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EDITORIAL

What is the benefit of computer-assisted image analysis of liver fibrosis area?

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Liver fibrosis is usually semiquantitatively assessed in liver biopsy specimens by the numerical system of Scheuer [1], the Metavir group [2], or Ishak [3]. Fibrosis is staged as F0, no fibrosis; F1, portal fibrosis without septa; F2, portal fibrosis and few septa; F3, numerous septa without cirrhosis; and F4, cirrhosis. Staging mainly depends on the degree of the architectural changes of liver structure.

Computer-assisted image analysis of the stained fibrosis area in liver biopsy specimens is a method for quantitatively measuring the amount of liver fibrosis [4]. It is not used for the clinical assessment of liver fibrosis in general, but is often used in the assessment of fibrosis in animal models. Its low popularity in clinical practice may be attributed to the complexity of the method.

The fibrosis stage as determined by the numerical systems and the relative area of fibrosis measured by computer-assisted image analysis usually correlate well to each other. However, discrepancy between the two sometimes occurs. Which of the two is more useful in clinical practice may depend on the objectives of assessing liver fibrosis.

The current study by Isgro et al. showed that collagen proportionate area (CPA) has a better relationship with liver stiffness measurement (LSM) and with hepatic venous pressure gradient (HVPG) compared with the Ishak stage. They also reported that CPA at 1-year post-transplantation in hepatitis C virus-infected patients predicts subsequent clinical decompensation more accurately than Ishak stage or HVPG [5]. They conclude that CPA should be the histological parameter with which to compare LSM and other non-invasive fibrosis markers and also be used to subclassify cirrhosis.

Nitta et al. [6] also reported the good correlation between LSM and fibrosis area measured by image analysis in the patients with chronic hepatitis C, while LSM and Metavir score yielded better correlation. Xie et al. [7] reported that fibrosis area measured by image analysis significantly correlated with model for end-stage liver disease score, serum bilirubin levels and prothrombin time in the patients with hepatitis B virus-related decompensated cirrhosis.

Arima et al. [8] reported that 42 % of chronic hepatitis C patients with pretreatment F3-4 who obtained sustained virological response by interferon (IFN) therapy had decreased fibrosis assessed by the numerical staging system, while the fibrosis area measured by image analysis decreased in 92 %. Thus the computer-assisted image analysis of liver fibrosis is more sensitive to measure the reduction of liver fibrosis after IFN treatment than the numerical system.

In conclusion, the relative fibrosis area measured by computer-assisted image analysis is suitable for the comparison with newly developing non-invasive methods for fibrosis assessment, such as LSM. It is also useful to assess the degree of severe fibrosis in cirrhosis for predicting prognosis and to assess the change of fibrosis after antiviral treatment or in natural courses. It is better to add computer-assisted image analysis to the interpretation of liver biopsy in order to obtain valuable quantitative information in the specimens. The standardization and simplification of the method is needed in order that computer-assisted image analysis of fibrosis area will be widely used.

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Comparison of the Efficacy of Ribavirin Plus Peginterferon Alfa-2b for Chronic Hepatitis C Infection in Patients With and Without Coagulation Disorders

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Many patients with coagulation disorders are infected with hepatitis C virus (HCV) that advances to end stage liver disease, resulting in an increased number of deaths. The efficacy of ribavirin and peginterferon combination therapy for chronic HCV infection in patients with coagulation disorders has not been clarified fully. The aim of this study was to evaluate the efficacy and tolerability of combination therapy in this patient population compared with patients who are infected with HCV and do not have coagulation disorders. A total of 226 consecutive chronic hepatitis C patients were treated with combination therapy and divided into two groups: patients with (n = 23) and without coagulation disorders (n = 203). Clinical characteristics, sustained virological response rates obtained by an intention-to-treat analysis, and combination therapy discontinuation rates were compared between the two groups. The sustained virological response rates did not differ significantly between patients with and without coagulation disorders (65.2% vs. 47.8% by intention-to-treat analysis). According to a multivariate analysis, age, alanine aminotransferase, gamma-glutamyltransferase, and HCV genotype were associated significantly with a sustained virological response, whereas whether a patient had a coagulation disorder did not affect the sustained virological response. In conclusion, combination therapy for chronic hepatitis C was comparably effective between patients with and without coagulation disorders and did not result in adverse bleeding. ***J. Med. Virol. 85:228–234, 2013.*** © 2012 Wiley Periodicals, Inc.

KEY WORDS: chronic hepatitis C; interferon; ribavirin; coagulation disorders; hemophilia

INTRODUCTION

Hepatitis C virus (HCV) infection is a widespread viral infection that often leads to chronic hepatitis, cirrhosis, and hepatocellular carcinoma. Until the 1980s, most patients with coagulation disorders became infected with HCV because of the extensive use of untreated factor concentrate. Some of these patients were infected with both hepatitis C and human immunodeficiency virus (HIV) [Brettler et al., 1990; Troisi et al., 1993; Yee et al., 2000; Franchini et al., 2001]. These patients with liver diseases and persistent abnormal transaminase progress to end stage liver disease, resulting in an increased number of liver disease-related deaths. In cases of co-infection with the HIV, the progression of liver disease is more rapid [Sanchez-Quijano et al., 1995; Soto et al., 1997; Benhamou et al., 1999; Ragni and Belle, 2001; De Luca et al., 2002] with a higher mortality rate than

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during HCV monoinfection [Darby et al., 1997; Yee et al., 2000]. The need for treating infection with HCV in patients with coagulation disorders is increasing worldwide.

Sustained virological responders who are negative for serum HCV RNA 6 months after the end of treatment with interferon (IFN) are likely to remain in virological and biochemical remission with histologic improvement [Marcellin et al., 1997; Shiratori et al., 2000]. In addition, IFN therapy reduces the risk of hepatocellular carcinoma among virological or biochemical responders [Imai et al., 1998; Ikeda et al., 1999; Yoshida et al., 1999]. Ribavirin is now used generally in combination with IFN or pegIFN to treat chronic hepatitis C and combination therapy is more effective than IFN monotherapy [Lai et al., 1996; McHutchison et al., 1998; Poynard et al., 1998; Manns et al., 2001].

Previous studies have investigated the efficacy of IFN monotherapy in patients with coagulation disorders and chronic hepatitis C [Makris et al., 1991], and the efficacy of combination therapy with ribavirin and PegIFN in patients with coagulation disorders [Fried et al., 2002a; Mancuso et al., 2006; Posthouwer et al., 2007]. However, there are no reported comparisons of this combination therapy between patients infected with HCV with and without coagulation disorders. In this study, the efficacy and tolerability of ribavirin plus pegIFN were evaluated retrospectively in patients with coagulation disorders and chronic hepatitis C and the results were compared with the responses of patients infected with HCV but without coagulation disorders.

MATERIALS AND METHODS

Patients and Methods

A total of 226 consecutive patients with chronic hepatitis C and a high viral load (serum HCV RNA levels greater than 100 kilo-international units [KIU]) were treated with a combination of pegIFN and ribavirin between December 2004 and March 2007 at Nagoya University Hospital and Ogaki Municipal Hospital. These patients included 23 patients with coagulation disorders (17 with hemophilia A, 4 with hemophilia B, and 2 with von Willebrand disease). All patients were under 75 years old, were anti-HCV antibody-positive, and had serum HCV RNA levels greater than 100 KIU/ml by quantitative PCR assay (Amplicor GT-HCV Monitor Version 2.0; Roche Molecular Systems, Pleasanton, CA) within 12 weeks preceding the therapeutic period. Patients were excluded if they had pretreatment hemoglobin (Hb) levels <10 g/dl, tested positive for serum hepatitis B surface antigen, a history of drug addiction, alcohol abuse, autoimmune hepatitis, primary biliary cirrhosis, a serious psychiatric or medical illness, or were pregnant. To exclude patient bias, only complete cohorts from each hospital were enrolled. HCV genotypes were determined by PCR using genotype-specific primers [Okamoto et al., 1994; Simmonds et al., 1994].

