td>
</tr>
<tr>
<td>miR-15a/miR-16-1</td>
<td>Down</td>
<td>Bcl-2, Cyclin D1</td>
<td>Inhibits cell proliferation</td>
</tr>
<tr>
<td>miR-15b</td>
<td>Down</td>
<td>Bcl-2</td>
<td>Inhibits cell proliferation</td>
</tr>
<tr>
<td>miR-22</td>
<td>Down</td>
<td>CDKN1A</td>
<td>Inhibits cell proliferation</td>
</tr>
<tr>
<td>miR-26a/c</td>
<td>Down</td>
<td>IL-6</td>
<td>Inhibits cell proliferation</td>
</tr>
<tr>
<td>miR-29c</td>
<td>Down</td>
<td>TNFAIP3</td>
<td>Inhibits cell proliferation and promotes apoptosis</td>
</tr>
<tr>
<td>miR-101</td>
<td>Down</td>
<td>DNMT3A</td>
<td>Downregulates DNA hypermethylation</td>
</tr>
<tr>
<td>miR-122</td>
<td>Down</td>
<td>NDRG3, GALNT10, Cyclin G1, PTTG1</td>
<td>Promotes cell apoptosis, inhibits cell proliferation and invasion</td>
</tr>
<tr>
<td>miR-129-2</td>
<td>Down</td>
<td>SOX4</td>
<td>Reduces cell proliferation and clonogenicity</td>
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<td>miR-132</td>
<td>Down</td>
<td>Akt</td>
<td>Inhibits cell proliferation</td>
</tr>
<tr>
<td>miR-145</td>
<td>Down</td>
<td>HDAC2, ADAM17</td>
<td>Inhibits cell proliferation and cell invasion</td>
</tr>
<tr>
<td>miR-148a</td>
<td>Down</td>
<td>HPIP, mTOR</td>
<td>Inhibits cell growth, epithelial-to-mesenchymal transition, invasion, and metastasis</td>
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<tr>
<td>miR-152</td>
<td>Down</td>
<td>DNMT1</td>
<td>Reduces global DNA hypermethylation</td>
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<tr>
<td>miR-199-a-3p</td>
<td>Down</td>
<td>mTOR, c-Met</td>
<td>Blocks G1-S transition of the cell cycle, thereby inhibiting cell growth, induces cell apoptosis, impairs invasion capability</td>
</tr>
<tr>
<td>miR-205</td>
<td>Down</td>
<td>E2F1</td>
<td>Inhibits cell proliferation</td>
</tr>
<tr>
<td>Oncogene-like miRNAs</td>
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<td></td>
<td></td>
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<tr>
<td>miR-17-92</td>
<td>Up</td>
<td>E2F1</td>
<td>Enhances cell growth and anchorage-independent growth</td>
</tr>
<tr>
<td>miR-18a</td>
<td>Up</td>
<td>ESR1</td>
<td>Suppresses ERα synthesis and stimulates cell proliferation</td>
</tr>
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<td>miR-21</td>
<td>Up</td>
<td>PTEN, PDCD4</td>
<td>Promotes cell growth and anchorage-independent growth</td>
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<tr>
<td>miR-27a</td>
<td>Up</td>
<td>Unknown</td>
<td>Enhances cell proliferation, activates cell cycling, Promotes migration and invasion</td>
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<tr>
<td>miR-29a</td>
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<td>PTEN</td>
<td>Promotes cell invasion/migration</td>
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<td>miR-143</td>
<td>Up</td>
<td>FNDC3B</td>
<td>Promotes cell invasion and tumor metastasis</td>
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<td>miR-155</td>
<td>Up</td>
<td>SOX6</td>
<td>Promotes cell growth</td>
</tr>
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<td>miR-181</td>
<td>Up</td>
<td>Fas, E2F5</td>
<td>Inhibits cell apoptosis and promotes tumor cell growth</td>
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<tr>
<td>miR-222</td>
<td>Up</td>
<td>p27 (kip1), PTEN</td>
<td>Promotes cell growth and migration</td>
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<tr>
<td>miR-224</td>
<td>Up</td>
<td>SMAD4</td>
<td>Promotes cell growth, migration and invasion</td>
</tr>
<tr>
<td>miR-602</td>
<td>Up</td>
<td>RASSF1A</td>
<td>Inhibits cell apoptosis and promotes cell growth</td>
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</tbody>
</table>

