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Hepatology Research

Hepatology Research 2011; **41**: 1216–1222 doi: 10.1111/j.1872-034X.2011.00881.x

Original Article

Suppressor of cytokine signal 3 and IL28 genetic variation predict the viral response to peginterferon and ribavirin

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Aim: The aim of this study was to investigate the relationship among the expression of suppressor of cytokine signaling 3 (SOCS 3) in the liver, the SNPs in the IL28B locus, and the outcome of interferon therapy.

Methods: Prior to interferon treatment, we immunostained 67 liver specimens from chronic hepatitis C (CHC) patients who were receiving peginterferon alpha-2b/ribavirin therapy for suppressor of cytokine signaling 3 (SOCS3), and compared the expression of SOCS3, IL28 polymorphisms and other clinical factors between the patients and compared their eventual outcomes.

Results: Significant differences between the low SOCS3 group and high SOCS3 group were found in age, as well as in the platelet, transaminase, gamma-glutamyl transpeptidase levels. The incidence of high SOCS3 was not significantly different between subjects with the TT genotype and the TG genotype (TT : TG = 71%:29%, $P = 0.250$). In a multivariate analysis, age (≥65 years old) (odds ratio 0.221 [0.120–0.966], $P = 0.045$), IL28B gene (genotype TT) (odds ratio 5.422 [1.254–23.617], $P = 0.024$) and SOCS3 (high) (odds ratio 0.308 [0.104–0.948], $P = 0.040$) were significant predictors of the interferon response. In patients with the TT genotype, those with low SOCS3 immunostaining showed a high sustained virological response (69%), while the sustained virological rate was low (27%) in the patients with high SOCS3 immunostaining.

Conclusions: Using a combination of the SOCS3 immunostained area in the liver and the expression of IL28B single nucleotide polymorphisms might be a useful predictor of hepatitis C virus clearance by interferon therapy.

Key words: hepatitis C virus, IL28B, interferon, suppressor of cytokine signaling 3

INTRODUCTION

APPROXIMATELY 200 MISSION people worldwide are infected with hepatitis C virus (HCV). In Japan, about 2 million people are chronically infected, and HCV is the leading cause of hepatocellular carcinoma (HCC). The current standard care for chronic hepatitis C (CHC) is a combination of peginterferon-α (PEG-IFN) and ribavirin. This treatment is effective in approximately 40–50% of CHC patients with a high viral load of genotype 1.[1–5] This therapy is costly and frequently associated with side effects. Therefore, predicting the outcome of interferon therapy is important.

Several factors, such as gender, body mass index, the presence of steatosis and liver fibrosis, drug adherence and viral factors including the serum quantity of HCV RNA and HCV genotype have been reported to be significantly associated with the treatment outcome.[2,6–11] Among viral factors, Akuta *et al.* recently reported that the substitution of the HCV core amino acid was a predictor for the effect of interferon and ribavirin combination therapy.[2,12] Among the host factors, recent reports showed that genetic variations near the IL28 gene (rs8099917, rs1297860) on chromosome 19 were predictors of the virological response to 48-week PEG-IFN plus ribavirin combination therapy in individuals

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Received 4 March 2011; revision 16 July 2011; accepted 24 July 2011.

with HCV, and also affected the clinical outcome, including spontaneous clearance of HCV.[13–15]

We previously reported that the expression of suppressor of cytokine signaling 3 (SOCS3), which is related to insulin resistance, impairs the response to interferon treatment and might be a useful predictor of HCV clearance by interferon therapy.[16]

In this study, we examined the relationship among the expression of SOCS 3 in the liver, single nucleotide polymorphisms (SNPs) in the IL28B locus, and the outcome of interferon therapy.

METHODS

NEEDLE BIOPSIES OF the liver were obtained from 67 patients with positive HCV antibodies prior to interferon treatment at Nagasaki University Hospital and National Hospital Organization (NHO) Nagasaki Medical Center. Twenty of 67 cases were also examined in a previous study.[16] All patients with genotype 1b received weekly injections of PEG-IFN. The clinical data of the patients are summarized in Table 1. Liver biopsy was performed by needle puncture for diagnostic purposes. The diagnosis of each case was independently confirmed histologically by liver pathologists according to the Japanese chronic hepatitis classification criteria (New Inuyama classification). According to these criteria, mild activity was defined as A0 or A1, severe activity as A2 or A3, mild fibrosis as F0 or F1, and severe fibrosis as F2, F3, or F4. Fatty changes in >5% of all areas were defined as steatosis.

Table 1 Clinical backgrounds of the patients

Age	56.8 ± 9.3
Gender	Male : Female = 37:30
BMI (kg/m^2)	23.5 ± 2.9
Viral load (KIU/mL)	2320 ± 1519
White blood cell (/uL)	5074 ± 1713
Hemoglobin (mg/dL)	14.1 ± 1.3
Platelet (×10^3/uL)	167.3 ± 75.6
AST (IU/L)	77.1 ± 45.2
ALT (IU/L)	101.2 ± 56.3
γGTP (IU/L)	70.6 ± 65.5
HCV core 70 wild	40 cases
HCV core 91 wild	50 cases
Steatosis (>5%)	37 cases
A (0–1:2–3)	36:31
F (0~1:2~4)	22:45

ALT, alanine aminotransferase; AST, aspartate aminotransferase; BMI, body mass index; γGTP, gamma-glutamyl transpeptidase; HCV, hepatitis C virus.

All patients received PEG-IFN (Schering-Plough, Tokyo, Japan) + ribavirin (Schering-Plough, Tokyo, Japan) therapy for 48 weeks. The patients who were treated with a dose of PEG-IFN or ribavirin reduced by more than 20% were excluded from the study. PEG-IFN (1.5 μg/kg) was administered once per week, and the ribavirin dose was titrated according to body weight. A sustained virological response (SVR) was defined as undetectable HCV RNA at 6 months after the end of interferon treatment.

Of 38 patients who could not achieve an end-of-treatment response, 28 patients required a re-elevation of their viral loads regardless of the fact that the HCV-RNA levels were temporarily negative, and 10 patients did not achieve an HCV negative result during the entire treatment period.

SOCS3 immunohistochemistry

All tissue samples were fixed in 10% neutral buffered formalin and then embedded in paraffin, and 4 μm thick serial sections were cut from each paraffin block. In the immunohistochemical study, an anti-SOCS3 antibody (dilution 1:100, Affinity BioRegents, Golden, CO, USA) was used for SOCS3. Immunohistochemistry was performed with the labeled streptavidin biotinylate antibody (LSAB) method and a commercially available kit (Histofine, SAB-PO(R); Nichirei Corporation, Tokyo, Japan). The area immunostained for SOCS 3 was divided according to the number of immunoreactive cells per unit area. Immunoreactive cases were classified as those with less than 30% of the hepatocellular cells stained (low SOCS3 group) and those with 30% or more of the cells stained (high SOCS3 group), because our previous study showed that staining of more than 30% of the area was a significant predictor of viral clearance.[16]

Genetic variation near the IL28B gene

Genotyping for replication was performed by use of the Invader assay or direct sequencing. In this study, genetic variation near the IL28B gene (rs8099917), which was previously reported to be a predictor of the virological response was investigated.[13]

Statistical analysis

The SPSS 9.0 for Windows statistical software program was used to assess correlations among multiple variables. When appropriate, clinical and laboratory data

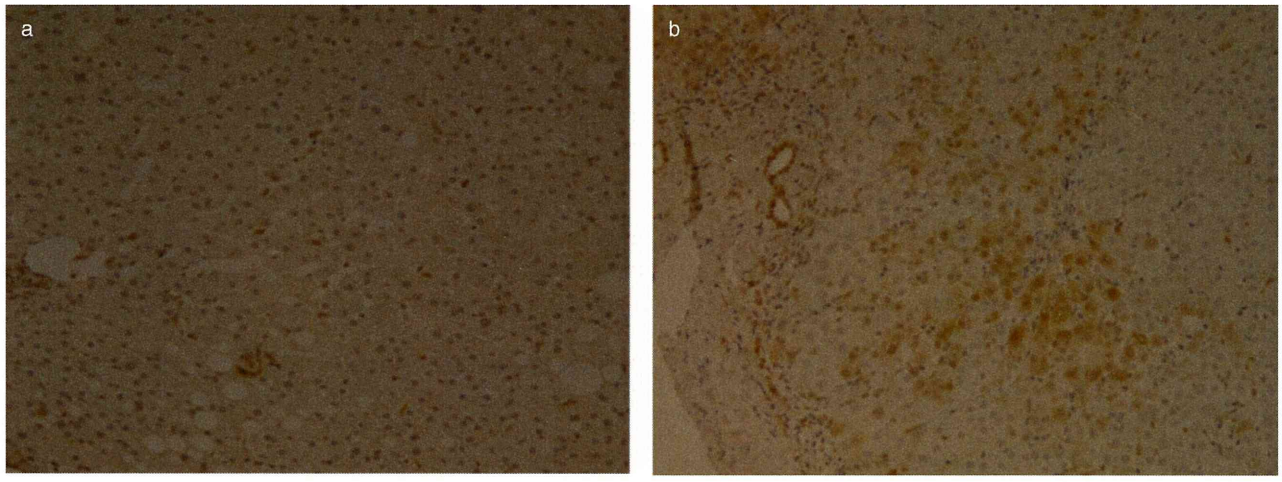

Figure 1 (a) This case showed less than 5% suppressor of cytokine signaling 3 (SOCS3) immunostained areas (low immunostaining). (b) This cases showed about 50% SOCS3 immunostaining areas (high immunostaining).

were compared with the Student's *t*-test or the Mann–Whitney test. A *P*-value of <0.05 was considered to be statistically significant.

RESULTS

Immunostaining of SOCS3 in the liver (Figs 1,2)

IMMUNOSTAINING FOR SOCS3 was mainly seen in the periportal area. Less than 30% SOCS3 immunostained areas were found in 36 cases (54%) and areas with 30% or more immunostaining for SOCS3 were found in 31 cases (46%).

