Genetics of *IL28B* and HCV—response to infection and treatment

C. Nelson Hayes, Michio Imamura, Hiroshi Aikata and Kazuaki Chayama

Abstract | The *IL28B* locus attracted the attention of HCV researchers after a series of genome-wide association studies independently identified a strong association between common *IL28B* polymorphisms and the outcome of PEG-IFN-α plus ribavirin combination therapy in patients chronically infected with HCV genotype 1. This association was subsequently replicated for other HCV genotypes and has been linked to spontaneous eradication of HCV, development of steatosis and biochemical changes (such as altered levels of γ-glutamyl transpeptidase and LDL). Despite the introduction of direct-acting antiviral drugs, *IL28B* genetics are likely to play a part in patient selection and treatment decisions—moving towards a personalized approach to therapy. In HCV-infected patients with the so-called favourable *IL28B* genotype (rs12979860 CC; associated with better treatment response), hepatic expression levels of *IL28B* and interferon-stimulated genes seem to be reduced at baseline, but are induced more strongly after IFN-α administration, perhaps resulting in more effective elimination of the virus. Clarification of the mechanisms underlying these biological phenomena will lead to improved understanding of the antiviral effects of IFN-λ and, ideally, to the development of better therapies against HCV infection. This Review summarizes current understanding of the role of *IL28B* in HCV infection and response to therapy.

Hayes, C. N. *et al. Nat. Rev. Gastroenterol. Hepatol.* **9**, 406–417 (2012); published online 29 May 2012; doi:10.1038/nrgastro.2012.101

Introduction

Shortly after the identification of HCV in 1989,[1] the development of HCV antibody tests—and thus improved screening and diagnosis—began to dramatically reduce the number of new cases of HCV infection by increasing awareness of this condition and by preventing transmission of HCV by blood transfusion or transplantation.[2] However, in 2011, an estimated 130–170 million people were chronically infected with HCV, putting them at an increased risk of cirrhosis, hepatocellular carcinoma and liver failure.[3] Despite the high costs and substantial toxicity of PEG-IFN-α plus ribavirin combination therapy, fewer than half of patients infected with the most common HCV genotype are able to achieve a sustained virological response (SVR),[4] which is defined as undetectable HCV RNA 6 months after the end of treatment. Although telaprevir and boceprevir are expected to greatly improve the rate of SVR, these direct-acting antiviral agents must currently be administered in combination with interferon (IFN)-α and ribavirin to help suppress viral breakthrough.[5] Identification of factors affecting response to IFN-α therapy, therefore, remains an important goal.

In 2009, a series of independent studies reported that patients infected with HCV genotype 1b who had a common variant in the *IL28B* locus (rs12979860 CC or rs8099917 TT) were significantly ($P < 7.1 \times 10^{-08}$) more likely to respond to PEG-IFN-α plus ribavirin combination therapy than patients with other *IL28B* variants.[6–8] Such patients were also more likely to spontaneously resolve acute HCV infection without treatment.[9] These results have added a new dimension to HCV research and offer the potential for more personalized and effective therapy. In the 2 years since the publication of these landmark papers, hundreds of studies have examined the role of *IL28B* polymorphisms in HCV infection and treatment. This Review summarizes some of the major findings of the role of the *IL28B* locus in HCV infection, describing background information on *IL28B* and the part IL-28B (also known as IFN-λ3) plays in the elimination of HCV and response to therapy.

IL28 gene family and innate immunity

The type III IFN-λ family consists of three members: the cytokines IL-29, IL-28A and IL-28B (also known as IFN-λ1, IFN-λ2 and IFN-λ3, respectively). Although functionally an IFN, these cytokines are structurally related to the IL-10 family of cytokines.[10] Discovered in 2003 by computational prediction, the *IL28A*, *IL28B* and *IL29* genes are located in a cluster on chromosome 19 (Figure 1).[11,12] Amino acid sequences of the two isoforms of IL-28 (IL-28A and IL-28B) have 96% homology, both being 81% identical to the amino acid sequence of IL29.[12] As with IFN-α, the three IFN-λs can be triggered by viral infection and induce antiviral and antitumour activity through both innate and adaptive immune system pathways.[13,14] As shown in Figure 2a, although both IFN-α and IFN-λ family cytokines signal through

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Competing interests
The authors declare no competing interests.

the Jak–STAT (Janus kinase–signal transducer and activator of transcription) pathway[11,15] and activate an overlapping set of IFN-stimulated genes (ISGs),[16] fundamental differences exist in gene expression between IFN-α and IFN-λ.[17] Whereas IFN-α binds to the constitutively expressed type I IFN receptor, IFN-λ cytokines bind to a heterodimer of the IL-10 and IL-28 receptors (IL10R and IL28R, respectively),[11] the latter of which is only expressed in restricted cell types, including hepatocytes, epithelial cells and plasmacytoid dendritic cells.[18] Although both types of IFN induce expression of many of the same genes, the change in ISG expression in response to IFN-λ tends to be weaker overall but increases steadily over time,[16] whereas IFN-α triggers an early peak in ISG expression followed by a rapid decline.[19] This phenomenon seems to result from the distinct kinetics of IFN-λ-mediated activation of STAT,[19] involving differences in transcription factor remodelling efficiency[16] and greater dependence on the NF-κB pathway.[20] Therefore, differences in ISG expression through type I and III IFNs are possible under specific conditions.[20]

Key points

- The 130–170 million people chronically infected with HCV have an increased risk of cirrhosis, hepatocellular carcinoma and liver failure
- Several single nucleotide polymorphisms upstream of the *IL28B* gene are associated with spontaneous clearance of HCV and improved response to PEG-IFN-α plus ribavirin combination therapy
- In patients with the so-called favourable *IL28B* allele (rs12979860 CC), associated with better response to therapy, HCV RNA levels decline rapidly with treatment and IFN-α therapy induces strong interferon-stimulated gene (ISG) expression
- In patients with unfavourable *IL28B* genotypes (rs12979860 CC/TT), ISG expression tends to be refractory to further IFN stimulation, resulting in poor response to IFN therapy
- *IL28B* genotype might also predict response to telaprevir triple therapy, although it might not be as effective at predicting the treatment response in this scenario as with PEG-IFN-α plus ribavirin combination therapy

Effects of *IL28B* polymorphisms

An inherent limitation of genome-wide association studies (GWAS; Box 1) is the difficulty in tracing the link between changes at a single base and differences in the resulting phenotype. Understanding the genetic basis of differences in resolution of HCV infection is yet more complex because it involves coordinated activity between innate and adaptive immune effectors and is affected by multiple host and viral factors. The fairly strong independent effect of *IL28B* polymorphisms therefore suggest a role in the high-level regulation of antiviral defence against HCV. The effects of *IL28B* polymorphisms have been investigated for a number of aspects of response to HCV infection and treatment, including response to therapy, natural elimination of the virus, and changes in gene expression and lipid metabolism.

PEG-IFN-α plus ribavirin combination therapy

Striking differences in HCV clearance and response to treatment among ethnic groups,[21] as well as among patients infected with the same HCV inoculum,[22] have long suggested a role for host genetic factors. Early candidate gene studies identified single nucleotide polymorphisms (SNPs) in genes encoding proteins involved in response to HCV infection—including osteopontin, MxA (also known as MX1), OAS1, EIF2AK2 (also known as PKR), IFN-α receptor 1, and MAPKAPK3[23–26]—but practical insights gained from these studies have been limited. SNPs are defined as base pair variants at a specific genomic position that have a frequency greater than 1%.[27] As the number of SNPs examined increases, the probability of detecting spurious associations also increases sharply and a drawback of candidate gene studies, in particular, is the need to select appropriate target genes prior to analysis, limiting the ability to detect novel associations. Advances in high-throughput screening, however, have made it possible to screen representative SNPs across the entire genome using GWAS. This 'hypothesis-free' approach can detect SNPs associated with disease phenotype or response to treatment without requiring *a priori* candidate gene selection. Nonetheless, most SNPs are thought to have small, cumulative effects that require large sample sizes to be detected, and results of GWAS often fail to be replicated in other populations. Although the importance of ethnicity in treatment outcome suggests a genetic basis, the simultaneous independent discovery of a common variant upstream of the *IL28B* gene and the magnitude of its effect on treatment outcome was unusual (Table 1).[6–8]

Ge *et al.*[6] published the first report of an association between a common polymorphism on chromosome

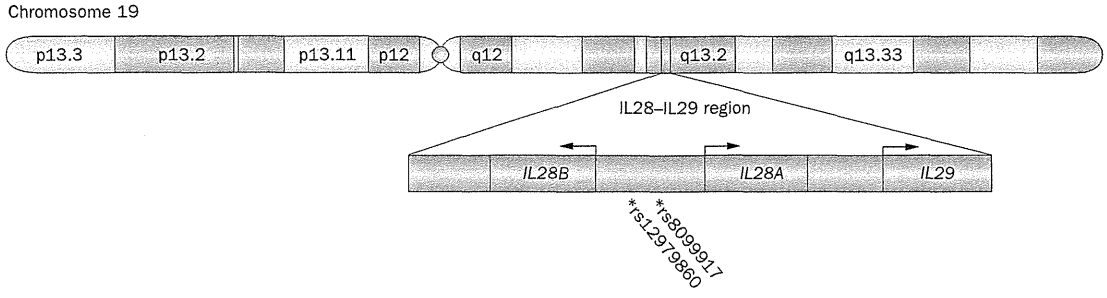

Figure 1 | The *IL28–IL29* locus on chromosome 19. The genes encoding the three members of the IFN-λ family, IL28A (IFN-λ2), IL28B (IFN-λ3) and IL29, (IFN-λ1) are clustered together on chromosome 19. The most important and validated SNPs with respect to response to IFN-α therapy, rs12979860 and rs8099917, are upstream of both *IL28B* and *IL28A* (owing to their antiparallel orientation), but are physically closer to *IL28B*.

