Inducible protein-10 as a predictive marker of antiviral hepatitis C treatment
A systematic review
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WJH covers topics concerning liver biology/pathology, cirrhosis and its complications, liver fibrosis, liver failure, portal hypertension, hepatitis B and C and inflammatory disorders, steatohepatitis and metabolic liver disease, hepatocellular carcinoma, biliary tract disease, autoimmune disease, cholestatic and biliary disease, transplantation, genetics, epidemiology, microbiology, molecular and cell biology, nutrition, geriatric and pediatric hepatology, diagnosis and screening, endoscopy, imaging, and advanced technology. Priority publication will be given to articles concerning diagnosis and treatment of hepatology diseases. The following aspects are covered: Clinical diagnosis, laboratory diagnosis, differential diagnosis, imaging tests, pathological diagnosis, molecular biological diagnosis, immunological diagnosis, genetic diagnosis, functional diagnostics, and physical diagnosis; and comprehensive therapy, drug therapy, surgical therapy, interventional treatment, minimally invasive therapy, and robot-assisted therapy.

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Inducible protein-10 as a predictive marker of antiviral hepatitis C treatment: A systematic review

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Data sharing statement: The technical appendix, and dataset are available from the corresponding author at nina.weis@regionh.dk.

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Abstract

AIM
To investigate interferon-γ-inducible protein-10's (IP-10) potential to anticipate rapid (RVR)- and sustained virological responses (SVR) to chronic hepatitis C (CHC) treatment.

METHODS
We included case series examining RVR or SVR in relation to 24 or 48 wk treatment for CHC, in patients treatment free for at least six months, with genotype 1 or 4, and in relation to 24 wk treatment for genotype 2 and 3, with pegylated interferon in combination with ribavirin. Patients had to have both a baseline IP-10 level as well as a hepatitis C virus (HCV)-RNA determination 4 wk after treatment initiation or 24 wk after end of treatment. Studies including patients with liver diseases other than CHC, human immunodeficiency virus-infection, treatment with immunosuppressants or cytostatica, alcohol dependency or active intravenous drug-use were excluded. We found 81 articles by searching the MEDLINE and EMBASE databases. Eight studies were eligible for inclusion. Their quality were assessed using an 18 point checklist for case series, developed using a modified Delphi technique. Information was extracted from the articles, and no raw data was requisitioned. The review protocol was
registered at the International Prospective Register of Systematic Reviews (reg. number: CRD42014008736).

RESULTS
Three studies reported on baseline IP-10 level in association with RVR. A significant association was found for HCV genotype 1 infection by two studies. Only two studies reported on HCV genotype 4 infected and genotype 2 and 3 infected patients, respectively. A trend was seen for an association between RVR and baseline IP-10 for genotype 4, while no association was found for genotype 2 and 3. Seven studies provided information regarding baseline IP-10 and SVR. Following the pattern regarding rapid virological response all five studies examining SVR in relation to baseline IP-10 levels for HCV, genotype 1 infected patients showed a significant association. Likewise a significant association was seen for HCV, genotype 4 infected, while no association was found for HCV, genotype 2 and 3 infected. Though only two studies examined the association for HCV genotype 4 infected and HCV genotype 2 and 3 infected respectively.

CONCLUSION
We found indications of a possible association between baseline IP-10 level and virological responses in patients with CHC genotype 1 and 4.

Key words: Chronic hepatitis C; Inducible protein-10's; Sustained virological response; Interferon-γ-inducible protein-10; CXCL-10; Chemokine; Genotype; Pegylated interferon; Ribavirin; Rapid virological response

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Core tip: This is the first systematic review examining the association between baseline levels of interferon-γ-inducible protein-10 (IP-10) and virological response to treatment with pegylated interferon and ribavirin among patients chronically infected with hepatitis C virus, genotype 1-4. We found a possible correlation for genotype 1 and 4 infected patients, indicating that baseline IP-10 levels could predict which patients, infected with genotype 1 or 4, would have the highest likelihood of benefitting from antiviral treatment with pegylated interferon and ribavirin. These findings can be especially relevant in countries, where treatments with direct acting antivirals are not readily applicable.


INTRODUCTION
Every year 3-4 million individuals are infected with hepatitis C virus (HCV) of whom only 20%-35% clear the infection, meaning that 2.4-3.2 million individuals remain chronically infected, defined as detectable HCV-RNA in two consecutive measurements ≥ six months apart. Globally, the prevalence of chronic hepatitis C (CHC) is estimated to 150 million people, with CHC being the leading cause of chronic liver disease[11]. CHC can lead to formation of connective tissue (fibrosis) in the liver. However, the rate and severity of the inflammation and fibrosis vary[2,3]. Though only 5%-20% of HCV infected patients develop cirrhosis, these patients have an increased risk of developing hepatocellular carcinoma, a condition responsible for more than 300000 deaths annually[4].