Denotes endogenous expression in HBV-infected liver tissues or HBV-infected cell lines. Down: downregulate; Up: upregulate; STAT1: signal transducer and activator of transcription 1; Fut2: fucosyltransferase 2; CDKN1A: cyclin-dependent kinase inhibitor 1A; IL-6: interleukin 6; TNFAIP3: tumor necrosis factor alpha-induced protein 3; DNMT3A: DNA methyltransferase 3A; NDRG3: N-myc downstream-regulated gene 3; GALNT10: UDP-N-acetyl-α-D-galactosamine polypeptide N-acetylgalactosaminytransferase-10; SOX4: sex-determining region Y box 4; HDAC2: histone deacetylase 2; IGF1R: insulin-like growth factor 1 receptor; ADAM17: ADAM metallopeptidase domain 17; HPIP: pre-B cell leukemia transcription factor-interacting protein; mTOR: mechanistic target of rapamycin; DNMT1: DNA methyltransferase 1; E2F1: Estrogen receptor 1; PTEN: phosphatase and tensin homolog; PDCD4: programmed cell death 4; FNDC3B: fibronectin type III domain containing 3B; SOCS1: suppressor of cytokine signaling 1; SOX6: Sex-determining region Y box 6; E2F5: E2F transcription factor 5; SMAD4: SMAD family member 4; RASSF1A: Ras-associated domain family member 1A.
miRNAs as diagnostic biomarkers of HBV-related liver disease

One of the major challenges in HBV research is identifying effective noninvasive biomarkers of HBV-related liver disease. Such markers can allow for rapid intervention and improved patient outcomes after curative treatment. The discovery of cell-free circulating miRNAs, which were able to mirror pathophysiological conditions in human bodily fluids, has opened new avenues for application of miRNAs as biomarkers for liver disease. Moreover, their accessibility and high stability in the circulatory system make them ideal biomarkers for the diagnosis of disease at an early, presymptomatic stage. Several studies have analyzed miRNA profiles in sera from HBV carriers in order to identify useful biomarkers (Table 3). Zhang et al. selected miRNA biomarkers from patients with HBV infection, patients with skeletal muscle disease, and healthy subjects. They showed that increased serum miR-122 levels correlated with histopathologic alterations and appeared earlier compared with alanine aminotransferase (ALT) levels, which remained within the reference intervals.113 Also, increased serum miRNA-122 levels were more specific for liver injury than for other organ damage.114 Other studies showed that serum miR-122 may allow for discrimination of HCC patients from healthy subjects but was not useful for distinguishing HCC cases from HBV carriers.114,115 Serum miR-223 together with miR-125b-5p have been reported as promising biomarkers of very early HBV-positive HCC, even in advanced stages of liver disease due to chronic hepatitis B.116 Other miRNAs have been suggested to have great diagnostic value. Serum miR-124 levels have been found to be significantly higher in HBV-infected patients with considerable liver necroinflammation than HBV-patients without or with mild necroinflammation.117 In addition, after antiviral therapy, serum miR-124 levels considerably declined, in association with histological improvement.117 Huang et al. showed that serum miR-29 levels were significantly higher in patients with minimal fibrosis than patients with liver cirrhosis (LC), suggesting that patients with minimal liver inflammation tended to express higher serum miR-29 levels than those with advanced inflammation.118 MiR-18a has been shown to have a significant diagnostic value for HBV-related HCC screening.119 MiR-18a yielded an area under the curve (AUC) of receiver operating characteristic (ROC) of 0.88 (specificity: 75%; sensitivity: 86%) in discriminating HBV-related HCC from healthy controls, and an AUC of ROC of 0.78 (specificity: 70%; sensitivity: 77%) in discriminating HBV-related HCC from chronic hepatitis B or HBV-related LC.119 A recent study by Xie et al. reported that miR-101 can serve as a potential biomarker to differentiate HBV-HCC from HBV-LC.120 Serum miR-101 is downregulated in HBV-HCC patients compared with HBV-LC patients. ROC analysis of serum miR-101 yielded an AUC of 0.98 (specificity: 96%; specificity: 90%) when differentiating between HBV-HCC and HBV-LC.120 Interestingly, serum miR-101 was superior to alpha-fetoprotein (AFP) for diagnosing HBV-HCC derived from HBV-LC. Combining serum miR-101 with AFP had no advantage over serum miR-101 alone for detecting HBV-HCC derived from HBV-LC.120 The frequent finding of dysregulated miRNAs in HBV-related HCC has sparked several research groups to conduct searches to identify a panel of serum miRNAs that may be potentially useful in the diagnosis of HBV-related HCC. Zou et al. identified a serum miRNA panel (miR-122, miR-192, miR-21, miR-223, miR-26a, miR-27a, and miR-801) that provided a high diagnostic accuracy of HBV-related HCC and was able to successfully distinguish HCC patients from chronic hepatitis and liver cirrhosis patients and healthy cases.121 Furthermore, Li et al. successfully identified 13 HBV-specific miRNAs that can clearly discriminate not only HBV cases from healthy controls and HCV cases but also HBV-positive HCC cases from controls and HBV cases.122 Six of these miRNAs (miR-1, miR-25, miR-92a, miR-206, miR-375, and let-7f) were significantly elevated in HCC cases, and two miRNAs, miR-375 and miR-92a, were previously identified as HBV-specific. In addition, the use of three of these miRNAs (let-7f, miR-25, and miR-375) as biomarkers, clearly separated HCC cases from controls, and miR-375 alone had an AUC of ROC of 0.96 (specificity: 96%; sensitivity: 100%) for HCC diagnosis.122

