



Published in final edited form as:

Gastroenterology. 2019 January ; 156(2): 311–324. doi:10.1053/j.gastro.2018.07.057.

Development of Direct-acting Antiviral and Host-targeting Agents for Treatment of HBV Infection

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Abstract

Hepatitis B virus (HBV) infection affects about 300 million people worldwide. Although antiviral therapies have improved the long-term outcomes, patients often require life-long treatment and there is no cure for HBV infection. New technologies can help us learn more about the pathogenesis of HBV infection and develop therapeutic agents to reduce its burden. We review recent advances in development of directing-acting antiviral and host-targeting agents, some of which have entered clinical trials. We also discuss strategies for unbiased high-throughput screens to identify compounds that inhibit HBV and for repurposing existing drugs.

Keywords

functional cure; DAA; drug; screening

Despite the availability of effective vaccine, hepatitis B virus (HBV) is a major public health threat, with about 300 million people chronically infected worldwide. These individuals are at high risk for developing liver cirrhosis and hepatocellular carcinoma (HCC)^{1, 2}. There are 2 classes of approved treatments for chronic HBV infection: nucleos(t)ide reverse transcriptase inhibitors (NRTIs), also known as nucleos(t)ide analogs (NUCs), and interferon alpha (IFNA). Both are effective but have limitations³. We review the latest strategies for curing HBV infection, the HBV life cycle, and potential drug targets. These include direct viral targets (by directing-acting antiviral agents) and host factors (by host-targeting agents) that are required for productive HBV infection. For a review of immune modulatory approaches, see XX (insert as new reference #3).

HBV Therapies and Goals

NRTIs target the reverse transcriptase activity of virus polymerase, limiting its replication. However, these drugs do not cure the infection, must be taken life long, and have risks of

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resistance and toxicity⁴. IFNA is the only approved treatment for HBV infection that has a distinct duration. IFNA increases the antiviral immune response, inhibits virus entry into cells, induces partial degradation of HBV covalently closed circular DNA (cccDNA), epigenetically suppresses cccDNA transcription, and inhibits post-transcription steps and virion secretion⁵. However, patients have a low rate of response to IFNA and its side effects are often difficult to tolerate⁴. Second-generation NRTIs, such as entecavir and tenofovir, potently suppress HBV replication but have little effect on the level and activity of cccDNA, which has a long half-life and can persist for decades in the liver despite suppression of viral replication³. This limitation necessitates prolonged (possibly indefinite) treatment with this class of anti-HBV drugs. Derivatives of tenofovir, such as prodrugs with improved pharmacological properties, have been developed and may reduce some side effects⁶. Despite these limitations, antiviral treatment can reverse liver fibrosis and even cirrhosis, prevent complications, and reduce though not eliminate the risk of HCC⁷.

Chronic HBV infection might be completely cured by inhibiting the virus replication intermediate—the cccDNA, and blocking reinfection. The goal is to achieve a functional cure—a state that resembles the natural recovery from HBV infection. This is defined as: persistently undetectable HBV DNA in serum, loss of HB surface antigen (HBsAg), preferably with seroconversion (development of anti-HBs), and normal liver enzymes and histology after stopping treatment, which is rarely achieved with treatments that do not directly target cccDNA¹.

HBV Life Cycle and Therapeutic Targets

HBV is an enveloped DNA virus that specifically targets human hepatocytes (Figure 2). HBV infects hepatocytes via the low-affinity interaction between determinant(s) of the viral envelope protein and heparan sulfate proteoglycans on hepatocytes. This interaction brings the preS1 protein in proximity to the solute carrier family 10 member 1 (SLC10A1 or NTCP); the resulting high-affinity interaction with the bile acid-binding pocket of NTCP facilitates virus entry^{8–10}. NTCP, responsible for the liver tropism of HBV and hepatitis D virus (HDV), is expressed only on the basolateral and sinusoidal membranes of hepatocytes. However, overexpression of human NTCP by mouse hepatocyte lines does not confer their susceptibility to HBV infection¹¹. Additionally, HepG2-NTCP clones that express similarly high levels of ectopic NTCP have varying efficiencies of HBV infection¹². These findings indicate that additional cell factors are required for efficient HBV infection.

The process of virus entry into hepatocytes is an attractive target for development of antiviral agents. HBV entry can be inhibited by heparin, small molecule compounds, and IFNA-induced factors that bind heparan sulfate proteoglycans in cell cultures^{8, 13, 14}. Myrcludex-B, a synthetic N-myristoylated lipopeptide derived from HBV preS1 protein, competes with the virus for binding to NTCP. This agent prevents HBV and HDV infection and in cells and animal models^{15, 16}. HBV enters hepatocytes via endocytosis. Caveolin and clathrin participate in HBV entry into HepaRG cells and immortalized primary human hepatocytes^{17, 18}. Viral particles are then transported from early to late endosomes, mediated by RAB5 and RAB7, which are probably required for nucleocapsid release from the

envelope¹⁹. Chemicals such as chlorpromazine specifically block clathrin-mediated endocytosis to inhibit HBV entry^{17, 18}.

After entry and uncoating, virus capsids migrate along microtubules to the nuclear periphery²⁰. With diameters of 36 nm (below the limit for transport by the nuclear pore complex)²¹, the HBV capsids pass through nuclear pores and enter the nuclei. The passage is mediated by interactions among the cellular transport receptors of the importin family²². The capsids are retained on the nuclear side of the nuclear pore complex by strong interaction with nucleoporin 153, a protein in the nuclear basket that participates in nuclear transport via importin beta²³. Nocodazole, which depolymerizes microtubules, inhibits nuclear import of capsids and thereby suppresses virus replication²⁰.

