VEGFR-1, VEGFR-2, and VEGFR-3. VEGFR-2 is the principal receptor that promotes the proangiogenic action of VEGF-A and has been the principal target of antiangiogenic therapies, although additional studies have underlined the importance of signaling through VEGFR-1. In 2 phase 3, placebo-controlled, randomized trials, sorafenib treatment significantly improved the time to tumor progression (TTP) and overall survival (OS) of patients with advanced HCC.[3,4] In those trials, however, no statistically significant pretreatment factors that predicted responses after patients started receiving sorafenib were identified.[5] Therefore, in clinical practice, it is extremely important to identify a predictive post-treatment biomarker that is associated with the treatment efficacy of sorafenib and the prognosis of patients after they start receiving sorafenib.

In general, the efficacy of treating solid tumors with systemic chemotherapy agents is assessed by radiologic findings. In 2010, Lencioni and Llovet published a modification of the Response Evaluation Criteria in Solid Tumors (RECIST).[6] However, the modified RECIST can be used only for typical HCC. Advanced HCCs often have atypical vascular patterns; therefore, evaluating tumor response to sorafenib is difficult with radiologic findings alone. Alternatively, α-fetoprotein (AFP) is the most popular tumor marker for HCC, and it has been reported that early AFP responses are a useful surrogate marker for predicting treatment response and prognosis in patients with advanced HCC who receive cytotoxic and antiangiogenic agents.[7-9] However, approximately 30% of patients with advanced HCC in the Sorafenib HCC Assessment Randomized Protocol (SHARP) trial had normal AFP concentrations.[10] Therefore, the identification of a new biomarker that can complementarily predict the efficacy of sorafenib and the prognosis of patients is necessary.

In a mouse model, an increase in hepatic VEGF levels was observed at 24 hours, 72 hours, and 120 hours after the administration of sorafenib,[11] suggesting that a change in VEGF levels may also occur during sorafenib therapy in humans. Therefore, we evaluated plasma VEGF changes during sorafenib treatment in patients with advanced HCC to determine whether VEGF has potential as a new biomarker for the prediction of treatment efficacy and prognosis after sorafenib administration.

MATERIALS AND METHODS

Patient Selection

Between December 2009 and August 2012, 95 consecutive patients with advanced, inoperable HCC received treatment with sorafenib at Musashino Red Cross Hospital. The diagnosis of HCC was based on guidelines established by the Liver Cancer Study Group of Japan[12] and the American Association for the Study of Liver Diseases[13] or by pathologic examination. According to these guidelines, a diagnosis of HCC is confirmed by histology or by characteristic radiologic findings, such as typical arterial enhancement of the tumor followed by a washout pattern in the images in the portal venous phase or the equilibrium phase on dynamic spiral computed tomography (CT) imaging or contrast-enhanced magnetic resonance imaging. Inclusion criteria were predefined as follows: 1) patients were alive 8 weeks after beginning treatment; and 2) patients had plasma VEGF and serum AFP concentrations evaluated at baseline, at 4 weeks, and at 8 weeks. Of 95 patients, 23 were unavailable for a week-8 VEGF measurement for the following reasons: 7 patients stopped sorafenib therapy because of erythema multiforme (grade 2-3) and started other therapies (radiation therapy or cytotoxic chemotherapy) within 1 month after starting sorafenib, 4 patients moved to another location before week 8, 5 patients refused to undergo a plasma VEGF measurement at week 8, and 7 patients were not available for obtaining VEGF concentration results. These 23 patients and 9 other patients who died within 8 weeks were excluded from the study. Hence, in total, 63 patients fulfilled the inclusion criteria. At enrollment, all patients had metastatic or locally advanced HCC that was not amenable to surgery or locoregional therapies, including transcatheter arterial chemoembolization (TACE) and local ablation. Written informed consent was obtained from all patients, and the ethics committee at Musashino Red Cross Hospital approved the study in accordance with the Declaration of Helsinki.

Sorafenib Treatment

The initial daily dose of sorafenib was 800 mg in 28 patients, 400 mg in 28 patients, and 200 mg in 7 patients. A reduced initial dose was allowed for patients who had the following factors: advanced age (≥80 years), gastrointestinal varices with a risk of bleeding, low body weight (<50 kg), and a poor performance status (≥2). In total, 60 patients underwent multiphase-multidetector CT imaging before starting sorafenib, 1 month after starting sorafenib, and every 3 months thereafter. Radiologic responses to therapy were evaluated according to modified RECIST. In all patients, serial measurements of plasma VEGF and serum AFP concentrations were performed before and after the receipt sorafenib and every month thereafter, with an allowance of ± 1 week. The endpoint of the current study was OS. In the follow-up visit after sorafenib administration, the medication was discontinued if progressive disease

(PD) was identified despite treatment, if intolerable adverse events occurred, or if inappropriate liver function was observed. Other palliative treatments or best supportive care were provided subsequently. An AFP response was defined as a decrease ≥20% in the serum AFP concentration during 8 weeks of treatment.