All patients were treated with 1.5 μg/kg of pegIFN α-2b (Peg-Intron®, MSD, Tokyo, Japan) once weekly for 24 weeks in patients infected with HCV genotype 2 or 3 and for 48 weeks in patients infected with HCV genotype 1 or 4. For the 17 patients infected with HCV genotype 1, the treatment duration was extended to 72 weeks because of higher efficacy compared to that obtained after 48 weeks of treatment, but only in cases in which HCV RNA was positive at 12 weeks and negative at 24 weeks from the start of therapy. Treatment was discontinued when a patient's Hb concentration fell below 8.5 g/dl because of drug-induced hemolytic anemia or when a patient's white blood cell count fell below 1,000/mm^3, neutrophil count fell below 500/mm^3, or platelet count fell below 50,000/mm^3. Some patients discontinued treatment because the virus could not be eradicated after 24 weeks, as determined by the physician. The pegIFN alfa-2b dose was reduced to 50% of the assigned dose when the white blood cell count was below 1,500/mm^3, the neutrophil count below 750/mm^3 or the platelet count below 8,000/mm^3. Oral ribavirin (Rebetol®, MSD, Tokyo, Japan) was administered for the same duration as pegIFN at 600 mg/day for patients who weighed 60 kg or less, 800 mg/day for those who weighed more than 60 kg but less than 80 kg, and 1,000 mg/day for those who weighed more than 80 kg during the treatment period. The ribavirin dose was reduced by 200 mg/day when the patient's Hb concentration fell below 10 g/dl because of drug-associated hemolytic anemia. Ribavirin was discontinued when pegIFN therapy was discontinued. Informed consent was obtained from each patient and the study was performed in accordance with the 1975 Declaration of Helsinki.

Liver Histology

Pretreatment liver biopsy specimens were classified based on a fibrosis scale of F0 to F4 (F0, no fibrosis; F1, portal fibrosis without septa; F2, few septa; F3, numerous septa without cirrhosis; and F4, cirrhosis) and in terms of necroinflammatory activity on a scale of A0 to A3 (A0, no histological activity; A1, mild activity; A2, moderate activity; and A3, severe activity) [Bedossa and Poynard, 1996; Fried et al., 2002b]. In patients with coagulation disorders, a liver biopsy was performed using factor concentrate, provided the patients gave informed consent.

Assessment of Efficacy

The virological response was assessed by a qualitative HCV RNA assay with a lower sensitivity limit of 100 copies/ml (Amplicor HCV version 2.0; Roche Molecular Systems). According to the qualitative HCV RNA results, responses were defined as a sustained virological response if no HCV RNA was detected at the end of the 24-week follow-up period after the treatment was completed. A patient was considered to have an end of treatment virological response if no HCV RNA was detected at the end of treatment.

Comparison of Characteristics and Treatment Efficacy Between Patients With and Without Coagulation Disorders

Sex ratio, age, body weight, body mass index (BMI), baseline serum alanine aminotransferase (ALT) levels, gamma-glutamyltransferase (GGT), pretreatment Hb level, platelet counts, HCV genotype and viral load, histologic activity, and fibrosis were compared between patients with and without coagulation disorders. The sustained virological response rates obtained by an intention-to-treat analysis and per-protocol analysis, ribavirin and pegIFN dose reduction rates, and combination therapy discontinuation rates were compared between the two groups. The end of treatment virological response rate was obtained by intention-to-treat and per-protocol analyses and then compared between the two groups. Next, the variable accession method in a multivariate analysis was used to examine factors associated with a sustained virological response after combination therapy, including the following factors: sex, age, BMI, baseline serum ALT, GGT, platelet counts, genotype, HCV RNA concentration, and presence of a coagulation disorder.

Because efficacy differed by the HCV genotype and the patient age, and since all coagulation disorder patients were male, the analysis focused on male, age-matched patients infected with HCV genotype 1. The characteristics and efficacy of treatment were compared in males, and age-matched patients with and without coagulation disorders who were infected with HCV-genotype 1.

Statistical Analysis

Values are expressed as the means ± SDs. Between-group differences in mean quantitative values were analyzed by Student's *t*-test, and differences in nonparametric data were analyzed by the Mann–Whitney *U*-test. Differences in proportions were examined by the Chi-squared test. Multiple logistic regression analysis was used to identify factors related to a sustained virological response. All statistical analyses were performed using SAS software (SAS Institute, Cary, NC). All P values were two-tailed, and $P < 0.05$ was considered statistically significant.

RESULTS

Patient Characteristics

The patients included 127 men and 99 women aged 22–74 years (mean ± SD, 54.7 ± 11.6). The mean age of patients without coagulation disorders was 56.3 ± 10.9 years and most patients were in their 50s and 60s. In contrast, the mean age of patients with coagulation disorders was 41.5 ± 9.8 years with an age distribution ranging from 20 to 50 years. The clinical characteristics of the two study groups are shown in Table I. All patients with coagulation disorders in this study were male because of inherited, sex-linked hemophilia, and two patients in this study had male von Willebrand disease. Patients with coagulation disorders were significantly younger than patients without coagulation disorders ($P < 0.0001$). Although body weight was not different between the two groups, patients with coagulation disorders had a significantly lower BMI than patients without coagulation disorders. Patients without coagulation disorders were infected with HCV genotypes that are not unique to Japan, such as genotypes 1a, 3a, and 4a. Four patients with coagulation disorders were infected with human immunodeficiency virus and one of these patients had achieved a sustained virological response.

Response to Therapy

The ribavirin dose reduction rate tended to be higher in patients without coagulation disorders than in patients with coagulation disorders ($P = 0.0643$). The treatment discontinuation rate did not differ significantly between the two groups. As a result, the sustained virological response rate by an intention-to-treat analysis did not differ significantly between the

TABLE I. Clinical Characteristics of Patients Treated With Combination Therapy

	Total patients (n = 226)	Patients without coagulation disorders (n = 203)	Patients with coagulation disorders (n = 23)	*P* value
Sex ratio (male/female)	127/99	104/99	23/0	<0.0001
Age (years)	54.7 ± 11.6	56.3 ± 10.9	41.5 ± 9.8	<0.0001
Body weight (kg)	60.2 ± 11.1	60.5 ± 11.5	60.5 ± 8.1	0.9972
Body mass index	22.9 ± 3.1	23.1 ± 3.1	21.5 ± 2.5	0.0226
Baseline serum ALT (IU/L)	63.3 ± 56.8	60.9 ± 54.9	84.4 ± 69.1	0.0598
GGT (IU/L)	54.2 ± 63.9	51.4 ± 62.2	78.6 ± 74.4	0.0526
Hemoglobin (g/dl)	14.1 ± 1.3	14.1 ± 1.3	14.4 ± 1.3	0.2714
Platelets ($\times 10^4/\mu l$)	17.8 ± 5.2	17.7 ± 5.2	19.0 ± 5.6	0.2597
Genotype (1a/1b/2a/2b/3a/4a)	7/160/40/15/3/1	0/150/39/14/0/0	7/10/1/1/3/1	<0.0001
HCV RNA (KIU/ml)	1,898.0 ± 1,448.3	1,923.1 ± 1,464.5	1,676.6 ± 1,305.1	0.4404
Activity (A0/A1/A2/A3)	2/108/71/11	2/101/64/11	0/7/7/0	0.3442
Fibrosis (F0/F1/F2/F3)	17/104/49/22	16/97/45/20	1/7/4/2	0.5351

ALT, alanine aminotransferase; GGT, gamma-glutamyltransferase; HCV RNA, hepatitis C virus RNA; KIU, kilo-international units.

TABLE II. Efficacy of Combination Therapy

	Total patients (n = 226)	Patients without coagulation disorders (n = 203)	Patients with coagulation disorders (n = 23)	*P* value
SVR rate (intention-to-treat)	49.6 (112/226)	47.8 (97/203)	65.2 (15/23)	0.1130
SVR rate (per-protocol)	54.4 (111/204)	52.7 (97/184)	70.0 (14/20)	0.1405
ETR rate (intention-to-treat)	84.1 (190/226)	84.7 (172/203)	78.3(18/23)	0.4218
ETR rate (per-protocol)	89.1 (179/201)	89.6 (163/182)	84.2 (16/19)	0.4772
Ribavirin dose reduction rate	44.2 (100/226)	46.3 (94/203)	26.1 (6/23)	0.0643
PegIFN dose reduction rate	34.1 (77/226)	33.5 (68/203)	39.1 (9/23)	0.5891
Combination therapy discontinuation rate	9.8 (22/226)	9.4 (19/203)	13.0 (3/23)	0.5722

SVR, sustained virological response; ETR, end of treatment virological response; PegIFN, peginterferon.

two groups. The sustained virological response rate of patients with coagulation disorders by a per-protocol analysis was higher than that of patients without coagulation disorders, but there was no significant difference. In addition, based on both intention-to-treat and per-protocol analyses, the end of treatment virological response rate did not differ significantly between the two groups (Table II).

Factors associated with a sustained virological response in combination therapy were determined by a multivariate analysis. HCV genotype 1 and 4 versus 2 and 3 ($P = 0.001$, odds ratio 4.353 [95% CI, 1.810–10.469]), baseline serum GGT ($P = 0.003$, odds ratio 1.018 [1.006–1.030]), age ($P = 0.006$, odds ratio 1.053 [1.015–1.093]), and baseline serum ALT ($P = 0.014$, odds ratio 0.991 [0.983–0.998]) were associated significantly with a sustained virological response, but whether or not a patient had a coagulation disorder was not associated significantly with a sustained virological response.

