Genome-wide association study identified \textit{ITPA/DDRGK1} variants reflecting thrombocytopenia in pegylated interferon and ribavirin therapy for chronic hepatitis C

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Hematologic abnormalities during current therapy with pegylated interferon and ribavirin (PEG-IFN/RBV) for chronic hepatitis C (CHC) often necessitate dose reduction and premature withdrawal from therapy. The aim of this study was to identify host factors associated with IFN-induced thrombocytopenia by genome-wide association study (GWAS). In the GWAS stage using 900K single-nucleotide polymorphism (SNP) microarrays, 303 Japanese CHC patients treated with PEG-IFN/RBV therapy were genotyped. One SNP (rs11697186) located on \textit{DDRGK1} gene on chromosome 20 showed strong associations in the minor-allele-dominant model with the decrease of platelet counts in response to PEG-IFN/RBV therapy \cite{P58.1731029;OR=4.6}. These associations were replicated in another sample set ($n=391$) and the combined $P$-values reached $5.29 \times 10^{-17}$ ($OR = 4.5$). Fine mapping with 22 SNPs around \textit{DDRGK1} and \textit{ITPA} genes showed that rs11697186 at the GWAS stage had a strong linkage disequilibrium with rs1127354, known as a functional variant in the \textit{ITPA} gene. The

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**INTRODUCTION**

Chronic infection with hepatitis C virus (HCV) presents a significant health problem worldwide, with ~2.3% of the world population, i.e. more than 120–130 million people, being infected (1). Only 20–30% of HCV-infected individuals recover spontaneously. The remaining 70–80% go on to develop chronic infection, being at significant risk for progressive liver fibrosis and subsequent liver cirrhosis (LC) and hepatocellular carcinomas (HCC). Successful treatment of chronic hepatitis C (CHC) leads to a reduction of liver fibrosis stage of patients, and also prevents HCC development (2).

Antiviral treatment has been shown to improve liver histology and decrease incidence of hepatocellular carcinoma in CHC (3,4). Current therapy for CHC consists of treatment with pegylated interferon (IFN), which acts both as an antiviral and as an immunoregulatory cytokine, and ribavirin (RBV), an antiviral pro-drug that interferes with RNA metabolism (5,6). However, <50% of patients infected with HCV genotype 1 treated in this way achieve a sustained viral response (SVR) or cure of the infection (5,7). Older patients with liver fibrosis showed a significantly lower SVR rate due to poor adherence resulting from adverse events and laboratory abnormalities (8–10). In particular, hematologic abnormalities often necessitate dose reduction, and premature withdrawal from therapy in 10–14% of patients (5,11–14). New drugs and therapeutic approaches for CHC are actively developed and several candidates are in early trial phase (15,16). Given this background, effective pre-treatment screening for predictive biomarkers with the aim of evaluating possible risks over benefits of currently available treatment will avoid these side effects in patients who will not be helped by treatment, as well as reduce the substantial cost of treatment.

The completion of the Human Genome Project has led to the advent of a new era of scientific research, including a revolutionary approach: the genome-wide association study (GWAS). Several recent studies, including our study, have demonstrated marked associations between single-nucleotide polymorphisms (SNPs) within and around *IL28B* gene, which codes for IFN-λ3 (16–21). Another recent study indicated that genetic variants of *ITPA* gene leading to inosine triphosphatase (ITPA) deficiency could protect against hemolytic anemia (HA) in CHC patients receiving RBV (22).

In Japan, HCV-infected patients are relatively old and some of them have had severe fibrosis (9). Thrombocytopenia is one of the critical adverse events by IFN-based therapy among liver cirrhotic patients (23), because low platelet count (PLT), i.e. <30.0 (10^3/l), would be a risk factor for any bleeding, as well as it would lead to poor treatment efficiency due to the initial or early dose reduction of PEG-IFN. Based on its pathogenesis, drug-induced thrombocytopenia is usually due to bone marrow suppression, immune-mediated destruction and platelet aggregation (24). In this study, we firstly found that genetic variants in the *ITPA/DDRGK1* genes were associated with IFN-induced thrombocytopenia, and then examined the correlation between IFN-induced thrombocytopenia and RBV-induced HA in Japanese CHC patients under PEG-IFN/RBV treatment.