Until recently, the standard of care for CHC was lengthy dual therapy with pegylated interferon plus ribavirin (peg-IFN/RBV), either as 180 μg peg-IFN-α-2a weekly or peg-IFN-α-2b 1.5 μg/kg per week in combination with ribavirin 15 mg/kg per day (minimum 1000 mg daily and maximum 1400 mg daily), fixed doses of 1000 mg for patients < 75 kg and 1200 mg for patients > 75 kg with genotype 1 or 4 or flat dosing of 800 mg daily for genotypes 2 and 3 - a treatment with modest success rates, severe adverse events and variation in treatment response between genotypes[4]. Therefore, a great effort has been put into identifying biomarkers to predict rapid virological response (RVR), defined as undetectable serum HCV-RNA at week four of antiviral treatment, and sustained virological response (SVR), defined as the undetectable HCV-RNA 24 wk after discontinuing antiviral treatment. One of the most promising chemokine biomarker candidate is interferon-γ inducible protein-10 (IP-10). Both intrahepatic IP-10 mRNA and plasma levels of IP-10 are elevated in individuals with CHC[10,11], strongly indicating that intrahepatic IP-10 is the source of plasma IP-10. Several studies have suggested that pretreatment levels of IP-10 have the capability to predict RVR and SVR[12,13]. In addition, hepatic inflammation and fibrosis have been shown to correlate with IP-10 levels[14,15], and it has been proposed, that plasma levels of IP-10 can predict the risk of fibrosis progression[16]. Later years have seen the forthcoming of the new direct acting antivirals (DAA), and all current treatment recommendations for CHC patients from the European Association for the Study of the Liver contain at least one DAA[14]. The current DAA are the NS5B polymerase inhibitor, sofosbuvir, the NS3/4A protease inhibitor simeprevir and the NS5A-replication-inhibitors daclatasvir and ledipasvir or the so-called 3D regimen containing the dual NS3/4A protease inhibitors Paritaprevir/Ritonavir; the NS5A inhibitor Ombitasvir and the NS5B palm polymerase inhibitor Dasabuvir. This has yielded the possibility for treating CHC patients with interferon free, all-oral regimens, with high SVR-rates and fewer adverse events[14-18]. Despite of these great advantages, the cost of DAA will without doubt substantially delay their introduction as standard treatment in low and middle-income countries by years to come. Moreover, even in high income countries, treatment with DAA therapy is reserved for patients with advanced liver disease, despite the fact that a majority of patients are expected to benefit from the treatment. Therefore,
peg-IFN/RBV treatment still has a role to play in treatment of patients with CHC, and the need for markers that can predict successful treatment outcomes to peg-IFN-α/RBV are still needed.

Several studies have independently shown an association between virological response and baseline IP-10 concentrations for CHC patients infected with genotype 1 and 2[19-21]. However, the association seems to be lacking for CHC patients, infected with HCV genotype 2 and 3[21,22]. Despite this being the case, a systematic review to address and clarify the differences in IP-10 properties, in relation to the different HCV genotypes, is missing. The aim of this systematic review was therefore to examine IP-10’s ability to predict RVR and SVR in patients with CHC genotypes 1-4 treated with peg-IFN/RBV. We succeeded in doing so, with data presented in the following.

**MATERIALS AND METHODS**

On initiation of this review a protocol was made and registered at the International Prospective Register of Systematic Reviews (PROSPERO) - registration number: CRD42014008736. Protocol can be found at https://www.crd.york.ac.uk/PROSPERO/.

**Literature search**

Using the search profiles listed in the Appendix I in the supporting information, suitable literature was identified in MEDLINE and EMBASE. The first article sorting was performed by rating the article headlines, while the second sorting was performed on abstract level. Papers passing both sorting rounds were considered for the review, and thoroughly scrutinized based on pre-defined inclusion and exclusion criteria as listed below. The initial search provided 81 articles; 34 in MEDLINE and 47 in EMBASE. After the first- and second-sorting, 14 articles remained from MEDLINE and 14 articles from EMBASE of which 10 were duplicates. One article was found by manual searching the references, bringing the total number of articles after the third sorting to 19. During the third sorting, 11 articles were excluded[6,8,22-30]. This left 8 studies for inclusion[7,9,21,31-34]. Overveiw of the entire sorting process is shown in Figure 1.

**Inclusion criteria**

Case series examining RVR or SVR in relation to 24 or 48 wk treatment with either 180 μg Peg-IFN-α-2a per week or peg-IFN-α-2b 1.5 μg/kg per week in combination with ribavirin 15 mg/kg per day (minimum 1000 mg daily and maximum 1400 mg daily) or fixed doses of 1000 mg for patients < 75 kg and 1200 mg for patients > 75 kg, in CHC patients infected with HCV, genotypes 2 or 3, treatment free for at least six months prior to inclusion, with both a baseline IP-10 level- and HCV-RNA determination 4 wk after treatment initiation to assess RVR and/or 24 wk after end of treatment to assess SVR.

Case series studies examining RVR or SVR, in relation to 24 wk treatment with either 180 μg Peg-IFN-α-2a per week or peg-IFN-α-2b 1.5 μg/kg per week in combination with ribavirin 800 mg daily or fixed doses of 1000 mg for patients < 75 kg and 1200 mg for patients > 75 kg, in CHC patients infected with HCV, genotypes 2 or 3, treatment free for at least six months prior to inclusion, with both a baseline IP-10 level- and HCV-RNA determination 4 wk after treatment initiation to assess RVR and/or 24 wk after end of treatment to assess SVR.

**Exclusion criteria**

Liver diseases other than CHC, Co-infection with human immunodeficiency virus (HIV), co-infection with hepatitis B virus (HBV), alcohol dependency (regular intake of ≥ 75 g/d), active intravenous drug-use, treatment with immunosuppressants or cytostatica and prior treatment for CHC within the last 6 mo.

**Quality assessment**

The quality of the 8 included articles were appraised using an 18 point checklist for case series, developed using a modified Delphi technique[35]. Each criterion can be answered with “yes”, “no” or “partially reported/unclear”, with the 18 criteria being weighted equally. In line with a pilot study conducted testing the assessment tool, we choose to rate studies with 14 or more “yes responses” as “high-quality studies”, and studies with 13 or less “yes responses” as “low-quality studies”. No studies were excluded on the basis of the criteria scores. The full checklist can be found in the Appendix I in the supporting information. Table 1 shows the sum score of the checklist. The baseline demographics regarded as important for the appraisal of the studies were: Number of patients included, patient ethnicity, patient age, male/female ratio, HCV RNA, liver enzyme level [alanine transaminase (ALT) or aspartate transaminase (AST)], body mass index (BMI), genotype, liver fibrosis stage and distribution on interleukin 28B (IL28B) single nucleotide polymorphism (SNPs).