Characteristics and Response of Male, Age-Matched Patients Infected With HCV Genotype 1

The clinical characteristics of the two study groups in the male, age-matched patients infected with HCV genotype 1 are shown in Table III. Body weight, BMI, and Hb levels were significantly lower in patients with coagulation disorders than patients without coagulation disorders ($P = 0.0003$, 0.0027, and 0.0103, respectively).

The treatment discontinuation rate of patients with coagulation disorders did not differ between the two groups. The sustained virological response rate by intention-to-treat and per-protocol analyses did not differ significantly between the two groups (Table IV). Factors associated with a sustained virological response in the male, age-matched, genotype 1 patients treated with combination therapy were determined by a multivariate analysis. BMI ($P = 0.036$, odds ratio 1.810 [1.041–3.145]) and baseline serum GGT ($P = 0.037$, odds ratio 0.981 [0.963–0.999]) were associated significantly with a sustained virological response, but whether or not a patient had a coagulation disorder was not associated significantly with a sustained virological response.

Adverse Events

The reasons for discontinuing combination therapy and the times at which the therapy was discontinued are shown in Table V. Once treatment was discontinued, therapy was not restarted even after the initial symptoms or illness disappeared. There were no bleeding episodes in the patients with coagulation disorders, including patients who received a liver biopsy.

TABLE III. Clinical Characteristics of Male, Age-Matched Patients With Genotype 1 Treated With Combination Therapy

	Total patients (n = 36)	Patients without coagulation disorders (n = 18)	Patients with coagulation disorders (n = 18)	*P* value
Age (years)	42.8 ± 8.0	44.9 ± 5.9	40.7 ± 9.3	0.1136
Body weight (kg)	66.1 ± 11.0	73.4 ± 9.3	60.4 ± 8.7	0.0003
Body mass index	22.7 ± 2.8	24.3 ± 2.3	21.4 ± 2.5	0.0027
Baseline serum ALT (IU/L)	69.8 ± 54.3	63.5 ± 31.7	76.2 ± 70.5	0.4919
GGT (IU/L)	72.7 ± 64.2	74.3 ± 71.1	71.2 ± 58.5	0.8869
Hemoglobin (g/dl)	14.9 ± 1.2	15.4 ± 1.0	14.4 ± 1.2	0.0103
Platelets ($\times 10^4/\mu l$)	19.3 ± 5.4	18.8 ± 4.5	19.8 ± 5.6	0.5773
HCV RNA (KIU/ml)	2,050.8 ± 1,273.4	2,322.8 ± 1,249.1	1,778.8 ± 1,273.5	0.2044
Activity (A0/A1/A2/A3)	0/12/11/0	0/6/5/0	0/6/6/0	0.6723
Fibrosis (F0/F1/F2/F3)	2/11/8/2	1/5/4/1	1/6/4/1	0.9392

ALT, alanine aminotransferase; GGT, gamma-glutamyltransferase; HCV RNA, hepatitis C virus RNA; KIU, kilo-international unit.

TABLE IV. Efficacy of Combination Therapy in Male, Age-Matched Patients With Genotype 1

	Total patients (n = 36)	Patients without coagulation disorders (n = 18)	Patients with coagulation disorders (n = 18)	*P* value
SVR rate (intention-to-treat)	58.3 (21/36)	61.1 (11/18)	55.6 (10/18)	0.7353
SVR rate (per-protocol)	69.0 (20/29)	64.7 (11/17)	75.0 (9/12)	0.5551
ETR rate (intention-to-treat)	77.8 (28/36)	83.3 (15/18)	72.2 (13/18)	0.4227
ETR rate (per-protocol)	93.1 (27/29)	88.2 (15/17)	100.0 (12/12)	0.2182
Ribavirin dose reduction rate	22.2 (28/36)	16.7 (3/18)	27.8 (5/18)	0.7175
PegIFN dose reduction rate	36.1 (13/36)	27.8 (5/18)	44.4 (8/18)	0.2979
Combination therapy discontinuation rate	5.6 (2/36)	0 (0/18)	16.7 (3/18)	0.0704

SVR, sustained virological response; ETR, end of treatment virological response; PegIFN, peginterferon.

DISCUSSION

A previous randomized trial in patients infected with HCV with inherited bleeding disorders showed that the sustained virological response rate improved significantly for patients who were treated with IFN and ribavirin compared to those treated with IFN alone [Fried et al., 2002a]. In addition, both chronic hepatitis C patients with and without coagulation disorders responded similarly to pegIFN and ribavirin combination therapy [Franchini et al., 2006; Posthouwer et al., 2006]. However, the efficacy and tolerability of this combination therapy differed based on the HCV genotype as well as the age, gender, and race of the patients; therefore it is difficult to compare patients with and without coagulation disorders under the same conditions. No report has examined that patients infected chronic hepatitis C with and without coagulation disorders at the same institution and during the same observation period. In addition, there are no reports on the efficacy of combination therapy in patients with chronic hepatitis C with and without coagulation disorders in age-matched patients infected with HCV genotype 1. Therefore, a retrospective study was conducted to evaluate the efficacy and tolerability of ribavirin plus pegIFN in chronic hepatitis C patients with and without coagulation disorders. In the per-protocol analysis, there were no significant differences, but the sustained virological response rate was higher in patients with coagulation disorders than in patients without coagulation disorders. Mancuso et al. [2006] reported that combination therapy with pegIFN alfa-2b plus ribavirin is highly efficacious in hemophiliacs with chronic hepatitis C. In an overall analysis, patients with coagulation disorders had a lower mean age than patients without coagulation disorders. In addition, the BMI of the patients with coagulation disorders was lower than that of patients without coagulation disorders. A multivariate analysis showed that the HCV genotype, baseline serum GGT, age, and baseline ALT were factors associated significantly with a sustained virological response and whether patients had coagulation disorders was not associated with a sustained virological response. Age, especially younger than 40 years old, was a good predictive factor for a sustained virological response, as was reported previously [Poynard et al., 2000; Fried et al., 2002b].

TABLE V. Reasons for Discontinuing Combination Therapy

Reason	Number	Weeks after starting treatment
Patients with coagulation disorders		
Peritonitis due to appendicitis	1	16
Pneumoniae	1	18
No HCV eradication	3	24, 28, 29
IDDM	1	44
Patients without coagulation disorders		
Fatigue	5	1, 2, 4.9, 19
Bleeding from duodenal varies	1	8
Dizziness	1	12
Palpitation	1	13
Cholecystitis	1	16
Symptom of Parkinson's disease	1	16
Fundal hemorrhage	1	17
Hepatocellular carcinoma	2	19, 21
Suspicion of Interstitial pneumonia	1	20
Gastric cancer	2	21, 36
Self-discontinuation	1	24
Neutropenia	1	25
Eruption	1	25
No HCV eradication	7	24, 25, 25, 27, 28, 29, 29

These results suggest that male patients who are infected with HCV genotype 1 and have coagulation disorders will have a higher sustained virological response than patients without coagulation disorders, if the coagulation disorder patients do not discontinue treatment. However, these results do not account for the differences in age. Therefore, male, age-matched patients infected with HCV genotype 1 were evaluated. The characteristics that differed between patients with and without coagulation disorders were body weight, BMI and baseline Hb levels.

In male, age-matched patients infected with HCV genotype 1, the sustained virological response rate based on both intention-to-treat and per-protocol analyses was not different between patients with and without coagulation disorders.

Using a multivariate analysis, whether patients had coagulation disorders was not associated significantly with a sustained virological response. Only BMI and GGT were identified as factors associated with a sustained virological response to combination therapy in male, age-matched patients infected with HCV genotype 1. A previous report showed that GGT levels may represent a surrogate marker of tumor necrosis factor-alpha expression in the liver and explain the importance of serum analyses to in predict the treatment outcome [Taliani et al., 2002]. Several studies revealed that GGT is one predictor of a sustained virological response [Taliani et al., 2002, 2006; Villela-Nogueira et al., 2005]. In western countries, obesity and a high BMI are associated with the absence of a sustained virological response to combination therapy of pegIFN or IFN with ribavirin [Bressler et al., 2003; Camma et al., 2004]. However, in Japan, most of the patients who are treated with combination therapy are not obese and have lower BMIs than patients in western countries. In this population, the mean BMI was 22.7 $\pm$ 2.8. In this low BMI population, a higher BMI would be associated with a sustained virological response. However, the reason why a low BMI is associated with the absence of a sustained virological response has not elucidated.

Adverse effects are thought to increase in patients with coagulation disorders; however, there was not a significant difference in adverse effects necessitating discontinuation of pegIFN and ribavirin between patients with and without coagulation disorders (13.0% vs. 9.4%). In addition, severe adverse effects and bleeding adverse effects were not associated with coagulation disorders. A previous report showed that IFN and ribavirin combination therapy may reduce the use of clotting factors in hemophilia patients with chronic hepatitis C [Honda et al., 2005; Yamamoto et al., 2006]. Ribavirin may reduce the side effect of bleeding during combination therapy. In this study, patients with coagulation disorders did not experience an adverse effect of bleeding.