**RESULTS**

*Genetic variants associated with IFN-induced thrombocytopenia*  

In this study, we conducted a GWAS to identify host genes associated with the decrease of platelets in response to PEG-IFN/RBV treatment in 303 Japanese HCV patients (107 patients with the decrease of PLT versus 196 patients without the decrease of PLT based on the criteria described in Materials and Methods), using a genome-wide SNP typing array (Affymetrix SNP 6.0 for 900K SNPs). The characteristics of patients for each GWAS stage and replication stage are summarized in Table 1. Figure 1 shows a genome-wide view of the single-point association data based on allele frequencies. One SNP (rs11697186) located on *DDRGK1* gene on chromosome 20 showed strong associations in the allele frequency model (*P* = 8.17 × 10^-9) with the decrease of PLT in response to PEG-IFN plus RBV treatment. The association reached genomewide level of significance [Bonferroni criterion *P* < 8.40 × 10^-8 (0.05/595052)], and another SNP (rs6139030) near *ITPA* gene had a marginal significance (*P* = 4.30 × 10^-7, in Table 2).

To validate the results of the GWAS stage, 22 SNPs were selected for the replication in a set of 391 Japanese HCV patients with and without platelet reduction (Supplementary Material, Table S1). The associations of the original significant SNP (rs11697186) and the marginal SNP (rs6139030) at the GWAS stage were replicated in the second set of 391 patients in the minor-allele-dominant model [*P* = 5.88 × 10^-10, odds ratio (OR) = 4.6 for rs11697186; *P* = 3.83 × 10^-10, OR = 4.3 for rs6139030, Table 2]. The combined *P*-values for both stages reached 5.29 × 10^-17 (OR = 4.5; 95% CI = 3.1–6.5) and 1.33 × 10^-15 (OR = 3.9; 95% CI = 2.8–5.5), respectively (Table 2).

*Genetic variants associated with RBV-induced anemia*  

We also conducted a GWAS to identify host genes associated with a quantitative change in hemoglobin (Hb) levels from baseline to week 4 of PEG-IFN/RBV treatment in the above 303 Japanese HCV patients (94 patients with an Hb reduction of ≥3 g/dl at week 4 and 209 patients without Hb reduction), using a genome-wide SNP typing array (Affymetrix SNP 6.0 for 900K SNPs). Two SNPs (rs11697186 and rs6139030)
located on DDRGK1 gene and ITPA gene on chromosome 20 showed strong associations in the allele frequency model ($P = 3.29 \times 10^{-10}$ and $P = 2.56 \times 10^{-9}$) with Hb reduction in response to PEG-IFN plus RBV treatment (Table 3).

The above 22 SNPs were selected for the replication study and fine mapping, including rs1127354, which was reported by the US group (22) to be strongly associated with Hb reduction (Supplementary Material, Table S2). All SNPs were genotyped using the DigiTag2 assay in an independent set of 391 Japanese HCV patients (21). The associations of the original SNPs were replicated in the second set of 391 Japanese HCV patients with quantitative change in Hb in response to PEG-IFN/RBV treatment [137 patients with Hb reduction versus 254 patients without Hb reduction (Table 3)].

Table 1. Clinical characteristics of patients in this study

<table>
<thead>
<tr>
<th></th>
<th>GWAS ($n = 303$)</th>
<th>Replication ($n = 391$)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age (years)</td>
<td>57.4 (9.7)</td>
<td>56.8 (9.9)</td>
</tr>
<tr>
<td>Sex (M/F)</td>
<td>151/152</td>
<td>209/182</td>
</tr>
<tr>
<td>Weight (kg)</td>
<td>60.6 (10.4)</td>
<td>61.3 (10.7)</td>
</tr>
<tr>
<td>Body mass index</td>
<td>23.5 (3.1)</td>
<td>23.7 (4.1)</td>
</tr>
<tr>
<td>Baseline Hb (g/dl)</td>
<td>14.1 (1.4)</td>
<td>14.1 (1.4)</td>
</tr>
<tr>
<td>Baseline platelet count (10^9/l)</td>
<td>151.3 (54.3)</td>
<td>159.7 (55.0)</td>
</tr>
<tr>
<td>Baseline ALT (IU/l)</td>
<td>83.5 (79.4)</td>
<td>86.8 (71.9)</td>
</tr>
<tr>
<td>Baseline creatinine (mg/dl)</td>
<td>0.70 (0.15)</td>
<td>0.72 (0.16)</td>
</tr>
<tr>
<td>Baseline liver fibrosis (F0–2/F3–4)</td>
<td>153/77/73</td>
<td>175/59/43</td>
</tr>
</tbody>
</table>