**RESULTS**

**Patient baseline demographic**

All information was extracted from the articles, no raw data was requisitioned. Overall, presentation of baseline demographic data was missing in one study. Instead, this study provided baseline demographics in the following subpopulations: IL28 rs12979860 (CC, CT, TT), rs12980275 (AA, AG, GG), rs8099917 (TT, TG, GG)[34]. Only baseline characteristics for rs12979860 are reported in the review, as these were representative for the study population. All studies provided baseline information on total number of patients included, gender and age. Four studies failed to provide BMI[7,9,10,34], and four studies did not supply exact information regarding patient ethnicity[7,9,10,32]. Information regarding number of patients included, ethnicity, age, male/female ratio, and BMI is reported in Table 2. ALT or AST values were not reported by two studies[33,34], one of these however stated that all patients included had two
serum ALT values above the upper limit of normal within 6 mo of treatment initiation\(^3\). Effect on liver parenchyma and HCV-RNA load are shown in Table 3. Regarding fibrosis stage, four studies used the Ishak score\(^7,31,33,34\), two studies used the Scheuer score\(^9,32\), and two studies used the Metavir staging system\(^19,21\). Overview of genotype and fibrosis stage is presented in Table 4. Information regarding treatment regimens can be found in Table 5. Four studies provided information on IL28B SNP distribution. An overview of SNPs can be seen in Table 6.

**Rapid virological response**

An overview is presented in Table 7. Lagging et al\(^3\) (2011) examined IP-10’s ability to predict virological response and treatment outcome in 170 patients with genotype 1, from the DITTTO-HCV study group. After six weeks, patients were randomized to individualized treatment, or continued on the standard combination therapy as no sub analysis on SVR for patient receiving therapy, corresponding with the review’s inclusion criteria for the course of 24-48 wk, was provided. Only results regarding RVR are featured in the review. The study found that patients obtaining RVR had significantly lower median baseline IP-10 levels than patients without a RVR. These findings were similar to results reported by Fattovich et al\(^21\) that patients infected with HCV, genotype 1, who achieved RVR, had a significant lower mean baseline IP-10, than those who did not. However, this association was not seen for patients infected with HCV genotype 2 or 3. The study also enrolled genotype 4 infected patients, but due to insufficient numbers (\(n = 15\)), these were excluded. Al-Ashgar et al\(^19\), 2013 studied the relationship between IP-10 and virological response in patients infected with genotype 4, and showed a trend

Figure 1  Flow chart depicting the sorting of articles. The chart depicts the number of articles found by searching the MEDLINE and EMBASE databases 04.15.2014, the number of articles excluded during the first and second sorting, the number of duplicates, the number of articles found by manual searching references, and the number of articles excluded in the third sorting, with indication of the reason for exclusion. Articles progressing down the chart from the original search to final inclusion are marked with green boxes, articles found by manual search are marked with blue boxes, and articles excluded are marked with red boxes. SVR: Sustained virological responses; RVR: Rapid virological responses; CHC: Chronic hepatitis C; HCV: Hepatitis C virus.
SVR

An overview is presented in Table 2. Following the pattern regarding RVR, all five studies examining SVR in relation to baseline IP-10 levels for HCV genotype 1 infected patients showed a significant association.

Apolinario et al[31] enrolled 63 Spanish patients from clinical trials and out patient clinics. Forty-three patients had genotype 1, while 20 had a non-1 genotype. Among the 43 HCV genotype 1 infected patients, mean baseline IP-10 levels were significantly lower in patients who reached a SVR compared to those who did not. Because some of the genotype non-1 infected patients received 48 wk of therapy, the results for these are not provided in Table 7. Diago et al[7] also found a significant association between mean baseline IP-10 and SVR for their overall population of Spanish patients. An association that remained significant, when the analysis was restricted to HCV genotype 1 infected patients. The same significant association between lower baseline IP-10 and SVR of the patients were infected with HCV, genotype 1, and 4 infected patients included, which was surprising, as three quarters provide separate results for the group of genotype non-1 patients included, which was surprising, as three quarters of the patients were infected with HCV, genotype 1, and could very well be the reason for finding a significant correlation in the overall population, when all genotypes were analyzed together. In line with this, Apolinario et al[31] stated that no associations was found for their genotype non-1 group. However lacking differentiation into sub genotypes, compromise the value of information, especially as no association were found for HCV, genotype 2 or 3 infected[21], and both studies reporting on genotype 4 infected patients[19,32] found significant lower IP-10 levels of than in SVRs. Interestingly, a sub analysis, performed by Al-Ashgar et al[31] on genotype 4a and 4d, showed that this correlation was present for genotype 4d (465.9 pg/mL ± 349.1 vs 904.9 pg/mL ± 523.1, P < 0.001), but not for genotype 4a (564.7 pg/mL ± 288.9 vs 568 pg/mL ± 384.9, P = 0.300). Derbala et al[32] failed to provide information on the exact levels of IP-10, and instead provided a graphic depiction, which could not be interpreted to adequate results.

DISCUSSION

Several studies have independently shown levels of IP-10 to be associated with both RVR and SVR to peg-IFN/RBV treatment for CHC patients infected with HCV, genotype 1 and 4, but not for genotype 2 and 3. We conducted this systematic review to assess variation in IP-10’s predictive ability for RVR and SVR to peg-INF/ RBV treatment in patients chronically infected with HCV genotypes 1-4.

Our main findings indicate that a correlation exist between baseline IP-10 and SVR- and in part for RVR - for genotype 1 and possibly for genotype 4, however not for genotype 2 or 3.