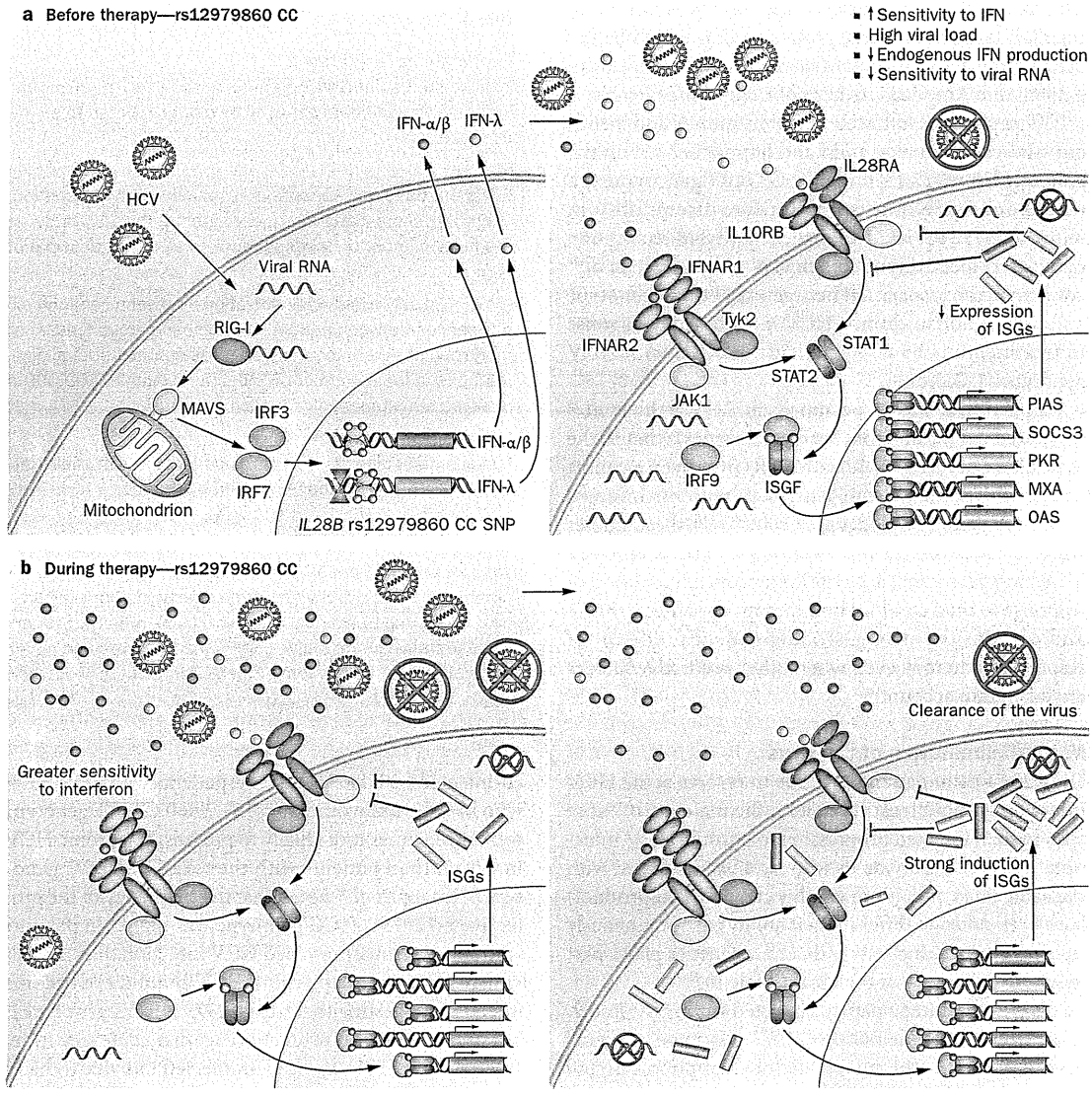

Figure 2 | Potential role of the favourable *IL28B* genotype in the response to interferon therapy. **a** | Intracellular HCV RNA is detected by surveillance molecules of the innate immune system, including the RIG-I–IFIH1 pathway, which causes the adaptor protein MAVS to induce expression and secretion of IFN-α, IFN-β and IFN-λ via IRFs. IFNs are recognized by receptors on the cell surface and initiate a signal cascade that results in induction of a large number of ISGs that collectively establish an antiviral state hostile to viral replication. IFN-α and IFN-β are recognized by IFNAR, whereas IFN-λ is recognized by the IL10R–IL28R receptor complex. Both receptors activate the Jak-STAT pathway, which induces the translocation of an ISGF complex to the nucleus, where it binds to the interferon-stimulated response elements of multiple ISGs. In individuals with the favourable allele (rs12979860 CC), the presence of viral RNA seems to induce only weak expression of IFN-λ, which in turn induces weak ISG expression. Although the response might be sufficient to clear the virus at low viral loads, the cell seems fairly tolerant of the virus and high viral loads can accumulate. **b** | During treatment, however, when IFN-α is administered, IFN signal transduction is unimpeded and results in strong ISG induction. As a result, these patients tend to respond well to therapy and are able to clear the virus efficiently. Abbreviations: IFIH1, IFN-induced helicase C domain-containing protein 1; IFNAR, IFN-α/β receptor 1; IL10R, IL-10 receptor; IL28R, IL-28 receptor; IRF, IFN regulatory factor; ISG, IFN-stimulated gene; ISGF, IFN-stimulated gene factor; Jak, Janus kinase; MAVS, mitochondrial antiviral-signalling protein; MXA, myxovirus resistance protein 1 (also known as MX1); OAS, 2′5′-oligoadenylate synthase; PIAS, E3 SUMO-protein ligase PIAS; PKR, protein kinase RNA-activated (also known as EIF2AK2); RIG-I, retinoic-acid inducible protein I; SOCS3, suppressor of cytokine signaling 3; STAT, signal transducer and activator of transcription.

19 and SVR on the basis of an analysis of a large cohort of white, African American and Hispanic patients with chronic HCV genotype 1 infection who were treated with 48 weeks of combination therapy with PEG-IFN-α plus ribavirin.[6] The rs12979860 SNP identified in this study is located in a noncoding region 3 kb upstream of *IL28B*. Patients homozygous for the major allele with the so-called favourable genotype (rs12979860 CC) were twice as likely to achieve an SVR as patients with the minor risk allele (rs12979860 TT or CT) following combination therapy.

The frequency of the major allele was proportional to the SVR rate across ethnic groups and explained half of the difference in SVR rates between African-American patients and American patients of European descent.

This report was followed by publication of independent studies by Tanaka *et al.*[7] and Suppiah *et al.*[8] on the role of rs8099917 (TT versus GT/GG genotypes), a neighbouring SNP in strong linkage disequilibrium with rs12979860, in 314 Japanese and 848 Australian patients, respectively. A fourth GWAS by Rauch *et al.*[28] confirmed the association between rs8099917 genotype and progression to chronic HCV infection and response to treatment in 465 white patients infected with HCV genotypes 1, 2, 3 or 4.

Using a candidate gene approach, McCarthy *et al.*[29] replicated the findings of Ge and colleagues[6] (that is, the association of rs12979860 with SVR) in a diverse cohort of 231 white and African-American patients infected with HCV genotypes 1, 2, or 3. Collectively, these studies suggest that either the rs12979860 CC or the rs8099917 TT genotype confers a 2–3-fold improved likelihood of response to dual combination therapy for chronic HCV and remains the strongest independent predictor of response to therapy even when other predictive factors are taken into account.[6,28]

Box 1 | Glossary terms for genome-wide studies

Candidate gene approach
Prior to the use of GWAS, genetic association studies were often performed by sequencing candidate genes known or suspected to be involved in with a disease or condition.

SNP
SNPs are base pair variants at a specific genomic location. Typically, only common SNPs with a population frequency greater than 1% or 5% are considered, due to the large number of samples required to detect associations involving rare SNPs.

GWAS
GWAS typically examine associations between common single nucleotide differences between patients in a disease group (cases) and a healthy group (controls) or other dichotomous classifications. Using high-throughput array-based methods, a large number of SNPs (for example, 500,000 or 1 million) can be assayed simultaneously for each patient.

Linkage disequilibrium
Linkage disequilibrium refers to combinations of alleles at different loci that occur together more often than expected by chance.

Causative SNP versus tagging SNPs
Due to linkage disequilibrium, GWAS can detect associations between a response variable and multiple SNPs in a region of DNA. In many cases, only one or a small number of SNPs directly affect the phenotype (for example, by changing an amino acid or altering transcription factor binding affinity). SNP arrays are based on a representative set of tagging SNPs that are expected to fall within linkage blocks that collectively cover most of the genome but may not include the causative SNPs.

Abbreviations: GWAS, genome-wide association studies; SNP, single nucleotide polymorphism.

Natural elimination of the virus

Only 20–30% of patients are able to resolve acute HCV infection without treatment, with the majority of those who remain infected progressing to chronic HCV infection.[9] However, individuals who have been infected with the same HCV inoculum (in this case, tainted product) have been noted to differ in their ability to spontaneously resolve the virus, suggesting that host genetics play a part in natural clearance of the virus (Table 2).[22]

In a GWAS of 1,362 patients infected with HCV, Rauch *et al.*[28] found that the rs8099917 TT genotype (patients homozygous for the major allele) strongly predicted spontaneous clearance of HCV infection. Thomas and colleagues[9] examined whether the SNP identified in the Ge *et al.*[6] study (rs12978860) was also associated with spontaneous clearance. They genotyped 1,008 patients with acute HCV infection and found that those with the rs12979860 CC genotype were more likely to spontaneously clear the virus than those with rs12979860 CT or TT genotype.[9] Tillmann *et al.*[30] also confirmed these results in a study of 136 German women, in whom spontaneous clearance occurred more often in patients with the CC genotype than either non-CC (CT or TT) genotype. Patients with a non-CC genotype were more likely to spontaneously clear the virus when they developed jaundice, but jaundice was not associated with viral clearance in patients with the CC genotype.[30]

Ruiz-Extremera and colleagues[31] examined the role of *IL28B* polymorphisms on vertical transmission of HCV between mother and child and found that whereas *IL28B* genotype in the mother and child are unrelated to vertical transmission, children with the rs12979860 CC genotype were more likely to spontaneously clear HCV genotype 1 infection. In a study of 138 Brazilian patients co-infected with HCV and HIV, patients with acute HCV who had the unfavourable rs12979860 CT/TT genotype were three times more likely to progress to chronic HCV infection than patients with the rs12979860 CC genotype.[32] Knapp *et al.*[33] noted that the frequency of the protective rs12979860 CC genotype was higher in patients who spontaneously resolved HCV infection than in individuals who were exposed to HCV but did not become infected, suggesting that the rs12979860 CC genotype is not associated with protection against acute infection. Interestingly, HCV-exposed uninfected individuals had a high frequency of killer cell immunoglobulin-like receptor 2DL3:group 1 HLA-C (KIR2DL3:HLA-C1),[33] which highlights the importance of the innate immune system in antiviral defence and suggests other heritable factors might be involved.