The above 22 SNPs were selected for the replication study and fine mapping, including rs1127354, which was reported by the US group (22) to be strongly associated with Hb reduction (Supplementary Material, Table S2). All SNPs were genotyped using the DigiTag2 assay in an independent set of 391 Japanese HCV patients (21). The associations of the original SNPs were replicated in the second set of 391 Japanese HCV patients with quantitative change in Hb in response to PEG-IFN/RBV treatment [137 patients with Hb reduction versus 254 patients without Hb reduction (Table 3)].

The mean quantitative reduction of blood cells from the baseline according to the ITPA rs1127354 genotype is shown in Figure 2. As the rs1127354 was also strongly associated with a quantitative change in Hb in response to PEG-IFN/RBV treatment (Table 3).

The mean quantitative reduction of blood cells from the baseline according to the ITPA rs1127354 genotype is shown in Figure 2. As the rs1127354 genotypes AA/CA were independently associated with a higher degree of reactive increase of the platelet count due to a lower degree of the reactive increase of the platelet count than those without anemia (P = 0.0001 in Fig. 5A). Within a subgroup of patients with the rs1127354 genotypes CC, patients with anemia still had a significantly higher degree of reactive increase of the platelet count than those without anemia ($P = 0.0001$ in Fig. 5C), and a similar result was obtained in a subgroup of patients without anemia (Fig. 5D). To elucidate the significant factors associated with the rs1127354 genotypes by multivariate analysis, the rs1127354 genotypes AA/CA were independently associated with protection against the reduction in Hb and more reduction in platelet counts at week 4 due to a lower degree of the reactive increase of the platelet count (OR = 0.029; 95% CI = 0.009–0.092; $P < 0.0001$, OR = 4.73; 95% CI = 3.04–7.37; $P < 0.0001$, respectively). Indeed, the reactive increase of the platelet count through weeks 1–4 was positively correlated with a high platelet count at the baseline and anemia (Hb reduction ≥3.0 g/dl) at week 4, but was negatively correlated with rs1127354 genotypes AA/CA and a platelet count reduction of ≥30 (10^9/l) at week 4 (Table 4).

**Table 1. Clinical characteristics of patients in this study**

| Age (years) | 57.4 (9.7) | 56.8 (9.9) |
| Sex (M/F)   | 151/152   | 209/182   |
| Weight (kg) | 60.6 (10.4) | 61.3 (10.7) |
| Body mass index | 23.5 (3.1) | 23.7 (4.1) |
| Baseline Hb (g/dl) | 14.1 (1.4) | 14.1 (1.4) |
| Baseline platelet count (10^9/l) | 151.3 (54.3) | 159.7 (55.0) |
| Baseline ALT (IU/l) | 83.5 (79.4) | 86.8 (71.9) |
| Baseline creatinine (mg/dl) | 0.70 (0.15) | 0.72 (0.16) |
| Baseline liver fibrosis (F0–2/F3–4) | 153/77/73 | 175/59/43 |