In conclusion, treatment of chronic hepatitis C with combination therapy was effective comparably between patients with and without coagulation disorders and there were no adverse effects of bleeding.

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Prevalence of Hepatitis C Virus Genotype 1a in Japan and Correlation of Mutations in the NS5A Region and Single-Nucleotide Polymorphism of Interleukin-28B With the Response to Combination Therapy With Pegylated-Interferon-Alpha 2b and Ribavirin

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Hepatitis C virus (HCV) genotype 1a is rare in Japanese patients and the clinical characteristics of this genotype remain unclear. The interferon (IFN) sensitivity-determining region (ISDR) and single-nucleotide polymorphisms (SNPs) of interleukin-28B (IL28B) among patients with HCV genotype 1b are associated with IFN response, but associations among patients with genotype 1a are largely unknown. This study investigated the clinical characteristics of genotype 1a and examined whether genomic heterogeneity of the ISDR and SNPs of IL28B among patients with HCV genotype 1a affects response to combination therapy with pegylated-IFN-α2b and ribavirin. Subjects comprised 977 patients infected with HCV genotype 1, including 574 men and 412 women (mean age, 55.2 ± 10.6 years). HCV was genotyped by direct sequencing of the 5′-untranslated region and/or core regions and confirmed by direct sequencing of the NS5A region. HCV genotypes 1a (n = 32) and 1b (n = 945) were detected. Twenty-three (71.9%) of the 32 patients with genotype 1a were patients with hemophilia who had received imported clotting factors. Prevalence of genotype 1a after excluding patients with hemophilia was thus 0.9%. Of the 23 patients with genotype 1a who completed IFN therapy, 11 (47.8%) were defined as achieving sustained virological response. Factors related to sustained virological response by univariate analysis were IL28B and ISDR. In conclusion, HCV genotype 1a is rare in Japan. The presence of IL28B genotype TT, and more than two mutations, in the ISDR are associated with a good response to IFN therapy in patients with HCV genotype 1a. ***J. Med. Virol. 84:438–444, 2012.*** © 2012 Wiley Periodicals, Inc.

KEY WORDS: hepatitis C virus; genotype 1a; NS5A; IL 28B; interferon

INTRODUCTION

Hepatitis C virus (HCV) is a member of the Flaviviridae family and causes chronic hepatitis that can develop into cirrhosis and hepatocellular carcinoma [Seeff, 2002]. HCV infection is a significant global health problem, affecting 170 million individuals worldwide. HCV can be divided into six genotypes and several subtypes according to genomic heterogeneity [Simmonds et al., 2005]. Each genotype shows a unique distribution and clinical characteristics such

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as interferon (IFN) responsiveness [Ghany et al., 2009]. HCV genotypes 1b, 2a, and 2b are the major types encountered in Japan [Enomoto et al., 1990; Hayashi et al., 2003]. Genotype 1a is common worldwide, but is rare in Japan except among individuals with hemophilia who have received imported clotting factors [Fujimura et al., 1996; Otagiri et al., 2002; Hayashi et al., 2003]. The prevalence and clinical characteristics, including IFN responsiveness, of Japanese patients with HCV genotype 1a are unclear. HCV NS5A protein reportedly includes a domain associated with IFN response. This domain, located in the NS5A region of HCV genotype 1b, is closely associated with response to IFN therapy and is known as the IFN sensitivity-determining region (ISDR) [Enomoto et al., 1996]. IFN acts to inhibit viral replication by inducing double-stranded RNA-dependent protein kinase (PKR). The ISDR is located at the 5′ end of the PKR-binding domain and is inhibited by PKR in vitro [Gale et al., 1998]. ISDR heterogeneity of genotype 1b is thus an important factor that may affect response to IFN [Enomoto et al., 1996; Nakano et al., 1999; Pascu et al., 2004; Hayashi et al., 2011a]. Several studies have reported a relationship between ISDR and IFN responsiveness among patients with HCV genotype 1a [Hofgärtner et al., 1997; Zeuzem et al., 1997; Kumthip et al., 2011; Yahoo et al., 2011]. However, this remains controversial for genotype 1a, and the utility of ISDR sequences for predicting IFN responsiveness has not been investigated for HCV genotype 1a in Japan due to the rarity of this genotype. Both genetic heterogeneity of the HCV genome and host genetics contribute to IFN responsiveness. Several genome-wide association studies have thus been performed to clarify host factors associated with IFN responsiveness, revealing that interleukin-28B (IL28B) polymorphisms are strongly associated with response to IFN therapy [Ge et al., 2009; Suppiah et al., 2009; Tanaka et al., 2009; Thomas et al., 2009]. Combined use of the single-nucleotide polymorphisms (SNPs) of IL28B and amino acid substitutions in the core region and ISDR could thus improve the prediction of response to IFN in patients with HCV genotype 1b [Akuta et al., 2011; Hayashi et al., 2011b; Kurosaki et al., 2011]. However, the effects of a combined evaluation of the SNPs of IL28B and amino acid substitutions in the ISDR in patients with HCV genotype 1a on IFN response are unclear. The aim of the present study was to determine whether genomic heterogeneity of the ISDR and SNPs of IL28B among patients with HCV genotype 1a affect response to combination therapy with pegylated-IFN-α2b and ribavirin.

PATIENTS AND METHODS

A total of 977 patients (569 men, 408 women) with chronic hepatitis C genotype 1 and high viral load (<100 KIU/ml) who were treated at Nagoya University Hospital and affiliated hospitals were enrolled in this study. Mean age of patients was 55.1 ± 12.2 years (range: 18–75 years). None of the patients had a history of chronic alcohol abuse, autoimmune disease, or metabolic disease. Patients with active intravenous drug use and immigrants were excluded from this study. The core region (aa 30–110) and ISDR (aa 2,209–2,248) of HCV were examined by direct sequencing. SNPs of IL28B (rs8099917) were identified using a real-time polymerase chain reaction (PCR) system. Patients received subcutaneous injections of pegylated-IFN-α2b (1.5 μg/kg) once each week along with oral ribavirin (600 mg/day for patients <60 kg, 800 mg/day for 60–80 kg, 1,000 mg/day for >80 kg) for 48 weeks. Patients who became negative for HCV-RNA between 16 and 36 weeks after initiating IFN treatment had the IFN treatment extended to 72 weeks, in accordance with Japanese guidelines [Kumada et al., 2010]. HCV-RNA levels in serum samples were examined at 12 weeks, at the end of IFN therapy, and at 6 months after the end of treatment. Serum was stored at −80°C for virological examination at pretreatment. Early virological response was defined as HCV-negative status at 12 weeks. Patients who were persistently negative for serum HCV-RNA at 24 weeks after withdrawal of IFN treatment were considered to show sustained virological response. Written informed consent was obtained from each patient, and the study protocol conformed to the ethical guidelines of the 1975 Declaration of Helsinki.

Virological Analysis

HCV-RNA quantitative viremia load was determined by PCR. HCV was genotyped by direct sequencing of the 5′-untranslated region and/or core regions as described previously and confirmed by direct sequencing of the NS5A region [Otagiri et al., 2002; Dal Pero et al., 2007; Hayashi et al., 2011a]. Genotypes were classified according to the nomenclature proposed by Simmonds et al. [2005]. Direct sequencing of the core and NS5A-ISDR regions was performed as reported previously [Dal Pero et al., 2007; Hayashi et al., 2011a]. In brief, RNA was extracted from 140 μl of serum using a commercial kit (QIAamp Viral RNA Kit; Qiagen, Valencia, CA) and dissolved in 50 μl of diethylpyrocarbonate-treated water. RNA (10 ng) was used for reverse transcription with oligos and random hexamer primers with a commercial kit (iScript cDNA Synthesis Kit; Bio-Rad, Hercules, CA). The HCV core region and NS5A-ISDR were amplified by nested PCR. In brief, each 50-μl PCR reaction mixture contained 100 nM of each primer, 1 ng of template cDNA, 5 μl of GeneAmp 10× PCR buffer, 2 μl of dNTPs, and 1.25 U of AmpliTaq Gold (Applied Biosystems, Foster City, CA). Primers for the core region were: sense, 5′-GGGAGGTCTCGTAGACCGTGCACCATG-3′ and antisense, 5′-GAGMGGKATRTACCCCATGAGRTCGGC-3′. Primers for the NS5A-ISDR were: sense, 5′-GCCTGGAGCCCTTGTAGTC-3′ and