Even though high viral load is associated with poor response to treatment,[34] multiple studies have reported an association between high viral load and the favourable *IL28B* genotype (rs12979860 CC).[6,29,35–37] One potential explanation for this phenomenon is that patients with the favourable allele might be able to spontaneously clear the virus when the viral load is below a certain threshold. As a result, patients with the favourable *IL28B* genotype presenting with low viral loads might be relatively uncommon. Understanding how an individual SNP enables some patients to efficiently clear the virus in the absence of therapy should yield insight into the regulation of antiviral defences.

Change in viral load

Although the *IL28B* SNP remains the strongest pretreatment predictor of SVR,[38] on-treatment predictors such

Table 1 | Associations between *IL28B* homozygous major allele and response to HCV therapy

Study	SNP	Total number of patients	Odds ratio	*P* value	Population	HCV genotype
SVR with PEG-IFN-α plus ribavirin combination therapy						
Ge *et al.* (2009)[6]	rs12979860 CC	1,137	3.10	1.21×10^{-28}	White, African American, Hispanic	1
Suppiah *et al.* (2009)[8]	rs8099917	293	1.98	7.06×10^{-8}	White	1
Tanaka *et al.* (2009)[7]	rs8099917	142	12.10	3.11×10^{-15}	Japanese	1
Rauch *et al.* (2010)[28]	rs8099917	465	5.20	5.47×10^{-8}	Swiss	1–4
McCarthy *et al.* (2010)[29]	rs12979860 CC	231	5.80	9.00×10^{-6}	White, African American	1–3
Thompson *et al.* (2010)[38]	rs12979860 CC	1,671	5.20	$<1.00\times10^{-4}$	White, African American, Hispanic	1
Ochi *et al.* (2011)[37]	rs8099917	594	2.46	6.52×10^{-8}	Japanese, Taiwanese	1, 2
SVR with telaprevir triple therapy						
Akuta *et al.* (2010)[96]	rs8099917	66	10.60	$<1.00\times10^{-3}$	Japanese	1
Chayama *et al.* (2011)[70]	rs8099917	94	8.33	1.40×10^{-2}	Japanese	1
SVR with combination therapy for non-1b HCV genotypes*						
Mangia *et al.* (2010)[63]	rs12979860 CC	268	1.76	1.13×10^{-6}	White	2, 3
Asselah *et al.* (2011)[64]	rs12979860 CC	164	3.32	8.00×10^{-4}	Egyptian, European, sub-Saharan African	4
Kawaoka *et al.* (2011)[65]	rs8099917	83	4.35	2.00×10^{-2}	Japanese	2
Lindh *et al.* 2011[66]	rs12979860 CC	341	NA	2.00×10^{-2}	White	2, 3
Sakamoto *et al.* (2011)[67]	rs8099917	129	3.96	1.04×10^{-1}	Japanese	2
Sarrazin *et al.* (2011)[68]	rs12979860 CC	267	2.80	9.00×10^{-3}	German population	2, 3

Representative studies are shown, along with results based on the most significant SNP (rs12979860 or rs8099917), sample size, *P* value, odds ratio with respect to the favourable allele (if reported), study population, and viral genotype. *Initial *IL28B* studies focused mainly on the difficult-to-treat genotype 1 with 48 weeks of PEG-IFN-α plus ribavirin combination therapy. Other genotypes may respond better to therapy, and treatment guidelines may differ slightly with respect to stopping rules and overall duration of therapy.[97] Abbreviations: NA, not available; SVR, sustained virological response.

as rapid virological response (RVR; that is, undetectable HCV RNA by week 4 of therapy) are more directly linked to treatment outcome (Table 2).[39,40] When the effect of RVR is taken into account, *IL28B* genotype might no longer be an important predictor of treatment outcome,[41] especially during infection with HCV genotypes other than 1b.[42] However, *IL28B* genotype influences on-treatment predictors in several ways. On the one hand, initial baseline viral load tends to be higher in patients with the favourable *IL28B* genotype.[6,34–37] On the other hand, these patients seem to clear the virus more efficiently at each time point examined (for example, 48 h,[43] 4 weeks,[34] 12 weeks,[44] and so on). Consequently, patients with the favourable *IL28B* genotype are more likely to achieve RVR,[38,39,45] and even among patients who fail to achieve RVR, *IL28B* genotype remains the strongest predictor of SVR.[38,44] *IL28B* genotype might be linked to higher death rates of infected hepatocytes in patients with the favourable genotype[43] as well as lower daily viral production rates,[46] which could partially explain the improved efficiency of virological response in those with the *IL28B* CC genotype compared with non-CC *IL28B* genotypes.

ISG expression and viral replication

Both IFN-α and IFN-λ induce expression of hundreds of target ISGs and, subsequently, an antiviral state. Consequently, ISG expression might be the best predictor of treatment response regardless of *IL28B* genotype,[47] although genotyping one or a few *IL28B* SNPs is probably more practical than assaying ISG expression levels. Unexpectedly, however, hepatic ISG expression was found to be markedly higher in patients with the unfavourable *IL28B* allele,[48] and patients with high baseline ISG expression levels were found to respond poorly to IFN-α therapy.[49] Hepatic expression of several ISGs—including *MXA* (also known as *MX1*), *EIF2AK2*, *OAS1* and *ISG15*—was lower in patients with the favourable *IL28B* genotype than in those with the unfavourable *IL28B* genotype;[50] conversely, expression of genes that suppress the antiviral state were reduced.[51] However, Shebl *et al.*[52] found no evidence of an association between *IL28B* genotype and ISG expression in hepatocytes from uninfected individuals, implying that the association between *IL28B* genotype and ISG expression in the liver does not reflect normal expression levels in healthy individuals.[52] HCV infection in nonresponders might result in continual, but ineffectual, intrahepatic ISG expression, including expression of IFN-signalling inhibitors. Cells with such preactivated ISGs might not only fail to effectively clear the virus, but might have reduced sensitivity to therapeutic IFN-α (Figure 3).[49,53]

Biochemical changes and hepatic steatosis

During chronic HCV infection, differences in the cytokine profiles induced by the *IL28* polymorphisms

Table 2 | Associations between *IL28B* homozygous major allele and host response to HCV

Study	SNP	Total number of patients	Odds ratio	*P* value	Population	HCV genotype
Spontaneous clearance of HCV infection						
Thomas *et al.* (2009)[9]	rs12979860 CC	1,008	3.03	$<1.00\times10^{-12}$	European and African ancestry	1
Grebely *et al.* (2010)[71]	rs8099917 TT	163	3.78	4.40×10^{-2}	Australian	1–3
Montes-Cano *et al.* (2010)[72]	rs12979860 CC	731	3.13	6.20×10^{-5}	Spanish	NA
Tillmann *et al.* (2010)[30]	rs12979860 CC	136	NA	$<1.00\times10^{-3}$	German women	1b
Knapp *et al.* (2011)[33]	rs12979860 CC	397	2.97	1.00×10^{-4}	UK	NA
Rauch *et al.* (2010)[28]	rs8099917 TT	1,362	2.31	6.07×10^{-9}	Swiss	1–4
Improved rapid and early viral dynamics (RVR, EVR)						
Thompson *et al.* 2010[38]	rs12979860 CC	1,671	NA	$<1.00\times10^{-4}$	White, African American, Hispanic	1
Bochud *et al.* (2011)[41]	rs12979860 CC	242	NA	7.00×10^{-3}	White	1–3
Hayes *et al.* (2011)[35]	rs12979860 CC	817	1.37	1.40×10^{-8}	Japanese	1
Lin *et al.* (2011)[44]	rs12979860 CC	191	NA	$<1.00\times10^{-3}$	Taiwanese	1
Stattermayer *et al.* (2011)[45]	rs12979860 CC	682	NA	$<1.00\times10^{-3}$	Austrian	1–4
Ochi *et al.* (2011)[37]	rs8099917 TT	594	NA	6.70×10^{-5}	Japanese, Taiwanese	1, 2
Increased baseline viral load						
Ge *et al.* (2009)[6]	rs12979860 CC	1,475	NA	1.20×10^{-10}	White, African American, Hispanic	1
McCarthy *et al.* (2010)[29]	rs12979860 CC	231	2.13	6.10×10^{-3}	White, African American	1–3
Lindh *et al.* (2011)[66]	rs12979860 CC	341	NA	$<1.00\times10^{-3}$	White	2, 3
Ochi *et al.* (2011)[37]	rs8099917 TT	594	2.46	1.00×10^{-2}	Japanese, Taiwanese	1, 2
Increased viral clearance rate and death rates among infected hepatocytes						
Hsu *et al.* (2011)[46]	rs8099917 TT	145	NA	$<2.34\times10^{-2}$	Taiwanese	1, 2
Scott *et al.* (2011)[43]	rs12979860 CC	20	NA	4.00×10^{-2}	White, African American	1, 3

Representative studies are shown, along with results based on the most significant SNP (rs12979860 or rs8099917), sample size, *P* value, odds ratio with respect to the favorable allele (if reported), study population, and viral genotype. Abbreviations: EVR, early virological; NA, not available; RVR, rapid virological response; SVR, sustained virological response.

lead to altered biochemical and inflammatory states (Table 3).[54] Patients with an unfavorable *IL28B* genotype have been shown to have an increased risk of HCV-associated cirrhosis and more severe fibrosis.[55,56] However, Marabita *et al.*[57] reported that when the date of infection is taken into account, *IL28B* genotype is no longer associated with rate of fibrosis progression.