**Relationship between ITPA rs1127354 genotypes and treatment outcome due to dose reduction of PEG-IFN or RBV**

In this population, a multivariate analysis showed that SVR was significantly associated with *IL28B* TT-genotype (OR
6.12 (2.78–13.46), \( P < 0.0001 \) as well as platelet counts \( \text{OR} 1.18 (1.11–1.26), \ P < 0.00001 \). We analyzed whether the rs1127354 genotype could influence the treatment outcome by PEG-IFN/RBV therapy. When analyzed in the patients available for treatment outcome (172 with \( \text{ITPA} \)-AA/CA and 450 with \( \text{ITPA} \)-CC), the percentage of patients receiving 80% of the expected PEG-IFN and RBV dose at baseline and week 4 was not significantly different among the rs1127354 genotypes. However, the rate of SVR tended to be higher in patients with \( \text{ITPA} \)-AA/CA genotype than those with \( \text{ITPA} \)-CC (48.8 versus 37.3%), because the relapse rate was lower in patients with \( \text{ITPA} \)-AA/CA. To investigate the influence on treatment outcome by dose reduction of PEG-IFN, in a subgroup of patients with low platelet counts (<10) at baseline (19 with \( \text{ITPA} \)-AA/CA and 53 with \( \text{ITPA} \)-CC) we analyzed the treatment outcome according to rs1127354 genotypes. The SVR rate was very low in each group (21.1% in \( \text{ITPA} \)-AA/CA and 17.0% in \( \text{ITPA} \)-CC), because many patients had the initial dose reduction of PEG-IFN (<80% of standard dose)—36.8% of patients with \( \text{ITPA} \)-AA/CA and 44.6% of patients with \( \text{ITPA} \)-CC genotype. Further prospective studies are required among the pre-cirrhotic or cirrhotic patients with low platelet counts.

**DISCUSSION**

Recent genome-wide association studies, including our study on HCV infection, have identified two important host genetic variants: the SNP in \( \text{IL28B} \) gene, which is strongly associated with response to therapy for chronic genotype 1 HCV infection (16–21), and the SNP in \( \text{ITPA} \) gene, which precisely predicts RBV-induced anemia in...
European-American population (22) and Japanese population (26). The genetic variation of ITPA causing an accumulation of inosine triphosphate (ITP) has been shown to protect patients against RBV-induced anemia during treatment for CHC infection. A recent report showed the biologic mechanism that ITP confers protection against RBV-induced ATP reduction by substituting for erythrocyte GTP, which is depleted by RBV, in the biosynthesis of ATP (25).

### Table 3. Two SNPs (rs11697186 and rs6139030) significantly associated with quantitative change in Hb levels from baseline to week 4 of PEG-IFN/RBV treatment

<table>
<thead>
<tr>
<th>dbSNP</th>
<th>Nearest gene</th>
<th>MAFa</th>
<th>Allele (1/2)</th>
<th>Stage</th>
<th>Patients with quantitative change in Hb</th>
<th>Patients without quantitative change in Hb</th>
<th>OR (95% CI)b</th>
<th>P-valuec</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>11</td>
<td>12</td>
<td>22</td>
<td>11</td>
</tr>
<tr>
<td>rs11697186</td>
<td>DDRGK1</td>
<td>0.15 (T)</td>
<td>T/A</td>
<td>GWAS</td>
<td>0 (0.0)</td>
<td>3 (3.3)</td>
<td>89 (96.7)</td>
<td>3 (1.5)</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Replication</td>
<td>0 (0.0)</td>
<td>2 (1.5)</td>
<td>134 (98.5)</td>
<td>6 (2.5)</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Combined</td>
<td>0 (0.0)</td>
<td>5 (2.2)</td>
<td>223 (97.8)</td>
<td>9 (2.0)</td>
</tr>
<tr>
<td>rs6139030</td>
<td>ITPA</td>
<td>0.17 (C)</td>
<td>T/C</td>
<td>GWAS</td>
<td>88 (93.6)</td>
<td>6 (6.4)</td>
<td>0 (0.0)</td>
<td>125 (59.8)</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Replication</td>
<td>134 (97.8)</td>
<td>3 (2.2)</td>
<td>0 (0.0)</td>
<td>143 (56.3)</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Combined</td>
<td>222 (96.1)</td>
<td>9 (3.9)</td>
<td>0 (0.0)</td>
<td>268 (57.9)</td>
</tr>
</tbody>
</table>

aMinor allele frequency and minor allele in 184 healthy Japanese individuals.
bOR for the minor allele in a dominant model.
cP-value by χ² square test for the minor allele dominant model.