The frequency and distribution of the SOCS3 expression are shown in (Fig. 2)

Correlation between SOCS3 immunostaining and clinicopathlogical factors

A significant difference between low and high SOCS3 groups was found in age (low : high = 54.5 ± 9.8:59.5 ± 8.1, $P = 0.028$), the levels of platelets (low : high = 189.5 ± 90.0:141.6 ± 41.3, $P = 0.009$), aspartate aminotransferase (AST) (low : high = 94.5. ± 56.0:62.1 ± 33.5, $P = 0.003$), alanine aminotransferase; (ALT) (low : high = 85.8 ± 52.4:119.0. ± 56.3, $P = 0.015$), gamma-glutamyl transpeptidase (γGTP) (low : high = 48.8 ± 53.5:94.7 ± 70.6, $P = 0.004$). The incidence of steatosis (low : high = 33%: 81%, $P = 0.001$), severe activity (low : high = 27%: 67%, $P = 0.001$) and sever fibrosis (low : high = 52%: 84%, $P = 0.006$) was significantly higher in the SOCS3 high

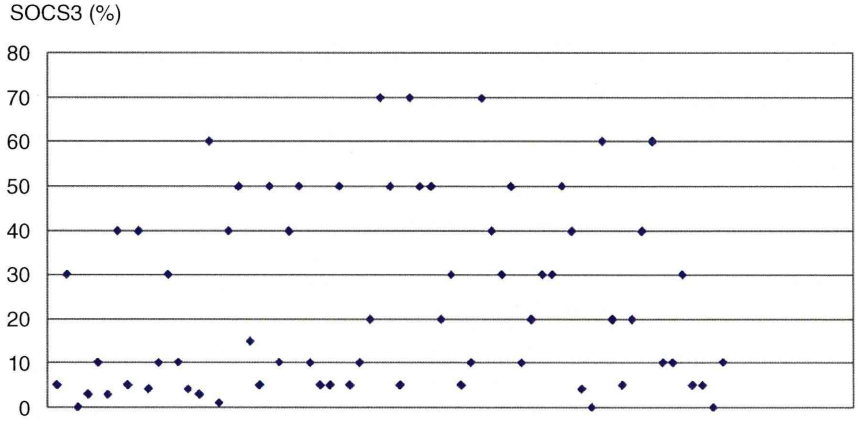

Figure 2 The distribution of the SOCS3 immunostaining area is shown.

Table 2 Comparison of the suppressor of cytokine signaling 3 (SOCS3) immunostaining groups

	SOCS3 high 31 cases	SOCS3 low 36cases	*P*-value
Age	59.5 ± 8.1	54.5 ± 9.8	0.028
Gender (male)	16 (53%)	21 (58%)	0.581
BMI (kg/m^2)	23.3 ± 2.2	23.6 ± 3.5	0.719
Viral load (KIU/mL)	2139 ± 1367	2475 ± 1950	0.427
White blood cell (/uL)	4935 ± 1386	5039 ± 1384	0.765
Hemoglobin (mg/dL)	14.1 ± 1.1	14.0 ± 1.3	0.570
Platelet (×10^3/uL)	141.6 ± 41.3	189.5 ± 90.0	0.009
AST (IU/L)	94.5. ± 56.0	62.1 ± 33.5	0.003
ALT (IU/L)	119.0 ± 56.3	85.8 ± 52.4	0.015
γGTP (IU/L)	94.7 ± 70.6	48.8 ± 53.5	0.004
Core 70 wild	17 (55%)	23 (63%)	0.451
Core 91 wild	23 (74%)	27 (75%)	0.939
Steatosis	25 (81%)	12 (33%)	0.001
Activity (severe)†	21 (67%)	10 (27%)	0.001
Fibrosis (severe)‡	26 (84%)	19 (52%)	0.006
IL28 TT rs8099917	22 (71%)	29 (80%)	0.358

†Severe activity was defined as A2 or A3.
‡Severe fibrosis was defined as F2, F3, or F4.
ALT, alanine aminotransferase; AST, aspartate aminotransferase; BMI, body mass index; γGTP, gamma-glutamyl transpeptidase; HCV, hepatitis C virus.

immunostaining group than in the SOCS3 low immunostaining group. No significant difference was observed between the SOCS3 low and high groups in any of the other clinical factors (age, body mass index [BMI], viral load, white blood cell count, hemoglobin, substitution of the core 70, 91) (Table 2).

Comparison of SOCS3 expression and the genetic variation of IL28B gene

No significant difference in the genetic variation of the IL28 TT genotype was observed between the SOCS3 low and high immunostaining groups (low : high = 80%: 71%, $P = 0.250$).

Assessment of SOCS3 expression and genetic variation in IL28 as predictors of a sustained virological response

The age of patients in the non responder (NR) group was significantly higher than that in sustained virological response (SVR) group (SVR : NR = 52.3 ± 11.5: 59.6 ± 6.1, $P = 0.003$).

The incidence of the IL28 TT genotype was significantly lower, and that of SOCS3 high immunostaining group was significantly higher in the NR group than in the SVR group (Table 3).

As determined by a logistic regression analysis, the significant predictor of an SVR was high age (≥65 years old) (odds ratio 0.221 [0.120–0.966], $P = 0.045$), the IL28 TT genotype (odds ratio 5.422 [1.254–23.617], $P = 0.024$) and SOCS3 (high) (odds ratio 0.308 [0.104–0.948], $P = 0.040$) (Table 4).We found that two of nine (22%) patients with the IL28 TG genotype and SOCS3 high immunostaining showed a SVR, while one of seven (14%) patients with the IL28 TG genotype and SOCS3 low immunostaining, six of 22 (27%) patients with the IL28 TT genotype and SOCS3 high immunostaining, and 20 of 29 (69%) patients with the IL28 TG genotype and SOCS3 low immunostaining showed a SVR (Fig. 3).

DISCUSSION

RECENT IMPROVEMENTS IN the efficiency of antiviral therapy have led to approximately 50% of patients with HCV genotype 1 achieving sustained viral clearance.[1–5] However, some patients are refractory to interferon therapy. A recent study reported that the presence of genetic variation near the IL28B gene (rs8099917, rs1297860) can be used as a pretreatment predictor of virlogical response to a 48-week PEG-IFN plus combination therapy in patients with HCV geno-

Table 3 Factors associated with the response to peginterferon-α (PEG-IFN) and ribavirin

	SVR 29 cases	NR 38 cases	*P*-value
Age	52.8 ± 11.0	59.8 ± 6.4	0.002
Gender (male)	17 (58%)	20 (52%)	0.625
BMI (kg/m^2)	23.9 ± 3.1	22.9 ± 3.1	0.190
Viral load (KIU/mL)	2188 ± 1764	2420 ± 1689	0.587
White blood cell (/uL)	4816 ± 1427	5225 ± 1287	0.242
Hemoglobin (mg/dL)	14.1 ± 1.1	14.0 ± 1.3	0.626
Platelet (×10^3/uL)	176.5 ± 52.8	160.3 ± 89.2	0.350
AST (IU/L)	75.5 ± 36.1	78.3 ± 51.5	0.795
ALT (IU/L)	108.9 ± 56.8	95.3 ± 56.0	0.333
γGTP (IU/L)	63.9 ± 61.9	75.7 ± 68.6	0.464
Core 70 wild	20 (69%)	20 (53%)	0.176
Core 91 wild	21 (72%)	29 (71%)	0.173
IL28 TT rs8099917	26 (90%)	25 (65%)	0.022
steatosis	14 (47%)	23 (61%)	0.452
Activity (severe)†	10 (34%)	21 (64%)	0.091
Fibrosis (severe)‡	18 (62%)	27 (71%)	0.437
SOCS3 (Positive)	8 (27%)	23 (61%)	0.015

†Severe activity was defined as A2 or A3.
‡Severe fibrosis was defined as F2, F3, or F4.
ALT, alanine aminotransferase; AST, aspartate aminotransferase; BMI, body mass index; γGTP, gamma-glutamyl transpeptidase; HCV, hepatitis C virus; NR, non responder; SOCS3, suppressor of cytokine signal 3; SVR, sustained virological response.

type 1.[13–15] We previously reported that SOCS3 was a factor associated with the response to PEG-IFN treatment.[16] We compared these factors and clarified their usefulness as predictors of PEG-IFN plus combination therapy.

In the laboratory data from our patients, a significant difference between the groups with weak and strong SOCS3 staining was found in the level of AST, ALT, and platelets. These laboratory data suggested that the SOCS3 immunostained area was significantly associated with the presence of inflammation and the fibrosis stage. Indeed, in a pathological study, the inflammation and fibrosis stage were significantly different between the low and high SOCS3 immunostaining groups. This finding was consistent with our previous study that showed that the SOCS3 immunostained area was influenced by inflammation and the fibrosis stage.[16]

Table 4 Results of a multilogistic regression analysis

	Odds ratio	*P*-value
Age (>65 years)	0.221 (0.120–0.966)	0.045
IL28 TT	5.422 (1.254–23.617)	0.024
SOCS3 (low)	0.308 (0.104–0.948)	0.040

SOCS3, suppressor of cytokine signal 3.

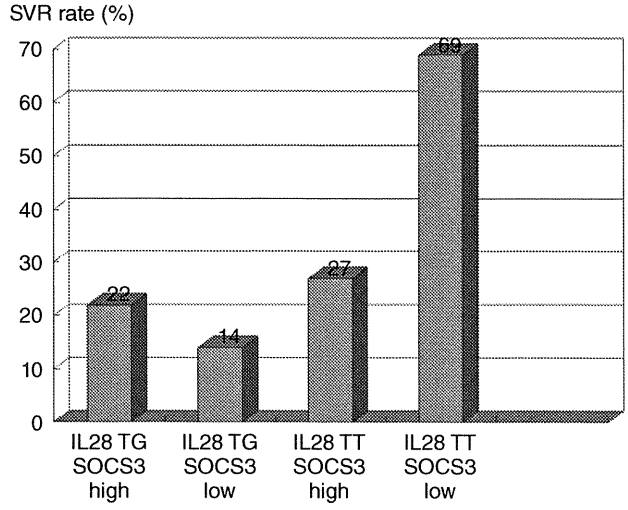

Figure 3 A total of 12.5% of patients with IL28 TG and suppressor of cytokine signaling 3 (SOCS3) high immunostaining showed a sustained virological response (SVR), 20% of patients with IL28 TG and SOCS3 low immunostaining, 31% of patients with IL28 TT and SOCS3 high immunostaining, and 68% of patients with IL28 TG and SOCS3 low immunostaining showed a SVR.