Disassembly of capsids at the nuclear pore results in the release of the virus's relaxed circular DNA (rcDNA) genome into the nucleus, where the partially double-stranded rcDNA is converted into cccDNA. Little is known about the detailed mechanisms of this process. Inhibition of HBV polymerase by nucleos(t)ide analogs does not block cccDNA formation in models of HBV infection, so cellular DNA repair enzymes rather than viral polymerases might be responsible for cccDNA formation¹⁶. This multi-step process involves the removal of covalently attached viral polymerase and an RNA primer from the positive strand, cleavage of terminally redundant sequences from the negative strand, repair of the incomplete positive strand, and ligation of both DNA strands. A DNA repair enzyme, tyrosyl-DNA-phosphodiesterase 2 (TDP2), removes the covalently bound viral polymerase from HBV and rcDNA in the nucleus²⁴. However, TDP2-knockout cells can still be infected by human HBV, indicating that other TDP-related proteins contribute to this activity²⁵. Flap-endonuclease 1 (FEN1) can remove the 5'-flap structure from rcDNA and might contribute to cccDNA formation²⁶. DNA polymerase κ (POLK) was found to complete the positive strand DNA synthesis of the rcDNA²⁷, whereas DNA ligase 1 and 3 contribute to formation of cccDNA during de novo HBV infection²⁸. Although POLK is important for maintenance of genomic stability²⁹, DNA ligase inhibitors, which are being developed as anti-cancer agents³⁰, might be developed for treatment of chronic HBV infection, if the side effects are tolerable.

HBV cccDNA is stable and has a long half-life in infected cells, so its clearance, a marker of a complete cure, has been difficult to achieve. High doses of IFNA or lymphotoxin beta receptor agonists induce non-cytolytic degradation of cccDNA from infected primary human hepatocytes or HepaRG cells, through induction of nuclear deaminase apolipoprotein B mRNA editing enzyme catalytic subunit (APOBEC) 3A or 3B^{31, 32}. The lymphotoxin pathway is active in livers of patients with chronic HBV infection³³. However, increased expression of genes that regulate the lymphotoxin pathway, including APOBEC3 enzymes, are not associated with a lower cccDNA content³³. Interestingly, upregulation of APOBEC3A in the liver correlates with an antiviral response in patients treated with IFNA³⁴. Unfortunately, because of IFNA's side effects, it may not be feasible to increase the dose to achieve this goal. Recently, overexpression of APOBEC3G in a Cre-mediated HBV recombinant cccDNA cell line resulted in cccDNA loss. This indicates that there could be ways to induce cccDNA degradation without IFNA treatment³⁵.

Although cell proliferation can cause cccDNA loss in animal models³⁶, HBV cccDNA is stably maintained as a mini-chromosome in infected hepatocytes. Loaded with histone and non-histone proteins, cccDNA serves as a template for RNA polymerase 2-mediated transcription of 4 viral RNAs, via the cell's transcription machinery³⁷. HBV cccDNA transcription is controlled by 4 promoters (the core, pre-S1, pre-S2/S, and × promoters) and 2 enhancers. Enhancer I mediates the activation of an early transcript (HBx mRNA), whereas enhancer II mediates expression of late transcripts³⁸. IFN-induced tripartite motif 22 (TRIM22) inhibits HBV core promoter activity and thereby HBV gene expression and replication in cells and animal models³⁹.

Several liver-enriched transcription factors and nuclear receptors bind the HBV promoter or enhancer elements and regulate HBV transcription. PreS1 promoter contains binding sites for hepatocyte nuclear factor (HNF)1 and HNF3^{40–43}. Transcription from the pre-S2/S promoter is mediated by transcription factor SP1 and it is also responsive to retinoid × receptor alpha (RXRA), peroxisome proliferator-activated receptor alpha (PPARα), and HNF4A^{44, 45}. Enhancer 1 contains binding sites for HNF1, HNF3, and CCAAT-enhancer-binding protein (CEBP)^{46–48}. In addition, the pre-C/C promoter and both enhancers contain binding sites for nuclear receptors including HNF4A, RXRS, PPARα, the nuclear receptor subfamily 2 group F member (NR2F2 or COUPTF) 1 and 2, and nuclear receptor subfamily 2 group C member 1 (NR2C1 or TR2)^{41, 42, 49}. Compounds that target these transcription factors suppress HBV replication^{16, 50}.

Epigenetic modifications to HBV cccDNA mini-chromosomes, such as DNA methylation and histone modifications, affect transcription of HBV cccDNA. HBV can induce methylation of cell and virus DNA, by induction of DNA methyltransferases⁵¹. Hypoacetylation of the cccDNA-associated H3 and H4 histones and recruitment of the cell's HDAC1 onto cccDNA are associated with low HBV replication in cells and in animal models⁵². Cell factors involved in epigenetic modifications, including cAMP responsive element binding protein (CREB), E1A binding protein p300 (p300), lysine acetyltransferase 2B (KAT3B or PCAF), CREB regulated transcription coactivator 1 (CRTC1), lysine acetyltransferase 2A (KAT2A or GCN5), and YY1 transcription factor (YY1) bind to cccDNA and promote its transcription^{53–55}. On the other hand, signal transducer and activator of transcription (STAT) 1 and 2, HDAC1, sirtuin 1 (SIRT1), SIRT3, protein arginine methyltransferase (PRMT) 1 and 5, enhancer of zeste 2 polycomb repressive complex 2 subunit (EZH2), defensin alpha 1 (DEFA1 or HP1), and structural maintenance of chromosomes (SMC) 5 and 6 interact with cccDNA to inhibit HBV cccDNA transcription^{53, 56–62}.

