R E V I E W

An update on small molecule inhibitors of the HCV NS5B polymerase: effects on RNA synthesis *in vitro* and in cultured cells, and potential resistance in viral quasispecies

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Abstract: Chronic infection by the hepatitis C virus (HCV) can lead to liver cirrhosis and hepatocellular carcinoma. There is currently no prophylactic vaccine against HCV, and the treatment is currently limited to modified interferon and ribavirin. The RNA-dependent RNA polymerase (RdRp) of HCV is an attractive target for inhibitor development, and this has led to active efforts in the development of nucleoside and non-nucleoside inhibitors. The HCV polymerase is also one of the model systems for detailed analysis of how RdRp structure affects the mechanism of RNA synthesis. This review summarizes current efforts with inhibitors targeting the HCV RdRp and how the various inhibitors affect the mechanism of RNA synthesis.

Keywords: HCV infection, RdRp, nucleoside inhibitors, subgenomic replicons, ProTides, ribavirin, allosteric site

Introduction and overview

HCV was identified to be the causative agent of non-A-non-B viral hepatitis in the late 1970s. Infection can be through contaminated blood and all means of exposure that range from drug use to needle pricks. The virus can also be transmitted through unprotected sex.[1] Approximately 80% of the acute infections will become chronic, leading to liver cirrhosis and hepatocellular carcinoma.[2] Men are about twice less likely to clear the virus during the acute phase of infection than women.[3] Recurring infection in the same individual can take place, likely due to reinfection by variants of the virus (quasispecies) arising from error-prone replication.[4] By the year 2000, HCV had infected over 170 million people worldwide and become the leading cause for liver transplants in the United States (US).[5]

The molecular clone of the virus was reported in 1989 by Houghton and coworkers.[6] Efforts to inhibit HCV infection, with focus on HCV replication, have been active ever since. Over the past 20 years, significant progress has been made in understanding HCV biology. In addition, companies both large and small have devoted many resources to developing therapies for HCV infection. While pegylated interferon, which generally targets the immune system, and the purine analog ribavirin are used against HCV and can be effective in approximately half of the individuals, this treatment is not specific to HCV infection and is associated with significant side effects.[7] A safe and effective inhibitor specific to HCV and a prophylatic vaccine against it are not yet available. Much work remains to be done on both the basic and applied aspects of HCV infection.

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This review provides an update on the mechanism of RNA synthesis by the HCV RdRp nonstructural protein 5B (NS5B), including the recent biochemical and structure-function studies on its required role in RNA synthesis, and a summary of the NS5B inhibitors. A feature of viruses that replicate with error-prone mechanisms, however, is that resistance will rapidly develop. Using the information available in HCV genome databases, we examined whether strains resistant to polymerase inhibitors already exist in the genotypes and subtypes of HCV.

The hepatitis C virus

HCV is an enveloped virus with a positive-strand RNA genome from the Flaviviridae family. Related viruses include other important human and animal pathogens, such as dengue virus, West Nile virus, and bovine viral diarrhea virus (BVDV). The HCV genome is ~9.6 kb in length and encodes a polyprotein of over 3,000 amino acids that is cleaved by host and HCV-encoded proteases into 10 structural and non-structural components (Figure 1A). The 5' untranslated RNA sequence (UTR) contains an internal ribosome entry site that recruits host ribosomes to translate the viral genome. The 5'UTR, 3'UTR, and the protein-coding region have important cis-acting replication elements to regulate genomic RNA synthesis.[8]

Based on the paradigm established by human herpes virus and the AIDS virus, replication-associated enzymes are important targets for antiviral development. The key enzyme for HCV RNA synthesis is NS5B, the RNA-dependent RNA polymerase that replicates the viral genome. NS5B works in a membrane-associated complex that also contains NS3 (protease-helicase), NS4A (NS3-coactivator), NS4B (key protein for the formation of the membranous web that houses the replication complex), and NS5A (a dsRNA-binding
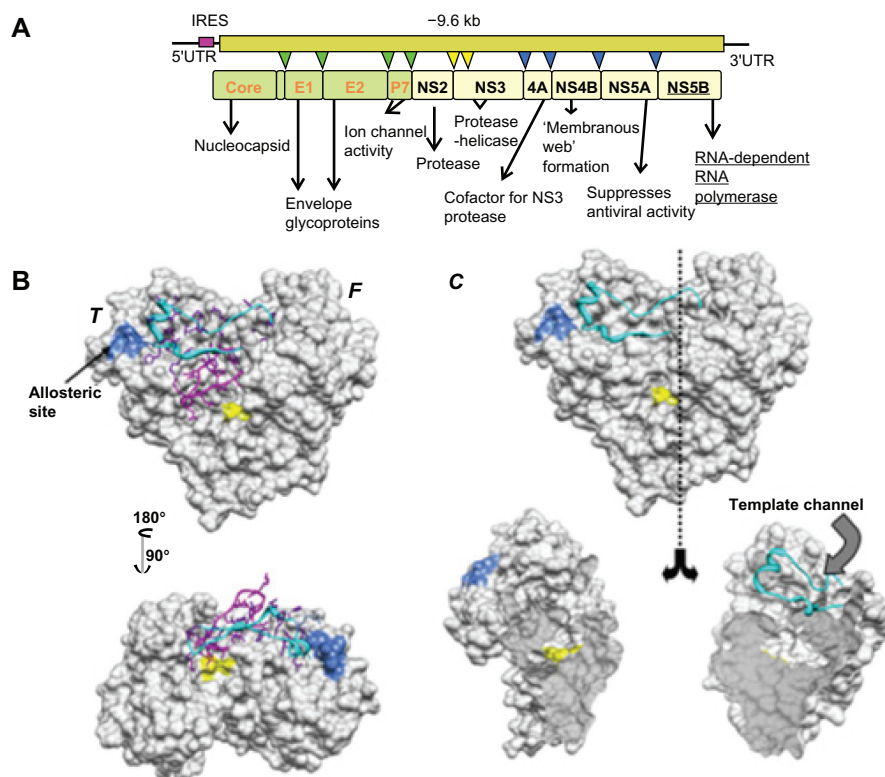

Figure I HCV polyprotein cleavage and the closed conformation of NS5B. **A**) The organization of the HCV genome and the scheme for HCV polyprotein cleavage. The positive sense RNA is schematically depicted on the top in mustard yellow. The internal ribosome entry site (IRES) is depicted as a purple box in the 5' UTR. The polyprotein sequence is shown in green for structural proteins and yellow for non-structural proteins. The green inverted triangles represent cleavage by the host signal peptidases. The core protein is further processed at its C-terminus by the ER signal peptide peptidase (little blue arrow). The NS2 protease separates itself from NS3 and the remaining polyprotein by autoproteolysis (yellow triangle). The remaining polyprotein is cleaved by NS3 protease by using NS4A as the cofactor (blue triangles). The putative functions of the individual proteins are indicated below each protein. **B**) The crystal structure of HCV NS5B Δ35 (PDB ID 1QUV) shown as surface representation with the fingers (F), thumb (T) and palm (P) domains. The allosteric GTP binding site in the thumb domain of HCV NS5B is colored light blue. This site is a low affinity GTP binding site identified by crystal soaking experiments, with an apparent K_d of 200–400 μM.[33] The residues involved with GTP binding at this site are P495, V499, R503, R32, and S29. R32 and S29 are at the apex of the Δ1 loop. The two loops that regulate RNA synthesis are shown as ribbons. The Δ1 loop is in cyan and the Δ2 loop is in magenta. The active site GDD residues in the palm domain are colored yellow. **C**) The template channel in NS5B is a region within the closed conformation of the enzyme that starts at the top in between the junction of the thumb and fingers domains and extends into the active site and emerges out in between the palm and thumb domains. The bottom image shows a cut away representation of NS5B exposing the template channel along a vertical axis (dashed line in top image).

protein that stimulates NS5B activity as well as inhibits cellular signaling).[9,10] These subunits can recognize important cis-acting regulatory sequences in the HCV genome.[8] These proteins also have additional roles during the infection process that are independent of RNA synthesis, such as interference with the signals for the host innate immune responses and perturbation of normal cell cycle control.[11–14] Therefore, targeting the viral replication enzymes could prevent the virus from affecting normal cellular processes as well as inhibiting HCV RNA synthesis.