Three studies provided information on baseline IP-10 in relation to RVR[19,21,34]. Studies reporting on HCV, genotype 1 infected patients, found significant lower baseline IP-10 values in patients achieving RVR compared to those who did not[21,34]. Only a trend, failing to reach significance, was described between baseline IP-10 and RVR in genotype 4 infected patients[19] and no significant relation was found in relation to genotype 2 or -3[21]. Seven studies provided information on baseline IP-10 in relation to SVR[7,19,21,31,33]. All five studies reporting on HCV genotype 1 infected patients[7,9,21,31,33] found significantly lower IP-10 levels of RV than non-SVR. Diago et al[7] did not provide separate results for the group of genotype non-1 patients included, which was surprising, as three quarters of the patients were infected with HCV, genotype 1, and could very well be the reason for finding a significant association in the overall population, when all genotypes were analyzed together. In line with this, Apolinario et al[31] stated that no associations was found for their genotype non-1 group. However lacking differentiation into sub genotypes, compromise the value of information, especially as no association were found for HCV, genotype 2 or 3 infected[21], and both studies reporting on genotype 4 infected patients[19,32] found significant lower baseline IP-10 level in their populations, when comparing patients achieving SVR vs non-SVR. It should be noted, that while Fattovich et al[31] considered two-sided P-values < 0.05 as statistical significant, only results of statistical tests with a P-value < 0.01 were considered of interest, because of the multiple comparisons between subjects with and without SVR. Therefore IP-10 was not considered to be associated with SVR, for HCV genotype 3 infected individuals, even though the p-value was found to be 0.02.

One study observed that the greatest difference in IP-10 levels was found at week 4. Patients, who at this
Table 2 Baseline total patient number, number of male patients, mean age, body mass index and ethnicity for the 8 included studies

<table>
<thead>
<tr>
<th>Ref.</th>
<th>Patients</th>
<th>Mean age</th>
<th>BMI</th>
<th>Ethnicity</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Males</td>
<td>(yr)</td>
<td>(kg/m²)</td>
<td></td>
</tr>
<tr>
<td>Apolinario et al[8]</td>
<td>40</td>
<td>41 (±9.3)</td>
<td>Information not provided</td>
<td>Information not provided</td>
</tr>
<tr>
<td>Lagging et al[9]</td>
<td>169</td>
<td>252</td>
<td>Information not provided</td>
<td></td>
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<tr>
<td>II.28B rs12979860 CC</td>
<td>64</td>
<td>41.6 (± 10.1)</td>
<td>25.1 (± 3.6)</td>
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</tr>
<tr>
<td>II.28B rs12979860 CT</td>
<td>77</td>
<td>41.9 (± 9.5)</td>
<td>25.0 (± 3.5)</td>
<td></td>
</tr>
<tr>
<td>II.28B rs12979860 TT</td>
<td>28</td>
<td>41.9 (±11.4)</td>
<td>25.0 (± 3.5)</td>
<td></td>
</tr>
<tr>
<td>Diago et al[10]</td>
<td>77</td>
<td>42 (± 9.7)</td>
<td>Information not provided</td>
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</tr>
<tr>
<td>Fattovich et al[11]</td>
<td>133</td>
<td>46 (± 11)</td>
<td>24.7 (± 3.8)</td>
<td>226</td>
</tr>
<tr>
<td>Kurelac et al[12]</td>
<td>17</td>
<td>41.5 (± 12.4)</td>
<td>23.7 (21.9-25)</td>
<td>46</td>
</tr>
<tr>
<td>Darling et al[13]</td>
<td>176</td>
<td>48.4 (± 7.4)</td>
<td>Information not provided</td>
<td>138</td>
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<tr>
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<td>144</td>
<td>46.47 (± 8.83)</td>
<td>30.18 (± 5.05)</td>
<td>Information not provided</td>
</tr>
<tr>
<td>Al-Ashgar et al[15]</td>
<td>41</td>
<td>38.7 (± 11.5)</td>
<td>Information not provided</td>
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</tbody>
</table>

1Study did not provide baseline characteristics for their entire population, but instead provided baseline demographics in accordance with IL-28 genotype (only baseline characteristics for rs12979860 are reported in the review, as these were representative for the study population); 2253 was reported to be enrolled, however when adding the males and female patients, it sums to 252; 3Only 226 out of 280 patients had serum available for IP-10 testing; 4Median (25-75 percentiles); 5Mean (SD); 651 patients from clinical trials had Spanish nationality; 7Egyptian nationality; 8Saudi nationality; 95% of the original DITTO patient population were Caucasian. BMI: Body mass index.

Table 3 Hepatitis C virus-RNA and patient liver enzyme status for the 8 included studies

<table>
<thead>
<tr>
<th>Ref.</th>
<th>HCV-RNA</th>
<th>Liver enzyme level n Limit</th>
<th>All patients n Limit</th>
<th>AST n Limit</th>
<th>ALT n Limit</th>
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<tbody>
<tr>
<td>Apolinario et al[8]</td>
<td>High viral load</td>
<td>28 ≥ 6.3 log IU/mL</td>
<td>35 &lt; 6.3 log IU/mL²</td>
<td>118 IU/L (± 64) $</td>
<td></td>
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<tr>
<td>Lagging et al[9]</td>
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<td></td>
<td></td>
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<tr>
<td>II.28B rs12979860 CC</td>
<td></td>
<td>6.3 log IU/mL (± 0.8)$</td>
<td>Information not provided</td>
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<td>II.28B rs12979860 CT</td>
<td></td>
<td>6.1 log IU/mL (± 0.7)$</td>
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<tr>
<td>II.28B rs12979860 TT</td>
<td></td>
<td>5.9 log IU/mL (± 0.8)$</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Diago et al[10]</td>
<td>85 ≥ 5.7 log IU/mL</td>
<td>52 &lt; 5.7 log IU/mL²</td>
<td>117.2 IU/L (± 81.6)$</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Fattovich et al[11]</td>
<td>147 ≥ 5.6 log IU/mL</td>
<td>5.74 log IU/mL (± 0.9)$</td>
<td>Information not provided</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Kurelac et al[12]</td>
<td></td>
<td>5.55 log IU/mL (5.52-6.1)$</td>
<td>92 IU/L (± 78)$</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Darling et al[13]</td>
<td></td>
<td>6.66 log IU/mL (± 6.76)$</td>
<td>90.9 IU/L (72.9)$</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Darbala et al[14]</td>
<td>45 ≥ 5.78 log IU/mL</td>
<td>19 &lt; 5.78 log IU/mL²</td>
<td>38 IU/L (27-51)$</td>
<td>51 IU/L (34-87)$</td>
<td></td>
</tr>
<tr>
<td>Al-Ashgar et al[15]</td>
<td></td>
<td>67.5 IU/L (43.5-106.8)$</td>
<td>56.0 IU/L (52.0-86.0)$</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