Interestingly, a study by Novellino et al. provided evidence that HBV subviral particles carry hepatocellular miRNAs to be released from HBV-infected cells into the blood. The experimental strategy consisted on the isolation of HBV subviral
anti-HBV drugs, including IFN to liver cirrhosis and HCC. Achieving this goal is done by quality of life and increase survival by preventing progression. The goal of hepatitis B treatment is to improve patients.

miRNA-based therapy for HBV-related liver disease

The goal of hepatitis B treatment is to improve patients’ quality of life and increase survival by preventing progression to liver cirrhosis and HCC. Achieving this goal is done by sustained suppression of HBV replication, which is accompanied by reduced histological activity of chronic hepatitis, leading to decreased risk of disease progression. The current anti-HBV drugs, including IFNα and nucleos(t)ide analogues, may effectively suppress HBV replication and induce remission of liver disease. However, the side effects of IFNα and the emergence of viral resistance during long-term therapy with nucleos(t)ide analogues make these therapeutic approaches far from satisfactory. Furthermore, after treatment withdrawal, most patients do not manifest durable control of infection and viral reactivation occurs. The persistence of intrahepatic cccDNA, the template of viral transcription, is the main cause of viral reactivation, given that IFNα and nucleos(t)ide analogues are unable to eradicate cccDNA from the liver. Therefore, developing novel antivirals that improve viral clearance with minimal side effects and potentially eradicate cccDNA is required for a cure or durable control of HBV infection.

The close relationship between miRNA expression and HBV-related liver disease has fueled an interest in exploiting miRNAs as therapeutic targets for the control and eradication of hepatitis B. Ely et al. have taken advantage of the natural RNA polymerase II-mediated transcriptional control of cellular miRNAs and designed RNA polymerase II promoter casquettes that transcribe anti-HBV primary miRNA (pri-miR)-122 and pri-miR-31 shuttles. These findings suggested that HBV subviral particles provide a new noninvasive tool for liver-specific miRNA profiling, allowing for the study of dynamic changes in hepatocellular miRNA expression during HBV infection in serum samples.

### Table 3. Clinical relevance of miRNAs in the diagnosis of HBV-related liver disease

<table>
<thead>
<tr>
<th>miRNA</th>
<th>Expression</th>
<th>Clinical relevance</th>
</tr>
</thead>
<tbody>
<tr>
<td>miR-18a</td>
<td>Up</td>
<td>Biomarker to detect HCC patients from healthy subjects and patients with chronic hepatitis or liver cirrhosis</td>
</tr>
<tr>
<td>miR-29</td>
<td>Down</td>
<td>Biomarker of severe liver necroinflammation and cirrhosis</td>
</tr>
<tr>
<td>miR-101</td>
<td>Up</td>
<td>Biomarker to differentiate HBV-HCC from HBV-liver cirrhosis</td>
</tr>
<tr>
<td>miR-122</td>
<td>Up</td>
<td>Biomarker of severe liver necroinflammation</td>
</tr>
<tr>
<td>miR-124</td>
<td>Up</td>
<td>Biomarker for considerable liver necroinflammation in patients with chronic hepatitis B, particularly in those with normal or mildly increased ALT level</td>
</tr>
<tr>
<td>miR-125b-5p and miR-223-3p</td>
<td>Up, Down</td>
<td>Biomarkers of HBV-positive HCC in very early, even at chronic hepatitis B stage of liver disease</td>
</tr>
<tr>
<td>miR-122, miR-192, miR-21, miR-223, miR-26a, miR-27a, and miR-801</td>
<td>Up</td>
<td>Biomarkers to detect HCC patients from those with chronic hepatitis, liver cirrhosis and healthy cases</td>
</tr>
<tr>
<td>let-7f, miR-25, and miR-375</td>
<td>Up</td>
<td>Biomarkers for HBV infection and HBV-related HCC</td>
</tr>
</tbody>
</table>

1Denotes serum miRNA level in patients with HBV-related HCC compared to patients with chronic hepatitis, liver cirrhosis or healthy controls.
2Denotes serum miRNA level in patients with moderate-to-severe liver necroinflammation compared to those with no or mild necroinflammation.