Systems to study HCV replication

Ever since the identification of the viral origin of Hepatitis C, a number of significant challenges have hampered the development of effective antivirals.[6,7,15,16] HCV did not have a model system to study its infection since it could only infect humans and chimpanzees. This required a number of less than optimal substitutes, including immune-defective mice with transplanted human livers.[17] A recent advance may result from the identification of the tree shrew as a host,[18] although the efficacy of this system remains to be tested.

Until 2005, HCV could not replicate efficiently in cultured cells. In 1999, Lohmann et al developed a substitute system for HCV, a selectable subgenomic replicon system.[19] Subgenomic replicons are viral mini-genomes that lack the genes encoding structural proteins, but have genes encoding fully functional nonstructural proteins that can express reporter genes in the human hepatocyte cell lines, Huh7 and its derivative Huh7.5. Huh7.5 was found to have a defect in the innate immune receptor, RIG-I.[20–22] Mutations in NS5A, NS3, and NS4B were necessary for the replicons to multiply in cells to higher levels (named as replication enhancing mutations or REMs).[23] These adaptive mutations helped the full-length viral genome to replicate in cells, but they failed to produce infectious viral particles.[24] Nonetheless, the HCV replicon systems opened the door for cell-based screens for HCV inhibitors and for the identification of mutations that are altered in their responses to inhibitors.

In 2005, a study of the full HCV infection beyond RNA replication was made possible by the isolation of a genotype 2a HCV strain which caused fulminant hepatitis in a Japanese patient. This strain was named JFH1.[25,26] JFH1 can successfully infect Huh7.5 cells and multiply without the need for REMs. Features of the JFH1 virus, however, are that it is not pathogenic in chimpanzees,[27] and it is not a candidate vaccine strain because of the prevalence of the 1a and 1b HCV infection in the western world. This leaves the subgenomic replicon system along with NS5B protein expressed

from heterologous systems as useful tools to understand the mechanism of RNA synthesis as well as for developing inhibitors targeting NS5B.

NS5B, the RNA-dependent RNA polymerase of HCV

Biochemical assays for RNA synthesis by NS5B have facilitated antiviral drug development and the complementary efforts to better understand the mechanism of HCV RNA synthesis. As with other polymerases, the analogy of a human right hand is useful in describing the domain architecture of NS5B with the thumb, the fingers, and the palm domains.[28,29] NS5B has the characteristic divalent metal binding motif that contains two consecutive aspartates in the palm domain.[30] The thumb and fingers domains are used to help regulate nucleic acid binding (Figure 1B). The 591-residue NS5B protein has a hydrophobic C-terminal tail of approximately 21 amino acids that tether the protein on to the membranes. These residues are dispensable for enzymatic activity, but needed for viral replication in cells.[31,32] NS5B lacking the C-terminal 21 residues (referred to as Δ21) is widely used in biochemical, structural, and inhibitor studies because it can be purified to homogeneity and does not require detergents in the buffer.[31,33–37] Furthermore, no significant differences between the enzyme kinetics of the full-length versus Δ21 enzymes were observed.[31,38] Another version that lacks 55 residues (referred to as Δ55) was initially used for biochemical and structural characterizations.[39] However, the Δ55 enzyme lacks a portion of the sequence that lines the active site, and its use has decreased over the years.

The first characterization of RNA synthesis by the HCV RdRp reported a primer-dependent activity wherein the non-HCV template formed a partial hairpin at the 3' end to allow the polymerase to extend by a copy-back mechanism.[40] Lohman et al[41] demonstrated that the recombinant RdRp can copy the full-length HCV plus strand genomic RNA by the same mechanism. Although these works established the polymerase activity of HCV RdRp, a copy-back mechanism cannot be relevant to HCV RNA replication since it would result in a deletion or other covalent modifications of the genome. A related RdRp from the BVDV was reported to initiate RNA synthesis by a *de novo* mechanism, suggesting the possibility that a similar *de novo* initiation mechanism existed for HCV RdRp.[42] *De novo* initiation was soon demonstrated for a recombinant HCV NS5B from both short synthetic RNA templates as well as from full-length and truncated plus-strand HCV genomic RNA.[43–46] A stable secondary structure is needed at the 3' end of the template RNA that will

promote more efficient *de novo* RNA synthesis, and a purine triphosphate, especially GTP (guanosine 5'-triphosphate), is the preferred initiating nucleotide.[35,43,46,47] High levels of GTP but not other NTPs (nucleotide triphosphates) have been found to stimulate *de novo* initiation.[48]

Structural and functional insights

A seminal start for the antiviral development effort against HCV was the elucidation of the structure of NS5B by X-ray diffraction of the C-terminally truncated versions of NS5B by three independent groups in 1999.[39,49,50] The palm domain has the conserved GDD residues that coordinate the divalent metal ions and carry out the nucleotidyl transfer reaction. Several crystal structures of NS5B in complex with inhibitors, NTPs, and a 5-nt ssRNA have been subsequently reported, but thus far no structural information is available for the ternary complexes involved in initiation and elongation.[51–55]

A unique feature of the HCV RdRp and that of related viral RdRps is that the thumb and the fingers domains are bridged by two loops called the Δ1 loop and Δ2 loop[28,56] (Figure 1B). These two loops are responsible for the closed conformation of the enzyme that results in a complete encircling of the active site from the front side (front side as viewed with the thumb domain at the left and fingers domain at the right side of the viewer in Figure 1B). The back side is covered by another loop called the β loop that forms part of the template channel. This loop extends toward the metal coordinating residues in the active site. This encircling of the active site will result in a well-defined template channel that can accommodate a ssRNA, but not a dsRNA (Figure 1C).[54]

Since the ternary complex of the RdRp will contain dsRNA, the closed structure solved by X-ray crystallography should transition to the more open one during the elongation stage of RNA synthesis. It was initially proposed that the β loop is used by the polymerase for this transition.[49] In fact, a study showed that a deletion of eight residues in the β loop allowed productive elongation from dsRNA templates whereas the wild type (WT) enzyme was not able to perform primer extension.[57] However, according to other predictions, if the β loop is pushed out of the template channel to accommodate the dsRNA, a large adjustment to the thumb domain should be necessary.[39,55]

The Δ1 loop in HCV NS5B contains about 35 residues (Figure 1B and 1C) and is largely a coil structure except for the region that contacts the thumb domain where a small helix (helix A) fits into a pocket defined by amino acids H428, I432, W397, A396, and several other residues. Amino acids in this loop are highly conserved and make important hydrophobic contacts with the thumb domain that will define the contours of the template channel.[55]

The model that the unique closed conformation of the enzyme was the one engaged in RNA synthesis was based on the ternary structure of the RdRp from phage ϕ6.[58] Further work found that mutations that disrupted the Δ1 loop and thumb domain interactions and therefore altered the closed conformation of the enzyme, were detrimental to RNA synthesis.[59] Therefore, it was speculated that this interaction is stable during the catalytic cycle of polymerization and that it may be used for the 'clamping movement' of the polymerase on the RNA template during elongation.[59] If true, this mechanism would be unique to HCV and related viral RdRps that have a Δ1 loop-like structure since other template-dependent polymerases do not possess a thumb and fingers bridging interaction during elongative RNA synthesis.[29,60] However, an 'open conformation' of a genotype 2a NS5B was crystallized by Biswal et al.[51] In this structure, the enzyme deviated from the closed structure due to changes in the interactions between the apex of the Δ1 loop and the thumb domain. The apex of the Δ1 loop formed a β sheet instead of the α helix that is evident in all other reported crystal structures of NS5B. This suggests that the tip of the Δ1 loop and thumb domain interactions may not be stable in solution. Additional biochemical experiments showed that an enzyme that has a deletion at the apex of the Δ1 loop was capable of primer extension from short RNA templates suggesting that an absolutely closed conformation of NS5B may not be a prerequisite for its catalytic activity.[61]

The allosteric site of NS5B

GTP is known to stimulate RNA synthesis by HCV NS5B at high concentrations.[48,55] Surprisingly, crystal soaking experiments identified a second site in the HCV NS5B that can bind GTP[33] (Figure 1B). The first site that is involved in polymerization exists in the palm domain, binds to all four NTPs, and has an affinity for GTP in the sub-micromolar range. The second site is found in the thumb domain adjacent to the pocket that interacts with the Δ1 loop and does have specificity for GTP. GTP bound to this site with an estimated Kd between 200–400 μM.[33] This latter site will henceforth be referred as the allosteric site.