**Figure 2.** Pairwise LD (r²) diagrams for DDRGK1 and ITPA. Lower panel shows estimates of pairwise r² for 22 SNPs selected in the replication study using the second set of 391 Japanese HCV patients with and without quantitative change in PLT levels from baseline to week 4 of PEG-IFN/RBV treatment.
In this study, two SNPs, rs11697186 and rs6139030, which were within and around DDRGK1 gene on chromosome 20, were strongly associated with thrombocytopenia as well as with Hb reduction at week 4. In clinical practice, the positive predictive value and negative predictive value by rs11697186 genotypes were 66.5 and 69.4% for thrombocytopenia, as well as 97.2 and 45% for RBV-induced anemia at week 4. As previously reported (22,26), a functional SNP (rs1127354) in the ITPA locus, which is in strong LD with rs11697186, was the most significant SNP associated with RBV-induced anemia and, in this study, IFN-induced thrombocytopenia in Japanese genetic populations. Note that severe Hb decline, which is mainly found in ITPA-CC patients, was inversely correlated with platelet reduction. This would contribute to an association between severe anemia and relative reactive increase of platelet count in this population, which attenuated the IFN effect on the platelet count. Our data supported a previous report which described that the current use of RBV, inducing severe anemia, might blunt the thrombocytopenic effect of IFNs as a result of reactive increase of platelet counts (27).

A previous paper showed hematological and bone marrow effects of RBV in rhesus monkeys (28). Hb values decreased significantly during RBV administration due to dose-related erythroid hypoplasia in bone marrow and returned to normal following withdrawal. On the other hand, increase of the platelet count occurred in both low- and high-dose treatment groups during RBV administration, with a fall of the platelet count to normal after drug withdrawal. The effect on platelet count was clearly dose related, with maximum counts rising to twice and three times above baseline levels in the low- and high-dose groups, respectively. This caused a significant increase of

Figure 3. ITPA rs1127354 genotypes and the quantitative reduction of blood cells from baseline. Mean reduction of (A) Hb levels, (B) platelet counts and (C) neutrophil leukocyte counts during treatment according to rs1127354 genotype is shown. Solid and dotted lines indicate patients with CC and AA/CA genotypes, respectively. Error bars indicate standard error. CC genotype had more reduction in mean Hb levels during therapy compared with the AA/CA genotype (*P < 0.0001 for weeks 2, 4, 8, 12). CC genotype had less of a reduction in mean platelet counts (*P < 0.0001 for weeks 2, 4, 8, and **P = 0.019 for week 12), and showed a reactive increase of platelet counts through weeks 1–4.

Figure 4. ITPA rs1127354 genotypes and reduction of platelet counts at week 4 of PEG-IFN/RBV therapy. The percentage of patients with platelet count reduction of >50 (×10^9/l) (black bar), 30–50 (×10^9/l) (gray bar) and <30 (×10^9/l) (white bar) at week 4 is shown for rs1127354 genotypes. The incidence of platelet count reduction of >50 and <30 was significantly lower in patients with the rs1127354 genotypes CC compared with AA/CA genotypes: 12 versus 35%, P < 0.0001, and 69 versus 31%, P < 0.0001, respectively.

In this study, two SNPs, rs11697186 and rs6139030, which were within and around DDRGK1 gene on chromosome 20, were strongly associated with thrombocytopenia as well as...
the platelet count associated with increased numbers of megakaryocytes. Additionally, the sequence homology of thrombopoietin (TPO) and erythropoietin (EPO) may explain the synergy of the physiologic role of TPO and EPO in platelet production. When EPO is elevated, as in iron deficiency anemia, an amino acid sequence similar to TPO may increase the platelet count (29).

Another possibility is a direct association between *ITPA* SNPs or the related SNPs with a strong LD and IFN-induced thrombocytopenia. *DDRGK1* (*DDRGK* domain-containing protein 1) is a novel C53/LZAP-interacting protein. C53/LZAP (also named as Cdk5rap3) is a putative tumor suppressor that plays important roles in multiple cell signaling pathways, including DNA damage response and NF-kappaB signaling (30); however, it remains largely unknown how the function of *DDRGK1* variants is regulated. Further studies are required to elucidate the possible association between *DDRGK1* variants and thrombocytopenia.