TABLE I. Clinical Characteristic of Patients With HCV Genotype 1a

	N = 32
Age (y.o.)	36.4 ± 2.2
Sex: male/female	28/4
AST (IU/L)	48.8 ± 33.6
ALT (IU/L)	64.6 ± 57.8
Platelet (10^4/μl)	18.8 ± 6.0
HCV RNA level (KIU/ml)	2607.4 ± 3072.2
Source (clotting factor/BTF/unknown)	23/2/7

AST, aspartate aminotransferase; ALT, alanine aminotransferase; HCV, hepatitis C virus.

antisense, 5′-CTGCGTGAAGTGGTGGAATAC-3′. Amplification conditions consisted of 10 min at 94°C, followed by 40 cycles of 94°C for 10 sec, 55°C for 30 sec, and 72°C for 30 sec in a thermal cycler (GeneAmp PCR System 9700; Applied Biosystems). The second PCR was performed using the same reaction buffer with the first-round PCR product as template, and the following sets of primers: for the core region, sense primer 5′-AGACCGTGCACCATGAGCAC-3′ and antisense 5′-TACGCCGGGGGTCAKTRGGGCCCCA-3′; and for the NS5A-ISDR, sense 5′-TGTTTCCCCCACGCACTAC-3′ and antisense 5′-TGATGGGCAGTTTTTGTTCTTC-3′. PCR products were separated by electrophoresis on 2% agarose gels, stained with ethidium bromide, and visualized under ultraviolet light. PCR products were then purified and sequenced with the second-round PCR primers using a dye terminator sequencing kit (BigDye Terminator v1.1 Cycle Sequencing Kit; Applied Biosystems) and an ABI 310 DNA Sequencer (Applied Biosystems).

Genotyping Analysis

Detection of SNPs for IL28B (rs8099917) was conducted using a real-time PCR system. In brief, genomic DNA was extracted from 150 μl of whole blood with a commercial kit (QIAamp DNA Blood mini Kit; Qiagen) and dissolved in 50 μl of diethylpyrocarbonate-treated water. DNA (10 ng) was used for PCR and genotyping of IL28B SNP (rs8099917) was performed by TaqMan allelic discrimination (ABI-Prism 7300 SDS software; Applied Biosystems) with TaqMan SNP Genotyping Assays provided by Applied Biosystems (C__11710096_10).

Statistical Analysis

Data are expressed as mean ± standard deviation (SD). The paired t-test was used to analyze differences in variables. A value of $P < 0.05$ was considered statistically significant. Statview 5.0 software (SAS Institute, Cary, NC) was used for all analyses.

RESULTS

Thirty-two of the 977 patients (3.3%) were infected by genotype 1a. Clinical characteristics of patients with genotype 1a are summarized in Table I. Twenty-three cases involved patients with hemophilia who had received imported clotting factors. The prevalence of genotype 1a after excluding patients with hemophilia was 0.9%. A comparison of clinical characteristics according to hemophilia status is shown in Table II. No significant differences were apparent among the two groups. Differences in clinical characteristics between genotypes 1a and 1b are shown in Table III. Males were more frequent among patients with genotype 1a (87.5%) than among those with genotype 1b (57.2%), as the majority of patients with genotype 1a were young male patients with hemophilia. Sequence alignments of the core region at codons 71 and 90 showed arginine and cysteine, respectively, in all patients. The HCV core region of genotype 1a was thus well-conserved, with no significant mutations at codons 71 or 90. This is not similar to previous findings for genotype 1b [Akuta et al., 2005, 2011; Hayashi et al., 2011a,b; Kurosaki et al., 2011]. Alignment of the amino acid sequence for NS5A-ISDR is shown in Figure 1. The sequence of the HCV-1 strain was defined as the consensus sequence of genotype 1a, and the number of mutations to the chosen consensus sequence in ISDR was used to analyze the ISDR system. Sequences of the HCV-1 strain and HCV-1 strain with only one amino acid substitution were defined as wild-type, while ISDR sequences with more than two amino acid substitutions were defined as mutant-type. Twenty-seven strains were defined as wild-type and 5 strains were defined as mutant-type. IL28B genotypes could be obtained for 25 patients, and IL28B alleles were TT (n = 14) and TG (n = 11). Twenty-three patients received pegylated-IFN-α2b plus ribavirin therapy. Twenty patients were treated for 48 weeks, and 1 patient was treated for 72 weeks. Two patients were withdrawn at 24 weeks due to a

TABLE II. Clinical Characteristic According to Hemophilia

	Patients with hemophilia (N = 23)	Patients without hemophilia (N = 9)	P-value
Age (y.o.)	37.1 ± 9.2	37.1 ± 16.3	0.9966
Sex: male/female	22/1	6/3	0.0572
AST (IU/L)	51.2 ± 34.8	41.9 ± 30.9	0.5072
ALT (IU/L)	68.2 ± 55.8	54.0 ± 66.1	0.5566
Platelet (10^4/μl)	18.4 ± 6.8	19.8 ± 3.0	0.5602
HCV levels (KIU/ml)	2599.6 ± 3108.0	2630.0 ± 3176.5	0.9812

AST, aspartate aminotransferase; ALT, alanine aminotransferase; HCV, hepatitis C virus.

TABLE III. Clinical Characteristic According to Genotypes

	Genotype 1a (N = 32)	Genotype 1b (N = 945)	*P*-value
Age (y.o.)	36.4 ± 2.2	55.9 ± 11.6	0.0001
Sex: male/female	28/4	546/408	0.0004
Patients with hemophilia	23	4	0.0001
AST (IU/L)	48.8 ± 33.6	59.9 ± 45.0	0.1745
ALT (IU/L)	64.6 ± 57.8	64.6 ± 57.8	0.9894
Platelet ($10^4/\mu l$)	18.8 ± 6.0	17.2 ± 6.0	0.0918
HCV levels (KIU/ml)	2607.4 ± 3072.2	2011.5 ± 1453.8	0.0642

AST, aspartate aminotransferase; ALT, alanine aminotransferase; PLT, platelet count; HCV, hepatitis C virus.

lack of response to IFN therapy. Frequency of early virological response, characterized by undetectable HCV at 12 weeks, was 30.4% (7/23). Virological response rate at the end of treatment was 47.8% (11/23). Finally, 11 of 23 patients (47.8%) achieved sustained virological response. Clinical characteristics were compared between patients who achieved sustained virological response and patients who did not (Table IV), revealing significant differences in two factors on univariate analysis: IL28B and ISDR.

DISCUSSION

The present study investigated 977 patients with genotype 1 using direct sequencing of core and NS5A regions, revealing that genotype 1a is rare (3.3%) in Japan. Of the 33 patients with genotype 1a, 23 (71.9%) were patients with hemophilia, confirming that the majority of cases with genotype 1a involve patients with hemophilia who have received imported clotting factors, as previously reported [Fujimura et al., 1996; Otagiri et al., 2002; Hayashi et al., 2003]. Analysis after excluding patients with hemophilia revealed the prevalence of genotype 1a in Japan was 0.9% (9/954). Recently, the distributions of HBV genotypes have been changing in Japan due to international exchange [Hayashi et al., 2007; Matsuura et al., 2009]. However, prevalences of HCV genotypes have remained stable because of the different modes of infection involved. The present study revealed that 11 (47.8%) of 23 patients achieved sustained virological response. The IFN responsiveness of HCV genotype 1a in Japanese patients was reported in 1999 from Okinawa, a far southern island in Japan [Sakugawa et al., 1997]. That study reported that the rate of sustained virological response tended to be higher in patients with genotype 1a than in those with genotype 1b, but no significant differences were identified because of the small number of patients with genotype 1a. Low virological response rates in both genotypes 1a and 1b were confirmed in the present Japanese patients, as in Caucasian patients [Manns et al., 2001; McHutchison et al., 2009]. No significant differences in sustained virological response rate were seen between genotypes 1a and 1b. Discriminating between genotypes 1a and 1b thus seems to have little clinical relevance in terms of IFN responsiveness. Viral factors associated with sustained virological response, including HCV genotype, have been studied most frequently studied and mutations in the core and NS5A regions of HCV genotype 1b have been associated with response to IFN therapy [Akuta et al., 2005, 2010, 2011; Okanoue et al., 2009; Nakagawa et al., 2010; Toyoda et al., 2010; Hayashi et al., 2011a; Hayes et al., 2011; Kumthip et al., 2011; Kurosaki et al., 2011]. These viral factors could improve prediction of sustained virological response for genotype 1a, as in 1b. Amino acid substitutions at positions 70 and 91 of the HCV core region in genotype 1b have been related to IFN responsiveness, liver steatosis, hepatic oxidative stress, insulin resistance, and carcinogenesis [Akuta et al., 2005, 2007, 2009; Tachi et al., 2010]. These substitutions may have substantial impacts on

