A Genetic Variant in the Interleukin 28B Gene Is a Major Predictor for Sustained Virologic Response in Mexican Patients with Chronic Hepatitis C Virus Infection

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Received for publication March 30, 2015; accepted July 9, 2015 (ARCMED-D-15-00205).

Background and Aims. The IL28B single nucleotide polymorphism (SNP) rs12979860 is a major predictor of treatment outcomes in hepatitis C virus (HCV) infection, but its distribution widely varies among populations and ethnicities. We undertook this study to investigate the distribution of IL28B SNP rs12979860 in Mexican patients with HCV infection and to assess its usefulness in predicting response to pegylated interferon-alpha and ribavirin (PegIFN-α/RVB) therapy.

Methods. Three hundred and fifty patients with chronic HCV infection were studied. The frequency of sustained virologic response (SVR), non-responders and relapses following a course of standard therapy was longitudinally assessed in 295 of these patients. IL28B SNP rs12979860 was genotyped from genomic DNA using real-time RT-PCR. The number needed to treat (NNT) to achieve a SVR was calculated.

Results. Seventy six (22%) patients were CC homozygous, 210 (60%) were heterozygous and 64 (18%) showed TT homozygosity for the IL28B SNP rs12979860. After a standard course of PegIFN-α/RVB, 69% of patients with the CC genotype, 46% of the heterozygous group and 38% of those with the TT genotype (p = 0.001) achieved a SVR. Conversely, the percentage of non-responders was 15, 43, and 48% (p < 0.0001), respectively. The NNT to achieve a SVR was strongly influenced by the IL28B rs12979860 genotype and ranged from 2–10.

Conclusions. The IL-28B rs12979860 CC genotype was found in 22% of Mexican patients chronically infected by HCV. Genotyping IL28B SNP rs12979860 is useful to predict the response to a standard regimen with PegIFN-α/RVB, especially in those infected with HCV genotype 1. © 2015 IMSS. Published by Elsevier Inc.

Key Words: Hepatitis C virus, Interleukin 28, Interferons, SNP rs12979860.

Introduction

Infection with hepatitis C virus (HCV) is now a well-recognized, leading cause of progressive liver damage worldwide. In Mexico, the overall prevalence of HCV infection has been estimated at 1.4%, with genotype 1 as the most commonly found (1,2). Acute HCV infection...
may progress to a chronic infection in ~80% of individuals; of them, 20–30% will develop cirrhosis and its complications or hepatocellular carcinoma (3).

In Mexico, a combination of pegylated interferon-alpha (PegIFN-α 2a or 2b) plus ribavirin (RBV) is the available therapy for chronic hepatitis even when this strategy is successful in <50% of patients infected with HCV genotype 1; in contrast, the rate of sustained virologic response (SVR) is nearly 80% in those patients infected with HCV genotypes 2 and 3 (4).

In addition to the inherent characteristics of each viral genotype, a variety of intrinsic factors in the host plays an important role in the development and progression of HCV infection. Several independent genome-wide association studies have identified a small number of single nucleotide polymorphisms (SNP) located in and near the IL28B gene that are associated with spontaneous viral clearance and the rate of response to treatment (5). The IL28B gene encodes the interleukin 28B (IL-28B), a powerful antiviral cytokine which is often called type III interferon lambda-3 (IFN-l3). In particular, the IL28B SNP rs12979860 demonstrates a critical role in the development of HCV infection (6,7). Indeed, the IL-28B rs12979860-C allele increases the probability to achieve spontaneous viral clearance during acute infection as well as SVR following a standard regimen of PegIFN-α/ RBV in chronic active hepatitis; in contrast, the IL-28B rs12979860-T allele is associated with lack of response to therapy and progression of HCV infection (7,8).

The distribution of IL28B rs12979860 genotypes shows a great diversity depending upon the geographical location and racial substrate. A study performed by Thomas et al. with >2000 individuals from different ethnic substrates were genotyped for the IL28B rs12979860 demonstrates that East Asian populations have the highest frequency of C alleles, Europeans have intermediate frequencies, whereas Africans have the lowest (7). In a similar manner, Ge et al. found that the lowest frequency of alleles associated with spontaneous viral clearance in African-Americans and highest frequencies in populations from East Asia, whereas intermediate frequencies were observed in European-Americans and Hispanics (9).