Multivariate analysis demonstrated that rs1127354 in the *ITPA* gene was independently associated with RBV-induced severe anemia and IFN-induced thrombocytopenia. This finding suggests that rs1127354 would be a useful marker to predict these hematological side effects by PEG-IFN/RBV therapy, indicating that genetic testing of *ITPA* variant might be applied to establish personalized dosages of PEG-IFN/RBV therapy. The rate of SVR tended to be higher in patients with *ITPA*-AA/CA genotype than those with *ITPA*-CC in this population. This might reflect decreased treatment efficacy (higher relapse rate) due to dose reduction of RBV in patients with *ITPA*-CC genotype. Our recent paper also demonstrated that the incidence of early dose reduction was significantly higher in *ITPA*-major (CC) patients as expected and, more importantly, that a significantly higher SVR rate was achieved in *ITPA*-hetero/minor (CA/AA) patients with HCV non-1b or low viral load strains (31) and in a subset of Japanese patients with the favorable TT genotype at rs8099917 of *IL28B* (32). Taken together, our results indicate that the *ITPA* minor variant A is not only a protective allele against PEG-IFN and RBV treatment-associated anemia in Japanese population, but also a significant predictor of SVR in certain HCV strains that show good response to IFN. The possible mechanism of protection against RBV-induced hemolysis is that ITP deficiency or low-activity variants against RBV-induced ATP reduction by substituting for erythrocyte GTP (25). On the other hand, half of the *ITPA*-major (CC) patients did not develop a significant Hb decline. This finding suggests other low-frequency *ITPA* variants or SNPs in other enzymes that are involved in erythrocyte purine nucleoside metabolism.

In Japan, the older HCV-infected patients developing liver fibrosis have been prevalent (mean age 62 years) (9). Thrombocytopenia by PEG-IFN/RBV therapy could lead to poor treatment efficiency among such Japanese patients with LC due to the initial or early dose reduction of PEG-IFN. In fact, ~40% of such population in this study had the initial dose reduction of PEG-IFN, resulting in a low SVR rate. Splenectomy or embolization of the splenic artery might be one of the options to increase the SVR rate, but a sufficient treatment outcome had not been obtained at present (35). Based on the recently accumulated SNP data, if patients had favorable *IL28B* genotype and *ITPA*-CC (lower reduction of platelet counts), a standard dose of PEG-IFN might be available for

**Table 4. Multivariate analysis of factors associated with reactive increase of platelets ≥20 (10^9/l) through weeks 1–4**

<table>
<thead>
<tr>
<th></th>
<th>OR</th>
<th>95% CI</th>
<th>P-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Baseline platelet counts</td>
<td>1.168</td>
<td>1.101–1.239</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>ITPA AA/CA</td>
<td>0.379</td>
<td>0.168–0.856</td>
<td>0.0196</td>
</tr>
<tr>
<td>Platelet reduction ≥30 (10^9/l) at week 4</td>
<td>0.051</td>
<td>0.021–0.120</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>Hb reduction ≥3.0 g/dl at week 4</td>
<td>1.602</td>
<td>0.914–2.809</td>
<td>0.0996</td>
</tr>
</tbody>
</table>

**Figure 5.** Reactive increase of platelet counts through weeks 1–4. Box plots of reactive increase of platelet count through weeks 1–4 according to the degree of anemia at week 4 are shown for all patients (A) and a subgroup of patients with the rs1127354 genotypes CC (B). Patients with anemia (Hb reduction ≥3.0 g/dl) at week 4 had a significantly higher degree of reactive increase of platelet count than those without anemia (P < 0.0001). Box plots of reactive increase of platelet counts according to the rs1127354 genotype CC are shown for all patients (C) and a subgroup of patients without anemia (D) (Hb reduction <3.0 g/dl) at week 4. Patients with the rs1127354 genotypes CC had a significantly high degree of reactive increase of platelet counts compared with those with genotypes AA/CA (P < 0.0001).
the patients with lower platelet counts and the SVR rate might be increased due to sufficient dose of PEG-IFN.

Several STAT-C agents (specifically targeted antiviral therapies for hepatitis C) are being tested for clinical efficacy against hepatitis C (12,13,15,16). Most experts believe that when new drugs are approved to treat hepatitis C, they will be used in combination with PEG-IFN and RBV. Moreover, recent clinical trials, including NS3 protease inhibitors, have shown that PEG-IFN plus RBV would be necessary to achieve optimal treatment responses (12,13). Our present results may provide a valuable pharmacogenetic diagnostic tool for tailoring PEG-IFN and RBV dosing to minimize drug-induced adverse events and for further optimization of clinical anti-HCV chemotherapeutics.