An important function of HBx is to redirect the damage specific DNA binding protein 1 (DDB1) E3 ubiquitin ligase to SMC5 and SMC6 for degradation and thereby relieve this suppression⁶². Similarly, HBx counteracts SETDB1-mediated histone 3 di- and trimethylation (H3K9me3) and HP1 recruitment to activate cccDNA transcription⁶¹. HBx is therefore an attractive virus therapeutic target.

IFNA represses HBV by reducing active histone markers on the cccDNA mini-chromosome in HBV-infected primary human hepatocytes⁶³. The small molecule C646 also achieves this

effect, by specifically inhibiting p300 and CBP histone acetyltransferases⁶³. Drugs that modify epigenetic regulation have also been developed to treat patients with cancer or viral infections^{64–66}. These agents might be used to inactivate cccDNA in infected hepatocytes.

The HBV polymerase is translated from an internal AUG codon on pregenomic RNA (pgRNA), whereas translation of other HBV proteins is controlled by initiation codons located closest to the 5' end of their mRNA^{67, 68}. In response to binding of the polymerase to the packaging signal epsilon at the 5' end, core proteins complex with the pgRNA and viral polymerase complex and initiate capsid formation^{69, 70}. The heat shock protein 90 mediates the interaction between pgRNA and polymerase⁷¹. Serine arginine protein kinase might bind to the C-terminal domain of core protein and regulate subsequent phosphorylation to prevent self-assembly and nonspecific RNA packaging⁷². In addition, the human cytidine deaminase APOBEC3G is incorporated into viral particles through binding to the viral reverse transcriptase and might be a negative regulator of virus replication⁷³. Capsid assembly modulators (CAMs), which are small-molecule compounds that target core protein, are under development.

Inside the viral capsid, pgRNA is reverse transcribed into minus-strand DNA by the viral polymerase, with its terminal protein domain acting as a primer for initiation of reverse transcription⁷⁴. During negative-strand synthesis, degradation of the pgRNA template by the RNase H activity of polymerase occurs concomitantly. When the polymerase reaches the 5' end of pgRNA, a RNA oligomer remains, and is used as the primer for plus-strand DNA synthesis by the viral polymerase⁷⁵. For unknown reasons, plus-strand DNA synthesis is incomplete, occurring for approximately half the genome, which results in formation of the partially double-stranded rcDNA viral genome⁷⁶.

NRTIs, which target viral polymerase for DNA synthesis activity, are highly effective in inhibiting HBV replication. Additionally, entecavir, tenofovir, and clevudine can inhibit polymerase-mediated protein priming^{77, 78}. RNase H activity is essential and has specific enzymatic activity of viral polymerase, so it could be a good therapeutic target. Recently, several inhibitors of RNase H, including beta-thujaplicinol and hydroxylated tropolones, have been identified^{79–82}. These anti-HBV agents are under development and might be used in combination with existing treatments to achieve higher suppression of virus replication.

The fate of rcDNA-containing capsids varies, which may be regulated by L protein⁸³. They either are transported back to the nucleus to amplify the cccDNA pool or undergo envelopment to be released as progeny virions. HBV virion assembly is initiated with nucleocapsid transportation to the surface of the MVBs, through NEDD4 and adaptor related protein complex 1 subunit gamma 2 (AP1G2), and then buds into MVB through ESCRT complexes on contact with the HBV envelope proteins via endosomal sorting complex^{84–86}. MVB and/or MVB-derived exosomes then fuse with the plasma membrane to release HBV virion.

In addition to secretion of HBV virions (Dane particles), many incomplete subviral particles, including filaments and spheres, are released from infected hepatocytes. Interestingly, filaments and Dane particles share the same secretion pathway, whereas spheres self

assemble in the lumen of the endoplasmic reticulum and are released by the general secretory pathway^{87, 88}. Subviral particles can reach levels 10,000-fold higher than the Dane particles in the serum of HBV carriers, where they can act as immunological decoys⁸⁹. In addition, secreted particles containing HBV RNA^{90, 91} or no viral nucleic acid⁹² have been reported.

Bone marrow stromal cell antigen 2 (BST2 or TETHERIN), expressed by immune cells in response to interferon, blocks the egress of enveloped viruses, including HBV, by tethering budding virions on the cell surface via its membrane anchor domains⁹³. Inhibitors that target HBV secretion and budding are preclinical studies and clinical trials^{94, 95}. Nucleic acid polymers blocked the release of HBsAg from infected hepatocytes in patients with chronic HBV infection and HBV and HDV coinfection in a phase 2 trial^{96, 97}.

Persistent HBV replication is associated with integration of HBV sequences into the hepatocyte genome. This integration is believed to be caused by non homologous end joining or microhomology-mediated end joining of double-stranded linear HBV DNA (dsDNA)⁹⁸. Reverse transcription of the pgRNA occasionally forms dsDNA as an aberrant by-product; the dsDNA can be released as defective virions or integrated into host genome^{98, 99}. In most integrated HBV DNA, the HBV core promoter is separated from its open reading frame, resulting in replication-incompetent transcripts. On the other hand, HBV DNA integrated into the genome can still act as a template for HBsAg expression^{100, 101}.