Although the association between polymorphisms in the IL28B gene and the outcome of HCV infection is now recognized, the actual distribution and role of the rs12979860 genotypes among Latin American populations with an emphasis on Mexican patients is unclear (9–12).

New therapeutic molecules have been approved in the last year, which lead to IFN-free regimens that have advantages such as a high rate of SVR, shorter course of treatment and a low rate of side effects, with these management prognostic factors such as SNP IL28B could lose impact. Nonetheless, these treatment modalities are limited in our reality because they have a high cost. Until they become available in our Public Health Systems a therapy that involves Peg-IFN/RBV with/without telaprevir and boceprevir remains acceptable and SNP IL28B 12979860 C/T continues to be a strong predictor of therapeutic response (13–15).

In this study the distribution of IL-28B SNP rs12979860 C/T genotypes in a large cohort of Mexican patients with chronic HCV infection was investigated. The usefulness of each genotype as a prognostic marker of response to PegIFN-α/RBV therapy was also assessed.

Materials and Methods

Patients

The protocol was approved by the Institutional Ethics Committee on Biomedical Research in Humans of the Instituto Nacional de Ciencias Médicas y Nutrición Salvador Zubirán and Servicio de Gastroenterología, Endoscopia y Hepatología del Hospital de la UMAE, Hospital de Especialidades, Centro Medico Nacional Siglo XXI. Prior to their inclusion in the study, all patients signed informed consent according to WHO policies.

Study design was cross-sectional and included 350 patients with HCV infection. Patients were selected from the Departamento de Gastroenterología–Clínica de Hígado del Instituto Nacional de Ciencias Médicas y Nutrición Salvador Zubirán and from the Servicio de Gastroenterología, Endoscopia y Hepatología, UMAE, Hospital de Especialidades, Centro Médico Nacional Siglo XXI between January 2010 and January 2013.

Patients were included if they were >18 years old, had a biopsy with a METAVIR score <4 prior to treatment and received PegIFN/RBV. Documented viral response in accordance with the guidelines for the diagnosis and treatment of chronic HCV infection was evaluated. All patients were anti-HCV positive (by third-generation EIA immunoassays by Abbott, Wiesbaden, Germany). Genotype for HCV was tested by INNO-LiPA HCV II (Inogenetics, Zwijnaarde, Belgium) and baseline viral load (RNA-HCV) was tested by COBAS TaqMan HCV test (Roche Molecular Systems, Branchburg, NJ).

All patients, as well as their parents and grandparents, were born in Mexico. Five ml of peripheral blood was obtained from each patient to extract genomic DNA for SNP IL28B rs12979860 C/T genotyping. Response to antiviral therapy was documented.

Antiviral Treatment

Of the 350 patients enrolled, 295 (84%) received standard therapy and were followed over time. The standard regimen included a subcutaneous administration of 180 μg of PegIFN-α 2a on a weekly dose or PegIFN-α 2b: 1.5 μg/kg body weight each week plus RBV with a dose adjusted by body weight as follows: 1000 mg in patients <75 kg body weight, 1200 mg when body weight >75 kg for
48 weeks for hcv genotype 1 carriers. In those with genotype 2 or 3 a course of 24 weeks was carried. SVR was assessed at 24 weeks after finishing the therapeutic schedule.

Viral Load and Outcome Definitions

Viral load was defined as the total HCV-RNA copies in peripheral blood by real-time RT-PCR with the COBAS TaqMan HCV test (Roche Molecular Systems). Viral load was measured at 0, 12, 24, and 48 weeks after inclusion in the study as well as 6 months after the end of treatment in all patients receiving standard PegIFN-α/RBV therapy.

The outcomes of antiviral treatment were defined as follows: 1) non-responder: patient who remained with HCV-RNA persistently positive throughout course of treatment or in those with a decrease <2 log10 from the basal values during the first 12 weeks of treatment; 2) sustained virologic response (SVR): patient with a negative result for HCV-RNA 6 months after finishing the therapeutic schedule; 3) virologic relapse: patient in whom HCV-RNA decreased and remained below the limit of detection during treatment but became detectable after treatment cessation.