Lipid metabolism has an important role in HCV infection, and patients with high cholesterol levels tend to respond better to IFN therapy than those with lower cholesterol levels.[58] However, HCV infection and IFN administration both tend to depress cholesterol levels. Patients with the favourable *IL28B* genotype tend to have higher levels of total cholesterol, apolipoprotein B and LDL-cholesterol,[58] as well as a lower frequency of hepatic steatosis, than patients with the unfavourable *IL28B* genotype.[59]

Identification of the causative SNP

Many treatment-associated SNPs in the *IL28B* locus have been reported, although most studies have examined either rs12979860 or rs8099917.[28] Although rs12979860 seems to have better predictive value in some populations,[60] haplotypes that include both SNPs might be more accurate than either SNP individually.[61] This finding suggests that neither SNP is directly causative, but that both are linked to one, or more, as-yet-unidentified causative SNPs. Linkage disequilibrium (Box 1) is lowest in the African-American population, suggesting that examination of this group offers the best chance to identify the causative SNP.[6,62] Massively parallel sequencing has been used to identify new *IL28B* variants and Smith and colleagues[62] reported two SNPs—rs4803221 and rs7248668—that are more strongly associated with treatment failure than rs8099917. The authors do, however, point out that the high degree of homology among *IL28B* and *IL28A* complicates the task of unambiguous read mapping and increases the risk of detecting spurious associations.[62]

Although SNPs typically have little individual effect on treatment outcome, the minor allele (rs12979860 CT/TT) in the *IL28B* locus increases the risk of treatment failure 2–3-fold (observation based on references in Table 1), suggesting a direct effect on gene expression

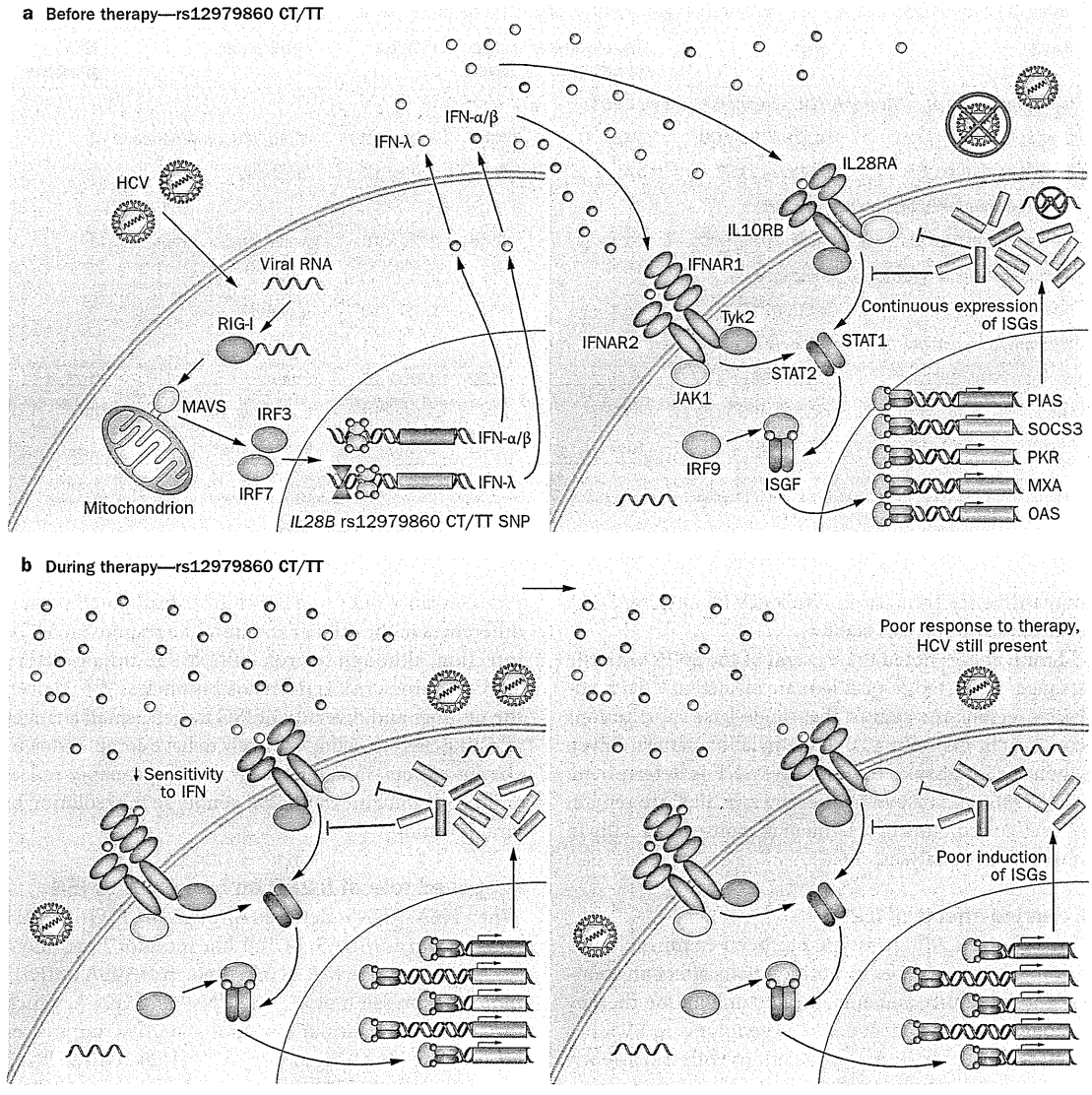

Figure 3 | Potential role of the unfavourable *IL28B* genotype in the response to interferon therapy. **a** | Intracellular HCV RNA is detected by surveillance molecules of the innate immune system, including the RIG-I–IFIH1 pathway, which causes the adaptor protein MAVS to induce expression and secretion of IFN-α, IFN-β and IFN-λ via IRFs. IFNs are recognized by receptors on the cell surface and initiate a signal cascade that results in induction of a large number of ISGs that collectively establish an antiviral state hostile to viral replication. IFN-α and IFN-β are recognized by IFNAR, whereas IFN-λ is recognized by the IL10R–IL28R receptor complex. Both receptors activate the Jak-STAT pathway, which induces the translocation of an ISGF complex to the nucleus, where it binds to the interferon-stimulated response elements of multiple ISGs. Unlike patients with the favourable *IL28B* (rs1297860 CC) genotype, in which viral RNA induces only modest ISG expression, patients with the unfavourable genotype (rs12979860 CT/TT) tend to have higher baseline ISG expression levels, suggesting continuous stimulation of the IFN signaling pathway in the presence of the virus. Nonetheless, the level of ISG expression seems to be insufficient to clear the virus, at the same time triggering negative regulation of the IFN signaling pathway through IFN-inhibitory molecules such as SOCS3 and PIAS. These pathways negatively regulate Jak-STAT signaling and make the cell less responsive to IFN signaling. **b** | As a result, even when IFN-α is administered as part of therapy, the cell is unable to induce a strong ISG expression, and the patient responds poorly to therapy. Abbreviations: IFIH1, IFN-induced helicase C domain-containing protein 1; IFNAR, IFN-α/β receptor 1; IL10R, IL-10 receptor; IL28R, IL-28 receptor; IRF, IFN regulatory factor; ISG, IFN-stimulated gene; ISGF, IFN-stimulated gene factor; Jak, Janus kinase; MAVS, mitochondrial antiviral-signalling protein; MXA, myxovirus resistance protein 1 (also known as MX1); OAS, 2'5'-oligoadenylate synthase; PIAS, E3 SUMO-protein ligase PIAS; PKR, protein kinase RNA-activated (also known as EIF2AK2); RIG-I, retinoic-acid inducible protein I; SOCS3, suppressor of cytokine signaling 3; STAT, signal transducer and activator of transcription.

resulting from a single base change. A number of possible mechanisms exist, and so far little evidence is available to reject some of the possibilities. The causative *IL28B* SNP might affect the strength, timing or specificity of *IL28B* expression by altering binding of transcription factors, enhancers or other regulatory elements, or it

Table 3 | Associations between *IL28B* homozygous major allele and biochemical and hepatic changes

Study	SNP	Total number of patients	Odds ratio	*P* value	Population	HCV genotype
Increased levels of cholesterol, LDL and apolipoprotein B100						
Li *et al.* (2010)[58]	rs12979860 CC	746	NA	8.90×10^{-10}	White, African American	1
Aizawa *et al.* (2011)[73]	rs8099917 TT	148	NA	6.40×10^{-3}	Japanese	1
Reduced frequency of hepatic steatosis						
Tillmann *et al.* (2011)[59]	rs12979860 CC	325	3.45	1.20×10^{-2}	White, African American	1
Reduced levels of γ-glutamyl transpeptidase						
Abe *et al.* (2010)[54]	rs8099917 TT	364	NA	1.00×10^{-3}	Japanese	1
Inflammatory activity, fibrosis and cirrhosis risk						
Barreiro *et al.* (2011)[76]	rs12979860 CT/TT	304	2.32	1.00×10^{-2}	Spanish	1, 3, 4
Fabris *et al.* (2011)[55]	rs12979860 CT/TT	412	NA	5.00×10^{-4}	Italian (white)	1–4
Falleti *et al.* (2011)[56]	rs12979860 CT/TT	629	1.68	$<5.00\times10^{-2}$	Italian (white)	1–4

Representative studies are shown, along with results based on the most significant SNP (rs12979860 or rs8099917), sample size, *P* value, odds ratio with respect to the favorable allele (if reported), study population, and viral genotype. Abbreviations: EVR, early virological; NA, not available; RVR, rapid virological response; SVR, sustained virological response.

may influence translation efficiency by altering DNA accessibility or mRNA stability.

Smith *et al.*[62] noted that several of the SNPs with the strongest reported associations are located in CpG regulatory regions and suggest that single-base substitutions could act by disrupting DNA methylation patterns. Even when the identity of the causative SNP is determined, rs12979860 and rs8099917 are, however, likely to remain as useful predictors of treatment response, especially in retrospective analyses.