Direct-acting Antivirals

Development of antiviral agents has largely focused on viral targets. The rationale was that these agents would have little or no cross-activity with human cells or proteins, and therefore be non-toxic. NRTIs are the backbone of treatment for chronic HBV infection. Although second-generation NRTIs efficiently suppress viral DNA synthesis, they do not eliminate the virus. There are several NRTIs in development that aim to improve upon existing NRTIs. These include besifovir¹⁰², metacavir¹⁰³, 2 prodrugs of tenofovir CMX157, and DA-2802 (see Table 1). Studies are needed to determine whether these NRTIs provide substantial advantages over current treatments.

Capsid inhibitors

Nucleocapsid formation and pgRNA packaging are critical steps of viral life cycle that might be targeted by antiviral agents. Two main classes of CAMs have been developed according to their mode of action on assembly. The phenylpropenamide and sulfamoylbenzamide chemical series interfere with pgRNA packaging and accelerate formation of immature empty capsid-like particles^{104–107}. Heteroaryldihydropyrimidine compounds induce formation of aggregated and aberrant capsid structures and also disrupt intact capsid^{108–112}(Figure 1). Clinical studies are underway to test CAMs, including JNJ-379, GLS4, ABI-H0731, NVR 3–778, Bay 41–4109, RO7049389, JNJ-440, AB-423, and QL-007 (see Table 1). AB-506 and ABI-H2158 are in preclinical studies. JNJ-379, administered for 28 days, was generally well tolerated and had potent antiviral activity at the doses evaluated¹¹³. ABI-H0731 was safe and well tolerated in a phase 1 trial, and once-daily doses had potent

antiviral activity¹¹⁴. Similarly, RO7049389 had robust anti-HBV activity in patients with chronic HBV infection, and was safe and well tolerated¹¹⁵.

RNA interference

RNA interference (RNAi) technology can be used to manipulate virus gene expression and might be developed for treatment. Briefly, small interfering RNAs (siRNAs) are designed to target specific viral mRNA sequences. After they are delivered into the hepatocytes, the siRNAs hybridize with viral mRNA, and the resulting double-stranded RNA is degraded¹¹⁶. The first siRNA against HBV to enter development was ARC-520¹¹⁷. Single and multiple doses of ARC-520 reduced HBsAg, HBeAg, HBcAg, and HBV DNA titers in HBV-infected chimpanzees and patients^{118, 119}. However, the observed HBsAg reductions were significantly lower in HBeAg-negative than in HBeAg-positive chimpanzees and patients. This could be because ARC-520 targets cccDNA-derived, but not integrated, transcripts. The second-generation siRNA, ARC-521,¹²⁰ was therefore developed. However, due to potential safety issue with the delivery platform, trials were terminated.

Using a proprietary, subcutaneously administered delivery vehicle, researchers at Arrowhead developed ARO-HBV, which is currently in a phase 1/2 trial. Other siRNAs, from different companies, are in phase 1 or 2 or preclinical studies (Table 1). Similar strategies include antisense oligonucleotides, locked nucleic acids, and RNA destabilizers, which are in development (Table 1). siRNAs against HBV are still in experimental stages—more studies are necessary to address the efficacy issues and safety concerns.

Gene editing

The genome editing tool, clustered regularly interspaced short palindromic repeats associated nuclease 9 (CRISPR/Cas9), has many innovative applications in different fields because of its potential for gene therapy. The CRISPR/Cas9 system comes from the immune system of bacteria and archaea, which detects and degrades foreign DNA from bacteriophages and plasmids¹²¹. Briefly, for gene editing, Cas9 is directed to its DNA target by base pairing between the guide RNA (gRNA) and DNA. A protospacer-adjacent motif (PAM) motif downstream of the gRNA-binding region is required for Cas9 recognition and cleavage. Cas9/gRNA cuts both strands of the target DNA, leading to double-strand DNA break repair. The promise of CRISPR/Cas9 as a tool for the cleavage and elimination, or at least inactivation, of HBV cccDNA and HBV genome integration, has prompted many studies. These have provided a clear proof of concept that this approach has the potential to treat or even cure patients with chronic HBV infection^{122–124}. Excision BioTherapeutics and Intellia Therapeutics announced their first CRISPR/Cas9 candidates for HBV infection (Table 1). However, off-target effects of the CRISPR/Cas9 system in patients are a concern¹²⁵. The p53-mediated DNA damage response induced during gene editing might also hamper its clinical applications¹²⁶.

Agents That Target Host Proteins

Despite the best effort to designing direct acting drugs that are highly virus-specific, off-target effects inevitably occur and cause side effects¹²⁷. Many of these can be managed with

thorough toxicology, pharmacokinetic, and pharmacodynamic studies. Furthermore, drug resistance often emerges when direct antivirals are used for extended time periods, leading to the requirement for combination regimens.

Nontoxic drugs have been developed that are effective in treatment of viral infections, including HBV. However, HBV has a small genome that encodes 4 major gene families, so it does not provide many targets for drug development. It is therefore important to study agents that target non-viral proteins or pathway required for HBV infection and replication (see Table 2). However, toxicity is a concern with this approach. Avoidance of toxicity requires a detailed understanding of the targeted pathways. Redundancy is often the rule rather than the exception in biology. When 1 pathway is inhibited, another often takes its place—either involving other members of the targeted pathway or separate pathways that overlap or converge with the targeted pathway. Differences in sensitivity of a virus vs human cells to disruption of a pathway can be exploited to achieve an acceptable therapeutic window. Viruses are less likely to become resistant to agents that target cell functions, although viruses can acquire mutations that reduce dependency on the targeted protein or pathway¹²⁸.