1Lagging et al provided baseline demographics in accordance with IL-28 genotype (only baseline characteristics for rs12979860 are reported in the review, as these were representative for the study population); 2Median (25-75 percentiles); 3Mean (SD); 4Median (IQR); 5Recalculated into log IU/mL. HCV-RNA is shown as number of patients with high or low viral load or as the mean or median for the entire population. Depending on the presentation in the original article, levels of ALT, AST or both are shown. HCV: Hepatitis C virus; ALT: Alanine transaminase; AST: Aspartate transaminase.

point had IP-10 levels higher than 250 pg/mL, had a 40-fold risk of not reaching SVR compared to patients with IP-10 levels lower than 250 pg/mL[3]. This might indicate, that IP-10 levels at treatment week 4, could be used to assess if peg-IFN/RBV treatment should be discontinued or not in genotype 1 patients - and perhaps could also be used to evaluate the need for adjacent DAA treatment (i.e., using a 4 wk lead in phase with peg-IFN/RBV treatment before apprising the need for DAAs). However, the small number of patients participating calls for caution when interpreting these results, and further studies of IP-10 levels at treatment week 4 should be encouraged.

One study[21] showed that the correlation between baseline IP-10 and SVR remained significant even when the population was grouped according to ethnicity (P < 0.001). The latter is interesting as AA ethnicity is otherwise considered an unfavorable prognostic factor for obtaining SVR[26,28], and might imply that IP-10 could help aid the decision as to whom would have the greatest potential benefit from peg-IFN/RBV treatment regardless of ethnicity. In this context it is interesting that it has previously been shown that HCV infected AA had higher IP-10 levels than corresponding CA patients, while uninfected AA had IP-10 levels similar to uninfected CA[28]. The effect of race on Interferon Stimulated Genes, once at the stage of CHC, should therefore be examined further.

Findings, regarding SVR for HCV genotype 2 and 3, followed the same pattern as the results for RVR with no association between baseline IP-10 and SVR present for genotype 2 or 3[21]. Supporting our findings, this lacking correlation in patients with HCV genotype 2 and 3, has also been shown when treating patients with standard and low (90 μg once weekly) peg-IFN/RBV regimens[22]. As mentioned, a significant correlation between IP-10 and SVR was reported by both studies, including HCV genotype 4 infected patients[20,32]. One of these[20] also performed differentiated analyses on HCV genotype 4
Table 4  Genotype and liver fibrosis stage for the 8 included studies

<table>
<thead>
<tr>
<th>Ref.</th>
<th>Genotype (n)</th>
<th>Method</th>
<th>Liver fibrosis stage</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>0 1 2 3 4 5 6</td>
</tr>
<tr>
<td>Lagging et al[12]</td>
<td>1701 231 491 111</td>
<td>Ishak score</td>
<td>11 61 65 30 15 20 14</td>
</tr>
<tr>
<td>IL28B rs12979860 CC</td>
<td>44 13 33 3</td>
<td>Ishak score</td>
<td>3 18 27 11 5 12 5</td>
</tr>
<tr>
<td>IL28B rs12979860 CT</td>
<td>96 7 15 5</td>
<td>Ishak score</td>
<td>7 35 27 17 7 6 6</td>
</tr>
<tr>
<td>IL28B rs12979860 TT</td>
<td>30 3 1 3</td>
<td>Ishak score</td>
<td>1 8 11 2 3 2 3</td>
</tr>
<tr>
<td>Diago et al[13]</td>
<td>103 9 25</td>
<td>Ishak score</td>
<td>106 31</td>
</tr>
<tr>
<td>Fattovich et al[14]</td>
<td>92 87 47</td>
<td>Metavir</td>
<td>121 21</td>
</tr>
<tr>
<td>Kurelec et al[15]</td>
<td>46</td>
<td>Ishak</td>
<td>34 12</td>
</tr>
<tr>
<td>Darling et al[16]</td>
<td>272</td>
<td>Ishak</td>
<td>220 52</td>
</tr>
<tr>
<td>Darbala et al[17]</td>
<td>159</td>
<td>Scheuer score</td>
<td>109 50</td>
</tr>
<tr>
<td>Ashgar et al[18]</td>
<td>64</td>
<td>Metavir</td>
<td>341 101</td>
</tr>
</tbody>
</table>

1Baseline information for the sub-analysis of IL28B rs12979860. Two hundred and fifty-two patients are reported to be enrolled, however adding the genotypes yields 253 patients. Likewise biopsies from 228 patients are described, however when adding the Ishak scores only yields 216 patients; 2Histology available for 44 patients; 3Lagging et al provided baseline demographics in accordance with IL-28 genotype (only baseline characteristics for rs12979860 are reported in the review, as these were representative for the study population). A box stretching over two or more genotypes or fibrosis stage, indicates that the number refers to the combined group.