Isolation of Genomic DNA and IL28B SNP rs12979860 Genotyping

Genomic DNA was isolated from peripheral blood using QIAamp DNA Blood Midi Kit (Qiagen, Valencia, CA) according to manufacturer’s instructions. Genomic DNA was quantified and adjusted at 10 ng/μl concentration in a NanoDrop 2000 spectrophotometer (Thermo Scientific, Rockford, IL). Genotyping for the IL28B SNP rs12979860 was performed from 50 ng/μl genomic DNA by real-time PCR using HybProbe probes according to the design of TIB Molbiol (TIB Molbiol, Berlin, Germany), and melting curves with FastStart DNA Master HybProbes kit (Roche Diagnostics, Mannheim, Germany). The reaction was performed in a total volume of 20 μl in a Light Cycler V2 thermocycler (Roche Diagnostics). Forty five amplification cycles were performed in the protocol. Each cycle included denaturation at 95°C for 10 sec, annealing at 60°C for 10 sec, and extension at 72°C for 15 sec. Finally, there was one cycle of melting curve denaturation at 95°C for 20 sec, annealing at 40°C for 20 sec, and 85°C with ramp rate of 0.2°C/sec with a cooling cycle at 40°C for 30 sec. Melting peak for the T allele was 51.80°C and for the C allele was 59.62°C.

Primer sequences used were IL28B (rs12979860) forward gCAggCTCAggTCATAcA, reverse CCCC TAACCTCtCAACGTc; sensor probe ggCgGAgAC CAggtTCgAATt-fl; anchor probe LC-CACTCCgCgCT CCCCCAgCAA-PH.

Statistical Analysis

 Frequencies and proportions were used to describe categorical data and differences were analyzed using the χ² test. Continuous variables were expressed as medians with interquartile range (IQR; 25th–75th percentile) and compared using the Kruskal-Wallis test with Dunn’s multiple comparisons post-test. Means with standard deviations were used to describe total viral load, and its differences were tested by one-way ANOVA with post-ANOVA comparison by the Tukey “honestly significant difference” test. The Hardy-Weinberg equilibrium model was applied and the testing deviation was performed using the Pearson χ² test for 1° of freedom (number of genotypes—number of alleles).

The number needed to treat (NNT; 95% confidence intervals 95% CI) to achieve an outcome was obtained for each IL28B rs12979860 genotype. This was calculated as the inverse of the absolute risk reduction (ARR) with the following formula: NNT = 1/ARR, where ARR = Control Event Rate (CER) − Experimental Event Rate (EER). An historical CER (SVR <2% following the use of placebo) was used for calculations (16).

All analyses were two-tailed and significance was set at p < 0.05. Graph Pad Prism v.6.0 (Graph Pad Software Inc., San Diego, CA) statistical software was used for calculations.

Results

Three hundred and fifty patients (210 females and 140 males) with an average age of 52.8 ± 11.6 years with a mean age of 52.8 ± 11.6 years were initially recruited (Figure 1). Baseline characteristics and biochemical measurements were available for 106 patients (Table 1). According to the distribution of IL28B rs12979860 alleles, median necroinflammatory activity was 2 (IQR 1–3) for CC homozygous, 1 (IQR 1–2) for heterozygous, and 1 (IQR 1–2; p = not significant [ns] for all comparisons)

Number of patients receiving standard PegIFN-α/RBV therapy and IL28B rs12979860 genotype. This was calculated as the inverse of the absolute risk reduction (ARR) with the following formula: NNT = 1/ARR, where ARR = Control Event Rate (CER) − Experimental Event Rate (EER). An historical CER (SVR <2% following the use of placebo) was used for calculations (16).

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Figure 1. Participant flowchart.
Table 1. Characteristics of 109 patients with HCV according to the IL28B genotype

<table>
<thead>
<tr>
<th>Variable</th>
<th>CC (n = 23)</th>
<th>CT (n = 63)</th>
<th>TT (n = 23)</th>
<th>p</th>
</tr>
</thead>
<tbody>
<tr>
<td>Female/Male, (65/44)</td>
<td>15/8</td>
<td>37/26</td>
<td>13/10</td>
<td>ns</td>
</tr>
<tr>
<td>Age (years), mean ± SD</td>
<td>52.5 ± 11.3</td>
<td>53.7 ± 11.6</td>
<td>52.2 ± 12.1</td>
<td>ns</td>
</tr>
<tr>
<td>ALT (IU/l)</td>
<td>71 (43.5–107)</td>
<td>69 (37.5–95)</td>
<td>76 (43.5–108)</td>
<td>ns</td>
</tr>
<tr>
<td>AST (IU/l)</td>
<td>48 (36–94.5)</td>
<td>47 (33.5–81)</td>
<td>52 (39.5–90.5)</td>
<td>ns</td>
</tr>
<tr>
<td>Liver biopsy</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Necroinflammatory activity</td>
<td>2 (1–3)</td>
<td>1 (1.2)</td>
<td>1 (1.2)</td>
<td>ns</td>
</tr>
<tr>
<td>METAVIR fibrosis stage</td>
<td>1 (0.5–3)</td>
<td>2 (1–3)</td>
<td>1 (1.2)</td>
<td>ns</td>
</tr>
<tr>
<td>Hepatitis C virus-RNA (IU/mL), mean ± SD</td>
<td>1.82E6 ± 2.79E6</td>
<td>2.30E6 ± 1.39E7</td>
<td>3.09E7 ± 2.2E8</td>
<td>ns</td>
</tr>
</tbody>
</table>