One example of a drug designed to target a cellular protein required for viral infection is maraviroc, which blocks CCR5 to prevent cell entry by HIV¹²⁹. Ribavirin, a broad-spectrum antiviral agent used to treat patients with HCV infection, is believed to potentiate the effects of interferon¹³⁰. Myrcludex B, which blocks NTCP, just completed a phase 2 trial of patients with HBV and HDV co-infection^{131, 132}. Cyclosporin A-like compounds, which probably interfere with NTCP-mediated HBV entry, are also in development¹³³. EYP001, a selective synthetic FXR agonist, prevents HBV infection of HepaRG cells and is in a phase 1 trial¹³⁴. GS-5801, a liver-targeted prodrug of a lysine demethylase-5 inhibitor, is in a phase 1 trial—it is one of the first epigenetic modifiers to be tested in patients with HBV infection¹³⁵. Glucosidase inhibitors and nucleic acid polymers, which prevent assembly and release of HBV particles, also in development^{96, 97, 136}.

Unbiased High-throughput Screen for Small Molecule HBV Inhibitors

With advances in high-throughput technologies and expansion of small molecule chemical libraries, researchers have begun to perform large-scale unbiased screens to identify compounds that inhibit HBV. Screens for antiviral compounds require a miniaturized platform of an infectious or replicating cell culture system coupled with a high-throughput read-out system needs to be developed first (see Figure 3). The overall system would have to identify HBV inhibitors with high levels of sensitivity, with reproducible and robust results. These systems have been developed for many viruses and yielded promising compounds for further development^{137, 138}.

For HBV, the building blocks for such a system are available. HBV infectious or replicating cell culture systems are established¹³⁹. Highly sensitive and specific assays to detect HBV replication are standard tools and can be readily applied to high-throughput screens. Several screens have already been developed and performed to identify HBV inhibitors¹⁴⁰.

It could also be possible to repurpose or reposition drugs that have already undergone substantial preclinical or clinical testing¹⁴¹. Drugs developed for a specific disorder can be used to treat other diseases that have overlapping pathogenic mechanisms. However, drugs affect multiple factors and pathways beyond the initial target for which they were developed. An unbiased screen of these drugs for those that inhibit HBV replication nor infection might identify new candidates. Collections of these drugs are currently available for this purpose¹⁴². This approach can markedly reduce the duration of drug development, which can last more than 10 years, because many of these drugs have already undergone toxicology and pharmacokinetic analyses. Efforts to repurpose drugs for antiviral development have been under way for viral infections and viral hepatitis^{143, 144}.

Immune-based Approaches

Immune cells and cytokines mediate cytolytic and non-cytolytic clearance of HBV infection⁵. Therapies that promote cytokine-mediated innate immune control of virus infection and restore adaptive immunity are important to develop. Agonists of toll like receptor 7 (TLR7), TLR8 and DExD/H-box helicase 58 (DDX58 or RIG-I) and therapeutic vaccines are in phase 1 and 2 trials (see Table 2). See ref XX for a detailed review of immune-based therapies for HBV infection (Gehring and Protzer reference).

Future Directions

Strategies to cure HBV infection have been met with renewed interest and energy by pharmaceutical and academic communities, partly because researchers have realized the limitations of treatment options and the unprecedented success of HCV therapy. Although HCV and HBV are different viruses, and challenges to curing their infections are virus are distinct, recent advances in technologies and expanded understanding of HBV infection have paved the way for exciting new directions for development of HBV therapies. Efforts to develop new classes of direct acting antivirals other than the traditional NRTIs are under way and some have entered clinical trials. Innovative approaches that focus on nontraditional viral targets, such as host targeting agents, warrant earnest consideration and should be pursued in parallel. Curing HBV infection is likely to require combination therapies that leverage our knowledge of the Achilles heel of the virus. Armed with new tools and technologies, coupled with increased understanding of HBV's pathogenic mechanisms, we should be able to cure HBV infection within the next decade.

Acknowledgment

This work was support by the Intramural Research Program of the National Institute of Diabetes and Digestive and Kidney Diseases, National Institutes of Health. Yuchen Xia is partly sponsored by ILCA-Bayer fellowship.