Cai et al[62] performed a systematic mutagenesis analysis of the allosteric site and found that none of the point mutations affected *de novo* initiation activity of NS5B *in vitro*. However, all of the mutations affected the replication of subgenomic replicons to various degrees, suggesting that the

allosteric site plays a crucial role in HCV replication in cells. By being adjacent to the Δ1 loop binding pocket in the thumb domain, the allosteric site could regulate the conformations of the NS5B that are relevant for RNA synthesis and possible interaction with cellular proteins (Figure 1B). Consistent with this model, residue H502 had been shown to be essential for homomeric interactions between NS5B subunits.[63] In addition, the allosteric site overlaps with the critical residues required for binding of inhibitors.[64,65]

Mechanism of RNA synthesis by HCV NS5B

In vitro RNA synthesis by the NS5B can be divided into at least four sequential stages: 1) assembly of productive initiation complexes (*de novo* initiation or primer extension complexes), 2) nucleotidyl transfer to synthesize the first or first few phosphodiester bonds, 3) processive elongation, and 4) termination of RNA synthesis. *In vitro*, the RdRp can also switch templates before termination, although the relevance of this activity in cells in not known. Under certain conditions, the HCV and other viral RdRps can also add non-templated nucleotides to the 3' terminus of the template.[34,66] While this activity can be relevant in the repair of deleted ends of the RNA, its biological relevance to HCV infection remains to be demonstrated. Finally, a property of RNA polymerases is the excision of an incorporated nucleotide in the presence of excess pyrophosphate and the HCV RdRp has been reported to also contain this activity.[67]

Although the crystal structures of the HCV RdRp provided an excellent starting point for understanding HCV RdRp RNA synthesis, the static closed conformation soon became insufficient to account for the requirements for RNA-dependent RNA synthesis. First, the template channels in the HCV RdRp and in φ6 polymerase were too narrow to accommodate the partial RNA duplexes that must be formed as a consequence of RNA synthesis.[55,61,68] Second, Ranjith-Kumar et al showed that the HCV RdRp could direct *de novo* initiated RNA synthesis from a circularized template.[69] Since a circularized RNA cannot thread a terminus into the active site, this observation suggests that the HCV polymerase could undergo a transition from the closed to an open conformation before template recognition. Third, *in vivo*, cyclophilins, a class of peptidyl-prolyl isomerases, are needed by NS5B likely to assist in template loading.[70] All of these results suggest that the closed conformation of the HCV RdRp is not the form that mediates a full round of HCV RNA synthesis either *in vitro* or in cells. Even structural analyses support a more dynamic model for HCV

RNA-dependent RNA synthesis. Biswal et al were able to capture a partially open conformation of the HCV RdRp using X-ray crystallography.[51] In addition, the BVDV RdRp was demonstrated to form a more open conformation due to the interaction between two subunits through the structural equivalent of the Δ1 loop.[56]

In *in vitro* conditions, NS5B can synthesize RNA by *de novo* initiation or primer extension mechanisms (Figure 2A). The K_M values for the NTPs involved in these two mechanisms are significantly different, suggesting that different conformations of NS5B are involved in these two modes of RNA synthesis.[71] Studies with the dengue virus RdRp also support this hypothesis wherein a higher temperature favors an open conformation of RdRp that could carry out primer extension, but not *de novo* initiation.[72]

Two models for HCV RdRp RNA synthesis are proposed based on the oligomeric state of the protein (Figure 2B): the closed monomer model and the oligomeric model. The closed monomer model posits that intramolecular interactions involving the Δ1 loop, Δ2 loop, and the β loop along with the C-terminal tail allow the polymerase to overcome the rate
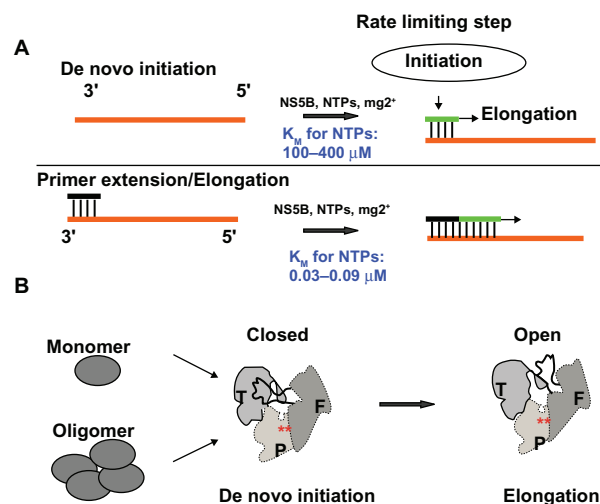

Figure 2 RNA synthesis mechanisms in NS5B. **A)** *De novo* initiation vs primer extension/elongation in NS5B. *De novo* initiation involves the recognition of the 3' end of the template RNA (red) by NS5B and initiation of RNA synthesis without the need for a primer. *De novo* initiation has two steps: initiation (involves the synthesis of a primer of 5–6 nt, shown as green) and elongation. Initiation is thought to be rate limiting. By contrast primer extension/elongation involves extension of a primer (black) along the length of a template (red) from a preformed primer-template RNA complex akin to the elongation step in *de novo* initiation. The newly extended RNA is shown as green. The K_M values shown are obtained from Ferrari et al[70] **B)**. Two models for *de novo* initiation by NS5B. The first model is based on the assumption that the Δ1 loop and thumb domain interactions are stable in a monomer. The second model is based on the idea that the Δ1 loop and thumb domain interactions are stabilized by oligomeric interactions between NS5B subunits. In both models, the closed conformation of the NS5B monomer is the form that is capable of *de novo* initiation, while steric clashes that result in the template channel when a dsRNA product is formed will push the enzyme to go into an open form where the Δ1 loop loses its original interactions with the thumb domain. T, P, and F refer to thumb, palm, and finger domains, respectively.

limiting initiation step of RNA synthesis and provide steric fit for specific recognition of the template RNA (Figure 2B). Once a nascent RNA reaches a sufficient length (~6–8 nt), the polymerase must transition to an open conformation likely by loosening its Δ1 loop and thumb domain interactions, after which, elongation ensues in the open conformation.[61] This mechanism may be relevant in several other RdRps which have the Δ1 loop like structures that connect the fingers and the thumb domains.[28,61]