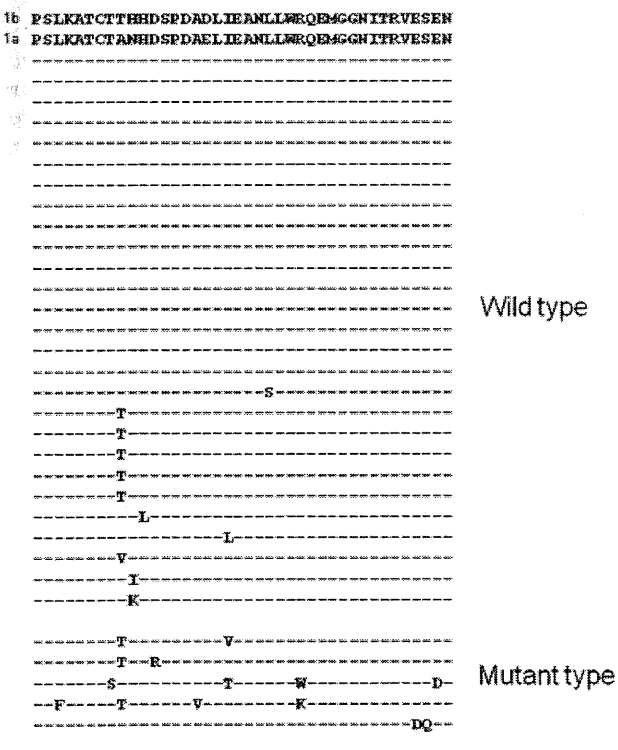

Fig. 1. Alignment of the amino acid sequence for the NS5A-ISDR. In the sequence alignment, dashes indicate amino acids identical to consensus sequence HCV1. Sequences of the HCV1 strain and HCV1 strains with one-nucleotide substitutions were defined as wild-type ISDR, and all other strains were defined as mutant-type ISDR. ISDR, interferon sensitivity-determining region.

TABLE IV. Univariate Analysis: Factors Predictive of Sustained Virologic Response

Factors	Sustained virologic response (n = 11)	Non-sustained virologic response (n = 12)	*P*-value
Age (y.o.)	37.9 ± 10.9	39.8 ± 11.3	0.6958
Gender: male/female	10/1	10/2	0.9999
ALT (IU/L)	78.2 ± 50.8	62.6 ± 68.1	0.5435
AST (IU/L)	51.4.4 ± 29.2	48.8 ± 40.4	0.8616
PLT ($\times 10^4/mm^3$)	19.0 ± 5.4	19.3 ± 5.7	0.8870
HCV RNA level (KIU/ml)	1323.1 ± 1077.3	2567.0 ± 2940.8	0.2481
ISDR: wild/mutant	7/4	12/0	0.0373
IL28B:TT/TG	9/1	4/8	0.0115

AST, aspartate aminotransferase; ALT, alanine aminotransferase; PLT, platelet count; HCV, hepatitis C virus; ISDR, interferon sensitivity-determining region; IL28B, interleukin 28B.

the pathogenesis of HCV genotype 1a infection. However, the HCV core region of genotype 1a is well-conserved and no significant mutations were seen in the core region, which is associated with IFN responsiveness. Several reports have also found that the HCV core region, including positions 70 and 91, of HCV genotype 1a is highly conserved [Alestig et al., 2011; Kumthip et al., 2011]. Mutations in the core region of genotype 1a would be rare, so this region might be unsuitable for routine clinical use, unlike in genotype 1b. However, the number of patients in this study was small, and large studies including from other countries are needed to clarify these issues. The ISDR in the NS5A region of HCV genotype 1b is closely associated with response to IFN therapy. ISDR mutations of genotype 1b are well known to be more important in predicting sustained virological response in Japanese patients than European patients [Hofgärtner et al., 1997; Zeuzem et al., 1997; Nakano et al., 1999; Pascu et al., 2004; Hayashi et al., 2011a]. European studies have failed to detect the specific amino acid substitutions in ISDR of genotype 1a associated with IFN responsiveness [Hofgärtner et al., 1997; Zeuzem et al., 1997]. In this study, sustained virological response was achieved in 36.8% of patients with wild-type ISDR and 100% of patients with mutant-type ($P = 0.0373$). The present analysis showed a close relationship between ISDR of genotype 1a and sustained virological response, as in genotype 1b. Recent investigations in Thailand and Iran have failed to identify the usefulness of ISDR for HCV genotype 1a in predicting sustained virological response [Kumthip et al., 2011; Yahoo et al., 2011]. The high virological response rate and low prevalence of patients with mutations in the ISDR do not favor the use of ISDR analysis in predicting IFN responsiveness [Herion and Hoofnagle, 1997; Yokozaki et al., 2011]. Rates of sustained virological response among these studies were much higher than those in the present study (68.4% and 75% vs. 47.8%). The mean number of mutations in patients who achieved sustained virological response in the studies by Kumthip et al. [2011] and Yahoo et al. [2011], and the present group were 1.4, 1.4, and 1.6, respectively. Differences in sustained virological response and the number of mutations to the ISDR might underpin this discrepancy in the evaluation of ISDR. Although the sample size in the present study was small, the results indicate that ISDR represents a strong indicator of progression to sustained virological response for patients with HCV genotype 1a. Amino acid substitutions in the ISDR of genotype 1a thus also play an important role in predicting sustained virological response in Japanese patients compared to patients from other countries. IL28B polymorphisms such as host genetics, as well as mutations in the HCV genome, contribute to IFN treatment outcomes. Rates of sustained virological response in patients in this study with TT and TG were 69.2% and 11.1%, respectively. The TG allele of the IL28B genotype was significantly associated with poor response to IFN therapy ($P = 0.0115$). SNPs of IL28B would regulate the expression of IFN-stimulated genes and affect IFN responsiveness. IL28B and ISDR thus exert independent effects on IFN responsiveness and both host and viral factors impacting IFN responsiveness would improve the prediction of sustained virological response. Several studies have thus reported that both the SNP of IL28B and mutations in the ISDR were associated with sustained virological response in patients with HCV genotype 1b [Akuta et al., 2011; Hayashi et al., 2011b; Kurosaki et al., 2011]. In the present study of HCV genotype 1a, among the 9 patients who had simultaneously the TG allele for IL28B and wild-type ISDR, only 1 achieved sustained virological response (11.1%). The best-sustained virological response was achieved in patients with mutant-type ISDR and the T allele (100%). The combination of SNPs for IL28B and mutations in ISDR may thus predict response to IFN therapy in patients with HCV genotype 1a as well as genotype 1b. Given the small sample size in this investigation, larger cohorts are needed to confirm the present results. Furthermore, infection with genotype 1a in Japanese patients is rare, making large-scale studies difficult to perform.

In conclusion, the prevalence of HCV genotype 1a is rare in Japan and the majority of cases involve patients with hemophilia. The TG genotype of IL28B is associated with poor response, while mutant-type ISDR is associated with good response to combination therapy with pegylated-IFN-α2b and ribavirin in patients with HCV genotype 1a. Combined use of both IL28B and ISDR could improve the prediction of IFN response.

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Predictive Value of Early Viral Dynamics During Peginterferon and Ribavirin Combination Therapy Based on Genetic Polymorphisms Near the *IL28B* Gene in Patients Infected With HCV Genotype 1b

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A study was carried out to determine whether early viral dynamics retain prediction of the outcome of peginterferon (PEG-IFN) and ribavirin combination therapy based on different genetic polymorphisms near the *IL28B* gene, the strongest baseline predictor of response to this therapy. A total of 272 patients infected with hepatitis C virus (HCV) genotype 1b were grouped according to genetic polymorphisms near the *IL28B* gene (rs8099917). The ability of reduced HCV RNA levels at 4 and 12 weeks after starting therapy to predict a sustained virologic response was evaluated based on these genotypes. Among patients with the TT genotype for rs8099917 (associated with a favorable response), the rates of sustained virologic response were higher in patients with a ≥ 3 $\log_{10}$ reduction in serum HCV RNA levels at 4 weeks after starting therapy ($P < 0.0001$). In contrast, among patients with the TG/GG genotype (associated with an unfavorable response), there were no differences in this rate based on the reduction in HCV RNA levels at 4 weeks. Early viral dynamics at 4 weeks after starting therapy retains its predictive value for sustained virologic response in patients with the TT genotype for rs8099917, but not in patients with the TG/GG genotype. Patients who are likely to achieve sustained virologic response despite unfavorable TG/GG genotype cannot be identified based on early viral dynamics during therapy. In contrast, lack of early virologic response at 12 weeks retains a strong predictive value for the failure of sustained virologic response regardless of *IL28B* polymorphisms, which remains useful as a factor to stop therapy. ***J. Med. Virol. 84:61–70, 2012.*** © 2011 Wiley Periodicals, Inc.