Table 5  Overview of the treatment regimens for pegylated interferon in combination with ribavirin, for the 8 studies included, in relation to dose and duration

<table>
<thead>
<tr>
<th>Ref.</th>
<th>Genotype</th>
<th>Duration</th>
<th>Interferon treatment</th>
<th>Ribavirin treatment</th>
</tr>
</thead>
<tbody>
<tr>
<td>Apolinaro et al[19]</td>
<td>Multi-centerpatients</td>
<td>1 48 wk</td>
<td>peg-INF-α2a once weekly 180 μg</td>
<td>800 μg per day or 1000 μg &lt; 75 kg, 1200 mg &gt; 75 kg per day 1000-1200 mg per day</td>
</tr>
<tr>
<td>Non-1</td>
<td>48 wk</td>
<td>peg-INF-α2b 1.5 μg/kg per week</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Out patients</td>
<td>24-48 wk</td>
<td>peg-INF-α2b 1.5 μg/kg per week</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Lagging et al[20]</td>
<td>1 6 wk1</td>
<td>peg-INF-α2a 1.5 μg/kg per week</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Diago et al[21]</td>
<td>1 48 wk</td>
<td>peg-INF-α2a 1.5 μg/kg per week or 180 μg peg-INF-α2a/week</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Fattovich et al[22]</td>
<td>1 and 4 24 wk</td>
<td>peg-INF-α2b 1.5 μg/kg per week or 180 μg peg-INF-α2b/week</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2 and 3</td>
<td>peg-INF-α2a/week</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Kurelec et al[23]</td>
<td>1 48 wk</td>
<td>peg-INF-α2b 1.5 μg/kg per week</td>
<td></td>
<td></td>
</tr>
<tr>
<td>24 wk</td>
<td>peg-INF-α2b 1.5 μg/kg per week</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Darling et al[24]</td>
<td>1 48 wk</td>
<td>peg-INF-α2a 1.5 μg/kg per week</td>
<td></td>
<td></td>
</tr>
<tr>
<td>24 wk</td>
<td>peg-INF-α2a 1.5 μg/kg per week</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Derbala et al[25]</td>
<td>4 48 wk</td>
<td>Peg-INF once weekly</td>
<td></td>
<td></td>
</tr>
<tr>
<td>1000-1200 mg per day</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Al-Ashgar et al[26]</td>
<td>1 48 wk</td>
<td>Peg-INF-α2a 1.5 μg/kg per week</td>
<td></td>
<td></td>
</tr>
<tr>
<td>1000 mg &lt; 75 kg, 1200 mg &gt; 75 kg per day</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

1After 6 wk, patients were randomized to differentiated treatment regimes; 2No further information on ribavirin treatment was provided; 3No further information on the subtype of peg-INF was provided. Apolinaro et al[19] feature patients from both an outpatient clinic as well as patients from two multicenter trials receiving different treatment regimens, illustrated by the segregation in the genotype column. peg-INF: Pegylated interferon.

subtypes, 4a and 4d, showing a significant association only for the latter (P = 0.330 and P < 0.001, respectively). It would have been interesting to examine if this was also the case for RVR, as it could be speculated that the association between baseline IP-10 and RVR in HCV genotype 4 infected patients failed to show significance, because both subtype 4a and 4d were analyzed as a whole. Therefore, subsequent studies making RVR and SVR assessments should be encouraged to perform differential analysis on individual viral subtypes, in order to uncover more specific associations. The setup for this study, did not allow us to investigate, what specific mechanisms account for the differences in correlation between baseline IP-10 and HCV genotype 1 and 4 compared with HCV genotype 2 and 3. However it is of great interest that these differences occur, and should be investigated further. Inversely patients infected with HCV genotype 2 or 3 generally has a more favorable response to treatment with PEG-IFN and RBV. Therefore, in a clinical setting the underlying mechanism might not be relevant, as genotype 2 and 3 patients would readily be treated, whereas clinicians might be more reluctant to initiate peg-INF treatment to genotype 1 and 4 - infected individuals and here IP-10 levels might help to show which patients should undergo treatment.

This review focused on the association between pretreatment IP-10 levels and virological responses. However, IL28B SNPs should be addressed when considering IP-10, as they are strongly linked with treatment response to Peg-INF/ RBV[39-45]. Especially are homozygote genotypes at markers rs8099917 (TT), rs12979860 (CC) and rs12980275 (AA) associated with a favorable outcome to treatment. While IL28B polymorphisms were not found to be predictive for treatment response in HCV genotype 2 and 3 infected individuals by Fattovich et al[21], pretreatment IL28B polymorphisms, HCV-RNA- and IP-10 levels independently predict RVR in HCV genotype 1 infected individuals, with RVR in turn being the strongest predictor of SVR. Combining the IL28B polymorphisms and HCV-
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Table 6  Overview of the marker distribution, in the four studies that supplied information on interleukin 28B single nucleotide polymorphism

<table>
<thead>
<tr>
<th>Ref.</th>
<th>Genotype (n)</th>
<th>rs12979860</th>
<th>rs12980275</th>
<th>rs8099917</th>
<th>rs11881222</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>AA</td>
<td>AG</td>
<td>GG</td>
<td>TT</td>
<td>TG</td>
</tr>
<tr>
<td></td>
<td>CC</td>
<td>CT</td>
<td>TT</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Lagging et al[21]</td>
<td>1 (253)</td>
<td>93</td>
<td>123</td>
<td>37</td>
<td>101</td>
</tr>
<tr>
<td>Fattovich et al[20]</td>
<td>1 (226)</td>
<td>1 (87)</td>
<td>33</td>
<td>44</td>
<td>15</td>
</tr>
<tr>
<td></td>
<td>1 (201)</td>
<td>25</td>
<td>21</td>
<td>1</td>
<td>25</td>
</tr>
<tr>
<td>Darling et al[30]</td>
<td>2 (87)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>3 (47)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Derbala et al[24]</td>
<td>4 (159)</td>
<td>57</td>
<td>77</td>
<td>25</td>
<td>96</td>
</tr>
</tbody>
</table>

Genotype column indicates specific genotype, and total number of patients with the specific genotype. Each marker column is divided into allelic distribution for the IL28B SNP genotype. SNP: Single nucleotide polymorphism.