Extended effects of *IL28B*

The role of *IL28B* genotype has been examined for a number of phenotypes in addition to its effect on spontaneous clearance and outcome of combination therapy (Tables 1–3). The effect of *IL28B* genotype on SVR has been replicated in diverse populations with consistently high odds ratios for outcome of therapy and spontaneous clearance (OR; range 2.5–12).[6–8,28,36–38] The effect seems to be strongest for difficult-to-treat HCV genotypes 1 and 4, but has also been reported for HCV genotypes 2 and 3, with intermediate ORs (1.5–4).[63–68] Initial evidence suggests that *IL28B* genotype might also be predictive of outcome after telaprevir triple therapy.[69,70] Multiple studies have also documented the effect of *IL28B* genotype on spontaneous clearance of the virus, although most studies have focused on patients of European ancestry[9,29,32,71,72] and few studies have examined the role, if any, of *IL28B* in exposed, uninfected individuals.[32]

IL28B genotype seems to be associated with differences in viral load early in treatment. As already mentioned, patients with the favourable genotype tend to have fairly high viral loads prior to treatment[6,35–37] that then rapidly decrease in the early weeks of therapy (for example RVR or early virological response).[34,37,38,41,44,45] The favourable *IL28B* genotype is also associated with biochemical differences, including increased cholesterol and LDL levels and reduced γ-glutamyl transpeptidase levels.[54,58,73] Differences in ISG expression levels,[48,50,74,75] viral clearance rate[46] and hepatocyte death rate[43] suggest differences in the cellular and immune response to HCV infection, although the role of *IL28B* in inflammatory activity, fibrosis risk and cirrhosis is unclear.[54–57,76] Given the number and diversity of ISG targets, small changes affecting IFN signalling are likely to have complex downstream effects. Further research will probably reveal additional roles for the *IL28B* genotype in resolution of viral infection.

Proposed role of *IL28B* on response to IFN

When HCV RNA is detected through the RIG-I–IFIH1 (also known as MDA5) or Toll-like receptor 3 pathways, the adaptor protein MAVS (also known as VISA or IPS1) induces expression of IFN-α, IFN-β and IFN-λ, which induce an intracellular antiviral state that suppresses viral replication (Figure 2a).[2,77–79] IFN-α and IFN-β signal through the IFN receptor (IFNAR), whereas IFN-λ signals through the IL10R–IL28R receptor complex.[11] Both receptors activate the Jak–STAT pathway, which upregulates a large number of ISGs by binding to the IFN-stimulated response element (ISRE; Figure 2a).[2] The underlying mechanism by which the rs12979860 SNP in the *IL28B* gene exerts its effect is not clear, but the unfavourable allele seems to lead to continuous activation of a subset of ISGs in the presence of intracellular HCV RNA.[53] Although this level of expression is not sufficient to effectively eliminate the virus from the cell, it might nonetheless upregulate IFN-inhibitory molecules such as SOCS3 and PIAS that negatively regulate Jak–STAT signalling, thereby reducing sensitivity to IFN signalling.[80] Therefore, the hepatocyte is not only unable to clear the virus from the cell but is unable to induce stronger ISG expression when IFN is administered during therapy.[53]

Several scenarios might arise in response to IFN therapy depending on the *IL28B* genotype of the host (Figures 2 and 3). In patients with the unfavourable genotype (rs12979860 CT/TT), prior to treatment, the

presence of viral RNA induces continuous ISG expression in hepatocytes. Although moderate ISG expression can partially impair viral replication, it also stimulates negative regulatory pathways that ultimately reduce IFN sensitivity. IFN-α administered during therapy fails to induce ISG expression strongly enough to eradicate the virus. As a result, the patient responds poorly to therapy (Figure 3). We are unaware of studies showing the long-term changes in ISG expression in patients with chronic HCV infection after IFN therapy. However, we speculate that ISG expression fails to return to preinfection levels as long as the virus remains active in the liver, which could contribute to the pathology of the disease and influence treatment options.

In those with the favourable *IL28B* allele (rs12979860 CC; Figure 2), prior to IFN-α treatment, the presence of HCV RNA seems to result in minimal IFN-λ expression. As a result, hepatocyte ISG expression remains low even in the presence of HCV RNA. Although this phenomenon might result in a higher baseline viral load in these patients than in patients with the unfavourable *IL28B* genotype, cells remain more sensitive to IFN. Therefore, IFN-α administered during therapy can result in stronger induction of ISG expression and more effective clearance of the virus.

Future perspectives

Therapeutic role of IFN-λ

In patients with the unfavourable *IL28B* genotype (rs12979860 CT/TT), increased constitutive expression of some ISGs could prevent cells from responding to IFN-α administered during therapy. However, IFN-λ signalling does not seem to become desensitized after prolonged stimulation, suggesting a role for IFN-λ in patients who fail to respond to IFN-α through ISG preactivation.[81] In an open-label study of 56 patients, Muir *et al.*[82] found that a 4-week course of PEG-IFN-λ (with or without ribavirin) was well tolerated and has clear antiviral activity with few adverse events.[82] The potent antiviral activity of IFN-λ coupled with reduced adverse effects owing to the restricted distribution of IFN-λ receptors suggest that it might serve as a less toxic alternative to IFN-α in HCV therapy.

Improved pretreatment predictive models

Although the *IL28B* SNP is currently the best single pretreatment predictor of SVR, not all patients with the favourable genotype achieve SVR, and some patients without it are nonetheless able to achieve SVR.[83,84] Therefore, this SNP alone might not be sufficiently discriminative to advise a course of treatment. SVR rates based on clinical studies could also be inflated because of requirements for a homogenous patient population with strict adherence to the treatment regimen,[6,62] whereas, in clinical practice, dose reductions, co-infection with HBV or HIV, and other complications might compromise the predictive effect of the *IL28B* SNP.

Useful prediction models must also take into account other host and viral factors that might influence outcome of treatment. Most current models use multivariate logistic regression, in which a number of continuous or categorical factors are evaluated simultaneously to find a minimal set of independent factors that can predict treatment outcome. A positive or negative coefficient is calculated for each factor in the model based on its effect size, and the probability of treatment success is calculated by multiplying the measured value for a factor by its coefficient and summing the results for all factors. The resulting sum is converted to a probability that represents the likelihood that the patient will respond successfully to therapy. Models can be evaluated in a test set by comparing the true positive rate with the true negative rate by plotting a receiver operating characteristic (ROC) curve and calculating the area under the curve (AUC). A model that accurately predicts success or failure for each patient would have an AUC of 1, whereas a model that over predicts or under predicts success will have a value less than 1 and a random model might have an AUC of 0.5.

When other independent factors are included (for example, age, sex, BMI, viral load, fibrosis stage, ISG expression and amino acid substitutions in viral proteins), current prediction models are able to achieve an ROC AUC approaching 0.85.[83,85,86] Although such models are certainly useful as a guide, an AUC of 0.85 implies that some patients who might respond to therapy will be predicted to fail and some patients who are not expected to respond to therapy may, nonetheless, successfully clear the virus.

Studies have also reported associations of *IL28B* with KIR (Killer-cell immunoglobulin-like receptors) and HLA genotypes,[87,88] CXC-chemokine ligand 10 (also known as IP-10)[89] and vitamin D levels.[90] These associations could further improve prediction accuracy by accounting for other genetic and environmental factors that influence the immune response and ability to respond to treatment. Predictive models are likely to become increasingly important as the number of alternative therapies increases and trade-offs between cost, risk of adverse effects and chance of success require more complex treatment decisions.

New therapies

The predictive role of *IL28B* SNPs is based on PEG-IFN-α plus ribavirin combination therapy. However, the treatment regimen for chronic HCV is currently undergoing a major change with the introduction of direct-acting antiviral agents.[5] Triple therapy with telaprevir or boceprevir is expected to dramatically improve the rate of SVR achieved,[5] raising the question of whether *IL28B* genotype will remain a useful predictor of treatment outcome. Initial data suggest that the favourable *IL28B* allele also predicts response to triple therapy (Table 1), but its predictive effect might not be as strong as for PEG-IFN-α plus ribavirin combination therapy.[70,91]

As an extension of the current standard of care, triple therapy still relies on IFN-α and ribavirin to suppress antiviral resistance.[5] Patients who fail to respond to IFN-α (owing to, for example, ISG preactivation) could also be more susceptible to antiviral resistance, and *IL28B* genotyping could help identify those patients who

are poor candidates for triple therapy. Not only might triple therapy be ineffective in such patients, but the lack of effective IFN response could fail to suppress the emergence of resistant strains, thereby complicating future treatment efforts and increasing the risk of horizontal transmission of resistant strains (for example, among high-risk subpopulations).

IL28B genotyping could also be useful in helping to predict and control recurrent HCV infection after liver transplantation, as re-infection with HCV following liver transplantation is common and requires post-transplant antiviral therapy.[92–94] The unfavourable *IL28B* genotype in recipients is associated with more severe recurrence of HCV infection, and *IL28B* genotypes of donors and recipients are independently associated with post-transplant treatment response, suggesting that donors with the favourable *IL28B* genotype might be preferentially allocated to HCV-infected patients.[93]

Conclusions

The role of *IL28B* in chronic HCV infection has been studied extensively following the identification of common genetic variants strongly predictive of treatment outcome in 2009. Results have been replicated in other populations and HCV genotypes, and predictive models have been developed that attempt to incorporate *IL28B* genotype into clinical decision-making. Even with the introduction of a new class of highly effective direct-acting antiviral agents, the *IL28B* SNP continues to serve as a useful predictor of treatment outcome and could help to establish treatment expectations and guide decisions for retreatment of prior nonresponders. Investigation of the underlying mechanism by which the *IL28B* genotype exerts its effect has yielded new insights into the regulation of antiviral defences that could have applications beyond the field of HCV research. Moving forward, the major challenge will be to incorporate this new knowledge into practical improvements in the clinic.