HCV, hepatitis C virus; SD, standard deviation; ns, not significant.
Values are expressed in median (interquartile range) unless otherwise specified.

Table 2. Characteristics of 350 patients according to the IL28B SNP rs12979860 genotype

<table>
<thead>
<tr>
<th>Variable</th>
<th>CC (n = 76)</th>
<th>CT (n = 210)</th>
<th>TT (n = 64)</th>
<th>p</th>
</tr>
</thead>
<tbody>
<tr>
<td>Female/Male, (210/140)</td>
<td>44/32</td>
<td>129/81</td>
<td>37/27</td>
<td>ns</td>
</tr>
<tr>
<td>Age (years), mean ± SD</td>
<td>52.5 ± 11.3</td>
<td>53.7 ± 11.6</td>
<td>52.2 ± 12.1</td>
<td>ns</td>
</tr>
<tr>
<td>HCV-RNA (IU/mL), mean ± SD</td>
<td>1.82E6 ± 2.79E6</td>
<td>2.26E6 ± 1.38E7</td>
<td>3.09E7 ± 2.2E8</td>
<td>ns</td>
</tr>
<tr>
<td>HCV genotype 1 (n = 246)</td>
<td>48</td>
<td>150</td>
<td>48</td>
<td></td>
</tr>
<tr>
<td>HCV genotype ≠ 1 (n = 104)</td>
<td>28</td>
<td>60</td>
<td>16</td>
<td></td>
</tr>
</tbody>
</table>

HCV, hepatitis C virus; SD, standard deviation; ns, not significant.

for TT homozygous. The METAVIR fibrosis stage was 1 (IQR 0.5–3), 2 (IQR 1–3), and 1 (IQR 1–2; p = ns for all comparisons), respectively. Similarly, no differences were found in serum concentration of alanine (ALT) or aspartate aminotransaminases (AST) between groups (Table 1). Prevalence of IL28B rs12979860 alleles were as follows: 76 (22%) individuals were CC homozygous, 210 (60%) were heterozygous, and 64 (18%) showed TT homozygosity (Table 2). A genotypic frequency of 0.27 was found for CC homozygosity, 0.49 for CT heterozygosity, and 0.23 for the TT homozygosity. Finally, allelic frequency for the C allele was 0.52, whereas this was 0.48 for the T allele. Notably, the study population was not in equilibrium for the IL28B rs12979860 alleles according to the Hardy-Weinberg theorem (p < 0.001).

The frequency of HCV genotypes were as follows: 246 (70%) patients were infected with HCV genotype 1, 90 (26%) by HCV genotype 2 and 13 (4%) with HCV genotype 3. Only one patient was infected with HCV genotype 5. There were no significant differences in the distribution of HCV genotypes according to each IL28B rs12979860 genotype (Table 2).

Of the 350 patients initially recruited, 295 (84%) received a regimen including PegIFN-α/RVB and antiviral therapy outcomes were analyzed over time. As noted in Table 3, 69% of patients with IL28B rs12979860-CC allele achieved a SVR. In heterozygous patients, SVR was 46%, and in TT homozygous patients the SVR was 38% (p = 0.001). Conversely, the percentage of patients who were non-responders was 15%, 43%, and 48% (p < 0.0001), respectively. Interestingly, when patients were stratified according to the IL28B SNP rs12979860 (CC vs. CT + TT), CC homozygosity was overrepresented in the group with SVR (31.7%) as compared to the group of non-responders (9.1%; p < 0.05). In contrast, TT homozygous individuals (TT vs. CT + CC) were distributed almost equally in the SVR (12%), non-responder (21%) and relapsers (18%; p = ns) groups.