Table 7  Overview of rapid virological response in the 3 studies providing information on baseline inducible protein-10’s, and hepatitis C virus RNA levels at week 4

<table>
<thead>
<tr>
<th>Ref.</th>
<th>Patients (n)</th>
<th>IP-10 measurement method</th>
<th>Genotype (n)</th>
<th>Baseline IP-10 concentration, grouped by rapid virological response (pg/mL)</th>
<th>Overall RVR (a)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>ELISA (Quantikine, R and D systems, Minneapolis, MN, United States)</td>
<td>1 (170)</td>
<td>222</td>
<td>401</td>
</tr>
<tr>
<td></td>
<td></td>
<td>ELISA (Quantikine, R and D systems, Minneapolis, MN, United States)</td>
<td>1 (92)</td>
<td>2.4 (± 0.28)</td>
<td>2.6 (± 0.25)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>ELISA (Quantikine, R and D systems, Minneapolis, MN, United States)</td>
<td>2 (87)</td>
<td>2.38 (± 0.31)</td>
<td>2.3 (± 0.30)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>ELISA (Quantikine, R and D systems, Minneapolis, MN, United States)</td>
<td>3 (47)</td>
<td>2.45 (± 0.23)</td>
<td>2.48 (± 0.39)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>ELISA (Quantikine, R and D systems, Minneapolis, MN, United States)</td>
<td>4 (64)</td>
<td>483.9 (± 261.6)</td>
<td>609.9 (±424.3)</td>
</tr>
</tbody>
</table>

1Entire patient population was 280, genotype 4 infected were removed from the analyses, and IP-10 results was available for 226 patients. IP-10: Inducible protein-10; RVR: Rapid virological response.

RNA yielded a specificity of 98% but a low sensitivity of 39%. By including IP-10 values in the equation, the sensitivity and the negative predictive value was raised from 81% to 94%, however lowering the positive predictive value from 87% to 76%. This is consistent with other findings in HCV genotype 1 infected, homozygous carriers of the favorable IL28B SNPs, with low IP-10 level, which also significantly predicted a first phase decline of HCV RNA, which translated into increased rates of RVR and SVR[30]. While the two latter studies was carried out solely on Caucasian patients infected with HCV genotype 1, the additive predictive effect has also been shown for both HCV genotype 1 infected AA and CA patients[31], and HCV genotype 4 infected patients[32], respectively. Although low in numbers, these results could indicate, that both variables should be considered in a clinical context, before initiating treatment with Peg-IFN/RBV in patients infected with HCV genotype 1 or 4. Further studies examining the association in HCV genotype 2 and 3 infected patients should be encouraged.

Conducting a systematic review with clear and stringent inclusion and exclusion criteria, is an obvious strength of this study, ensuring homogeneity between the studies included, hereby allowing an unbiased assessment of the current evidence. Another strength of our study was that we assessed the quality of the studies included, and provided a detailed declaration of the studies aim, method - including treatment regimens and duration, as well as baseline patient demographics for the individual studies - supplying a solid ground for interpreting the results put forth. Although some authors recommend the use of quality assessments, other consider them misleading[46], and there remains uncertainties about the relationship between methodology, validity and the use of sum scores to judge the quality of studies[47]. Therefore we chose not to exclude any articles based on their quality score (e.g., high quality or low quality), but instead presented the ratings of the studies in the review to serve as an objective guide to interpret the review’s results, rather than a tool for selecting studies for the review. As seen by the exclusion criteria, we wished to eliminate the possible uncertainties that could arise by including studies treating HIV/HCV - or HBV/HCV co-infected patients. Therefore, it should be mentioned that even though there was no indication towards inclusion of co-infected patients, three of the included studies, based in the United States, Croatia and Egypt, contained no clear exclusion criteria for HIV- or HBV- infection[31-33].

Only a limited number of articles fulfilled the in- and exclusion criteria to be assessed in this review. Hence, more work is needed to establish a sufficient ground for final conclusions to be made. Further, there was an overweight of studies that addressed the association between SVR and baseline IP-10 in CHC patients infected...
with HCV genotype 1, whereas there was only a small fraction addressing the association between SVR and baseline IP-10 for genotype 2, 3 and 4, as well as studies examining the relationship between RVR and baseline IP-10 constituting an insufficient base for assessing baseline IP-10’s predictive ability in these regards.

In this systematic review, we found correlations between baseline IP-10 levels and SVR in patients chronically infected with HCV genotype 1 and 4, while no such association was found for patients infected with HCV genotype 2 or 3. Likewise, we found indications of a possible correlation between baseline IP-10 and RVR for HCV genotype 1 infected patients, while no such association were found for HCV genotype 2 or 3 patients, and only a trend was found for HCV genotype 4 infected patients. However, the amount of information regarding baseline RVR for genotypes 1-4, and SVR’s relation with baseline IP-10 for genotypes 2, 3 and 4 were insufficient for final conclusions.

**COMMENTS**

**Background**

Until recently, the standard of care for chronic hepatitis C (CHC) patients was lengthy dual therapy with pegylated interferon plus ribavirin (peg-IFN/RBV), a treatment with modest success rates, severe adverse events and variation in treatment response between hepatitis C virus (HCV) genotypes. Therefore, efforts to identifying biomarkers that can predict virological responses to treatment have been made. Interferon-γ inducible protein-10 (IP-10) is one such promising marker, with several studies independently showing an association between virological response and baseline IP-10 concentrations for CHC patients infected with HCV genotype 1 and 4. However, the association seems to be lacking for CHC patients, infected with HCV genotype 2 and 3.

**Research frontiers**

IP-10 has been shown to be expressed at higher levels in HCV genotype 1 infected CHC patients with moderate to severe fibrosis compared to patients with mild or non fibrosis. Therefore, studies are being made to examine if this correlation is also found in HCV genotype 2 and 3 infected CHC patients. In addition to this, examinations of baseline IP-10 ability to predict fibrosis progression in CHC patients are pending. IP-10 research in relation to CHC is therefore expanding from the possible correlation between virological response to treatment with peg-IFN/RBV at baseline, to also include fibrosis score at baseline and fibrosis progression over time.