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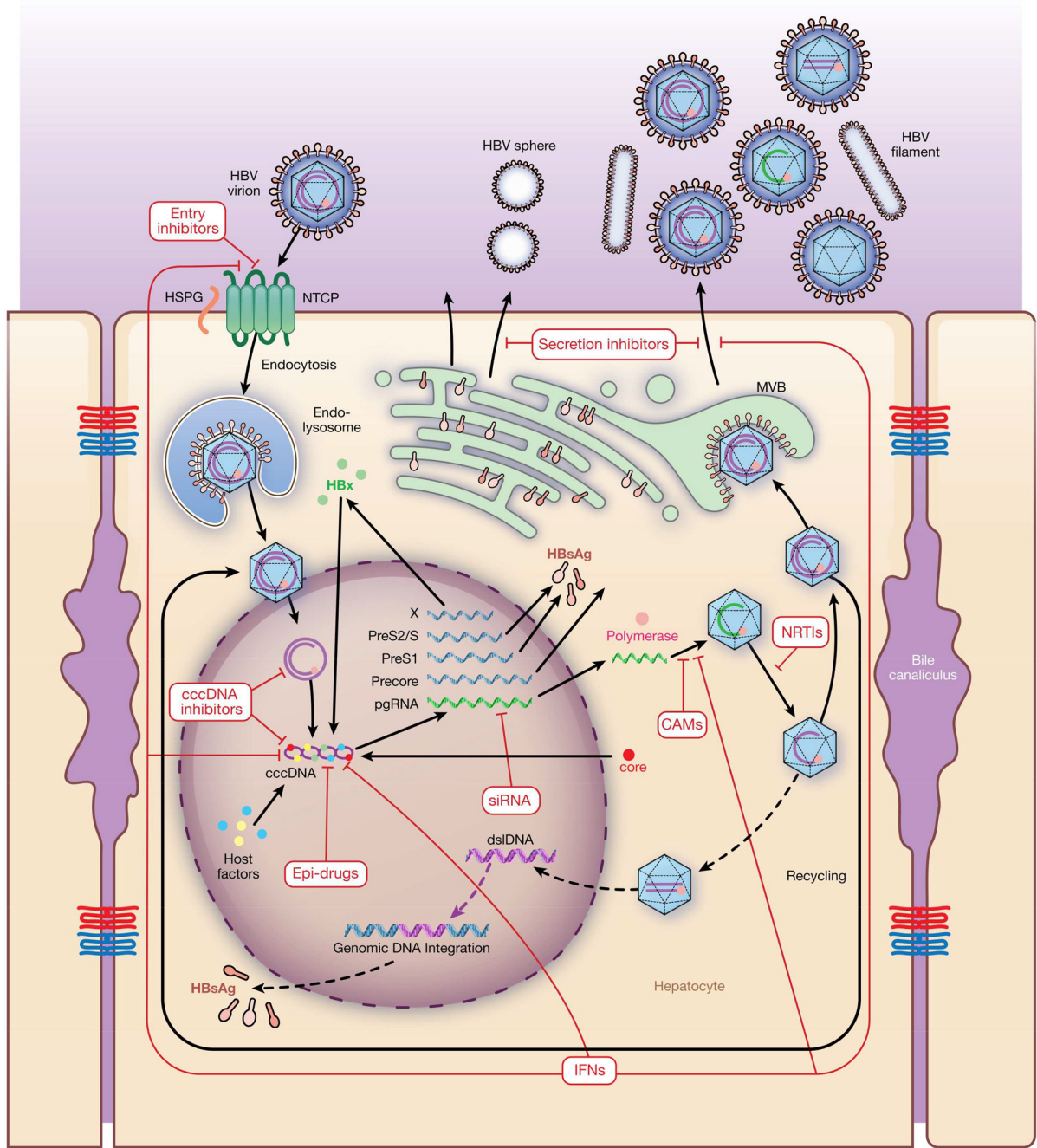


Figure 1. HBV Life Cycle and Therapeutic Targets

The HBV cycle includes virus attachment, entry, uncoating, trafficking to nucleus, cccDNA formation, transcription, translation, encapsulation, secretion, and integration. HBV infection is initiated via interaction with heparan sulfate proteoglycans (HSGP), resulting in a large envelope protein that binds NTCP. After internalization, viral capsids are released and then directed to the nucleus, where the HBV genomes are released. In the nucleus, relaxed circular DNA genomes are converted into cccDNAs, which can persist in the nucleus of infected cells as a mini-chromosome and serve as template for viral RNA transcription.

Viral mRNAs are transported to the cytoplasm, where they are translated into viral proteins. Together with the viral polymerase, the pgRNA is encapsulated and reverse transcribed within the nucleocapsid into progeny rcDNA. Mature nucleocapsids are then either directed to the MVB pathway for envelopment with HBV envelope proteins or re-directed to the nucleus to establish a cccDNA pool. dsIDNA that contains capsid is also produced that can be integrated into the cellular genome or released as defective virion. Drugs or antiviral agents designed to target different steps of the HBV life cycle are shown in red.