Moreover, a significant difference between the low and high SOCS3 groups was also found in the level of γGTP. Several previous reports showed that the level of γGTP was correlated with steatosis in the liver.[7,17] In this study, the presence of steatosis also was significantly different in the low and high SOCS3 immunostaining groups. Together with our results, these results demonstrated that the SOCS3 immunostained area in the liver was associated with obesity, insulin resistance, and hepatic steatosis.[18,19]

Although recent reports showed that genetic variation of IL28B was also associated with liver inflammation and fibrosis,[20] this was not associated with the SOCS3 immunostained area in the present study. The SOCS3 proteins are known for their role as negative regulators and inhibitors of Janus kinase-signal transducer and activator of transcription (JAK-STAT) signaling, where they mediate a classical negative feedback loop in the IFN-α/β receptor signaling pathway.[21,22] The mechanism that leads to the association between genetic variation of IL28B and the effect of interferon therapy is clear, because it has been demonstrated that IL28B inhibits hepatitis C virus replication through the JAK-STAT pathway.[23] Taken together, both the SOCS3 immunostained area and IL28B polymorphisms were associated with the JAK-STAT pathway, but the different factors might interfere with JAK-STAT signaling in different ways.

The NR rate to combination PEG-IFN plus ribavirin therapy in patients with the non-TT genotype was 10–20%. The value of NR for the prediction of the genetic variation of IL28B was therefore very high. On the other hand, the SVR rate in patients with the TG genotype was about 50%. The value of SVR prediction based only on the genetic variation of IL28B was therefore not as strong for this genotype.

The substitution of core amino acids was also reported to be a predictive factor for the response to interferon therapy and was significantly associated with the genetic variation of IL28B.[24] On the other hand, the SOCS3 immunostained area was independent of both of these factors. Thus, we suggested that using a combination of the SOCS3 immunostained area with the IL28B genotype can provide the best prediction of the response to PEG-IFN plus ribavirin therapy.

Indeed, in TT genotype patients, the SVR rate in the SOCS3 weak group was about 70%, and NVR rate in the SOCS3 low immunostained group was 27%. If a liver biopsy was performed, immunostaining for SOCS3 was easy, and provided a useful predictor of the response to interferon therapy.

Our study has some limitations. Our sample size was too small. Further large-scale studies are necessary to confirm the present results and to provide a better understanding of the interactions between the SOCS3 immunostained area and the genetic variation of IL28B.

In conclusion, a combination of the SOCS3 immunostained area in the liver and the assessment of the genetic variation of IL28B seem to be good predictors of the response to PEG-IFN plus ribavirin therapy.

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PLoS one

Highly Parallel and Short-Acting Amplification with Locus-Specific Primers to Detect Single Nucleotide Polymorphisms by the DigiTag2 Assay

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Abstract

The DigiTag2 assay enables analysis of a set of 96 SNPs using Kapa 2GFast HotStart DNA polymerase with a new protocol that has a total running time of about 7 hours, which is 6 hours shorter than the previous protocol. Quality parameters (conversion rate, call rate, reproducibility and concordance) were at the same levels as when genotype calls were acquired using the previous protocol. Multiplex PCR with 192 pairs of locus-specific primers was available for target preparation in the DigiTag2 assay without the optimization of reaction conditions, and quality parameters had the same levels as those acquired with 96-plex PCR. The locus-specific primers were able to achieve sufficient (concentration of target amplicon $\geq$5 nM) and specific (concentration of unexpected amplicons $<$2 nM) amplification within 2 hours, were also able to achieve detectable amplifications even when working in a 96-plex or 192-plex form. The improved DigiTag2 assay will be an efficient platform for screening an intermediate number of SNPs (tens to hundreds of sites) in the replication analysis after genome-wide association study. Moreover, highly parallel and short-acting amplification with locus-specific primers may thus facilitate widespread application to other PCR-based assays.

Citation: Nishida N, Mawatari Y, Sageshima M, Tokunaga K (2012) Highly Parallel and Short-Acting Amplification with Locus-Specific Primers to Detect Single Nucleotide Polymorphisms by the DigiTag2 Assay. PLoS ONE 7(1): e29967. doi:10.1371/journal.pone.0029967

Editor: Javier S. Castresana, University of Navarra, Spain

Received September 26, 2011; **Accepted** December 9, 2011; **Published** January 13, 2012

Funding: This work was supported by a KAKENHI [grant number 22710191] Grant-in-Aid for Young Scientists (B) from the Ministry of Education, Culture, Sports, Science, and Technology of Japan, and the Miyakawa Memorial Research Foundation. Partial support by the SENTAN program, Japan Science and Technology Agency, is also acknowledged. The funders had no direct role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Competing Interests: The authors have declared that no competing interests exist.

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Introduction

Polymerase chain reaction (PCR) is a commonly used technique in molecular biology. Several previously developed methods have employed multiplexed PCR in order to analyze genomic variations such as microsatellites or short tandem repeats (STRs), single nucleotide polymorphisms (SNPs) and insertions/deletions [1–3]. Multiplexed preparation of DNA templates in a single reaction is cost-effective, saving starting materials and run-time, while requiring careful optimization of assay conditions. The optimization process is highly empirical and time consuming, and depending on the combinations of markers, may or may not lead to successful assay development. For the conventional design of multiplex PCR, optimization of reaction conditions and careful pre-selection of targets are required in order to prevent excessive off-target priming by the numerous primers in the reaction. Moreover, the risk of generating errors in multiplex PCR, such as insufficient amplification, biased amplification and considerable primer-dimer formation within primers, tends to increase roughly as the square of the number of added primer pairs [4].

There are several approaches to resolving these drawbacks, including solid-phase assay formats (glass slide arrays, microbeads), oligonucleotides containing locked nucleic acid (LNA) residues and circularized amplification. Primers immobilized on the surface of the solid phase appear to markedly increase product yield on solid supports and may avoid the need for target pre-selection with a modification to enrich the input genomic DNA via a crude solution-phase multiplex PCR [5,6]. LNA pentamers showed high priming efficiency to achieve small biased priming in multiplex PCR [7]. Circularized amplification avoids generating artifacts associated with conventional multiplex PCR where two primers are used for each target [8]. This procedure was shown to perform a 96-plex amplification of an arbitrary set of specific DNA sequences. The arrayed primer extension-based genotyping method (APEX-2) allows efficient homogeneous 640-plex DNA amplification with locus-specific primers [9]. These approaches show effective consequences for multiplex amplification, however, a small number of approaches are practically used in the field of molecular genetics, presumably due to its cost and time consuming steps in preparation.

We developed the DigiTag2 assay for multiplex SNP typing as a simple and cost effective approach by combining multiplex PCR to enrich genetic regions including the target SNPs and an oligonucleotide ligation assay to encode all of the SNP genotypes into well-designed oligonucleotides designated DNA coded numbers (DCNs) [10]. For an effective primer design for multiplex PCR, there are several important physical properties for primer sequences, including melting temperature, Gibbs energy of duplex between primer and template, and interactions between primers and PCR amplicons. The DNA polymerase enzyme used in a multiplex PCR is one of the important factors for a successful unbiased amplification.

The DigiTag2 assay is a suitable approach to analyze an intermediate number of SNPs (tens to hundreds of locus) in the replication study after genome wide association study [11–12]. However, the most time consuming step for the DigiTag2 assay in a total running time of 13 hours is multiplex PCR for target preparation (5.5 hours). Here, we report an improved protocol for the DigiTag2 assay with a short-acting multiplex PCR through the use of Kapa 2GFast HotStart DNA polymerase, which reduces total running time and increases assay throughput. In this study, we also validate the applicability of the 192-plex PCR with locus specific primers to amplify the target regions from genomic DNA, which leads to save genomic DNA samples.

Methods

DNA samples

Genomic DNA samples from 96 unrelated healthy donors were obtained from the Japan Health Science Research Resources Bank (Osaka, Japan). All donors provided written informed consent and samples were anonymized. One microgram of purified genomic DNA was dissolved in 100 µl of TE buffer (pH 8.0) (Wako, Osaka, Japan), followed by storage at −20°C until use.

Primer design

A total of 192 pairs of primer were designed using the Visual OMP software version 7.1.0.0 (DNA software, Ann Arbor, MI, USA) with relatively long length (35–45-mer; average, 39.5-mer) to give amplicon sizes between 312 bp and 995 bp (average, 589 bp), each of which had an SNP site (Table S1). Prediction of DNA melting temperature was calculated using nearest-neighbor thermodynamic models. To avoid spurious amplification products, we employed a two-step protocol (denature and extension steps) using specifically designed primer pairs with an extension temperature at 68°C. The specificity of primer sequences was verified by Blat search in order to predict its location(s) on the human genome (GRCh37), and to confirm no unexpected SNP(s) within the primer sequence. The specificity of primer pairs was verified using MFE primer software, which can predict potential amplicon(s) generated from the human genome (GRCh37, up to 5 kb in amplicon size) [13]. All oligonucleotides (de-salted, 100 pmol/µl in TE (10 mM Tris-HCl, pH 8.0, 1 mM EDTA)) were purchased from Life Technologies (Carlsbad, CA, USA), and were stored at −20°C.

Multiplex PCR with Kapa 2GFast HotStart DNA polymerase

Multiplex PCR mix had a final volume of 10 µl, including 10 ng of genomic DNA, 25 nM each primer, 1.5× KAPA2G Buffer (including 2.25 mM Mg^{2+}), an additional 2.25 mM Mg^{2+} (final concentration of Mg^{2+}: 4.5 mM), 0.2 mM dNTPs and 0.4 U of Kapa 2GFast HotStart DNA polymerase (Kapa Biosystems, Woburn, MA, USA). PCR amplification was conducted using a TGradient (Biometra, Göttingen, Germany) or PTC-225 (MJ Research, Waltham, MA, USA) as follows: 95°C for 3 min, followed by 40 cycles of 95°C for 15 s and 68°C for 2 min. When necessary, the fragment length of PCR products was confirmed by capillary electrophoresis (Agilent 2100 Bioanalyzer, Agilent, Santa Clara, CA, USA) in order to evaluate PCR efficiency. The total running times for multiplex PCR with Kapa 2GFast HotStart DNA polymerase using TGradient and PTC-225 were 1 h 48 min 55 s and 2 h 6 min 59 s, respectively.