**Down:** downregulate; **Up:** upregulate
similar strategy, Chattopadhyay et al. developed linear expression cassettes that produced anti-HBV miRs shuttles. Silencing of HBV markers of replication was efficient (>75%) in cultured cells and in vivo. Furthermore, a knock down of approximately 95% HBV replication was attained in a hydrodynamic infection model. Together, these findings suggest that employing miRs shuttles is potentially valuable for treating HBV infection. However, besides antiviral efficiency, improvement of liver expression and efficient delivery of miRs shuttles is potentially important to limit nonspecific effects. In this context, Mowa et al. investigated the utility of the liver-specific murine transthyretin receptor (MTTR) Pol II promoter for expression of anti-HBV pri-miRs by incorporating MTTR promoter into the helper dependent adenoviral vectors (HDAds) carrying pri-miR expression cassettes. The results revealed that MTTR-expressed pri-miRs induced a knockdown of up to 94% of HBV replication in HBV transgenic mouse model and did not result in hepatotoxicity. Notably, HD Ads affected efficient delivery of pri-miRs targeting HBV. Another important property of HD Ads is their capacity for accommodating large transgene sequences. Therefore, as well as miRs activating cassettes, other anti-HBV elements may be incorporated into HD Ads to augment their therapeutic efficacy. Recent advances regarding the role of engineered gene-modifying enzymes such as transcription activator like effector nucleases (TALENs) and zinc finger nucleases in cleavage of HBV cccDNA have been impressive. These enzymes may be used in combination with HBV-targeting miRNAs activators to efficiently control or eradicate HBV infection. Another improvement in miRNA therapy is the use of lentiviral miRNA-based system (LVshHBS) expressing siRNAs targeting the HBsAg gene of HBV genome. LVshHBS significantly inhibited the HBsAg mRNA and protein levels in HepG2.2.15 cells, while HBsAg secretion into the culture supernatant was decreased by 70%. Also, in LVshHBS-transduced HepG2.2.15 cells, expression of genes involved in cell cycle and oncogenesis was downregulated, indicating that LVshHBS not only inhibited HBV replication but also inhibited the growth of HCC. Although these experimental studies have confirmed the capacity of miRNA-based antivirals to treat hepatitis B, adequate evaluation of their efficacy is required and further research is needed to determine their impact alone or in combination to other antiviral elements on HBV eradication.

Conclusions

In summary, this review adds to a growing body of evidence concerning the complex interactions between host-encoded miRNAs and HBV. MiRNAs are considered as important cellular regulatory molecules that profoundly modulate HBV genes expression. Their functions are mainly mediated by interacting with HBV transcripts, cellular genes, and signaling pathways that have a critical role in viral replication and pathogenesis. In turn, HBV modulates the expression of miRNAs in HBV-infected cells and promotes the development of liver disease and HCC. It is true that these findings regarding HBV-miRNA interactions have contributed to important progress in understanding HBV pathogenesis. However, further research is needed to clarify the mechanisms by which host miRNA expression is altered during HBV infection and the role of miRNA alterations in cellular functions and liver disease processes. Regarding clinical applications, altered expression profiles of cell-free circulating miRNAs in serum/plasma between the different stages of HBV-mediated liver disease have opened new insights into the utility of miRNAs as noninvasive biomarkers. This is particularly true in the diagnosis of liver inflammation and HCC at an early stage and to predict the risk of disease progression. Although a large number of miRNAs have been identified as promising biomarkers, it is only practical to use the most sensitive and specific ones with complementary functions in clinical settings. Additionally, it is very important to elucidate the mechanisms of how cell-free circulating miRNAs are changed in the serum/plasma of HBV-infected patients and whether these circulating miRNAs influence HBV pathogenesis. Understanding the role of altered miRNA expression either in serum or liver provides a strong basis for targeting miRNAs in the treatment of hepatitis B, and it is likely that miRNA-based therapies will be part of the therapeutic armamentarium against HBV in the future.

Conflict of interest

None

Author contributions

Review design (BK, SB), collection of data (BK), writing the manuscript (BK, SB), revising the article for important intellectual content (SB, HSA, SE).

References

Kitab B. et al.: MicroRNAs and HBV infection


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