Review criteria

A search for original articles published between 1989 and 2011 and focusing on *IL28B* polymorphisms was performed in MEDLINE and PubMed. The search terms used were "hepatitis C virus", "interleukin 28b", "interferon lambda", "genome-wide association study", "single nucleotide polymorphism", "interferon-stimulated gene", and "spontaneous clearance" alone and in combination. All articles identified were English-language, full-text papers. We also searched the reference lists of identified articles for further relevant papers.

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Acknowledgements

This work was supported in part by Grants-in-Aid for scientific research and development from the Ministry of Education, Culture, Sports, Science and Technology, and the Ministry of Health, Labour and Welfare, Government of Japan.

Author contributions

All authors contributed equally to researching data for the article, discussion of content and reviewing and/or editing the manuscript before submission.
C. N. Hayes and K. Chayama wrote the article.

Dual Therapy With the Nonstructural Protein 5A Inhibitor, Daclatasvir, and the Nonstructural Protein 3 Protease Inhibitor, Asunaprevir, in Hepatitis C Virus Genotype 1b–Infected Null Responders

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Patients with chronic hepatitis C virus (HCV) infection and previous null response to pegylated interferon (Peg-IFN) and ribavirin (RBV) have limited therapeutic options. HCV genotype 1 is the most common worldwide and the most difficult to treat; genotype 1b is the most common subtype of genotype 1 outside North America. The enhanced antiviral activity achieved by combining two direct-acting antiviral (DAA) agents may improve clinical outcomes. This open-label, phase IIa study included 10 patients with chronic HCV genotype 1b infection and previous null response (<2 $\log_{10}$ reduction in HCV RNA after 12 weeks) to Peg-IFN and RBV. Patients received dual DAA treatment for 24 weeks with the nonstructural protein 5A replication complex inhibitor, daclatasvir (60 mg once-daily), and the nonstructural protein 3 protease inhibitor, asunaprevir (initially 600 mg twice-daily, then subsequently reduced to 200 mg twice-daily). The primary efficacy endpoint was the proportion of patients with sustained virologic response (SVR) at 12 weeks post-treatment (SVR_{12}). Nine patients completed 24 weeks of treatment; 1 patient discontinued treatment after 2 weeks. In the 9 patients who completed the full course of treatment, HCV RNA was undetectable at week 8 and remained undetectable through the end of treatment; all 9 patients achieved SVR_{12} and SVR_{24}. HCV RNA also remained undetectable post-treatment in the patient who discontinued after 2 weeks. There was no viral breakthrough. Diarrhea and headache, generally mild, were the most common adverse events; transaminase elevations were reported in 3 patients, but did not result in discontinuation. *Conclusions*: Dual therapy with daclatasvir and asunaprevir, without Peg-IFN and RBV, can achieve high SVR rates in difficult-to-treat patients with HCV genotype 1b infection and previous null response to Peg-IFN and RBV. (HEPATOLOGY 2012;55:742-748)

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Chronic hepatitis C virus (HCV) infection affects approximately 180 million individuals worldwide and is a common cause of chronic liver disease and hepatocellular carcinoma (HCC) in Japan, the United States, and many European countries.[1,2] Among the six major HCV genotypes, genotype 1 is the most common and the most difficult to treat, and its two main subtypes may differentially influence therapeutic outcomes.[3,4] Genotype 1b is the most prevalent worldwide and predominates in Japan and China, whereas genotype 1a is most common in the United States; subtype prevalence in Europe is similar.[5-7]

Abbreviations: ALT, alanine aminotransferase; cEVR, complete early virology response: undetectable HCV RNA at week 12; DAA, direct-acting antiviral; EOTR, end-of-treatment response: undetectable HCV RNA at week 24; eRVR, extended rapid virologic response: undetectable HCV RNA at weeks 4 and 12; HCC, hepatocellular carcinoma; HCV, hepatitis C virus; IL28B, *interleukin-28B; INR, international normalized ratio; LLQ, lower limit of quantitation; NS3, nonstructural protein 3; NS5A, nonstructural protein 5A; Peg-IFN-α, pegylated interferon alpha; PCR, polymerase chain reaction; RBV, ribavirin; RVR, rapid virologic response: undetectable HCV RNA at week 4; SNP, single-nucleotide polymorphism; SVR, sustained virologic response: undetectable HCV RNA post-treatment; SVR_{12}, sustained virologic response 12 weeks post-treatment; SVR_{24}, sustained virologic response 24 weeks post-treatment; ULN, upper limit of normal.*

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Received July 22, 2011; accepted September 27, 2011.

This study was funded by Bristol-Myers Squibb. Editorial assistance for the preparation of the manuscript for this article was provided by Richard Boehme, Ph.D., of Articulate Science and was funded by Bristol-Myers Squibb.

Treatment of chronic HCV infection with pegylated interferon alpha (Peg-IFN-α) and ribavirin (RBV) elicits a sustained virologic response (SVR) in 40%-50% of treatment-naïve patients with genotype 1 infections; SVR rates in this population increase to 66% or 75% when boceprevir or telaprevir, respectively, is added to the regimen.[8-12] Response rates are influenced by viral load and genotype and by patient demographics, disease history, and genetics.[10] Peg-IFN/RBV retreatment of patients with previous nonresponse to Peg-IFN/RBV is frequently unsuccessful, with SVR rates of only 6%-9%.[13,14] Null responders are the subset of nonresponders who have responded most poorly to Peg-IFN/RBV, and their urgent need for more potent therapies has prompted the evaluation of regimens containing direct-acting antivirals (DAAs). SVR rates of 27% (genotype 1a) and 37% (genotype 1b) were achieved in null responders with a regimen combining telaprevir with Peg-IFN/RBV in a study of nonresponders.[15] These results suggest that DAA-containing regimens can benefit this population, but greater antiviral potency is needed to increase response rates further.

Combinations of two DAAs may overcome IFN nonresponsiveness in null responders by increasing antiviral activity and reducing the risk of developing resistance-associated variants.[16] In HCV-infected human hepatocyte chimeric mice, dual DAA treatment eradicated HCV without resistance, whereas resistance emerged rapidly with single DAA treatment.[17] In a clinical study that included null responders, marked antiviral effects were observed after 13 days of dual DAA treatment, supporting the evaluation of longer term dual DAA therapy reported in this study.[18] Daclatasvir (BMS-790052) is a first-in-class, highly selective nonstructural protein 5A (NS5A) replication complex inhibitor with picomolar potency and broad genotypic coverage; asunaprevir (BMS-650032) is a nonstructural protein 3 (NS3) protease inhibitor active against HCV genotypes 1a and 1b.[19,20] Daclatasvir and asunaprevir are associated with different resistance-associated variants, consistent with their different molecular targets, and showed no meaningful pharmacokinetic interactions in healthy volunteers.[20-22]

In a 24-week study of null responders in the United States, daclatasvir and asunaprevir demonstrated potent antiviral effects, both as a dual DAA regimen and in a quadruple regimen that included Peg-IFN/RBV.[23] Overall, 36% of dual-therapy recipients achieved SVR, including both of the 2 patients with genotype 1b infection. However, patients with genotype 1a experienced frequent viral breakthrough with the dual regimen and only 2 of 9 achieved SVR, suggesting subtype-associated differences in resistance barrier and response. We present the results of an open-label trial evaluating dual therapy with daclatasvir and asunaprevir in Japanese patients with chronic HCV genotype 1b infection and previous null response to Peg-IFN/RBV.

Patients and Methods

Study Design. This open-label, phase IIa study (clinicaltrials.gov identifier NCT01051414) evaluated the antiviral activity and safety of daclatasvir combined with asunaprevir in patients with HCV genotype 1 infection and previous null response to treatment with Peg-IFN/RBV, defined as <2 $\log_{10}$ reduction of HCV RNA after 12 weeks of therapy. This sentinel cohort provided safety data for review by an independent study safety committee before the enrollment of additional cohorts that will be described in a subsequent report. Written informed consent was obtained from all patients. The study was approved by institutional review boards at each site and was conducted in compliance with the Declaration of Helsinki, Good Clinical Practice Guidelines, and local regulatory requirements.

Patients. Patients eligible for enrollment in the sentinel cohort included men and women 20-75 years in age (women of childbearing potential were required to use adequate contraception) with chronic HCV genotype 1 infection for at least 6 months (all enrolled patients were genotype 1b because of the high prevalence of this subtype in Japan) and HCV RNA $\geq 10^5$ IU/mL. Eligible patients met criteria defining null responders and had no evidence of cirrhosis documented by laparoscopy, imaging, or liver biopsy within 2 years.

Patients were excluded if they had a history of HCC, coinfection with hepatitis B virus or human immunodeficiency virus, other chronic liver disease, or

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View this article online at wileyonlinelibrary.com.

DOI 10.1002/hep.24724

Potential conflict of interest: Nothing to report.

This article first published online ahead of print on 30 January 2012. The following corrections have since been made: "BMS-790052" has been replaced throughout with "daclatasvir"; "BMS-50032" has been replaced throughout with "asunaprevir". The article has been updated online and in print.

evidence of hepatic decompensation. Patients were also excluded if they had other severe or unstable conditions or evidence of organ dysfunction in excess of that consistent with the age of the patient, were unable to tolerate oral medication or had conditions that could affect the absorption of study drug, or were exposed to any investigational drug within 4 weeks of study participation or had any previous exposure to inhibitors of NS5A or NS3 protease. Laboratory findings that excluded participation were the following: alanine aminotransferase (ALT) >5× the upper limit of normal (ULN); total bilirubin ≥2 mg/dL; direct bilirubin >1.5× ULN; international normalized ratio (INR) ≥1.7; albumin ≤3.5 g/dL; hemoglobin <9.0 g/dL; white blood cells <1,500/mm^3; absolute neutrophil count <750/mm^3; platelets <50,000/mm^3; or creatinine >1.8× ULN.

Prohibited concomitant medications included inducers or inhibitors of cytochrome P450/3A4, non-study medications with anti-HCV activity, any prescription medication or herbal product not prescribed for a specific condition, liver-protection drugs, proton pump inhibitors, and erythropoiesis-stimulating agents. H_2 receptor antagonists were permitted, but administered ≥10 hours before or ≥2 hours after daclatasvir; other acid-modifying agents had to be taken ≥2 hours before or after daclatasvir.