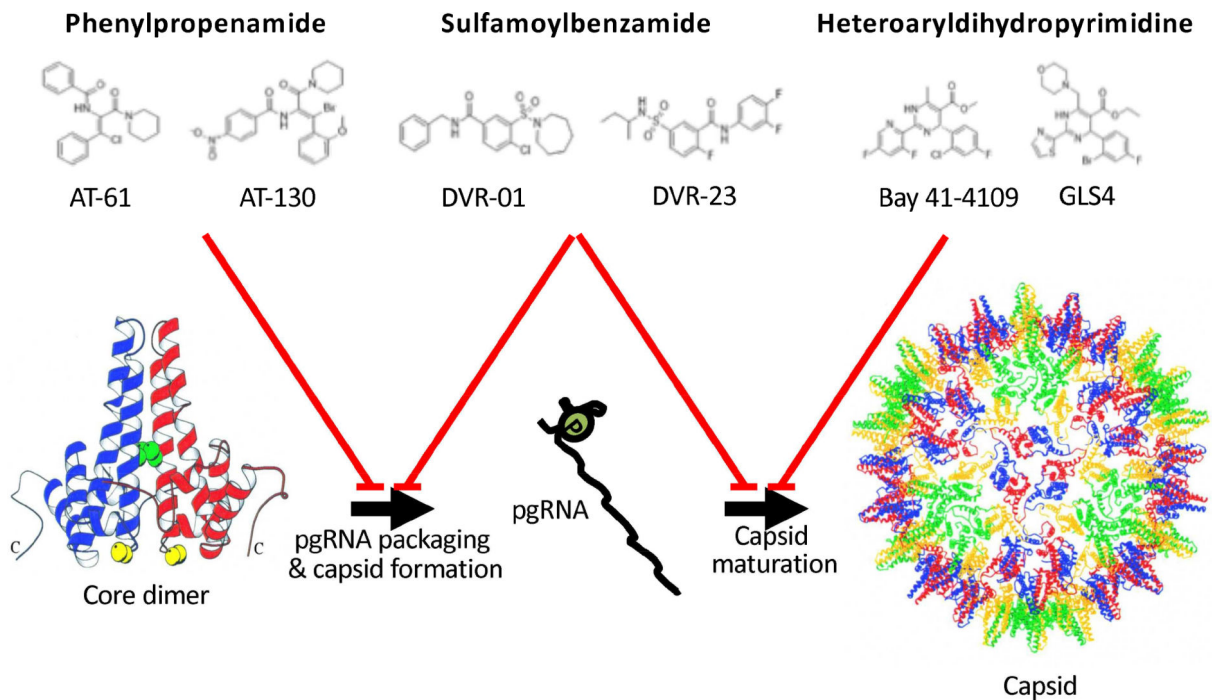


Figure 2. Types and Structures of HBV Capsid Inhibitors

(A) Representative compounds belong to phenylpropenamide, heteroaryldihydropyrimidine, or sulfamoylbenzamide family. (B) The targets of different compounds are: phenylpropenamide chemicals, which interfere with pgRNA packaging; heteroaryldihydropyrimidine compounds, which induce abnormal assembly of capsid; and sulfamoylbenzamide family serials, which target both. The target side of heteroaryldihydropyrimidine is shown with a black arrow. (Figure adapted from Wynne et al. *Mol Cell* 1999. with permission from Cell Press)

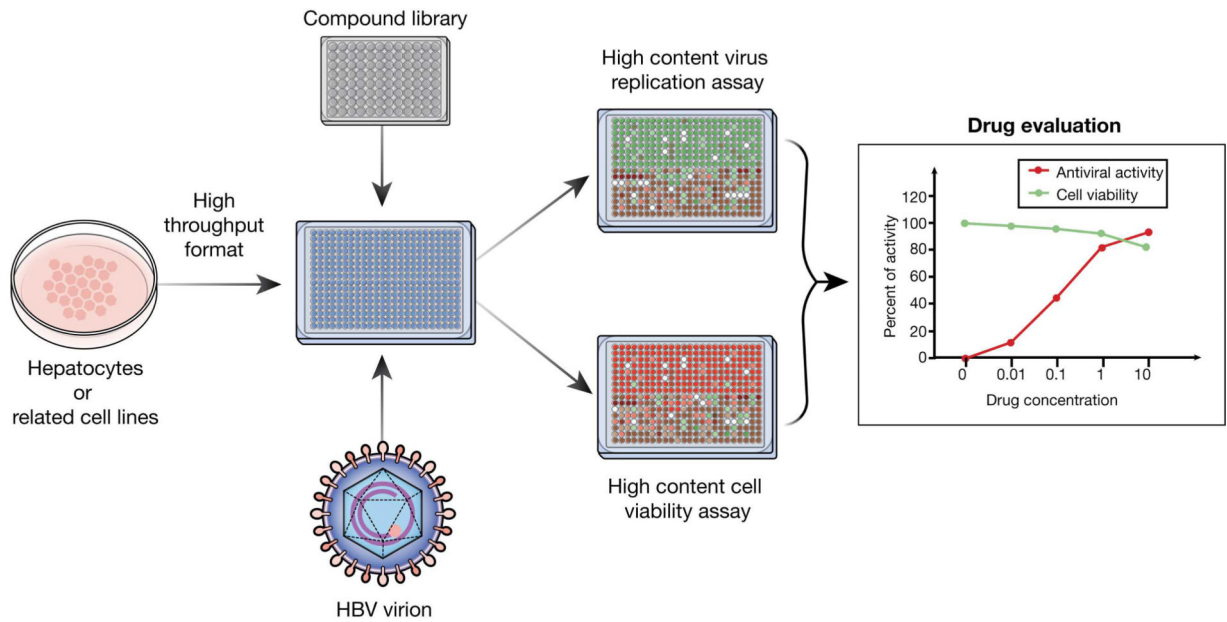


Figure 3. High-throughput Screen for Anti-HBV Compounds

A high-throughput screen for compounds that inhibit HBV involves culture of HBV-susceptible hepatocytes, followed by infection with HBV and addition of compound library. Compounds found to block HBV entry or replication in this assay can be validated in additional assays and for their effects on cell viability.

Table 1.