Multiplex PCR with QIAGEN Multiplex PCR Kit

Multiplex PCR mix had a final volume of 10 µl, including 10 ng of genomic DNA, 25 nM each primer, 1× Multiplex PCR Buffer (including 3.0 mM Mg^{2+}), 0.2 mM dNTPs and HotStar-Taq DNA polymerase (QIAGEN Multiplex PCR Kit; QIAGEN, Valencia, CA, USA). PCR amplification was conducted using a TGradient or PTC-225 as follows: 95°C for 15 min, followed by 40 cycles of 95°C for 30 s and 68°C for 6 min. The total running times for multiplex PCR with QIAGEN Multiplex PCR Kit using TGradient and PTC-225 were 5 h 27 min 53 s and 5 h 46 min 39 s, respectively.

96-plex genotyping by the DigiTag2 assay

The DigiTag2 assay performs multiplex SNP typing by encoding all of the SNP genotypes into well-designed oligonucleotides, designated DNA coded numbers (Figure 1, DCNs: D1_i, ED-1 and ED-2) [10]. The DCNs are assigned to the target SNPs in an unconstrained manner; therefore, the DNA chips prepared to read out the types of DCNs are universally available for any type of SNP without optimization of assay conditions. The DigiTag2 assay proceeds in four steps; target preparation, encoding, labeling and detection.

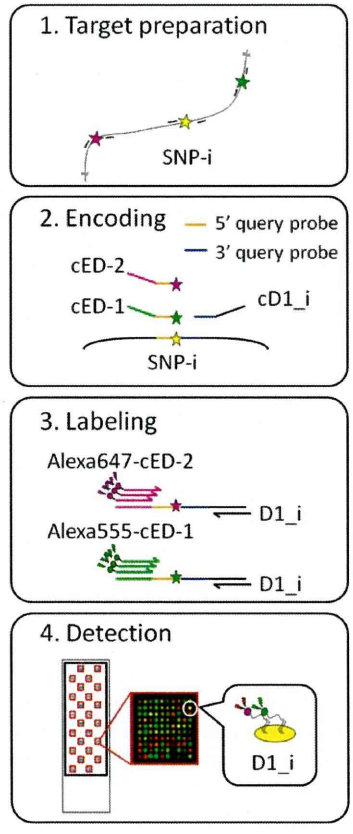

Figure 1. Schematic representation of the DigiTag2 assay. The assay has four steps: target preparation, encoding, labeling and detection. SNP genotypes are encoded into well-designed oligonucleotides, designated DNA coded numbers (DCNs: D1_i, ED-1 and ED-2). D1_i is a variable sequence assigned to each SNP. Reverse complement sequences are written by attaching the character 'c' before the sequence name.
doi:10.1371/journal.pone.0029967.g001

The encoding reactions had a final volume of 15 μl, including 0.5 μl of multiplex PCR products, 20 mM Tris-HCl, pH 7.6, 25 mM potassium acetate, 10 mM magnesium acetate, 10 mM DTT, 1 mM NAD, 0.1% Triton X-100 (1× Taq DNA ligase buffer) with 0.33 nM of each probe and 5 U Taq DNA ligase (New England BioLabs, Ipswich, MA, USA). Encoding reactions were conducted using a TGradient or PTC-225 under the following conditions: 95°C for 5 min, followed by 58°C for 15 min. The reaction was stopped by holding the temperature at 10°C.

The labeling reactions had a final volume of 12 μl, including 6 μl of ligation products, 0.5 μM each labeled primer (Alexa555-cED-1 and Alexa647-cED-2), 2.5 nM each D1 primer (D1_i), 50 mM KCl, 2 mM Mg^{2+}, 0.1 mM DTT, 0.2 mM each dNTP (N = A, G, C), 0.1 mM [^{3}H]-dTTP, 0.25 mg/ml activated salmon sperm DNA (1× *Ex Taq* Buffer) and 0.05 U of *Ex Taq*™ polymerase (TaKaRa, Shiga, Japan). Labeling reactions were conducted using a TGradient or PTC-225 under the following conditions: first held at 95°C for 1 min, followed by 30 cycles of 95°C for 30 s, 55°C for 6 min and 72°C for 30 s. The reaction was stopped by holding the temperature at 10°C. Total running times for labeling using TGradient and PTC-225 were 3 h 49 min 48 s and 4 h 8 min 48 s, respectively.

In the detection step, a hybridization mixture was prepared by mixing 6.25 μl of labeling products with 8.75 μl of hybridization buffer containing 0.5× SSC, 0.1% SDS, 15% formamide, 1 mM EDTA and 3.125 fmol of hybridization control (Alexa555-labeled D1_100 and Alexa647-labeled D1_100). The hybridization control was prepared for ensuring the hybridization step. Ten microliters of hybridization mixture was applied to each block on the universal DNA chip. Hybridization was carried out for 30 min at 37°C in a hybridization oven (ThermoStat plus; Eppendorf, Ham, Germany). After hybridization, glass slides were washed in washing buffer (0.1× SSC, 0.1% SDS) by shaking at 60 rpm for 3 min. Glass slides were consecutively washed in distilled water by shaking at 60 rpm for 1 min and then dried up by centrifugation at 500× g for 1 min. Hybridization images were scanned at photomultiplier voltages of 400 V for Alexa555 and 480 V for Alexa647 using a commercially available DNA chip scanner and fluorescence image analysis was performed using commercially available software (GenePix 4000B unit and GenePix Pro 4.1 software package; Molecular Devices, Sunnyvale, CA, USA).

Labeling with Kapa 2GFast HotStart DNA polymerase

The labeling reactions with Kapa 2GFast HotStart DNA polymerase had a final volume of 12 μl, including 6 μl of ligation products, 0.5 μM each labeled primer (Alexa555-cED-1 and Alexa647-cED-2), 2.5 nM each D1 primer (D1_i), 1.5× KAPA2G Buffer (including 2.25 mM Mg^{2+}), an additional 2.25 mM Mg^{2+} (final concentration of Mg^{2+}: 4.5 mM), 0.2 mM dNTPs and 0.4 U of Kapa 2GFast HotStart DNA polymerase. Labeling reactions were conducted using a TGradient or PTC-225 under the following conditions: first held at 95°C for 1 min, followed by 30 cycles of 95°C for 15 s, 55°C for 120 s and 72°C for 5 s. The reaction was stopped by holding the temperature at 10°C. The total running times for labeling using TGradient and PTC-225 were 1 h 29 min 48 s and 1 h 48 min 34 s, respectively.

Results

Singleplex PCR using 192 pairs of locus-specific primers

Singleplex PCR was conducted under the same reaction condition with multiplex PCR using 25 ng of genomic DNA to ensure target amplicon detection and to confirm the emergence of extra bands (unexpected amplicons). Singleplex PCR with 192 pairs of locus-specific primers revealed that most of the primer pairs are able to achieve sensitive detection (concentration of target amplicon ≥5 nM) and specific amplification without extra bands (concentration of unexpected amplicons <2 nM) except for 14 pairs of primers; low sensitivity (<5 nM) for 5 pairs of primers (61, 99, 102, 189 and 191) and low specificity with extra bands (≥2 nM) for 9 pairs of primers (40, 56, 62, 70, 91, 106, 149, 173 and 174) (Figure 2 and Table S2). Five pairs among the 9 low-specific primer pairs with extra bands (62, 70, 149, 173 and 174) resulted from heteroduplex formation of target amplicons during polyacrylamide gel electrophoresis. Despite the presence of extra bands, the remaining 4 pairs of low-specific primers had a target amplicon with a detectable concentration ≥5 nM.

Validation of efficacy of 192-plex PCR by 96-plex genotyping with the DigiTag2 assay

The DigiTag2 assay enables the simultaneous analysis of 96 target SNPs in: (1) multiplex PCR with locus-specific primers to amplify target genomic regions including target SNPs; (2) multiple oligonucleotide ligation assay with locus-specific probes to determine the genotype of each SNP; and (3) hybridization to the universal DNA chip tethered with probe sequences identical to D1_i (23-mer) (Figure 1) [10]. The validity of 192-plex PCR was assessed with 96 individual DNAs (population control samples) by comparing two sets of 96-plex genotype calls acquired from 96-plex PCR with those from 192-plex PCR (Table 1).

Conversion rate shows the proportion of successfully genotyped SNPs with fewer than 3 undetected samples after excluding low-quality genotyping data, which had more than 5 undetected SNPs in a total of 96 SNPs. However, the composition of failed SNPs in genotyping was not identical, and the conversion rate showed no differences between 192-plex PCR and 96-plex PCR. For the 1st set of 96 SNPs, 7 SNPs among 10 failed SNPs were matched between 192-plex PCR and 96-plex PCR, and for the 2nd set, 8 SNPs among the 9 failed SNPs were matched. The average call rate for successfully genotyped SNPs was over 99.79% for both sets of 96-plex genotyping, even if 192-plex PCR products were adopted for target preparation. Reproducibility was determined by independent genotyping with 96 individuals twice. As a consequence, four discordant genotype calls were observed in the duplicated genotyping data. Concordance of genotype calls between 192-plex PCR and 96-plex PCR was determined using 6,290 genotype calls for the 1st set and 7,884 genotype calls for the 2nd set. Consequently, 14,171 out of 14,174 genotype calls were matched by comparison with 83 SNPs for the 1st set and 86 SNPs for the 2nd set. In total, 3 discordant genotype calls were observed (Figure 3).