**Innovations and breakthroughs**

Despite the work done so far to correlate IP-10 levels to treatment response, this is our knowledge, the fist systematic review to address and clarify the differences in IP-10 properties, in relation to the different HCV genotypes and virological response. The authors found indications of correlations between baseline IP-10 levels and SVR in CHC patients infected with HCV genotype 1 and 4, but not in patients infected with HCV genotype 2 or 3. Likewise, the authors found indications of a possible correlation between baseline IP-10 and RVR for HCV genotype 1 infected patients, while no such association were found for HCV genotype 2 or 3 patients, and only a trend was found for HCV genotype 4 infected patients.

**Applications**

Despite of the great advantages with the new treatment options with direct acting antivirals (DAA), the cost of DAA will without doubt substantially delay their introduction as standard treatment in low and middle-income countries by

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**Table 8 Overview of sustained viral response in the 8 studies providing information on baseline inducible protein-10’s, and hepatitis C virus-RNA levels 24 wk after end-of- treatment**

<table>
<thead>
<tr>
<th>Ref.</th>
<th>Patients (n)</th>
<th>IP-10 measurement method</th>
<th>Genotype</th>
<th>Baseline IP-10 concentration, grouped by sustained virological response (pg/mL)</th>
<th>Overall SVR</th>
<th>SVR</th>
<th>Non-SVR</th>
<th>P-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Apolinar et al[31]</td>
<td>63</td>
<td>ELISA (OptEIA, Pharmingen, San Diego, CA, United States)</td>
<td>1 (43)</td>
<td>245 (± 154)</td>
<td>381 (± 138)</td>
<td>P &lt; 0.05 (mean ± SD)</td>
<td>36</td>
<td>27</td>
</tr>
<tr>
<td>Diago et al[32]</td>
<td>137</td>
<td>ELISA (Human immunoassay kit; BioSource Europe SA, Nivelles, Belgium)</td>
<td>1 (103)</td>
<td>347 (± 197.4)</td>
<td>476.8 (± 303.5)</td>
<td>P &lt; 0.01 (mean ± SD)</td>
<td>79</td>
<td>58</td>
</tr>
<tr>
<td>Fattovich et al[33]</td>
<td>226</td>
<td>ELISA (Quantikine, R and D systems, Minneapolis, MN, United States)</td>
<td>1 (92)</td>
<td>2.47 ± 0.23</td>
<td>2.65 ± 0.28</td>
<td>P &lt; 0.001 (log mean ± SD)</td>
<td>209</td>
<td>71</td>
</tr>
<tr>
<td>Kurelac et al[34]</td>
<td>46</td>
<td>ELISA (Quantikine, R and D systems, Minneapolis, MN, United States)</td>
<td>1 (46)</td>
<td>2.42 ± 0.21</td>
<td>2.67 ± 0.46</td>
<td>P &lt; 0.05 (log mean ± SD)</td>
<td>26</td>
<td>20</td>
</tr>
<tr>
<td>Darling et al[35]</td>
<td>272</td>
<td>ELISA (Quantikine, R and D systems, Minneapolis, MN, United States)</td>
<td>1 (272)</td>
<td>2.42 ± 0.21</td>
<td>2.67 ± 0.46</td>
<td>P &lt; 0.05 (log mean ± SD)</td>
<td>26</td>
<td>20</td>
</tr>
<tr>
<td>Derbala et al[36]</td>
<td>159</td>
<td>Lumines, Cytokine multiplex immunoassay kit (Merck Millipore, Billerica, MA, United States)</td>
<td>4 (159)</td>
<td>2.47 ± 0.23</td>
<td>2.65 ± 0.28</td>
<td>P &lt; 0.001 (log mean ± SD)</td>
<td>98</td>
<td>61</td>
</tr>
<tr>
<td>Al-Ashgar et al[37]</td>
<td>64</td>
<td>ELISA (Quantikine, R and D systems, Minneapolis, MN, United States)</td>
<td>4 (64)</td>
<td>2.47 ± 0.23</td>
<td>2.65 ± 0.28</td>
<td>P &lt; 0.001 (log mean ± SD)</td>
<td>41</td>
<td>23</td>
</tr>
</tbody>
</table>

1Entire patient population was 280, genotype 4 removed from the analyses, and IP-10 results was available for 226 patients Note that M. Derbala et al did not provide written specification on IP-10 levels for SVR compared to non-SVR, and only supplied a graphic depiction, which could not be interpreted to adequate results; 'SVR for the entire population.' P = 0.02. Only the results of statistical tests with a P value < 0.01 were considered of interest, because of the multiple comparisons between subjects with and without SVR. SVR: Sustained viral response; IP-10: Inducible protein-10.
years to come. In addition, DAA in high-income countries is still reserved for patients with advanced liver disease. Therefore, peg-IFN/RBV treatment still has a role to play in treatment of patients with CHC. Their findings of a possible correlation between baseline IP-10 mRNA levels and SVR in CHC patients infected with HCV genotype 1 and 4 but not for genotypes 2 and 3 could be beneficial in a clinical setting. Genotype 2 and 3 patients would readily be treated, as these patients generally have a favorable outcome to peg-IFN/RBV compared to genotype 1 and 4 infected individuals. In such patients, IP-10 levels might help to show which patients would have the best prognosis for a positive outcome to treatment.

Terminology
Interferon-γ-inducible protein-10, more commonly denoted IP-10 or CXCL10, is a non-ELR-CXC chemokine, binding to the CXC-receptor-3. It functions as a chemotactic, attracting T lymphocytes and NK cells to the site of inflammation. Within the liver, IP-10 mRNA is produced by hepatocytes in inflammatory areas, and both intrapathic IP-10 mRNA and plasma levels of IP-10 are elevated in individuals with CHC, indicating that intrapathic IP-10 is the source of plasma IP-10. The hypothesis therefore is that IP-10 can function as proxy for the level of liver inflammation, which in turns leads to fibrosis formation.

References


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