The oligomerization model posits that the closed conformation of NS5B is maintained by homomeric interactions between NS5B subunits, likely by stabilizing the Δ1 loop and thumb domain interactions. Since the closed conformation is only required for the initiation of RNA synthesis and multiple active sites may not be needed for *de novo* initiation (S Chinnaswamy, C Kao, manuscript in review), the oligomeric interactions between the NS5B monomers are thought to involve more than one interface as shown by Wang et al.[73] Interestingly, genotypic differences have been reported in oligomeric properties of NS5B and may have clinical implications.[74] For example, polymerase inhibitors that interfere with NS5B oligomerization may not be effective on certain HCV genotypes that rely to a lesser degree on NS5B homomeric interactions in order to overcome the rate limiting initiation step of RNA synthesis. The oligomeric model for RNA synthesis is also proposed for the well-studied poliovirus RdRp and for the norovirus RdRp.[75,76]

HCV NS5B inhibitors

Inhibitors of HCV NS5B can be broadly classified into four classes based on their chemical composition and/or mode of action. The first class consists of nucleoside or nucleotide analogs that act as competitors of NTPs during RNA synthesis. This class also includes the purine analog ribavirin, the only Food and Drug Administration (FDA) approved small molecule drug for the treatment of HCV, which has pleiotropic effects on both the cellular and viral enzymes (see below). The second class consists of non-nucleoside inhibitors that allosterically target the NS5B, and the majority of these inhibit the initiation stage of RNA synthesis. A third, small class has a distinct mechanism of inhibition in that its members covalently modify the residues near the active site of NS5B and inhibit its activity and some act by chelating the divalent metal ions needed by NS5B. A fourth and rapidly emerging class consist of compounds that target cellular proteins needed for HCV polymerase function. This class may have advantages in that the virus cannot rapidly evolve resistance to the inhibitors.

Nucleoside inhibitors (NI)

Nucleoside or nucleotide mimics are usually designed to cause premature chain termination during viral nucleic acid synthesis or to increase error in polymerization. Conversion of the nucleoside prodrugs to their triphosphorylated forms is required for inhibitory activity. Several nucleoside analogs have been studied in cells expressing HCV subgenomic replicons, and also in animal models.

Ribose C2' modifications

Nucleoside analogs with modifications at the C2' position of ribose may hold more promise as antivirals. A number of these compounds have progressed to clinical trials and can act in synergy with the interferon-ribavirin combination therapies.[77] 2' ribose modification of cytidine (2'-O-methyl) and adenosine (2'-C-methyl) (Figure 3) will result in potent inhibition of replication by the HCV subgenomic replicons by acting as 'non-obligate' chain terminators of RNA synthesis. That is, although the analogs retain the ribose 3'OH group for phosphodiester bond formation, they can induce structural constraints in the active site that lead to chain termination.[78] A resistant mutation in NS5B S282T was identified for the 2' ribose modified nucleoside analogs (Figure 4).[79] Biochemical characterization revealed that the resistance was due to reduced affinity to the compound and also an increased ability by the mutant polymerase to incorporate the nucleotide analog during elongation.

Migliaccio et al reported good oral bioavailability of 2'-C-methyl guanosine (2'-C-mG) and also synergistic inhibitory activity with interferon.[79] However, a 7-deaza modified 2'-C-mG suffered from poor cell penetration and inefficient phosphorylation by cellular kinases whereas a 7-deaza modification of 2'-C-methyl-adenosine resulted in a compound with improved pharmacokinetic properties and lower toxicity than its unmodified form.[80] MK0608 (7-deaza-2'-C-methyladenosine) has an EC_{50} of 0.25 μM in replicons and has showed promising results in animal studies.[81] PSI-6130 (2-deoxy-2'fluoro-2'-C-methylcytidine) and its prodrug form, R7128 that has a ribose 2' fluoro group modification have EC_{50}s of ~4.5 μM against the HCV NS5B subgenomic replicon and may be specific since they did not affect the BVDV subgenomic replicon.[82]

Other nucleoside modifications

In general, ribose 3'-deoxy modified nucleoside analogs, especially 3'-deoxy-GTP and 3'-deoxy-CTP (cytidine triphosphate), are good chain terminators of HCV NS5B RNA elongation *in vitro*, but they suffer from poor activation
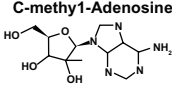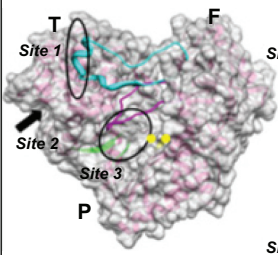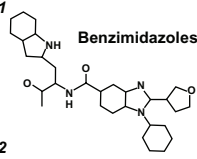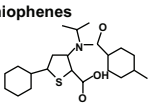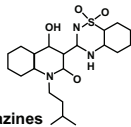
Figure 3 NI and NNI of NS5B. The figure tabulates the different NI and NNI of NS5B into their proposed or identified binding sites and their mechanism of inhibition (MOI). The NI bind in the active site as they are incorporated into the nascent RNA. NNI bind to three different sites in the polymerase. Site 1 overlaps with the binding region at the apex of the Δ1 loop on the thumb domain, while Site 2 is a hydrophobic cleft found ~10 Å beneath Site 1. Site 3, unlike the other two sites, is not on the surface of the enzyme and is located in the template channel and binds to different drugs. Residues from 360–370 are commonly referred to as the 'primer-grip' site as this region is thought to interact with the primer in an elongating polymerase (colored green). Benzofurans that are in Site 3 class bind to this region. Benzothiadiazines are thought to bind to residues close to the active site (like M414) in Site 3. The divalent metals that bind in the active site are shown as yellow spheres. The representative scaffolds of the different drugs are shown. T, P, and F refer to thumb, palm, and finger domains, respectively.

into their triphosphate forms in cells.[83] A 4' ribose-modified nucleoside, 4'-azidocytidine (R1479), and the modified version of 4'-azidocytidine have also been reported to be able to chain-terminate RNA synthesis by HCV NS5B.[84] This analog had a similar IC_{50} (in the range of 1.12–1.3 μM) to that of 2'-C-methyl-cytidine in subgenomic HCV replicon-expressing cells, and concentrations as high as 2 mM were not toxic to cells.[84] The S282T mutation did not affect the inhibitory effect of R1479. However, this analog has been discontinued due to safety issues.[81]

2'-C-methylcytidine (NM107) was found to inhibit BVDV polymerase with a K_i of 160 nM.[81] However, this drug did not have good oral bioavailability. A modification at the 3'OH of ribose, 3'-O-valinyl-2'-C-methylcytidine (valopicitabine or NM283) led to enhanced pharmacokinetic properties and has showed promise initially in clinical studies in HCV infection especially when combined with peg-IFN and ribavirin.[81] However, due to associated serious side effects the FDA has suspended clinical trials for NM283 in the US.[77]

Dihydroxypyrimidines that are thought to be pyrophosphate mimics have been reported to affect RNA synthesis by the HCV NS5B protein.[85,86] NS5B, like other RNA polymerases, can hydrolyze inhibitors incorporated into the nascent RNA strand by essentially reversing the polymerase

reaction in the presence of increased pyrophosphates. Therefore, inhibitors that can bind the pyrophosphates could impact HCV resistance to nucleotide or nucleoside analogs. Mutations G152E and P156L will decrease the ability of dihydroxypyrimidines to act as competitive inhibitors in HCV replicon replication.[85]

Ribavirin

The purine analog ribavirin is an FDA approved drug for treatment of HCV in humans and has been in use for more than a decade. In conjunction with pegylated interferon, ribavirin can clear HCV in approximately 50% of the treated patients, but many side effects exist.[87] Ribavirin may act by more than one mechanism, including by modulation of the immune response and an increase in the polymerase mutation rate when incorporated, causing an 'error catastrophe'.[87] Ribavirin may also act by inhibiting the host IMP dehydrogenase, which will in turn lower the GTP level in the cell. Interestingly, a Y415F mutation has been mapped in the template channel (Figure 4A) that can confer resistance to this purine analog, providing evidence for ribavirin binding to NS5B.[88]