Short-acting multiplex PCR by use of Kapa 2GFast HotStart DNA polymerase

Kapa 2GFast HotStart DNA polymerase was employed to perform multiplex PCR with the locus-specific primers for target preparation in genotyping with the DigiTag2 assay. To optimize reaction conditions with Kapa 2GFast HotStart DNA polymerase, singleplex PCR was conducted using 25 ng of genomic DNA with three randomly chosen pairs of locus-specific primers. The designed amplicon sizes for the three pairs of primers were 501 bp, 671 bp and 492 bp. We performed singleplex PCR using a two-step protocol (denature and extension steps) with varied extension periods (15 s, 30 s, 60 s and 120 s) and with varied Mg^{2+} concentrations (3.0 mM and 4.5 mM) (Figure 4). The most sensitive detection and highest levels of amplification for the three

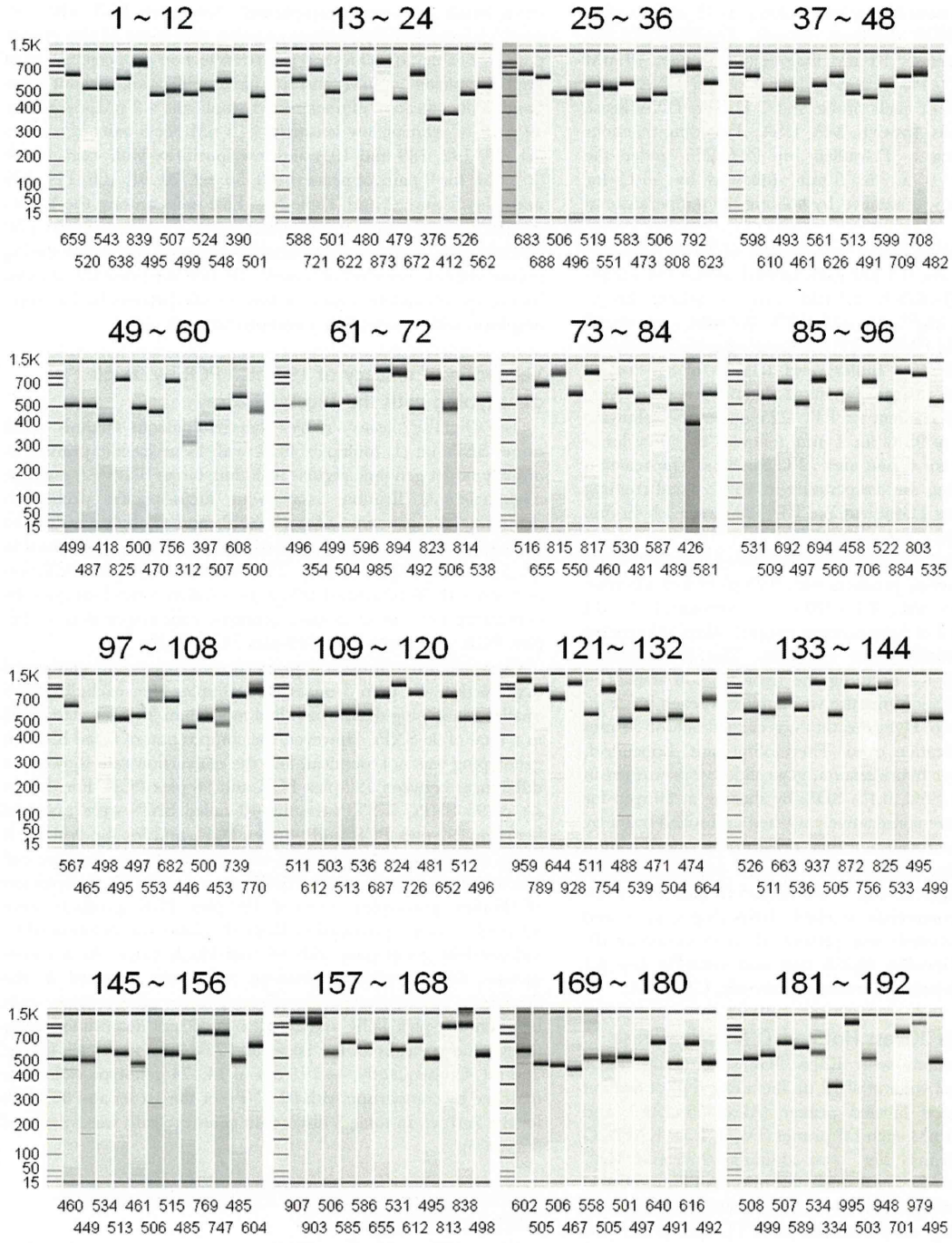

Figure 2. Electropherogram of singleplex PCR products with 192 pairs of locus-specific primers. The designed amplicon size is depicted below each lane.
doi:10.1371/journal.pone.0029967.g002

pairs of primers were observed with 120 s for the extension period and 4.5 mM for the Mg^{2+} concentration. The total running time for multiplex PCR with locus-specific primers was less than 2 hours, which is about 3 h 30 min shorter than the previous protocol (see MATERIALS AND METHODS).

The total running time of the DigiTag2 assay was markedly reduced when the labeling step was also conducted using Kapa 2GFast HotStart DNA polymerase instead of *Ex Taq* polymerase. When the DigiTag2 assay was conducted with Kapa 2GFast HotStart DNA polymerase for multiplex PCR and labeling step, the total running time of the assay was about 7 hours, which is about 6 hours shorter than the previously used protocol in combination with QIAGEN Multiplex PCR Kit for multiplex PCR and *Ex Taq* polymerase for the labeling step.

Table 1. Validation of efficacy of 192-plex PCR by 96-plex genotyping.

		192-plex PCR	96-plex PCR
1st set	Conversion rate	86/96 SNP	86/96 SNP
	Call rate	99.84% (7,728/7,740 genotype)	99.81% (6,695/6,708 genotype)
	reproducibility	99.99% (7,288/7,289 genotype)	100% (6,121/6,121 genotype)
	concordance	99.98% (6,289/6,290 genotype)	
2nd set	Conversion rate	87/96 SNP	87/96 SNP
	Call rate	99.79% (8,074/8,091 genotype)	99.79% (8,161/8,178 genotype)
	reproducibility	99.97% (7,792/7,794 genotype)	99.99% (7,712/7,713 genotype)
	concordance	99.97% (7,882/7,884 genotype)	

doi:10.1371/journal.pone.0029967.t001

Table 2 summarizes the quality parameters (conversion rate, call rate, reproducibility and concordance) when genotyping was conducted with 192-plex PCR or 96-plex PCR by use of Kapa 2GFast HotStart DNA polymerase. The conversion rate was slightly decreased when multiplex PCR was conducted in 192-plex form. However, the conversion rates were better than those observed when multiplex PCR was conducted with the QIAGEN Multiplex PCR Kit. The composition of failed SNPs in genotyping was not consistent for the 1st set of 96 SNPs, in which 4 SNPs were matched between 192-plex PCR and 96-plex PCR. For the 2nd set, a total of 8 failed SNPs in the 96-plex PCR were completely matched to those in the 192-plex PCR. When the composition of failed SNPs were compared between Kapa 2GFast HotStart DNA polymerase and QIAGEN Multiplex PCR Kit, the 1st set had 5 matched SNPs in a total of 8 failed SNPs for 192-plex PCR, and 4 matched SNPs in 5 failed SNPs for 96-plex PCR. From the 2nd set, 5 SNPs in a total of 9 failed SNPs were matched when 192-plex PCR was conducted and 4 SNPs in a total of 8 failed SNPs were matched when 96-plex PCR was conducted. The average call rate for successfully genotyped SNPs was over 99.76% for both sets of 96-plex genotyping, even if 192-plex PCR products were adopted for target preparation. The reproducibility was 100% for the 2nd set; however, three discordant genotype calls were observed for the 1st set. With regard to the concordance of genotype calls between 96-plex PCR and 192-plex PCR, only one discordant genotype call was observed in the comparison for the 1st set, and no discordant genotype calls were observed in the 2nd set.

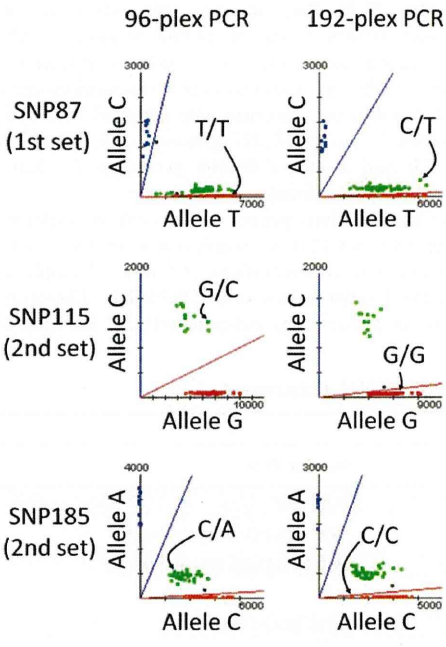

Figure 3. Scatter plots for three SNPs with 3 discordant genotypes. Scatter plots in genotyping with 192-plex PCR and 96-plex PCR are depicted side-by-side. The genotypes of discordant samples are indicated in the scatter plots by arrows.
doi:10.1371/journal.pone.0029967.g003

Table 3 shows the concordance rate in comparison with the genotype calls by the use of Kapa 2GFast HotStart DNA polymerase or QIAGEN Multiplex PCR Kit for multiplex PCR. For the 1st set, there were 4 discordant genotype calls with 96-plex PCR and 8 discordant genotype calls with 192-plex PCR. For the 2nd set of 96 SNPs, there was one discordant genotype call in genotyping with 96-plex PCR and 192-plex PCR.