KEY WORDS: chronic hepatitis C; early viral dynamics; genetic polymorphisms near the *IL28B* gene; peginterferon; response-guided therapy; ribavirin

INTRODUCTION

The current standard antiviral therapy for patients with chronic hepatitis C is combination therapy with peginterferon (PEG-IFN) and ribavirin [Ghany et al., 2009]. Although this treatment regimen has increased markedly the number of patients with a sustained virologic response, i.e., the eradication of hepatitis C virus (HCV), only 50% of patients infected with HCV genotype 1 achieved a sustained virologic response approximately.

Many investigators have examined factors that predict the treatment outcome of PEG-IFN and ribavirin combination therapy in patients infected with HCV genotype 1. In addition to the baseline factors, the response of HCV during combination therapy, i.e., the changes in serum HCV RNA levels after starting therapy, has been shown to be an important predictor of the treatment outcome [Zeuzem et al., 2001; Buti

Conflict of interest: None.

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et al., 2002; Berg et al., 2003], with the emphasis on "response-guided therapy" [Lee and Ferenci, 2008; Marcellin and Rizzetto, 2008]. Recent reports have emphasized the importance of evaluating the viral dynamics at 4 weeks after starting therapy to predict a sustained virologic response. A rapid virologic response, in which serum HCV RNA is undetectable at 4 weeks after starting therapy, has been the strongest predictive factor of a sustained virologic response reportedly [Martinez-Bauer et al., 2006; Poordad et al., 2008; de Segadas-Soares et al., 2009; Martinot-Peignoux et al., 2009]. In addition, the predictive value of reduced serum HCV RNA levels at 4 weeks after starting therapy has been clarified further, and a ≥ 3 $\log_{10}$ reduction in HCV RNA levels at 4 weeks after starting therapy has high predictive value that a patient will achieve a sustained virologic response as a final outcome, even in the absence of a rapid virologic response [Toyoda et al., 2011].

In contrast, the lack of an early virologic response, defined as either undetectable serum HCV RNA or HCV RNA levels decreased by >2.0 $\log_{10}$ from the pretreatment level at 12 weeks after starting therapy, has been the most important predictor for the failure of a sustained virologic response in patients infected with HCV genotype 1 reportedly [Fried et al., 2002; Davis et al., 2003]. Therefore, treatment may be discontinued in patients without an early virologic response at 12 weeks of treatment, according to the recommendation in the AASLD guidelines [Ghany et al., 2009].

More recently, several studies reported that genetic polymorphisms near the *IL28B* gene (rs8099917, rs12979860) on chromosome 19 affect the virologic response to PEG-IFN and ribavirin combination therapy in patients infected with HCV genotype 1 [Ge et al., 2009; Suppiah et al., 2009; Tanaka et al., 2009; McCarthy et al., 2010; Rauch et al., 2010]. Furthermore, genetic polymorphisms near the *IL28B* gene are the strongest baseline predictive factor of the final outcome of combination therapy. An additional report showed the effects of genetic polymorphisms near the *IL28B* gene on HCV viral dynamics during PEG-IFN and ribavirin combination therapy [Thompson et al., 2010].

Although early HCV viral dynamics during therapy was shown originally to have a high predictive value for a sustained virologic response in HCV genotype 1-infected patients before genetic polymorphisms near the *IL28B* gene were linked to a therapeutic response, it is not clear whether early viral dynamics retain their predictive value in light of this additional information. The purpose of the present study was to investigate whether response-guided therapy based on viral dynamics at 4 or 12 weeks after initiating therapy retains its ability to predict the final outcome of PEG-IFN and ribavirin combination therapy after accounting for genetic polymorphisms near the *IL28B* gene.

MATERIALS AND METHODS

Patients and Treatment

Between January 2007 and June 2008, a total of 402 patients with chronic hepatitis C received antiviral combination therapy with PEG-IFN and ribavirin for HCV infection at the Ogaki Municipal Hospital or the Nagoya University Hospital. Among these patients, 272 were infected with HCV genotype 1b and had pretreatment HCV RNA levels >5.0 $\log_{10}$ IU/ml based on a quantitative real-time PCR-based method for HCV (HCV COBAS AmpliPrep/COBAS TaqMan System; Roche Molecular Systems, Pleasanton, CA; Lower limit of quantification, 1.7 $\log_{10}$ IU/ml: Lower limit of detection, 1.0 $\log_{10}$ IU/ml) [Colucci et al., 2007; Pittaluga et al., 2008]. This study did not include any patients infected with HCV genotype 1a because this genotype is not found in the general Japanese population.

All patients were given PEG-IFN alpha-2b (Pegintron, Schering-Plough, Tokyo, Japan) weekly and ribavirin (Rebetol, Schering-Plough, Kenilworth, NJ) daily. The PEG-IFN and ribavirin doses were adjusted based on the patient's body weight. Patients weighing ≤ 45 kg were given 60 μg of PEG-IFN alpha-2b once a week, those weighing >45 and ≤ 60 kg were given 80 μg, those weighing >60 and ≤ 75 kg were given 100 μg, those weighing >75 and ≤ 90 kg were given 120 μg, and those weighing >90 kg were given 150 μg. Patients weighing ≤ 60 kg were administered 600 mg of ribavirin per day, those weighing >60 and ≤ 80 kg were given 800 mg per day, and those weighing >80 kg were administered 1000 mg per day. The PEG-IFN and ribavirin doses were modified based on the manufacturer's recommendations. All patients were scheduled to undergo 48 weeks of treatment. The treatment duration was extended up to 72 weeks in some patients. In addition, treatment was discontinued before 48 weeks in some patients who had a low likelihood of achieving an eradication of HCV due to the presence of serum HCV RNA at 24 weeks after starting therapy.

A sustained virologic response was defined as undetectable serum HCV RNA at 24 weeks after ending the therapy. A patient was considered to have relapsed when serum HCV RNA was detectable between the end of treatment and 24 weeks after completing treatment, although serum HCV RNA was undetectable during and at the end of therapy. Patients were considered to have non-response if serum HCV RNA was detectable at 24 weeks after initiating therapy (i.e., null response or partial response according to the American guidelines [Ghany et al., 2009]). Patients were considered to have a rapid virologic response if they had undetectable serum HCV RNA at 4 weeks after starting therapy. An early virologic response was defined as the disappearance or decrease in serum HCV RNA levels by at least 2 $\log_{10}$ at 12 weeks after starting therapy. Patients were considered to have a complete early virologic response if serum HCV RNA was undetectable at 12 weeks after starting therapy and a partial early virologic response if the serum

HCV RNA levels had decreased by at least 2 $\log_{10}$ at 12 weeks after initiating therapy. Patients were considered not to have an early virologic response if their HCV RNA levels did not decrease by more than 2 $\log_{10}$ at 12 weeks compared to the pretreatment levels. Patients were considered to have a slow virologic response if the serum HCV RNA became undetectable between 12 and 24 weeks.

The study protocol was in compliance with the Helsinki Declaration and was approved by the ethics committee of the Ogaki Municipal Hospital and the Nagoya University School of Medicine. Prior to initiating the study, each patient provided written informed consent to use the laboratory data, analyze genetic polymorphisms near the *IL28B* gene, and test stored serum samples.

Assessments of Serum HCV RNA Levels and Genetic Polymorphisms Near the *IL28B* Gene

After a patient provided informed consent, serum samples were obtained at the patient's regular hospital visits, just prior to initiating treatment, every 4 weeks during the treatment period, and during the 24-week follow-up period after treatment. Serum samples were stored at −80°C until further use. The HCV RNA levels were measured using a quantitative real-time PCR-based method for HCV (HCV COBAS AmpliPrep/COBAS TaqMan System).

Genotyping of rs 8099917 polymorphisms near the *IL28B* gene was performed using the TaqMan SNP assay (Applied Biosystems, Foster City, California) according to the manufacturer's guidelines. A predesigned and functionally tested probe was used for rs8099917 (C__11710096_10, Applied Biosystems).

Statistical analyses. Quantitative values are reported as the mean ± SD. In between-group differences were analyzed by the chi-square test. Univariate and multivariate analyses using a logistic regression model were performed to identify factors that predict a sustained virologic response, including age, sex, body weight, serum alanine aminotransferase activity, serum aspartate aminotransferase activity, serum gamma-glutamyl transpeptidase levels, serum alkaline phosphatase values, serum albumin levels, total serum bilirubin values, white blood cell counts, hemoglobin, platelet counts, hepatitis activity grade (A0 and A1 vs. A2 and A3), liver fibrosis grade (F0 and F1 vs. F2 and F3), pretreatment HCV RNA levels ($\geq$6.5 $\log_{10}$ vs. <6.5 $\log_{10}$), reduction in peginterferon dose and ribavirin dose, reduction in HCV RNA levels at 4 weeks after starting therapy ($\geq$3 $\log_{10}$ vs. <3 $\log_{10}$), and the type of an early virologic response. All *P*-values are two-tailed, and $P < 0.05$ was considered significant statistically.