Study Drug Dosing. All patients received oral combination therapy with daclatasvir and asunaprevir from the beginning of the study. Daclatasvir was dosed as two 30-mg tablets once-daily. Asunaprevir was initially dosed as three 200-mg tablets twice-daily; subsequently, the dose of asunaprevir was reduced to 200 mg twice-daily after reports of hepatic enzyme elevations in a clinical study of asunaprevir and Peg-IFN/RBV.[24]

Treatment was continued to week 24 for patients with HCV RNA below the assay lower limit of quantitation (LLQ; 15 IU/mL) on or after week 2; treatment was discontinued for patients with <2 $\log_{10}$ IU/mL decrease of HCV RNA from baseline or on or after week 2. For patients with viral rebound on or after week 2, or HCV RNA above LLQ on or after week 4, treatment was discontinued or weight-based Peg-IFN-RBV therapy was added for up to 48 additional weeks at the investigator's discretion, based on expected tolerance of Peg-IFN-RBV. Viral rebound was defined as an increase ≥1 $\log_{10}$ IU/mL from nadir at more than one time point or HCV RNA ≥15 IU/mL after declining to below that level.

Safety and Efficacy Assessments. Assessments, including HCV RNA, physical examination, vital signs, adverse events, laboratory tests, and review of concomitant medications, were conducted at screening, on study days 1 (baseline) through 7 and days 9, 11, and 14, at weeks 3, 4, 6, 8, 10, 12, 16, 20, and 24, and at post-treatment weeks 4, 8, 12, and 24. Twelve-lead electrocardiograms were recorded at all visits, except those at weeks 3 and 6. Additional pretreatment assessments included HCV genotype and host interleukin-28B (*IL28B*) genotype.

Serum HCV RNA levels were determined at a central laboratory using the Roche COBAS TaqMan HCV Auto assay (LLQ = 15 IU/mL; Roche Diagnostics KK, Tokyo, Japan). HCV genotype and subtype were determined at the central laboratory by polymerase chain reaction (PCR) amplification and sequencing. *IL28B* genotype was determined by PCR amplification and sequencing of the rs12979860 single-nucleotide polymorphism (SNP).

Outcome Measures. The primary efficacy endpoint was the proportion of patients with undetectable HCV RNA at 12 weeks post-treatment (SVR_{12}). Secondary endpoints included the proportions of patients with rapid virologic response (RVR; defined as undetectable HCV RNA at week 4), extended RVR (eRVR; undetectable HCV RNA at weeks 4 and 12), complete early virologic response (cEVR; undetectable HCV RNA at week 12), end-of-treatment response (EOTR; undetectable HCV RNA at week 24), and SVR at 24 weeks post-treatment (SVR_{24}).

The possible presence of HCV-resistance polymorphisms was analyzed using stored specimens. Resistance testing was performed on all samples at baseline and on samples indicative of virologic failure, defined as either (1) <2 $\log_{10}$ HCV RNA decrease from baseline at week 2, (2) virologic rebound (HCV RNA detectable after previously undetectable or ≥1 $\log_{10}$ increase from nadir), or (3) detectable HCV RNA at weeks 4 or 12 or at the end of therapy. Resistance analysis methodology included isolation of HCV RNA, PCR amplification, and population sequencing of HCV NS3 protease and NS5A domains.

Statistical Analysis. Categorical variables were summarized using counts and percents; continuous variables were summarized with univariate statistics.

Results

Patient Characteristics and Disposition. Twelve patients were screened; 2 patients failed to meet entry criteria (for HCC and elevated direct bilirubin, respectively), and 10 were enrolled and treated. Enrolled patients were generally older (median, 62 years); 6

Table 1. Baseline Demographic and Disease Characteristics

Parameter	Value
N	10
Age, median years (range)	62 (52-70)
Male sex, n (%)	4 (40)
Japanese race, n (%)	10 (100)
Host *IL28B* genotype,* n (%)	
CC	2 (20)
CT	8 (80)
HCV genotype 1b, n (%)	10 (100)
HCV RNA, mean $\log_{10}$ IU/mL (SD)	6.8 (0.61)
ALT, mean U/L (SD)	60.6 (32.9)
Platelets $\times$ 10^9 cells/mL, median (min, max)	150.5 (84.0, 166.0)
Total bilirubin, median mg/dL (min, max)	0.8 (0.6, 1.2)
Albumin, median g/dL (min, max)	3.9 (3.1, 4.2)
INR, median (min, max)	1.0 (1.0, 1.1)

*SNP rs12979860.

Abbreviation: *IL28B*, interleukin-28B; HCV, hepatitis C virus; SD, standard deviation; ALT, alanine aminotransferase; min, minimum; max, maximum; INR, international normalized ratio; SNP, single-nucleotide polymorphism.

were female and all were Japanese (Table 1). All enrolled patients were infected with genotype 1b, reflecting the predominance of this subtype in Japan, although the study protocol did not exclude patients with HCV genotype 1a.[6] Two patients were *IL28B* genotype CC (SNP rs12979860) and 8 were CT. Nine patients completed 24 weeks of therapy; 1 patient discontinued at week 2 because of a grade 4 total bilirubin elevation (see below). Among the 9 patients treated for 24 weeks, asunaprevir was dosed at 600 mg twice-daily for 12-21 weeks before the dose was reduced to 200 mg twice-daily (Fig. 1).

Virologic Response. Serum HCV RNA levels decreased rapidly in all patients (Fig. 2); mean reductions from baseline were 4.4 $\log_{10}$ IU/mL at week 1,

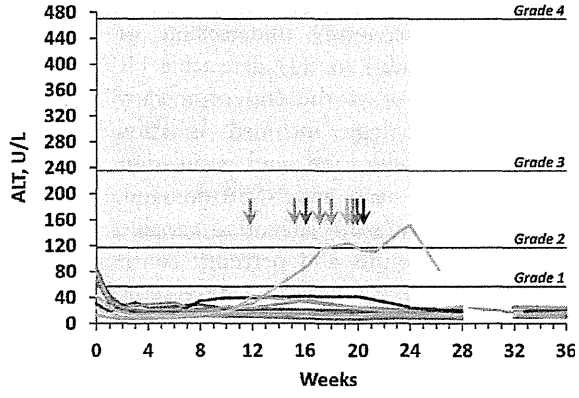

Fig. 1. ALT levels: individual patients. Serum ALT levels for the 9 patients who completed 24 weeks of treatment; the patient who discontinued at week 2 is not presented. Shaded area indicates the treatment period; arrows indicate the points at which the dose of asunaprevir was reduced from 600 to 200 mg twice-daily. Arrow and line colors are the same for each patient.

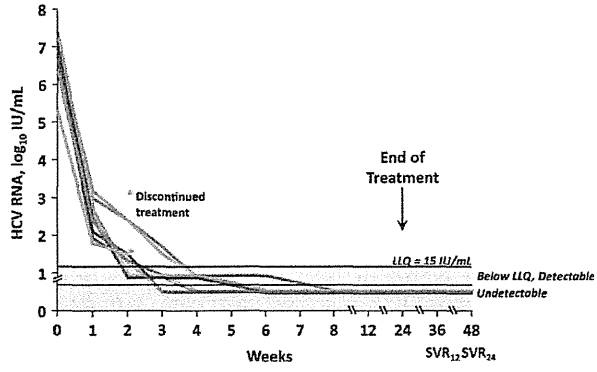

Fig. 2. HCV RNA levels: individual patients. Individual patient plasma HCV RNA levels during 24 weeks of treatment and through 24 weeks post-treatment (week 48) are shown. LLQ = 15 IU/mL.

5.3 $\log_{10}$ IU/mL at week 2, and 5.8 $\log_{10}$ IU/mL from week 4 through the end of treatment. At week 4, HCV RNA was undetectable (RVR) in 4 of 10 (40%) patients and below the assay LLQ in 9 of 10 (90%; Fig. 3). No patients qualified for discontinuation or addition of pegIFN/RBV. At week 8, HCV RNA was undetectable in 9 of 10 patients (all who remained on treatment) and remained undetectable through the end of treatment and follow-up. SVR_{12}, the primary endpoint, and SVR_{24} were achieved by 90% of patients, including all 9 who completed 24 weeks of therapy. The patient who discontinued treatment at week 2 had low-level HCV RNA at discontinuation (1.8 $\log_{10}$ IU/mL), but HCV RNA was undetectable at follow-up visits 2, 3, 4, 13, and 24 weeks after discontinuation.

Viral Breakthrough and Relapse. There was no viral breakthrough during treatment or relapse of HCV RNA post-treatment. Analysis of baseline samples revealed variants reported to confer minimal to low

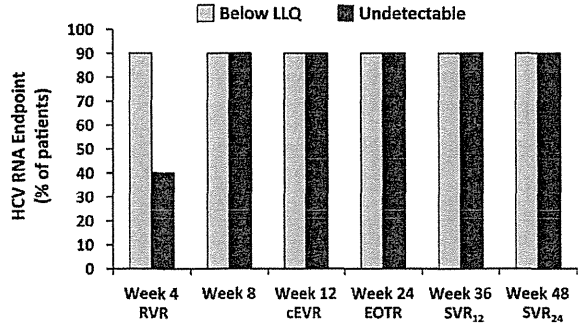

Fig. 3. HCV RNA endpoints. Categorical HCV RNA endpoints are indicated for the 10 study patients. One patient discontinued at week 2 and was counted as a treatment failure at the time points shown. However, HCV RNA was undetectable in this patient at 2, 3, 13, and 24 weeks post-treatment.