Resistance mutations to NI include S282T, S96T, and N142T (Figure 4A).[79,89] The S282T mutation confers resistance to 2'-C-methyl-cytidine and 2'-C-methyl-adenosine.
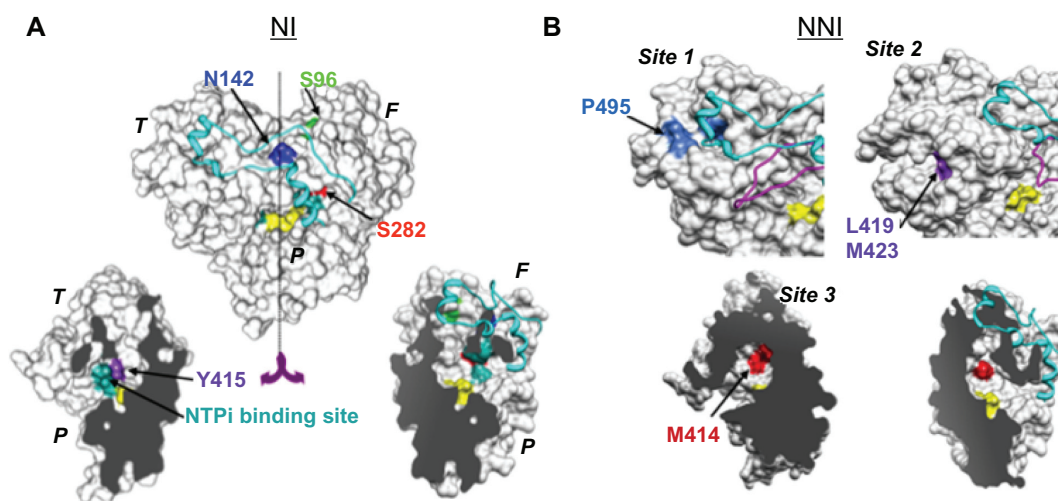
Figure 4 Locations of resistance mutations that arise in NS5B structure (PDB ID 1QUV) in the presence of different NI and NNI. **A**) S282T is a resistance mutation that arises in response to 2'-C-methyl-cytidine and 2'-C-methyl-adenosine nucleoside analogs; residue S282 is indicated in red. S96T and N142T mutations are resistant to 4'-azidocytidine (R1479) and are shown in different colors. Y415F is a resistance mutation commonly observed in response to ribavirin therapy. The Δ1 loop is shown in cyan and the active site GDD residues are colored yellow. The NTPi binding residues in the active site[88] are shown in light green. The bottom image shows the cut away representation of the polymerase exposing the template channel and the NTP tunnel. **B**) Resistance mutations arising in NS5B in the presence of NNI. Mutants conferring resistance to benzothiadiazines (NNI, Site 3) include M414T, C451R, G558R, and H95R, but only M414 is shown in the cut away representation of the polymerase. H95 is located outside of the template channel whereas other mutations are within the template channel. The Δ1 loop is in cyan and Δ2 loop is in magenta and the active site GDD residues are in yellow. T, P, and F refer to thumb, palm, and finger domains, respectively.

S282T also reduced the replicative capacity of subgenomic repicons to ~20% to that of WT.[79] S96T and N142T mutations confer resistance to R1479, and their presence severely debilitates subgenomic replicon capacity[89] and does not confer cross resistance to 2'-C-methyl-cytidine, suggesting a specific interaction in the binding pocket. The S282 residue is in close proximity to the residues in NS5B that bind to the NTPi (initiation nucleotide) (Figure 4A).[90] Mutations involving the NTPi-binding residues have yielded polymerases that are decreased in *de novo* initiation, but unaffected for primer extension activity.[91] This also suggests that the NTP binding pocket in the active site altered during elongation than during *de novo* initiation, consistent with the idea of a specific NTPi binding pocket during initiation. Residue S282 therefore has a specific interaction with the nucleotide analog inhibitors in the NTP binding pocket in order for a mutation at this residue to confer resistance. None of the mutations conferring resistance to NI lie outside the template channel (Figure 4A), suggesting that they do not allosterically influence the polymerase function, unlike non-nucleoside inhibitors (see below). Dinucleotide analogs targeting *de novo* initiation by NS5B have also been reported,[92] but no progress has been reported in their development.

ProTides

A significant issue pertaining to all nucleoside-based inhibitors is that they must be converted into the triphosphorylated form to be potent competitive inhibitors of nucleotide incorporation.[93] For HCV, cellular kinases are responsible for this conversion and the addition of the first phosphate (to form the nucleoside monophospate) is the rate-limiting step. One solution to increase conversion to the active inhibitor is to generate compounds that can be activated by cellular enzymes to contain a 5' monophosphate. However, these analogs need to contend with poor permeability through cellular membranes by the addition of lipophilic groups to the portion of the molecule that will be cleaved. Phosphoramidate analogs that can be converted to nucleotides, termed ProTides have shown recent promise. ProTides with 4'-azido modified uridines and inosines as well as lipophilic moieties can inhibit HCV replicon replication with low micromolar EC_{50} and CC_{50} (cytotoxicity) levels greater than 100 μM.[94,95] In combination with other chemical motifs known to be effective against HCV, ProTides could provide the next generation of NI with improved efficacy. This technology should be applicable to other nucleotide analogs and has already shown promise with DNA methyltransferases.[96]

Non-nucleoside inhibitors (NNI)

Several NNI have been identified that primarily target the initiation phase of RNA synthesis by NS5B, likely by preventing critical conformational adjustments in the enzyme needed for productive RNA synthesis. The NNI target two sites on the surface of the polymerase and one within the template channel. Site 1 involves the Δ1 loop and thumb domain interface ('finger-tip' region). Site 2 is in a pocket

in the thumb domain that is present beneath Site 1. Site 3 is in the template channel, and involves the 'primer-grip site' and the β loop (Figure 3).

Site 1

Benzimidazoles and indole derivatives bind to Site 1 and inhibit the initiation stage of RNA synthesis by NS5B.[53] Benzimidazoles were identified by Boehringer Ingelheim to inhibit NS5B noncompetitively with NTPs at low micromolar IC_{50} values.[53,97,98] This site also overlaps with the allosteric site that putatively binds GTP[33] (Figures 3 and 1B). Inhibitor binding at this site results in disruption of the inter-domain communication and displacement of the Δ1 loop.[53]

Benzimidazole and indole derivatives did not inhibit NS5B during the elongative mode of RNA synthesis and also were ineffective on preformed NS5B-RNA complexes.[64,99] Interestingly, the presence of RNA was required for binding of benzimidazoles to NS5B while preincubated binary complexes that should cause a stepwise loss of Δ1 loop-thumb domain interaction rendered the complex more resistant to the inhibitory effects of the benzimiazole and indole derivatives.[64,71] Notably, two residues, W397 and H428, that are critical for *de novo* initiation by NS5B[61] have side chains that chemically resemble the two classes of NNI that act at Site 1 (imidazole ring in H428 resembles benzimidazoles and indole ring in W397 resembles indoles). Substitutions of P495 to an Ala or a Leu also conferred resistance to benzimidazoles.[64]

The inability of the Site I NNI to inhibit NS5B involved in elongative RNA synthesis suggests that either the binding site is not available during elongation or that the Δ1 loop and thumb domain interactions are not required during elongative RNA synthesis.[53,64,99,100]

Plant-derived phytoestrogens have been shown to be effective against NS5B in biochemical assays and act as non-competitive inhibitors of NTPs and the template RNA.[101] The mechanism of action is thought to be similar to that of benzimidazole compounds based on structure-activity relationship studies.