MATERIALS AND METHODS

Patients

From April 2007 to April 2010, samples were obtained from 303 patients with chronic HCV (genotype 1) infection who were treated at 14 multi-center hospitals (liver units with hepatologists) throughout Japan. Each patient was treated with PEG-IFN-α2b (1.5 μg/kg body weight, subcutaneously once a week) or PEG-IFN-α2a (180 μg once a week) plus RBV (600–1000 mg daily according to body weight) for 48 weeks. Treatment duration was extended in some patients up to 72 weeks, according to the physicians’ preferences. The dose of PEG-IFN or RBV was reduced according to the recommendations on the package inserts or the clinical conditions of the individual patients. EPO or other growth factors were not given. Written informed consent was obtained from each patient and the study protocol conformed to the ethics guidelines of the Declaration of Helsinki and was approved by the institutional ethics review committees. HBsAg-positive and/or anti-HIV-positive patients were excluded from this study.

In the following stage of replication study, SNP genotyping in an independent set of 391 Japanese HCV patients treated with PEG-IFN plus RBV treatment was completed using the DigiTag2 assay (36). Twenty-two of the 23 SNPs were successfully analyzed and were used for SNP genotyping and data cleaning. All 22 SNPs in the replication study cleared HWE P-value >0.001.

Based on the above SNPs data obtained from 303 Japanese HCV patients, using the Affymetrix Genome-Wide Human SNP Array 6.0, we also performed GWAS between 94 patients with a quantitative change of >3 g of reduction in Hb and 209 patients without quantitative change in Hb levels from baseline to week 4 of PEG-IFN/RBV treatment. SNP genotyping in an independent set of 391 Japanese HCV patients with and without quantitative change in Hb levels from baseline to week 4 of PEG-IFN/RBV treatment (137 patients with quantitative change in Hb and 254 patients without quantitative change in Hb) was also completed using the DigiTag2 assay (36). Twenty-two of the 23 SNPs were successfully analyzed and were used for SNP genotyping and data cleaning.

An application of the Cochrane–Armitage test on all the SNPs showed the genetic inflation factor λ = 1.000 for thrombocytopenia and λ = 1.006 for anemia in the GWAS stage (Supplementary Material, Figs S1 and S2). In addition, principal component analysis was performed in 303 samples for the GWAS stage together with the HapMap samples (CEU, YRI, CHB and JPT) (Supplementary Material, Fig. S3). These results implied that the effect of population stratification was negligible, except one sample, which was excluded from further analysis.

Laboratory and histological tests

Blood samples were obtained at baseline, 1, 2, 4, 8 and 12 weeks after the start of therapy and for hematologic tests after the start of therapy and for hematologic tests, blood chemistry and HCV-RNA. Genetic polymorphism in the IL28B gene (rs8099917) was determined using the ABI TaqMan assay (Applied Biosystems, Carlsbad, CA, USA). Fibrosis was evaluated on a scale of 0–4 according to the METAVIR scoring system. The SVR was defined as an undetectable HCV-RNA level by qualitative PCR with a lower detection limit of 50 IU/ml (Amplicor, Roche Diagnostic Systems, CA, USA) or by Cobas Amplitrep/Cobas TaqMan assay (CAP/CTM) with a lower detection limit of
Statistical analysis

The observed association between an SNP and the decrease of platelets/quantitative change in Hb levels with response to PEG-IFN plus RBV treatment was assessed by χ² test with a two-by-two contingency table in three genetic models: allele frequency model, dominant-effect model and recessive-effect model. SNPs on chromosome X were analyzed by Fisher’s exact test. The association between ITPA polymorphisms and the degree of reduction in platelet counts and Hb levels at each time point during therapy were analyzed by Mann–Whitney U test. Multivariable regression analysis was used to analyze the factors associated with ITPA, the rs1127354 genotype, factors associated with platelet count reductions and factors associated with the reactive increase in platelet counts. IBM-SPSS software v.15.0 (SPSS, Inc., Chicago, IL, USA) was used for these analyses.

Possible heterogeneity in allele frequencies at rs1127354 was assessed by Tarone’s test. The association between the SNP and thrombocytopenia/anemia were analyzed by the Cochran–Mantel–Haenszel test. Both analyses were performed using the R (version 2.9.0) software (Supplementary Material, Table S3).

AUTHORS’ CONTRIBUTIONS


SUPPLEMENTARY MATERIAL

Supplementary Material is available at HMG online.

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