Table 2. On-Treatment Adverse Events Occurring in ≥2 Patients

Event	Patients, n (%)
Diarrhea	7 (70)
Headache	4 (40)
ALT increased	3 (30)
AST increased	3 (30)
Lymphopenia	2 (20)
Abdominal discomfort	2 (20)
Malaise	2 (20)
Pyrexia	2 (20)
Nasopharyngitis	2 (20)
Lipase increased	2 (20)
Back pain	2 (20)

Abbreviations: ALT, alanine aminotransferase; AST, aspartate aminotransferase.

levels of resistance to daclatasvir.[22] NS5A substitutions L28M and L31M were detected in 1 patient each, and Y93H was detected in 2 other patients. NS3 protease substitutions reported to confer resistance to telaprevir, boceprevir, and TMC-435 were detected[25]; T54S was identified in 1 patient, and Q80L was identified in 3. In 1 patient, both NS3 protease substitutions (T54S and Q80L) and an NS5A substitution (Y93H) were detected. There was no consistent association between detection of these variants and virologic outcomes.

Safety. The most frequently reported adverse events were diarrhea and headache, all of which were mild (grade 1) (Table 2). The patient who discontinued (see below) experienced multiple grade 3 or 4 adverse events and laboratory abnormalities on treatment. In the other 9 patients, there were no grade 3 or 4 transaminase elevations or other grade 3 or 4 events, no clinically relevant changes in electrocardiogram parameters, and no lymphopenia of any severity. Two transient grade 1 ALT elevations were reported, and 1 grade 2 elevation that began at week 16 and persisted until the end of treatment, after which it normalized within 2 weeks (Fig. 1). There were no notable differences in ALT before and after asunaprevir dose reduction.

There were two serious adverse events. A 54-year-old male was hospitalized with grade 3 pyrexia and persistent diarrhea 11 days after initiating study treatment. Loxoprofen was initiated, and body temperature normalized and diarrhea improved after 4 days. The patient remained on study treatment. The second event concerned a 60-year-old woman with a history of ulcerative colitis who discontinued study treatment after 2 weeks because of a grade 4 bilirubin elevation with multiple complicating features. Five days before discontinuation, she presented with infectious gastroenteritis and was treated with cefotiam and was subsequently hospitalized with fever, vomiting, and diarrhea. Meropenem, human serum albumin, and furosemide were initiated. At discontinuation of study drugs, laboratory findings included total bilirubin of 7.7 mg/dL and grade 3 lymphopenia and serum phosphorus reduction; transaminases and alkaline phosphatase were within normal ranges. In the week after discontinuation, white cell and eosinophil counts became elevated; total bilirubin improved and transaminases remained normal. Two weeks after discontinuation, grade 4 ALT and aspartate-aminotransferase elevations and a grade 3 lipase elevation were reported. Six weeks after discontinuation, bilirubin and transaminase elevations were resolved and lipase improved to within 2× ULN.

Discussion

This study assessed combination oral DAA therapy in a difficult-to-treat population with multiple adverse prognostic features, including HCV genotype 1b infection, primarily *IL28B* CT genotype, generally older age, and null response to previous Peg-IFN/RBV therapy.[10,13,14] These patients represent a group with a significant need for new therapeutic options.

A DAA-only therapeutic strategy may be particularly appropriate for null responders, who have previously shown only marginal response to Peg-IFN/RBV.[13,14] The combination of two highly potent DAAs cleared detectable virus rapidly in this study; HCV RNA was undetectable by week 8 in all 9 patients treated for 24 weeks. This outcome compares favorably with those observed when null responders received a combination of Peg-IFN/RBV and a single NS3 protease inhibitor, telaprevir or TMC435.[15,26] In these studies, HCV RNA remained detectable in 36% to approximately 50% of patients after 12 weeks.

HCV RNA remained undetectable 12 (SVR_{12}) and 24 weeks (SVR_{24}) post-treatment in all patients who completed treatment. This contrasts with the poor results obtained with Peg-IFN/RBV retreatment and the reported 37% SVR rate of genotype 1b null responders who received Peg-IFN/RBV and telaprevir.[10,13-15] Additional follow-up of patients from this study will assess whether SVR_{24} is predictive of long-lasting viral clearance with this dual DAA therapy, as it is with Peg-IFN/RBV. It is interesting that HCV RNA was persistently undetectable post-treatment in the patient who discontinued after only 2 weeks of treatment. With early discontinuation data from only this single case, at present, the result must be considered an anomaly. The factors that contributed to viral

clearance are uncertain, although the patient's *IL28B* CC genotype suggests increased sensitivity to endogenous interferon[27]; the possible influence of concurrent acute gastroenteritis or other complicating factors is unknown. However, coupled with the attainment of SVR_{12} in all other patients, this outcome suggests that required duration of therapy, which is currently predicated on data from Peg-IFN-based regimens, may need reassessment for DAA-only regimens, and, possibly, that certain patient populations can be treated for very short durations.

The high SVR rate is consistent with limited data from a related U.S.-based study, in which 2 of 2 null responders with HCV genotype 1b and who were treated with daclatasvir and asunaprevir achieved SVR_{24}.[23] However, only 2 of 9 patients with genotype 1a achieved SVR_{24} with the dual DAA regimen, compared with 9 of 10 patients who received both DAAs and Peg-IFN/RBV. These differences suggest that viral genotype can influence responses to DAA regimens that do not include Peg-IFN/RBV, and outcomes can be optimized with individualized therapy that considers viral genotype, among other factors. Because of the high SVR rate, the potential influence of other baseline and on-treatment parameters could not be assessed, other than to observe that unfavorable predictors of Peg-IFN/RBV response, such as older age and *IL28B* CT genotype,[27,28] had no measureable impact on outcomes.

There was no viral breakthrough on treatment. In view of the rapid emergence of resistance in some studies of short-term DAA monotherapy,[29,30] these findings support the concept that dual DAA therapy reduces the risk of viral breakthrough, in addition to increasing antiviral activity. Resistance analyses revealed that before treatment, some patients carried NS5A and NS3 polymorphisms predicted to reduce sensitivity to daclatasvir and some HCV protease inhibitors, respectively.[22,25] There was no clear relationship between the presence of these polymorphisms and minor interpatient differences in the rate of early virologic response; however, further study in larger patient cohorts will help determine whether baseline polymorphisms can influence virologic response with this regimen.

The adverse event profile of the dual DAA regimen compares favorably with the more frequent and severe events reported with Peg-IFN/RBV, although patient numbers in this study were limited. The mild diarrhea experienced by several patients has been reported previously with asunaprevir and is common with other drugs of this class.[15,18,24] Though a role for daclatasvir and/or asunaprevir in the two serious adverse events could not be ruled out and the investigator considered these events drug related, multiple confounding factors existed. The case of pyrexia was consistent with a viral infection and resolved with treatment. In the case of hyperbilirubinemia that led to discontinuation, the time course of laboratory abnormalities and related events suggests a link to the use of cefotiam and meropenem for treatment of infectious gastroenteritis. Both of these agents have been associated with vomiting, diarrhea, and hyperbilirubinemia.[31,32]

The asunaprevir dose was reduced during treatment because of transaminase elevations observed with 600 mg twice-daily in a concurrent study.[24] In this sentinel cohort, viral suppression was maintained in all patients after dose reduction, and no grade 3 or 4 transaminase elevations occurred during treatment at either dose of asunaprevir. One patient experienced grade 2 transaminase elevations that began at week 16 and persisted during treatment, despite asunaprevir dose reduction at week 19. Although these elevations were not severe, their rapid normalization post-treatment suggests a possible relationship to study treatment. None of the 9 patients treated for 24 weeks experienced transaminase elevations post-treatment. Although grade 4 transaminase elevations occurred 2 weeks post-treatment in the patient who discontinued, the timing of these events and multiple other complications suggest that they were not related directly to study treatment.

In conclusion, the combination of daclatasvir and asunaprevir achieved a high rate of SVR_{24} in patients with HCV genotype 1b infections and previous null response to Peg-IFN/RBV. These results support the concept that HCV infection can be cured with two DAAs without Peg-IFN/RBV, even in difficult-to-treat populations that lack robust IFN responsiveness. Further research will assess the benefits of DAA combinations in larger, more diverse patient populations.

Acknowledgment: The authors thank the patients and their families, research staff at all participating sites, and Bristol-Myers Squibb Research and Development colleagues.

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J Gastroenterol (2013) 48:1–12
DOI 10.1007/s00535-012-0714-9

REVIEW

Treatment of chronic hepatitis C virus infection in Japan: update on therapy and guidelines

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Received: 4 November 2012 / Accepted: 4 November 2012 / Published online: 28 November 2012

Abstract Hepatitis C virus (HCV) infection is a serious health problem leading to cirrhosis, liver failure and hepatocellular carcinoma. The recent introduction of telaprevir, which was approved in November 2011, in combination with peg-interferon and ribavirin is expected to markedly improve the eradication rate of the virus. However, side effects of triple therapy may be severe. In a phase three III clinical trial, 2250 mg of telaprevir, which is the same dosage used in clinical trials in Western countries, was given to Japanese patients. As this dosage is considered to be relatively high for Japanese patients, who typically have lower weight than patients in Western countries, reduction of telaprevir is recommended in the 2012 revision of the guidelines established by the Study Group for the Standardization of Treatment of Viral Hepatitis Including Cirrhosis published by the Ministry of Health, Labour and Welfare of Japan. Other protease inhibitors with fewer side effects are now in clinical trials in Japan. Alternatively, treatment of patients with combination of direct acting antivirals without interferon has been reported. In this review we summarize current treatment options in Japan and discuss how we treat patients with chronic HCV infection.

Keywords Telaprevir · Triple therapy · Antiviral resistance · Anemia · Dose reduction

Abbreviations

HCV	Hepatitis C virus
DAAs	Direct acting anti-virals
SVR	Sustained virological response
RVR	Rapid virological response

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Introduction

At least 1.5 million people in Japan and more than 200 million people worldwide are chronically infected with the hepatitis C virus [1, 2]. Due to an aging patient population, the health burden of chronic HCV infection in Japan is expected to increase over the next several decades [3]. Chronic infection develops in 60–80 % of symptomatic patients, leading to higher risk of cirrhosis, hepatocellular carcinoma, and end-stage liver disease. Chronic HCV infection is also one of the primary indications for liver transplantation [3], and ultimately 5–7 % of patients die from complications related to HCV infection [4–7].

The goal of HCV therapy is successful eradication of the virus and resolution of liver disease. Success is defined as