Site 2

Compounds based on the thiophene scaffold were originally identified by Shire Biochem Inc., as binding to NS5B in the thumb domain and inhibiting its activity.[102] Compounds derived from the leads in this class are generally hydrophobic, consistent with the hydrophobic nature of the binding site that involves residues L419, M423, L474, and W528 (Figure 4B). In the genotype 1b NS5B, no gross change in

the conformation of the enzyme was observed in the presence of the inhibitor,[52,103] however, the genotype 2a NS5B showed a pronounced change with the disruption of the helix A in the Δ1 loop that resulted in the formation of a β sheet.[51] Despite the availability of several crystal structures for the NS5B-inhibitor complex,[51,52,102,103] a clear MOA remains to be elucidated for this class of inhibitors. This site is speculated to be involved with NS5B oligomerization,[51,52,102] and inhibitor binding at this site may perturb function of the NS5B allosteric site.[103] Pyranoindoles that putatively bind at Site 2 inhibit the transition between initiation and elongation stage of RNA synthesis.[104]

Mutations conferring resistance to Site 2 NNI include L419M and M423T.[105] A minor population of drug-resistant clones carrying M423I and I482L were also observed in subgenomic replicons. When the mutations were introduced into WT replicons, all of them showed resistance to thiophene-2-carboxylic acid derivatives.[105] Although some inhibitors that act at Site 2 have exhibited low nanomolar IC_{50} values in biochemical assays, they generally had micromolar IC_{50} values in cell-based assays.

Site 3

Different classes of compounds have been described to bind to this site and inhibit NS5B (Figure 3). The first consists of derivatives of benzothiadiazines initially identified from the GlaxoSmithKline proprietary compound library[106] with 0.5 μm IC_{50} values in subgenomic replicons of genotype 1b. These compounds inhibit the initiation phase of RNA synthesis, but do not affect elongation or already assembled initiation complexes.[37,107] Benzothiadiazines inhibited *de novo* initiation by WT Δ21 with IC_{50} values about 5–10-fold less than those for primer extension.[37] Benzothiadiazines appear to act allosterically, as the inhibition is noncompetitive with GTP and RNA.[37,106]

Resistance mutations arising in HCV genotype 1b replicons after exposure to benzothiadiazines include M414T, C451R, G558R, and H95R (Figure 4).[37] Replicons with the M414T and H95R substitutions were unaffected for replication efficiency compared to the WT replicons, but replicons with the C451R and G558R substitutions replicated at very low levels in absence of compounds and interestingly, showed a dose-dependent increase in replication.[37] In biochemical RdRp assays, however, only M414T showed significant rescue from inhibition of RNA synthesis while H95R, C451R, and G558R did not.

Benzofuran-C3-carboxamide (HCV796) is a second class of drugs that bind at Site 3 and have a potent EC_{50} of

~9 nM in replicon cells.[108] Its binding site overlaps, but is not identical to that of benzothiadiazines. HCV796 binds several residues in the 'primer-grip' site (residues 360–370) including C366. Also L314, C316, and M414 and mutations in these residues render NS5B resistant to HCV796 both in replicons and in biochemical enzymatic assays.[109] HCV796 showed an excellent inhibitory profile in the chimeric mouse model[108] and was approved by the FDA for phase II clinical trials. However, it showed severe hepatocellular toxicity in humans and its development has therefore been discontinued.[110]

A third class of Site 3 binders include 1,5-benzodiazepines which have IC_{50} values of 3–9 µM in biochemical assays[111] and EC_{50}s of 12–32 µM in HCV replicon cells. Several of the NNI binding to all three sites described above are currently in clinical trials.

Miscellaneous NS5B inhibitors

Other classes of inhibitors based on aminorhodanine scaffold have been reported to inhibit NS5B by covalently modifying

C366 in the 'primer-grip' site (Figure 5).[112] Dicarboxylic and diketo acid derivatives could bind in the active site of NS5B.[113,114] These drugs act by chelating the active site magnesium ions as they act as pyrophosphate analogs. These compounds generally have poor cell permeability and may involve toxicity hence they have not been developed further.

Birroccio et al[65] showed that a DNA aptamer selected to bind to NS5B by the SELEX approach was able to inhibit its activity. They further showed that the DNA aptamer bound to the exposed basic patch of the allosteric site on the thumb domain (Figure 1B). RNA aptamers have also been identified to bind NS5B and inhibit its activity in biochemical assays and in HCV infected cells.[115] One aptamer, 27v, was competitive with RNA for binding to NS5B and prevented both initiation and elongation. A second aptamer, 127v, was non-competitive with RNA and inhibited only pre-elongation events in RNA synthesis by NS5B. It is likely that 127v also binds to the allosteric site and inhibits NS5B in a mechanism similar to Site 1 NNI.
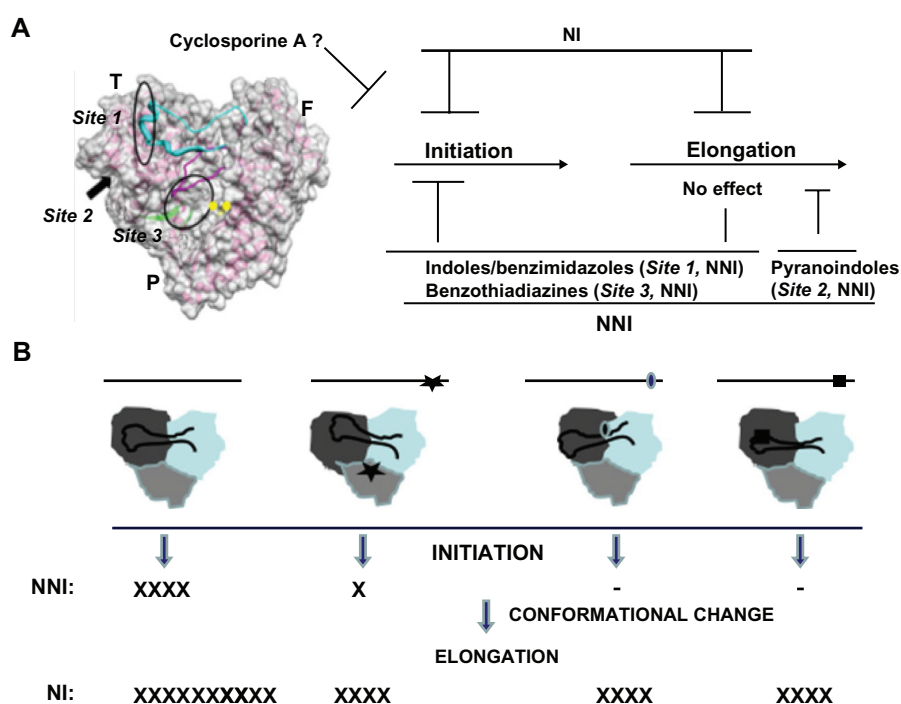

Figure 5 A summary of the effect of different NI and NNI on the mechanism of RNA synthesis by NS5B and the role of polymorphisms in therapeutic failures with NNI. **A**) NS5B PDB ID 1QUV is shown as described in Figure 3. NI target the active site of NS5B and get incorporated into the nascent RNA and hence are effective in blocking both initiation and elongation events. NNI generally target the initiation of RNA synthesis by NS5B and do not affect elongation. However, Howe et al[97] have reported that the pyranoindole class of drugs that bind to NNI Site 2 inhibit elongation, while synthesis of a 5 nt primer was not affected. Cyclosporine A prevents the interaction of cyclophilins with NS5B, however how cyclophilins manipulate NS5B's function is not clear. It is likely that cyclophilins help assemble productive initiation complexes by NS5B, and hence cyclosporine A may target initiation events in RNA synthesis. **B**) Presence of polymorphisms in the viral genome (black line) in the region encoding NS5B is shown as a star, an oval or a filled box. The resulting polymerases (the three domains are in different colors and the Δ1 loop is shown as a black line) have different conformations due to polymorphisms involving the drug binding sites and in other regions. NNI act during the initiation stage and their effect (denoted by Xs) are reduced in either polymerases with mutations in their binding sites or are difference in their conformations (number of Xs denotes the extent of inhibition). A conformational change occurs after initiation in NS5B and elongation ensues. NI that act as chain terminators target the elongating polymerase active site and get incorporated in the nascent RNA chain, and hence are not affected by the polymorphisms in NS5B and therefore are equally effective against NS5B of all genotypes.