Discussion

The locus specific primers sufficiently worked in a multiplex form under the same reaction conditions without any optimization processes, either 96-plex PCR or 192-plex PCR. We also found that either 96-plex PCR or 192-plex PCR could be accomplished within two hours through the use of Kapa 2GFast HotStart DNA polymerase. The total running time of the DigiTag2 assay was shortened by 6 hours over the original 13-hour long protocol using Kapa 2GFast HotStart DNA polymerase for both multiplex PCR and the labeling step. The quality parameters (conversion rate, call rate, reproducibility and concordance) observed in genotyping with the new protocol were the same as those observed in the original protocol using QIAGEN Multiplex PCR Kit for multiplex PCR and *Ex Taq* polymerase for the labeling step. The DigiTag2 assay worked with a conversion rate of over 93.2% (179 / 192 SNPs), average call rate of over 99.80% (16,789/16,823 genotypes) and reproducibility of over 99.99% (16,135/16,136 genotypes) using 96-plex PCR under the new protocol. The composition of successfully genotyped SNPs was different when the genotype calls were acquired using the different polymerases (Kapa 2GFast HotStart DNA polymerase and QIAGEN Multiplex PCR Kit), which would result from a varying amplification bias in multiplex PCR. We also found that 192-plex PCR with locus-specific primers worked in 96-plex genotyping with the DigiTag2 assay, giving the same quality parameter data as those observed in genotyping with 96-plex PCR. However, the

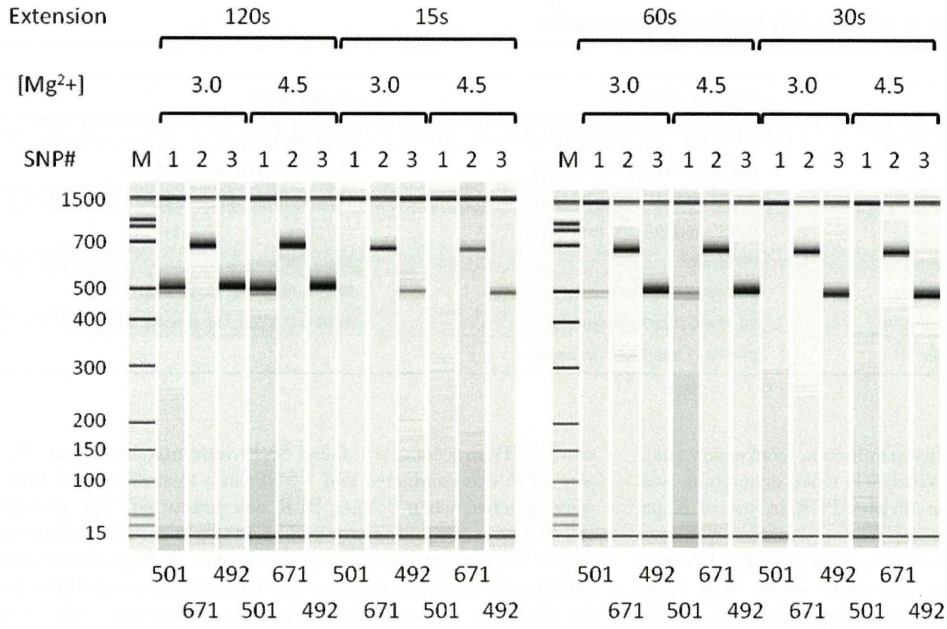

Figure 4. Electropherogram of singleplex PCR products using Kapa 2GFast HotStart DNA polymerase. Singleplex PCR was performed with varied extension periods (15 s, 30 s, 60 s and 120 s) and with varied Mg^{2+} concentrations (3.0 mM and 4.5 mM) using three pairs of locus-specific primers. The designed amplicon size is depicted below each lane.
doi:10.1371/journal.pone.0029967.g004

composition of successfully genotyped SNPs was not consistent between 192-plex PCR and 96-plex PCR, which may be explained by changing the interactions between primer pairs in 192-plex PCR and in 96-plex PCR. The composition of successful SNPs was not consistent when using different polymerases or multiplex systems in the multiplex PCR, which casts some shadows on the reliability of the assay. Regardless of the existing shadows, indeed, 96-plex and 192-plex PCR work with a high conversion rate in genotyping over 93.2%. To clear the existing shadows, it is necessary to continuously accumulate genotyping data.

In this study, fifteen discordant genotype calls were in total observed in the comparison of genotype calls with: i) duplicated genotyping data; ii) genotyping data by use of 192-plex PCR and 96-plex PCR; and iii) genotyping data with different types of polymerases (Table S3). Table S3 shows the genotype calls acquired 8 times under different conditions. All fifteen discordant genotype calls were analyzed with direct sequencing, of which 13 genotype calls were determined. In 8 of 15 discordant genotype calls, the genotype calls were completely different depending on the type of polymerase. The genotype calls acquired using Kapa 2GFast HotStart DNA polymerase were 100% concordant (6 of 6) with those acquired by direct sequencing. This suggests that SNP allelic bias in PCR amplification readily occurred with the QIAGEN Multiplex PCR Kit; however, the error rate in genotyping was only 0.04% (6 out of 14,886 genotypes). The remaining 7 discordant genotype calls were randomly observed in 1 out of 8 different conditions. This shows that the random error rates were almost equal in the genotype data acquired with both types of polymerases (4 out of 62,227 genotypes for QIAGEN Multiplex PCR Kit and 3 out of 66,008 genotypes for Kapa 2GFast HotStart DNA polymerase).

Among the five low-sensitivity primer pairs found on singleplex PCR (61, 99, 102, 189 and 191), no amplicons were detected by primer pair 189 and low concentrations (<5 nM) of amplicon were detected by the 4 other primer pairs (Table S2). Therefore, the SNP189 failed in genotyping, independently of the type of

Table 2. Validation of efficacy of 192-plex and 96-plex PCR with Kapa 2GFast HotStart DNA polymerase.

		192-plex PCR	96-plex PCR
1st set	Conversion rate	88/96 SNP	91/96 SNP
	Call rate	99.84% (8,259/8,272 genotype)	99.76% (8,443/8,463 genotype)
	reproducibility	99.97% (8,069/8,071 genotype)	99.99% (8,339/8,340 genotype)
	concordance	99.99% (7,982/7,983 genotype)	
2nd set	Conversion rate	87/96 SNP	88/96 SNP
	Call rate	99.91% (8,171/8,178 genotype)	99.83% (8,346/8,360 genotype)
	reproducibility	100% (7,705/7,705 genotype)	100% (7,796/7,796 genotype)
	concordance	100% (8,161/8,161 genotype)	

doi:10.1371/journal.pone.0029967.t002

Table 3. Concordance of genotype calls between Kapa 2GFast HotStart DNA polymerase and QIAGEN Multiplex PCR Kit.

		Kapa 2G	QIAGEN
1st set	96-plex PCR	99.94% (6,513/6,517 genotype)	
	192-plex PCR	99.89% (7,441/7,449 genotype)	
2nd set	96-plex PCR	99.99% (7,778/7,779 genotype)	
	192-plex PCR	99.99% (7,700/7,701 genotype)	

doi:10.1371/journal.pone.0029967.t003

polymerase and multiplicity in multiplex PCR (192-plex or 96-plex). However, the SNP191, which was amplified by primer pair 191, was successfully genotyped only when the QIAGEN Multiplex PCR Kit was used for the multiplex PCR. The concentration of amplicon amplified by primer pair 99 was the same as the 2.8 nM observed with the amplicon amplified by primer pair 191. SNP99, which was amplified by primer pair 99, was successfully genotyped independently of polymerase type and multiplicity in multiplex PCR (192-plex or 96-plex). These results suggest that the sensitivity in genotyping with Kapa 2GFast HotStart DNA polymerase was lower than the previously used protocol with QIAGEN Multiplex PCR Kit. These results would be explained by a biased amplification with the shortened protocol using Kapa 2GFast HotStart DNA polymerase, which tends to lead to a consequent biased genotyping. However, the investigated number of primer pairs would not be sufficient to decide the sensitivity in genotyping; therefore, it is necessary to continuously accumulate genotyping data. As the investigated number of primer pairs was only 192 (384 primers) in this study, melting temperature of each primer and the number of potential amplicons predicted by the MFE primer software were strongly associated with low sensitivity and low specificity in an amplification, respectively (multiple regression analysis, $P = 1.26 \times 10^{-37}$ and $P = 1.52 \times 10^{-21}$, respectively).

Through the use of Kapa 2GFast HotStart DNA polymerase, the genotype calls for 96 SNPs can be acquired in about 7 hours by the DigiTag2 assay. The genotyping platform with high conversion rate plays an important role for the replication studies to identify the disease associated genes from candidate loci found in the GWAS (genome-wide association study). The DigiTag2 assay with an improved protocol will be an efficient platform for screening an intermediate number of SNPs (tens to hundreds of sites) in the replication studies. Because of limitations in the variation of DNA coded numbers (DCNs), 192-plex genotyping is not available for the current DigiTag2 assay. However, 192-plex PCR can save genomic DNA samples and time for target preparation. Moreover, 192-plex PCR is also available for direct-sequencing and other PCR-based assays to amplify the target regions from genomic DNA.

Supporting Information

Table S1 Sequence information of 192 pairs of locus specific primer.
(XLSX)

Table S2 Results of singleplex PCR with 192 pairs of locus specific primer.
(XLSX)

Table S3 The 15 discordant genotype calls in 8 different conditions.
(XLSX)

Acknowledgments

We would like to thank M. Takasu for technical support, and H. Adachi, N. Tabei and J. Fujimiya (Dynacom Co., Ltd.) for assistance with primer and probe design.

Author Contributions

Conceived and designed the experiments: NN KT. Performed the experiments: YM MS. Analyzed the data: NN YM MS. Contributed reagents/materials/analysis tools: NN YM MS. Wrote the paper: NN KT.

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J Gastroenterol
DOI 10.1007/s00535-010-0322-5

ORIGINAL ARTICLE—LIVER, PANCREAS, AND BILIARY TRACT

Pretreatment prediction of response to peginterferon plus ribavirin therapy in genotype 1 chronic hepatitis C using data mining analysis

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Received: 22 June 2010 / Accepted: 21 August 2010

Abstract
Background This study aimed to develop a model for the pre-treatment prediction of sustained virological response (SVR) to peg-interferon plus ribavirin therapy in chronic hepatitis C.
Methods Data from 800 genotype 1b chronic hepatitis C patients with high viral load (>100,000 IU/ml) treated by peg-interferon plus ribavirin at 6 hospitals in Japan were randomly assigned to a model building ($n = 506$) or an internal validation ($n = 294$). Data from 524 patients treated at 29 hospitals in Japan were used for an external validation. Factors predictive of SVR were explored using data mining analysis.
Results Age (<50 years), alpha-fetoprotein (AFP) (<8 ng/mL), platelet count ($\geq 120 \times 10^9$/l), gamma-glutamyltransferase (GGT) (<40 IU/l), and male gender were used to build the decision tree model, which divided patients into 7 subgroups with variable rates of SVR ranging from 22 to 77%. The reproducibility of the model was confirmed by the internal and external validation ($r^2 = 0.92$ and 0.93, respectively). When reconstructed into 3 groups, the rate of SVR was 75% for the high probability group, 44% for the intermediate probability group and 23% for the low probability group. Poor adherence to drugs lowered the rate of SVR in the low probability group, but not in the high probability group.