In regard to the HCV genotype, 71/200 (35.5%) individuals with genotype 1 achieved a SVR, whereas 72/92 (76%; p < 0.05) patients infected with HCV other than genotype 1 achieved SVR. In a similar way, the viral load at baseline was 1.01E7 ± 1.1E8 in patients with HCV genotype 1 and 1.56E6 ± 3.3E6 (p < 0.05) in individuals infected with other HCV genotypes.

Finally, NNT to reach a SVR was calculated for the standard regimen with PegIFN-α/RVB. Analyses were made according to each IL28B rs12979860 genotype as well as each HCV genotype as shown in Table 4. The IL28B rs12979860 genotype strongly influenced the odds to achieve a SVR in patients infected with HCV genotype 1 but not in those infected with other HCV genotypes. The NNT to achieve a SVR was 2 for patients with HCV with a genotype other than type 1 irrespectively of the presence of CC, CT or TT IL28B rs12979860 genotypes. For patients with HCV genotype 1 and a TT homozygosity for the IL28B rs12979860, a NNT of 10 was found. A NNT of 4 was calculated for the heterozygous patients (p < 0.05 vs. TT alleles), and a NNT of 2 was observed for those homozygous to CC alleles (p < 0.05 for both comparisons).
Discussion

In Mexico as in other countries, treatment for HCV with Peg-IFN/RBV remains the main option for chronic infections. In this sense, SNP IL28B rs12979860 C/T could be considered as an important host factor for therapeutic decisions.

In our study we present a large cohort of Mexican patients. A total prevalence of 22% for the protective IL28B SNP rs12979860-C allele was found, accounting for 0.27 genotypic frequency of CC genotype and 0.52 allelic frequency for C allele. When NNT to achieve a SVR was analyzed, IL28B SNP rs12979860 genotype strongly influences the outcome following a conventional course of PegIFN-α/RBV but only in patients infected with HCV genotype 1.

The ability of viruses to infect and persist within an individual results largely from an intricate interaction between viral faculties to evade the host’s immune system and various intrinsic factors useful to remove pathogens. Regarding HCV infection, a small number of SNPs have been demonstrated as relevant in both the response to treatment and the spontaneous viral clearance (5). A seminal study performed in 2009 in which > 500,000 SNPs were assessed, IL28B SNP rs12979860 was described as the strongest predictor of spontaneous viral clearance (6). These results were later confirmed (17).

Different findings have been reported in relation to the distribution of IL28B SNP rs12979860. In our study, Mexican patients have a low frequency (0.52) of the protective C-allele in contrast to East Asian populations who have the highest frequency of the protective C-allele (~0.95). European Americans and Hispanics have intermediate frequencies (~0.7), with the lowest frequencies being observed among African-Americans (~0.42) (5,6,17). These findings may reflect the differences in the ancestry of each population and places our patients at an intermediate level between Hispanics and African-Americans in regard to the allelic frequencies observed.

Allelic frequencies could vary among populations from a similar geographical area. In our study we found a prevalence of 22%, closely related to the 24% prevalence previously reported in 84 Mexican patients by Martínez-Gómez (12). If we look at other studies performed in Latin America, we find 20% prevalence for CC homozygosity in IL28B rs12979860 in 99 Chilean patients (10) and 18% prevalence (in 102 patients) in a study from Argentina (11). In contrast, in Moroccan and Egyptian populations, a frequency of 67–68% for rs12979860-C allele was reported, significantly higher than the one observed in sub-Saharan African populations (23–55%) (7,18,19). Our findings suggest that Latin Americans from either South or North America are similar in terms of genetic variants in the IL28B SNP rs12979860 in contrast to regional discrepancies observed in Africa.

In relation to genotype, several studies have been consistent with the outcome that individuals with a CC genotype are more likely to achieve a SVR than those with a TT genotype. It has been described that patients with a European ancestry have a higher probability of being cured than patients with other ancestries. In this vein, we found that Mexican patients homozygous to the CC genotype have a >2-fold higher rate of SVR than those with the TT genotype. Moreover, the present study shows that the number of patients needed to treat to achieve a SVR is highly influenced by the rs12979860 genotype, at least in individuals infected with HCV genotype 1. Although two patients are needed to treat (HCV genotype 1) with the CC genotype to achieve a SVR, this number increases up to ten when the TT genotype is present; the NNT of 4 in heterozygous patients further supports the notion of a dose/effect relation for the SNP. If we analyze other Latin Americans patients (from different latitudes), better response rates are present when CC alleles are described (9–11). Notably, the relapse frequency was not associated with the IL28B genotype among our patients, although this phenomenon has been previously observed (5,17).