Direct-acting Antivirals for HBV in Development

Compound	Mechanism and Target	Stage of Development	Sponsor	Reference and Clinicaltrials.gov no
Besifovir	Polymerase	Phase 3, Approved in S. Korea	Il Dong Pharmaceutical; South Korea	102; NCT01937806
DA-2802 (tenofovir disoproxil orotate)	Polymerase	Phase 3	Dong-A ST Co., Ltd.; South Korea	NCT02967939
Metacavir	Polymerase	Phase 2	Guangzhou Yipinhong Pharmaceutical, China	103; NCT02965859
CMX157 (tenofovir Exalidex)	Polymerase	Phase 2	ContraVir Pharmaceuticals	NCT02710604
RNase H inhibitors	RNaseH	Preclinical	Arbutus	sponsor's web site
JNJ-379 (JNJ-56136379)	Capsid	Phase 2	Janssen Sciences, Belgium	NCT03361956
GLS4	Capsid	Phase2	HEC Pham, China	145; sponsor's web site
ABI-H0731	Capsid	Phase 1b/2a	Assembly	NCT03109730
NVR 3-778 (AL-3778)	Capsid	Phase 1/2	Novira	146; NCT02112799 NCT02401737
Bay 41-4109	Capsid	Phase 1	AiCuris, Germany	147; sponsor's web site
RO7049389	Capsid	Phase 1	Roche, Switzerland	NCT02952924
JNJ-440	Capsid	Phase 1	Alios Biopharma	NCT03439488
AB-423	Capsid	Phase 1	Arbutus	sponsor's web site
QL-007	Capsid	Phase 1	Qilu Pharmaceutical, China	NCT03244085
AB-506	Capsid	Preclinical	Arbutus	sponsor's web site
ABI-H2158	Capsid	Preclinical	Assembly	sponsor's web site
ARB-1467 (TKM-HBV)	siRNA	Phase 2	Arbutus	NCT02631096
ARO-HBV	siRNA	Phase 1/2	Arrowhead	NCT03365947
ALN-HBV	siRNA	Phase 1/2	Alnylam	sponsor's web site
LUNAR™-HBV	siRNA	Preclinical	Arcturus	sponsor's web site
Hepbarna (BB-HB-331)	siRNA	Preclinical	Benitec, Australia	sponsor's web site
ARC-520	siRNA	Terminated	Arrowhead	NCT02452528 NCT02604212 NCT02604199 NCT02738008 NCT02065336 NCT02577029
ARC-521	siRNA	Terminated	Arrowhead	NCT02797522
ARB-1740	siRNA	Terminated	Arbutus	sponsor's web site
IONIS-HBVLRx (GSK3389404)	Antisense oligonucleotide	Phase 2	Ionis Pharmaceuticals, with GlaxoSmithKline, United Kingdom	NCT03020745
IONIS-HBVRx (GSK3228836)	Antisense oligonucleotide	Phase 2	Ionis Pharmaceuticals, with GlaxoSmithKline, United Kingdom	NCT02981602

Compound	Mechanism and Target	Stage of Development	Sponsor	Reference and Clinicaltrials.gov no
RG6004 (RO7062931)	Locked Nucleic Acid	Phase 1/2	Roche, Switzerland	148; NCT03038113
AB-452	RNA destabilizer	Preclinical	Arbutus	sponsor's web site
EBT106	CRISPR	Preclinical	Excision BioTherapeutics	sponsor's web site
HBV	CRISPR	Preclinical	Intellia Therapeutics	sponsor's web site

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Table 2.

Agents that Target Host Factors in Development for Treatment of HBV Infection

Compound	Mechanism and Target	Stage of Development	Sponsor	Reference
Myrcludex B	entry	phase 2	Hepatera, Russia	NCT02888106 NCT02637999
GS-5801	epidrug	phase 1	Gilead	sponsor's web site
REP 2139	HBsAg	phase 2	Replicor, Canada	96, 97; NCT02565719
REP 2165	HBsAg	phase 2	Replicor, Canada	97; NCT02565719
RO7020322 (RG7834)	HBsAg	Terminated	Roche, Switzerland	149; NCT02604355
EYP001	FXR agonist	phase 1	Enyo Pharma, France	NCT03469583
APG-1387	apoptosis	phase 1	Asscentage Pharma, China	150; sponsor's web site
Birinapant	apoptosis	terminated	TetraLogic Pharmaceutical	NCT02288208
CRV431	cyclophilin inhibitor	preclinical	ContraVir Pharmaceutical	sponsor's web site
GS-9688	TLR8 agonist	phase 2	Gilead	NCT03491553
GS-9620	TLR7 agonist	phase 2	Gilead, USA	NCT02579382
RO6864018 (RG7795 and ANA773)	TLR7 agonist	phase 2	Roche, Switzerland	NCT02391805
RO7020531	TLR7 agonist	phase 1	Roche, Switzerland	NCT02956850
AL-034	TLR7 agonist	phase 1	Alios Biopharma	NCT03285620
AIC649	immune modulator	phase 1	AiCuris, Germany	151
Inarigivir (GS-999 and SB 9200)	RIGI and NOD2 agonist	phase 2	Spring Bank	NCT02751996 NCT03434353
INO-1800	therapeutic vaccine	phase 1	Inovio Pharmaceuticals	NCT02431312
TG1050	therapeutic vaccine	phase 1	Transgene, France	NCT02428400
HB-110	therapeutic vaccine	phase 1	Genexine, South Korea	152;NCT01641536 NCT00513968
HepTcell (FP-02.2)	therapeutic vaccine	phase 1	Altimmune	NCT02496897
JNJ-64300535	therapeutic vaccine	phase 1	Janssen Sciences, Belgium	NCT03463369
TomegaVax HBV	therapeutic vaccine	preclinical	TomegaVax	sponsor's web site
MVA-VLP-HBV	therapeutic vaccine	preclinical	GeoVax and CaroGen	sponsor's web site
GS-4774	therapeutic vaccine	terminated	Gilead	NCT02258581
LTCR-H2-1	T-cell receptor	preclinical	Lion TCR, Singapore	sponsor's web site
Thymalfasin	immune modulator	phase 4	Huashan Hospital, China	NCT03448744