Inhibitors that act indirectly on NS5B

Cyclosporin A (CsA) and derivatives have been used as immunosuppressants in organ transplant patients. It was a surprise that CsA was found to be effective against HCV replication in subgenomic replicon cells.[116] Given that CsA interacts with the class of peptidyl-prolyl isomerases named cyclophyllins, the latter were thought to be important for NS5B activity. In fact, cyclophylin B was found to increase RNA-binding by the HCV NS5B.[116] However, most follow-up studies showed that CsA likely acts on cyclophylin A (CypA) to negatively affect HCV replication through NS5B as well as other HCV replication proteins.[117,118] CypA may recruit NS5B to the replication complexes in the membranes[118] and through its isomerase activity, cause a conformational change in NS5B that increases RNA binding. There may also be a cyclophilin A-independent recruitment of NS5B to replication complexes, as would be expected if cyclophilins acted to modify NS5B conformation.[119] This activity may also act on other subunits of the HCV replicase like NS5A.[120] NS5B mutations that render resistance to CsA include I11V and I432V which are within or are in very close proximity to the Δ1 loop.[121] However, mutations like Q438R and E440G which are associated with the β loop were also found to confer CsA resistance.[121] CsA derivatives like NIM-811 and SCY-635 have generated much excitement in this novel class of NS5B inhibitors.[122,123] A recent report points out an association between estrogen receptors and NS5B in HCV replicon carrying cells, and the anti-estrogen drug tamoxifen disrupted this association in a manner similar to that of CsA.[124] It is presently unknown whether tamoxifen directly associates with NS5B. It is also of interest to note here that phytoestrogens were able to inhibit NS5B by a mechanism similar to that of Site 1 NNI.[94]

NS5B inhibitors and RNA synthesis

The inhibitory studies involving some of the compounds have also helped us gain a better understanding of the mechanism of RNA synthesis by NS5B. The indole/benzimidazole class of compounds binds to the 'finger-tip' region and since this region was thought to be critical to maintain the closed conformation of NS5B, it was thus quite revealing for the mechanism of RNA synthesis that they did not inhibit the phase corresponding to elongative RNA synthesis (Figure 5A).[64,99,100,107] Subsequent analysis revealed that the closed conformation of NS5B is only needed for *de novo* initiation, but not elongative RNA synthesis.[61] Site 1 compounds therefore bind at the 'finger-tip' region and prevent proper interaction between the fingers and thumb domains that is critical for initiation of RNA synthesis.[53]

Inhibitors that bind to Site 3 (particularly benzothiadiazines) also inhibited initiation by NS5B, but not the elongation stage of RNA synthesis despite acting at over 20 Å from the 'finger-tip' regions.[37] Site 3 compounds bind within the template channel, and none of the binding residues have been implicated in biochemical analysis to be specifically required for initiation. It is notable that C451 is a residue in the β loop that is thought to be required for proper positioning of the template in the active site[57] and a substitution to an arginine conferred resistance to benzothiadiazines. The benzofurans bind to the 'primer-grip' site and it is possible that this region may be involved with the optimal movement of the thumb and palm domains during initiation complex assembly. Biochemical evidence on the stage in RNA synthesis inhibited by the benzofuran drugs is not available. Site 3 binding compounds may prevent the formation of an overall closed structure in NS5B that will involve structures including the β loop and the 'primer-grip site'.

The RNA synthesis assay used could have affected some of the interpretations of the results concerning the modes of RNA synthesis.[37,64,99] While some studies used templates that could direct both *de novo* initiation and primer extension, others used heteropolymeric primer extension templates in their assays.[64,99] We would like to emphasize the importance to distinguish initiation that occurred by a *de novo* mechanism or whether the first nucleotide was added to a preexisting primer. *De novo* initiation refers to the formation of a phosphodiester bond between the first and second nucleotide. Once the nascent RNA is extended to be 6–8 nt in length, the polymerase ternary complex is thought to undergo some change to allow it to transition to a more processive elongative mode of RNA synthesis.[90] In contrast, assays that examined whether the inhibitors affected the ability of NS5B to extend from an oligonucleotide-primed template will not assess whether *de novo* initiation was affected, but will assess pre-elongation events like productive RNA binding.

A lesson learned from the effects of the inhibitors is that the mode of RNA synthesis by HCV NS5B appears to be intimately linked to the conformation of the polymerase. As stated, the monomeric polymerase may exist in the closed conformation where there is extensive interaction between the finger and thumb domains mediated by structures such as the Δ1 loop, the β loop, Δ2 loop, and the 'primer-grip site' with different regions of the enzyme contributing to the overall closed structure that is thought to be the one involved in *de novo* initiation (Figure 1B). Alternatively, initiation may be through an oligomeric complex consisting of two or more RdRp subunits that result in conformational changes

in each of the subunits that will favor initiation stages in RNA synthesis including productive RNA binding. Thus far, inhibitors that bind Site 1 and Site 3 appear to interfere with the closed NS5B conformation as per crystallographic evidence. Interestingly, they may perturb this conformation and then prevent proper initiation of RNA synthesis while allowing the polymerase to retain the ability to extend from a primed template. As oligomeric contacts between NS5B subunits are thought to be mediated by ionic interactions,[72] it may be a challenge to obtain suitable drugs with appreciable pharmacokinetic properties that will target the NS5B oligomerization step.

The role of cyclophilins in RNA synthesis by NS5B is not as clear, although they are needed to increase RNA binding by NS5B.[116,121] It is possible that the peptidyl-prolyl isomerase activity of cyclophilins could act on the proline residues in NS5B to change the conformation of the monomer molecule and/or higher order structures of NS5B and assist in productive binding to RNA, therefore influencing initiation rather than elongation RNA synthesis (Figure 5A). Notably, I432V and I11V conferred increased affinity for RNA binding, in support of the idea that cyclophyllin A is affecting the NS5B interaction with RNA.

HCV genotypic variation in inhibitor response

HCV exists as six known genotypes and a number of subtypes. Within the infected individual, significant differences in the viral sequences are commonly encountered, demonstrating that each subtype is a quasispecies.[125] NI that inhibit NS5B by effecting chain termination will do so primarily by targeting the elongation stage of RNA synthesis. In contrast, the majority of NNI target the conformation of the polymerase to prevent initiation. With these two mechanisms in mind, it is noteworthy that NI tend to be effective at approximately comparable levels among all HCV genotypes while NNI tend to exhibit genotypic-specific differences in responses.[76,125–129] In fact, significant differences in response to NNI have been noted within different viral sequences isolated from the same individual.[125] This suggests that different viral isolates have either mechanistic differences in the initiation complex assembly or variations in the binding pockets for NNIs.