Viral genotype 1 was the most common type of HCV found in Mexican patients. Unfortunately, this genotype has been consistently associated with the highest basal viral load and the lowest rate of SVR. Similar data have been consistently described in patients from Mexico and in

Table 3. Response to Peg-IFN α/RBV according to the IL-28B SNP rs12979860 genotype in 295 patients with HCV infection

<table>
<thead>
<tr>
<th></th>
<th>CC (n = 68)</th>
<th>CT (n = 179)</th>
<th>TT (n = 48)</th>
<th>p</th>
</tr>
</thead>
<tbody>
<tr>
<td>SVR, n (%) HCV 1: HCV ≠ 1</td>
<td>47 (69) 27:20</td>
<td>83 (46) 44:39</td>
<td>18 (38) 6:12</td>
<td>0.001</td>
</tr>
<tr>
<td>Non-responders, n (%) HCV 1: HCV ≠ 1</td>
<td>11 (15) 10:1</td>
<td>76 (43) 62:14</td>
<td>23 (48) 21:2</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>Relapsers, n (%) HCV 1: HCV ≠ 1</td>
<td>10 (16) 7:3</td>
<td>20 (11) 16:4</td>
<td>7 (16) 6:1</td>
<td>ns</td>
</tr>
</tbody>
</table>

HCV, hepatitis C virus; SVR, sustained virologic response; ns, not significant.

Table 4. NNT to achieve a SVR according to IL-28B SNP rs12979860 genotype as well as to HCV genotype*

<table>
<thead>
<tr>
<th>HCV genotype 1</th>
<th>CC</th>
<th>CT</th>
<th>TT</th>
</tr>
</thead>
<tbody>
<tr>
<td>HCV genotype other than 1</td>
<td>2</td>
<td>4</td>
<td>10</td>
</tr>
</tbody>
</table>

NNT, numbers needed to treat; SVR, sustained virologic response; HCV, hepatitis C virus.
*NNTs were rounded to the nearest higher or lower value.
populations from other regions around the world (9—11,20). Despite a high frequency of HCV genotype 1 and a relatively low frequency of the IL28B SNP rs12979860 CC genotype is found in Mexican populations, the widespread use of antiviral therapy should not be discouraged.

Contrariwise, it is necessary to characterize other factors that may improve therapeutic decisions in our patients. Prokunina-Olsson et al. described a dinucleotide variant ss469415590 (TT/DG) (21). This SNP is located upstream of INFL3 (II28B) and has been designated as interferon lambda 4 (INFL4). Reports suggest that it has a stronger prognostic value on dual therapy than IL28B rs12979860 in HCV-1 (22—24). In this scenario, it may be important to assess its usefulness in our population.

In the last year, new molecules for treatment of HCV have become available. These drugs, categorized as direct acting antiviral drugs (DAA), are mixed in different treatment options leading to IFN-free regimens with a reported SVR of 97—98%. For some populations RBV should be used in addition. This new treatment modality presents advantages such as a short course and few side effects. These drugs are not affected by the host genetic factors, specifically SNP IL28B 12979860 (13—15), but their cost is higher than past treatments, which makes them inaccessible to all patients. It is for these populations where we believe tests like SNP IL28B 12979860 could still be useful as a marker to predict treatment response. We hope in coming years that direct acting antiviral treatment will be used.

We are aware that our study has limitations such as the absence of healthy subjects as a control group, lack of individuals who had naturally cleared HCV, absence of long-lasting follow-up to determine the progression of HCV infection, the search for additional polymorphisms and haplotypes of the IL28B gene and other potential genes. However, our data add valuable information to better understand the relationship between IL28B and HCV infection, further supporting that IL28B may be a promissory therapeutic target in the coming years.

In conclusion, the IL-28B rs12979860 CC genotype is present in 22% of Mexican patients with chronic HCV infection and is a strong predictor of response to the current treatment course of PegIFN-α/RVB, especially in patients infected with HCV genotype 1.

References