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Published online: 10 September 2010

Conclusions A decision tree model that includes age, gender, AFP, platelet counts, and GGT is useful for predicting the probability of response to therapy with peg-interferon plus ribavirin and has the potential to support clinical decisions regarding the selection of patients for therapy.

Keywords Data mining · Decision tree · Alpha-fetoprotein · HCV · Peg-interferon

Introduction

The current standard therapy for genotype 1 chronic hepatitis C is 48 weeks of pegylated interferon (PEG-IFN) plus ribavirin (RBV) [1]. Sustained virological response (SVR), defined as undetectable HCVRNA post-treatment is regarded as a cure of chronic hepatitis C. However, the rate of SVR to this regimen is only 50% in patients with HCV genotype 1b and a high HCVRNA titer [2, 3]. Since PEG-IFN and RBV combination therapy is costly and accompanied by potential adverse effects, the ability to predict the possibility of SVR before therapy may significantly influence the selection of patients for therapy. A recent report revealed that single nucleotide polymorphisms located in the *IL28B* are strongly associated with a response to PEG-IFN plus RBV therapy [4–6]. Besides, the amino acid substitutions in the NS5A [7–9] or core region of HCV were also associated with response to therapy [10, 11]. Unfortunately, these host genetic and viral factors are not yet readily available for general application in actual clinical practice. Fibrosis of the liver is also an important predictor of response, but resources may be limited in some countries. Clinical and non-invasive parameters may be better suited for general practice, but there is no established means by which the likelihood of a response can be predicted prior to therapy.

Data mining is a method of predictive analysis that explores data, without setting the hypothesis, to discover hidden patterns and relationships in highly complex datasets and enables the development of predictive models. Decision tree analysis is a core component of data mining and predictive modeling [12], and it is utilized by decision makers in various fields of business. Recent publications on decision tree analysis indicate its usefulness for defining prognostic factors in various diseases such as prostate cancer [13], diabetes [14], melanoma [15, 16], colorectal carcinoma [17, 18], and liver failure [19]. The results of the analysis are presented as a tree structure, which is intuitive and facilitates the allocation of patients into subgroups by following the flow chart form [20]. We have recently reported the usefulness of decision tree analysis for the prediction of early virological response (undetectable HCVRNA within 12 weeks of therapy) to PEG-IFN and RBV combination therapy in chronic hepatitis C [21].

In the present study, we used decision tree analysis to explore baseline predictors of response to PEG-IFN/RBV therapy so that a pre-treatment algorithm could be created to discriminate chronic hepatitis C patients who are likely to respond to PEG-IFN/RBV therapy from those who are not. For the purpose of use in general practice, only clinical and non-invasive parameters were included in the analysis.

Materials and methods

Patients

This was a multicenter retrospective cohort study supported by the Japanese Ministry of Health, Labor and Welfare. Data were collected from a total of 800 chronic hepatitis C patients who received therapy for 48 weeks with PEG-IFN alpha-2b and RBV at Musashino Red Cross Hospital, Toranomon Hospital, Tokyo Medical and Dental University, Osaka University, Nagoya City University Graduate School of Medical Sciences, Yamanashi University, and their related hospitals. The inclusion criteria to be enrolled in this study were as follows (1) infection by genotype 1b, (2) HCVRNA higher than 100,000 IU/ml by quantitative PCR (Cobas Amplicor HCV Monitor v 2.0, Roche Diagnostic systems, CA), which is typically used for the definition of high viral load in Japan, (3) lack of co-infection with hepatitis B virus or human immunodeficiency virus, (4) lack of other causes of liver disease such as autoimmune hepatitis and primary biliary cirrhosis and (5) completion of at least 12 weeks of therapy. Patients received PEG-IFN alpha-2b (1.5 μg/kg) subcutaneously every week and were administered a weight-adjusted dose of RBV (600 mg for <60 kg, 800 mg for 60–80 kg, and 1,000 mg for >80 kg), which is the recommended dosage in Japan. Patients who were treated for more than 49 weeks were not included in the study. For the analysis, patients were randomly assigned to either the model building ($n = 506$) or the internal validation ($n = 295$) group. Consent was obtained from each patient. The study protocol conformed to the ethical guidelines of the Declaration of Helsinki and was approved by the institutional review committee. The baseline characteristics and representative laboratory test results are listed in Table 1. The overall rate of SVR was 47% in the model building set and 49% in the validation set. There were no significant differences in the clinical backgrounds between these 2 groups.

For external validation of the model, we collaborated with another study group supported by the Japanese Ministry of Health, Labor and Welfare. This multicenter study group consisted of 29 medical centers and hospitals

Table 1 Comparison of pre-treatment factors between model building and internal validation patients

	Model ($n = 506$)	Validation ($n = 295$)
Age (years)	56 (14–75)	55 (18–74)
Male gender[a]	261/506 (52%)	160/295 (54%)
Body mass index (kg/m^2)	22.9 (14.3–34.0)	23.2 (16.1–33.8)
Albumin (g/dl)	4 (2.7–5.0)	4 (2.8–4.9)
Creatinine (mg/dl)	0.7 (0.4–1.5)	0.7 (0.4–1.1)
AST (IU/l)	60 (11–370)	62 (11–240)
ALT (IU/l)	73 (11–413)	73 (14–390)
GGT (IU/l)	56 (10–328)	55 (7–409)
Total cholesterol (mg/dl)	173 (73–297)	171 (29–273)
Triglyceride (mg/dl)	105 (33–474)	109 (32–372)
White blood cell count (/μl)	4,745 (1,800–10,900)	4,823 (1,200–9,700)
Neutrophil count (/μl)	2,563 (667–7,870)	2,484 (508–7,579)
Red blood cell count (/μl)	448 (313–577)	451 (313–574)
Hemoglobin (g/dl)	14.1 (9.4–18.3)	14.1 (10.0–18.0)
Hematocrit (%)	41.7 (13.3–53.7)	41.9 (15.5–52.7)
Platelets (10^9/l)	164 (52–380)	158 (43–312)
AFP (ng/ml)	14.7 (0.9–680)	13 (0.8–323)
HCVRNA (10^3 IU/ml)	1,852 (100–5,100)	1,870 (100–5,100)
Fibrosis stage: F3–4	73/417 (18%)	48/247 (19%)

Data expressed as median (range) unless otherwise indicated

AST aspartate aminotransferase, *ALT* alanine aminotransferase, *GGT* gamma-glutamyltransferase, *AFP* alpha-fetoprotein

[a] Data expressed as number/available data (percentage)

belonging to the National Hospital Organization. A dataset collected from 524 patients who were treated with PEG-IFN alpha-2b/RBV was used as an external validation dataset, i.e., completely independent from the dataset that was used for model building.

Laboratory tests

Blood samples were obtained before therapy and at least once every month during therapy, and were used for hematologic tests, blood chemistry analysis and determination of HCV RNA. Pretreatment levels of HCV RNA were quantified by Cobas Amplicor (Roche Diagnostic Systems, Pleasanton, CA). SVR was defined as undetectable HCV RNA at week 24 after completion of therapy, as determined by qualitative PCR with a lower end detection limit of 50 IU/ml (Amplicor, Roche Diagnostic Systems). Liver biopsy was available in 664 patients. Fibrosis and activity were scored according to the METAVIR scoring system [22]. Fibrosis was staged on a scale of 0–4: F0 (no fibrosis), F1 (mild fibrosis: portal fibrosis without septa), F2 (moderate fibrosis: few septa), F3 (severe fibrosis: numerous septa without cirrhosis) and F4 (cirrhosis). Activity of necroinflammation was graded on a scale of 0–3: A0 (no activity), A1 (mild activity), A2 (moderate activity) and A3 (severe activity).

Statistical analysis

A database of pretreatment variables was created containing 6 variables from hematological tests (red blood cells, hemoglobin, hematocrit, white blood cells, neutrocytes and platelets), 8 variables from the blood chemistry test [creatinine, albumin, aspartate aminotransferase, alanine aminotransferase, gamma-glutamyltransferase (GGT), total cholesterol, triglyceride and alpha-fetoprotein (AFP)], serum level of HCV RNA and 3 variables for patient characteristics (age, gender and body mass index). Based on this database, the recursive partitioning analysis algorithm referred to as decision tree analysis was implemented to define meaningful subgroups of patients with respect to the possibility of achieving SVR.

Decision tree analysis is a family of nonparametric regression methods. Software is used to automatically explore the data to search for optimal split variables and to build a decision tree structure [23]. For the analysis, the entire study population was evaluated to determine which variables and cutoff points yielded the most significant division into 2 prognostic subgroups that were as homogeneous as possible for the probability of SVR. Thereafter, the same analytic process was applied to all newly defined subgroups. A restriction was imposed on the tree construction such that the procedure stopped when either no additional significant variable was detected or when the sample size was below 20. For this analysis, the data mining software IBM SPSS Modeler 13 (IBM SPSS Inc., Chicago, IL) was utilized. SPSS software v.15.0 (SPSS Inc., Chicago, IL) was used for multivariate logistic regression analysis.