Gu et al have shown differences in oligomeric properties and enzymatic activities in NS5B from genotype 1a and 1b.[73] It is likely that differences exist in the binding constants for NS5B oligomerization across genotypes to affect the efficiency of initiation of RNA synthesis. Pauwels et al[128] used biochemical assays to show that among the NNIs,

benzimidazoles (Site 1) did not show much variation in IC_{50} values across genotypes except that they were about 100-fold higher for genotype 2a and 2b. Site 2 and Site 3 inhibitors showed significant genotypic variation in responses, consistent with an altered binding site being responsible for the observed differences. For example, a polar residue at position 414 was not tolerated by the 2a NS5B to bind benzothiadiazines while a Q414M mutation partially restored the inhibition. In a similar observation 1,5-benzodiazipines were effective against only genotype 1a and 1b NS5B while Q414M mutation led to only a partial inhibition of the genotype 2a NS5B.[111]

Ludmerer et al amplified the NS5B sequences from patient sera, cloned the cDNAs into a genotype 1b con1 background and assessed them for sensitivity to different NI and NNI.[125] Interestingly, more than 90% of these sequences are split into two major groups of A218, C316, and Q464 (ACQ) which appear in con1, and S218, N316, and E464 which appear in BK isolate.[125] While NI affected all of the replicons, differences existed in the responses to NNI. For a patient treated with benzimidazoles, viruses with changes in NS5B sequences that responded with a difference of almost 20-fold to the drug were found. This difference was more pronounced with the patients with genotype 1b infection than with genotype 1a infection. Furthermore, benzothiadiazines were not effective on isolates from a patient with genotype 1b infection at three times the EC_{50} value (EC_{50} was determined for a consensus con1 NS5B). The response to thiophenes was somewhat uniform among different isolates in the same study.

Herlihy et al[127] found a variation of 0%–7% at the amino acid level in the NS5B sequences from the viral population present in each patient. In this study, replicons were constructed with a con1 background containing consensus NS5B sequences from non-genotype 1 viruses obtained from patient sera and then evaluated for their response to different NI and NNI. While NM107 (2'-C-methylcytidine) and a NS3 protease inhibitor elicited a similar response in chimeric replicons containing NS5B from different genotypes, differences were clear when NNI were tested. Benzimidazoles elicited a similar response in genotypes 1b, 3a, 4a, and 5a, but up to a 30-fold reduction in response from genotype 2a and 2b was noted. Thiophenes had an 8-fold reduction in response from genotype 5a compared to 1b, while genotypes 2b, 3a, and 4a did not have any significant response. Benzothiadiazines did not result in significant response from any of the genotypes at concentrations that were inhibitory to genotype 1b replicons. Interestingly, benzofuran (HCV796) that binds to Site 3 had a comparable response from all genotype

1 and non-genotype 1 NS5B-containing replicons. Notably, the C316Y mutation that confers resistance to HCV-796 is frequently present in viruses resistant to combinations of NS5B and NS3 inhibitor.[104]

These results collectively demonstrate that the viral quasispecies, as well differences between viral genotypes, can be major factors in therapeutic failures. NNI target the initiation complex formation in NS5B, and therefore are dependent on strict conservation of their binding sites for binding and inhibition (Figure 5B). Since NS5B lacks proofreading activity and readily incorporates mutations in the genome, polymorphisms are common in the NNI binding sites.[128] In contrast, NI compete for binding with the NTPs, which should make them effective against all of the HCV genotypes at similar levels.

Changes in the viral genome as well as the genetics of the infected individual could affect the response to the ribavirin-interferon combination therapy that is currently the only approved therapy for HCV infections.[7,130] The 'non-responders' to this combination therapy interestingly have viruses that have about 3-fold more hydrophobic sequences

in the viral proteins along with a pattern of co-varying residues.[131] These predictions remain to be tested in more defined systems. Clearly, more genomic analysis as well as studies in chimpanzees, or mice transplanted with human livers,[17] will be needed in order to improve the strategies for antiviral development against HCV.

Variations within the HCV NS5B sequence and potential impact on effects of NNI

The available data on the emergence of resistant mutations to various inhibitors of NS5B described above prompted us to examine the natural prevalence of these mutations in 480 HCV isolate sequences, which comprised 465 HCV isolate sequences deposited in the HCV database[132] and 15 genotype 6a sequences extracted from NCBI.[133] All the sequences used were complete genome sequences and were divided into the following genotypes further analysis: genotypes 1a, 1b, 1c, 2, 3, 4, 5a, and 6 (Table 1). In summary, genotypes 1a and 1b contained isolates with mutations in the residues that are putatively

Table 1 The presence of potential resistant mutations in the NS5B proteins of HCV from different genotype

Compound	Resistant Mutation	HCV genotype (number of NS5B sequences analyzed)							
		1a (166)*	1b (232)	1c (3)	2# (17)	3# (7)	4# (8)	5a (2)	6# (45)
2' ribose modified nucleoside analogs	S282T-1b	S/R (1)^					S/R (1)		
	S96T-1b								
	N142T-1b		N/S (23); **N/T (1)**						
Ribavirin	Y415F-1a	**Y/F (2)**	Y/F (3)			Y/F (2)			Y/F (1)
Benzimidazoles	P495A/L-1b								
Thiophene-2-carboxylic acid	L419M-1b		L/I (2)		L/V (3)	L/I (7)	L/I (8)		L/I (45)
	M423T/I/V-1b	M/A (1); **M/I (1)**						**M/I (2)**	
	I482L-1b	I/L (1)				I/L (7)	I/L (8)		**I/L (45)**
Benzothiadiazine	M414T-1b	M/V (1)	M/I (1)		M/Q (17)		M/I (2); M/V (6)		
	C451R-1b	C/Y (1); C/V (1)	C/R (1); C/N (1); C/H (3); C/I (7); C/S (1); C/T (22); C/Y (9); C/V (2)	C/V (2); C/T(1)	C/V (17)	C/T (1); C/V (6)	C/T (8)	C/V (2)	C/T(45)
	G558R-1b						G/E (1)		
	H95R-1b		H/L (1)						**H/R (1)**
Indole-N-acetamides	L392I-1b	L/F (5)	L/F (4); **L/I (5)**		L/I (13)				**L/I (1)**
	V494A-1b				**V/A (17)**	V/C (4); V/I (3)			**V/A (29);** V/M (1)
HCV-796	C316Y-1b		C/N (93); **C/Y (1)**						
Dihydroxypyrimidines	G152E-1b	P/A (2)	P/A (4); P/S (1)		P/A (13)	P/A (1); P/R (1)	P/A (1)		P/S (1)
	P156L-1b								

*The number of sequences analyzed in each genotype.^The numbers in parentheses indicate the number of the mutation identified in the data set. Grids left blank had no mutation identified in the analysis. The original residue from the typical HCV sequence is followed with the residue identified in one letter amino acid code. Mutations identified in red are identical or highly similar to those characterized to be resistant to the compounds. 2# includes genotype 2a, 2b, 2c, 2k; 3# includes genotype 3a, 3b, 3k; 4# includes genotype 4a, 4d; 6# includes genotype 6a–6q, 6t and one unassigned subtype.

involved with NNI that bind at Site 2 and Site 3. The residues that bind to Site 2 NNI, particularly L419, had polymorphisms in several HCV genotypes. The I482L mutation in Site 2 NNI was present in genotypes 1a, 3, 4, and 6. Residue C451 that is involved with binding to Site 3 NNI also had polymorphisms all of the HCV genotypes. Mutation Y415F that conferred resistance to ribavirin was characteristically found in all the genotypes except genotypes 1c, 2, and 5a. Mutations that contributed to resistance to Indole-N-acetamides, L392I and V494A, were in isolates from 1b, 2, and 6.[134] Interestingly, mutation C316Y that was commonly found in strains with resistance to HCV-796 was only found in genotype 1b and at a low frequency.[135] P156 that helped to confer resistance to the pyrophosphate mimic, dihydroxypyrimidines, was commonly found to be changed, although not to the leucine reported by Powdrill et al[85] However, the G152 residue did not vary across the genotypes. In brief, this analysis reveals that sequence variations that are already present in various HCV genotypes could significantly impact antiviral therapies.

Summary

This review summarized the structural and functional aspects of NS5B and how they impact both RNA synthesis and the development of inhibitors. Clearly much work remains before control of HCV infection is possible. It is also increasingly clear that any inhibitors that target NS5B must be used in combination with other HCV and/or cellular targets to affect the outcome of persistent HCV infection.

Acknowledgment

Disclosure

The authors report no conflicts of interest in this work.

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