RESULTS

The characteristics of the patients examined in this study are shown in Table I. Liver histology was evaluated according to the METAVIR score [The French METAVIR Cooperative Study Group, 1994]. Although some patients had a reduction in their PEG-IFN and ribavirin doses during therapy, respectively, all patients except for those who discontinued the therapy had more than 80% adhesion to both the PEG-IFN and ribavirin regimens. No patients discontinued the therapy because of adverse effects. The treatment duration was extended up to 72 weeks in 51 of 71 patients (71.8%) who exhibited a slow virologic response. As a final outcome, 118 patients (43.4%) achieved a sustained virologic response, 84 patients (30.9%) relapsed, and the remaining 70 patients (25.7%) had no response.

TABLE I. Characteristics of all Study Patients (n = 272)

Age (years)	56.0 ± 10.9
Sex (female/male)	139 (51.1)/133 (48.9)
Body weight (kg)	57.8 ± 10.5
Alanine aminotransferase (IU/L)	64.6 ± 56.4
Aspartate aminotransferase (IU/L)	53.9 ± 42.7
Gamma-glutamyl transpeptidase (IU)	48.5 ± 43.9
Alkaline phosphatase (IU/L)	267.9 ± 101.3
Albumin (g/dl)	4.04 ± 0.37
Total bilirubin (mg/dl)	0.79 ± 0.30
White blood cell count (/μl)	4892 ± 1333
Hemoglobin (g/dl)	14.0 ± 1.3
Platelet count ($\times 10^3$/μl)	163 ± 51
Liver histology-activity (A0/A1/A2/A3)*	3 (1.2)/136 (55.3)/ 92 (37.4)/15 (6.1)
Liver histology-fibrosis (F0/F1/F2/F3)*	27 (11.0)/114 (46.3)/ 70 (28.5)/35 (14.2)
Pretreatment HCV RNA concentration ($\log_{10}$ IU/ml)	6.35 ± 0.79
Reduction in the peginterferon dose	81 (29.8)
Reduction in the ribavirin dose	130 (47.8)
Final outcomes (sustained virologic response /relapse/ no response)	118 (43.4)/ 84 (30.9)/70 (25.7)

HCV, hepatitis C virus.
Percentages are shown in parentheses.
*Liver biopsy was not performed in 26 patients.

Reduction in Serum HCV RNA Levels at 4 Weeks after Starting Therapy and Treatment Outcome According to Genetic Polymorphisms Near the *IL28B* Gene

An analysis of genetic polymorphisms at rs8099917 near the *IL28B* gene indicated that 207 patients (76.1%) had a TT genotype, 3 patients had a GG genotype (1.1%), and the remaining 62 patients were TG heterozygote (22.8%). Table II shows the comparison of the background characteristics between patients with the favorable TT genotype and those with the unfavorable TG/GG genotype. As reported previously [Abe et al., 2010], gamma-glutamyl transpeptidase level was higher significantly in patients with the TG/GG genotype. As a final outcome, the rate of a sustained virologic response was higher significantly in patients with the TT genotype. Among 207 patients with the TT genotype, serum HCV RNA became undetectable in 19 patients (9.2%) at 4 weeks after starting therapy (a rapid virologic response). In the remaining 188 patients, the decrease in serum HCV RNA levels at 4 weeks after starting therapy ranged from 0.12

TABLE II. Characteristics of Study Patients According to the Genetic Polymorphisms Near the *IL28B* Gene

	Patients with TT genotype of rs8099917 (n = 207)	Patients with TG/GG genotype of rs8099917 (n = 65)	*P*-value
Age (years)	56.5 ± 10.4	54.4 ± 12.4	0.4112
Sex (female/male)	107 (51.7)/100 (48.3)	32 (49.2)/33 (50.8)	0.8384
Body weight (kg)	57.8 ± 10.9	57.8 ± 9.4	0.8361
Alanine aminotransferase (IU/L)	65.1 ± 53.3	62.8 ± 65.6	0.2548
Aspartate aminotransferase (IU/L)	53.6 ± 34.8	54.7 ± 62.0	0.3339
Gamma-glutamyl transpeptidase (IU)	44.2 ± 37.1	62.3 ± 59.0	0.0003
Alkaline phosphatase (IU/L)	263.1 ± 90.3	282.8 ± 129.9	0.3875
Albumin (g/dl)	4.04 ± 0.36	4.05 ± 0.43	0.8020
Total bilirubin (mg/dl)	0.79 ± 0.30	0.76 ± 0.32	0.3010
White blood cell count (/μl)	4826 ± 1333	5100 ± 1320	0.1608
Hemoglobin (g/dl)	13.9 ± 1.3	14.1 ± 1.4	0.3339
Platelet count ($\times 10^3/\mu l$)	161 ± 49	169 ± 57	0.3871
Liver histology-activity (A0/A1/A2/A3)*	2 (1.1)/98 (52.4)/ 74 (39.6)/13 (6.9)	1 (1.7)/38 (64.4)/ 18 (30.5)/2 (3.4)	0.3241
Liver histology-fibrosis (F0/F1/F2/F3)*	21 (11.2)/83 (44.4)/ 57 (30.5)/26 (13.9)	6 (10.2)/31 (52.5)/ 13 (22.0)/9 (15.3)	0.6401
Pretreatment HCV RNA concentration ($\log_{10}$ IU/ml)	6.37 ± 0.85	6.29 ± 0.55	0.0582
Reduction in the peginterferon dose	61 (29.5)	20 (30.8)	0.9644
Reduction in the ribavirin dose	101 (48.8)	29 (44.6)	0.5565
Final outcomes (sustained virologic response /relapse/ no response)	106 (51.2)/ 69 (33.3)/32 (15.5)	12 (18.4)/15 (23.1)/ 38 (58.5)	<0.0001

HCV, hepatitis C virus.
Percentages are shown in parentheses.
*Liver biopsy was not performed in 26 patients.

$\log_{10}$ to 5.71 $\log_{10}$ (mean, 3.12 $\log_{10}$). The reduction in serum HCV RNA levels was $\geq$3 $\log_{10}$ in 98 patients (47.3%), <3 $\log_{10}$ and $\geq$2 $\log_{10}$ in 52 patients (25.1%), <2 $\log_{10}$ and $\geq$1 $\log_{10}$ in 23 patients (11.1%), and <1 $\log_{10}$ in 15 patients (7.3%). Figure 1A shows the rate of a sustained virologic response according to the reduction in HCV RNA levels at 4 weeks after starting therapy in patients with the TT genotype. The rates were higher significantly in patients who achieved a rapid virologic response or had a $\geq$3 $\log_{10}$ decrease in

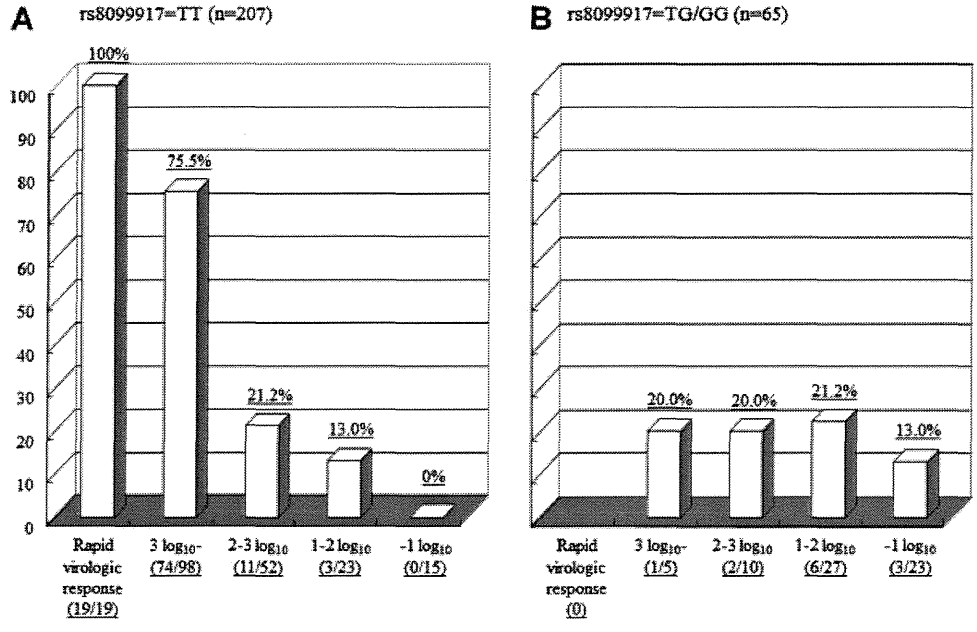

Fig. 1. The rate of sustained virologic responses (%) based on the reduction in serum HCV RNA levels at 4 weeks after starting therapy. **A**: Patients with the TT genotype for rs8099917, (**B**) patients with the TG/GG genotype for rs8099917.