Results

Decision tree analysis

Decision tree analysis was carried out on the model building dataset from 506 patients using 18 variables. Figure 1 shows the results. The analysis automatically selected 5 predictive variables to produce a total of 7 subgroups of patients. Age was selected as the variable of initial split with an optimal cutoff of 50 years. The possibility of achieving SVR was 41% for patients older than 50 compared to 70% for patients

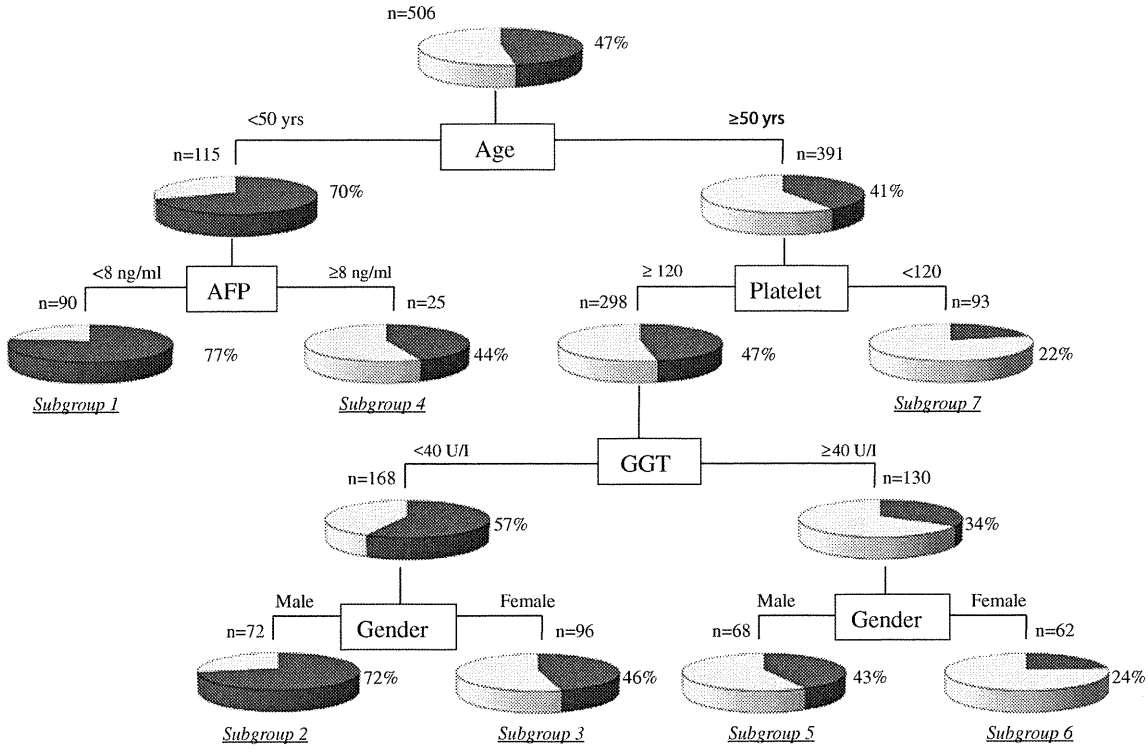

Fig. 1 Decision tree analysis. *Boxes* indicate the factors for splitting and the cutoff value for the split. *Pie charts* indicate the rate of SVR for each group. Terminal subgroups of patients discriminated by the analysis are numbered from 1 to 7. *AFP* alpha-fetoprotein, *GGT* gamma-glutamyltransferase

younger than 50. Among patients younger than 50, the level of serum AFP, with an optimal cutoff of 8 ng/ml, was selected as the variable of second split. Patients with lower AFP levels had a higher probability of SVR (77 vs. 44%). Among older patients, platelet count was selected as the second variable of split, with an optimal cutoff of 120×10^9/l. Patients with higher platelet counts had a higher probability of SVR (47 vs. 22%). Among patients with platelet counts higher than 120×10^9/l, GGT was selected as the third variable of split with an optimal cutoff of 40 IU/l. Patients with a lower GGT level had a higher probability of SVR (57 vs. 34%). Gender was selected as the fourth variable of split, with male gender being a predictor of a higher SVR probability (72 vs. 46% in patients with GGT levels <40 IU/l and 43 vs. 24% in those with GGT ≥40 IU/l). HCVRNA load was included in the analysis but was not selected as a significant variable.

The probabilities of SVR for the 7 subgroups derived by this process were highly variable. The subgroup of young patients (<50 years) with low serum AFP (<8 ng/ml) (subgroup 1) or the subgroup of older (≥50 years) male patients with high platelet counts ($\geq 120 \times 10^9$/l) and low serum GGT (<40 IU/l) (subgroup 2) showed the highest probability of SVR (72 and 77%), while the subgroup of older (≥50 years) patients with low platelet counts ($<120 \times 10^9$/l) (subgroup 7) and older (≥50 years) female patients with high serum GGT (subgroup 6) showed the lowest probability of SVR (22 and 24%).

Validation of the decision tree

The results of the decision tree analysis were validated with an internal validation dataset of 295 cases, which was independent of the model building dataset. Each patient in the validation set was allocated to subgroups 1–7 using the flow-chart form of the decision tree. The rates of SVR were 77% for subgroup 1, 71% for subgroup 2, 55% for subgroup 3, 44% for subgroup 4, 41% for subgroup 5, 17% for subgroup 6, and 30% for subgroup 7. The rates of SVR for each subgroup of patients were closely correlated between the model building dataset and the internal validation dataset ($r^2 = 0.925$) (Fig. 2a).

To further confirm the universality of the results, data collected from 524 patients by a collaborating study group were used for external validation. Thus, the dataset used for external validation was completely independent of the

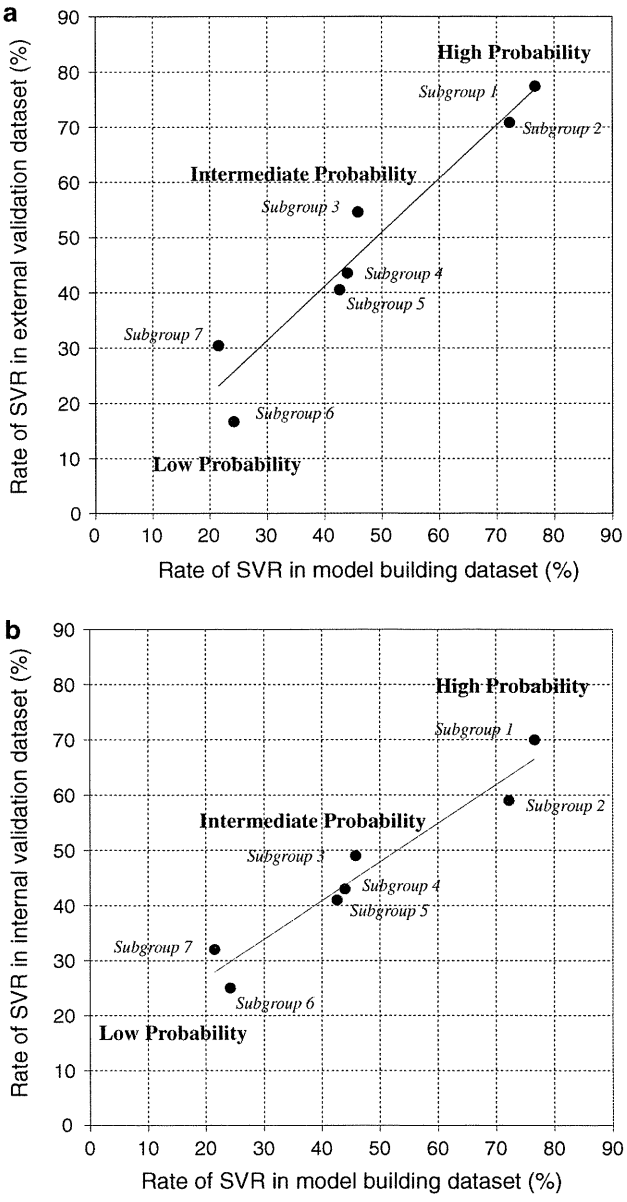

Fig. 2 Validation of the decision tree analysis by an internal and external validation dataset: subgroup-stratified comparison of the SVR rate. The rate of SVR in each subgroup was plotted. The *X* axis represents the model building, and the *Y* axis represents the validation datasets. **a** Internal validation and **b** external validation. There was a close correlation between the model building and the internal validation dataset (correlation coefficient $r^2 = 0.925$) and between the model building and the external validation dataset (correlation coefficient $r^2 = 0.936$)

original dataset used for model building. Each patient in the external validation set was allocated to subgroups 1–7 using the flow-chart form of the tree. The rates of SVR were 70% for subgroup 1, 59% for subgroup 2, 49% for subgroup 3, 43% for subgroup 4, 41% for subgroup 5, 25% for subgroup 6, and 32% for subgroup 7. The rates of SVR for each subgroup of patients were closely correlated

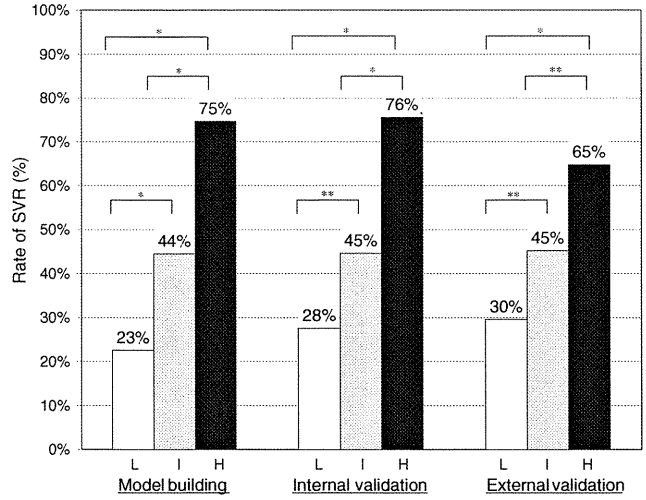

Fig. 3 Comparison of SVR rates between groups divided by the decision tree. The rate of SVR was compared among the 3 groups of patients divided by the decision tree analysis (*white*, *gray* and *black boxes*, indicating a low (*L*), intermediate (*I*) and high (*H*) probability group, respectively). The rate of SVR was significantly different among the 3 groups. $*p < 0.0001$, $**p < 0.001$

between the model-building dataset and the validation dataset ($r^2 = 0.936$) (Fig. 2b).

Construction of 3 groups according to the probability of SVR

Seven subgroups were reconstructed into 3 groups according to their predicted rates of SVR: the high probability group consisted of subgroups 1 and 2, the intermediate probability group consisted of subgroups 3, 4 and 5, and the low probability group consisted of subgroups 6 and 7. The rate of SVR was significantly different among the 3 groups (Fig. 3). The rate of SVR in the high probability group was consistently high: 75% for model building patients, 76% for internal validation patients and 65% for external validation patients. Conversely, the rate of SVR in the low probability group was consistently low: 23% for model building patients, 28% for internal validation patients and 30% for external validation patients. The rate of SVR in the intermediate probability group was 44% for model building patients, 45% for internal validation patients and 45% for external validation patients. Since 28–32% of patients were classified as high probability and 30–32% were classified as low probability, roughly 60% of patients were classified as having either a high or low probability of achieving SVR.

Effect of dose reductions of PEG-IFN and RBV on SVR

The cumulative dose of PEG-IFN and RBV was not included as a variable of analysis since the present study