Plasma VEGF Measurements

Serial serum samples were collected prospectively from each patient. Venous blood samples were drawn into a serum separator tube and centrifuged at ×1800*g* for 10 minutes, and plasma samples were stored at −80°C until measurement. Plasma VEGF concentrations were measured quantitatively using an enzyme-linked immunosorbent assay kit (Quantikine Human VEGF Immunoassay; R&D Systems, Minneapolis, Minn) according to the manufacturer's instructions. We defined a decrease in the plasma VEGF level >5% from the pretreatment level at 8 weeks as a "VEGF decrease."

Statistical Analysis

Categorical variables were compared using the chi-square test, and continuous variables were compared using the Mann-Whitney test. All tests of significance were 2-tailed, and P values < .05 were considered statistically significant. OS curves were calculated using the Kaplan-Meier method, and differences between groups were assessed using the log-rank test. OS was determined as the interval between the date of treatment initiation and either death or the last visit. A Cox proportional-hazards model was used to determine the factors associated with OS. In univariate analyses, clinical and biologic parameters (sex, age, etiology, albumin, bilirubin concentrations, Child-Pugh class, plasma VEGF concentrations, and serum AFP concentrations) and tumor factors (vascular invasion and distant metastasis) were included. A logistic regression model was used to identify the factors associated with 1-year survival after the receipt of sorafenib. All statistical analyses were performed using StatView (version 5.0) software (Abacus Concepts, Berkeley, Calif).

RESULTS

Patient Characteristics

In total, 63 patients were enrolled in this study, and their characteristics are listed in Table 1. The diagnosis of HCC was confirmed by histology in 11 patients and by typical radiologic findings based on established guidelines in the remaining 52 patients. In all, 51 patients had previously received other therapeutic modalities, including 22 patients who previously received radiofrequency ablation, 22 who previously underwent TACE, 1 who previously received transcatheter arterial chemoinfusion, and 6 who previously underwent hepatic resection. Twelve patients had received sorafenib as initial therapy for HCC. Among the 63 enrolled patients, 33 were seropositive for hepatitis C virus antibody, 8 were seropositive for hepatitis B surface antigen, and 22 were seronegative for both hepatitis C virus antibody and hepatitis B surface antigen. Eighteen patients had evidence of extrahepatic metastasis, and 18 had major vascular invasion. No patient was lost to follow-up in this study.

TABLE 1. Characteristics of Study Patients With Advanced Hepatocellular Carcinoma (n = 63)

Characteristic	Median [Range]
Age, y	70 [40-85]
Sex: No. of men (%)	53 (84.1)
Baseline AFP, ng/mL	114 [2.0-98440]
Baseline plasma VEGF, pg/mL	288 [60-1580]
Treatment duration, mo	4.1 [0.1-28.3]
Overall survival, mo	9.3 [2.0-30.9]

Abbreviations: AFP, α-fetoprotein; VEGF: vascular endothelial growth factor.

Pretreatment Plasma VEGF Concentration and Prognosis and Extent of Hepatocellular Carcinoma

Pretreatment plasma VEGF concentrations in the 9 patients who died within 8 weeks were significantly higher than in the patients who survived beyond 8 weeks (813 ± 630 pg/mL vs 384 ± 18 pg/mL; P = .0024). Consistent with a previous study (the SHARP trial; Llovet et al[3]), our data suggested that the pretreatment plasma VEGF concentration is a useful prognostic factor for sorafenib therapy. However, there was no significant difference in OS between patients who had pretreatment plasma VEGF concentrations ≤450 pg/mL (n = 46) and those who had concentrations >450 pg/mL (n = 17; P = .731). The pretreatment plasma VEGF concentration could not predict prognosis for the patients who survived beyond 8 weeks.

We compared the size and extent of HCC between patients who had low plasma VEGF concentrations (≤450 pg/mL) and high plasma VEGF concentrations (>450 pg/mL). No difference was observed in the size or extent of HCC at baseline between patients with lower versus higher pretreatment plasma VEGF concentrations.

Association Between Changes in Plasma VEGF Concentrations and Overall Survival

The median OS assessed by the Kaplan-Meier method was 16.3 months for all 63 patients enrolled in the study

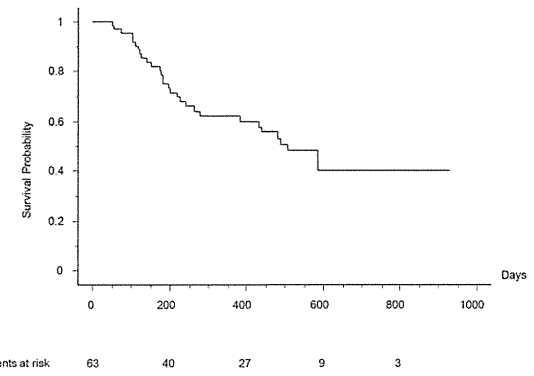

Figure 1. This Kaplan-Meier plot illustrates overall survival for all patients in the study.

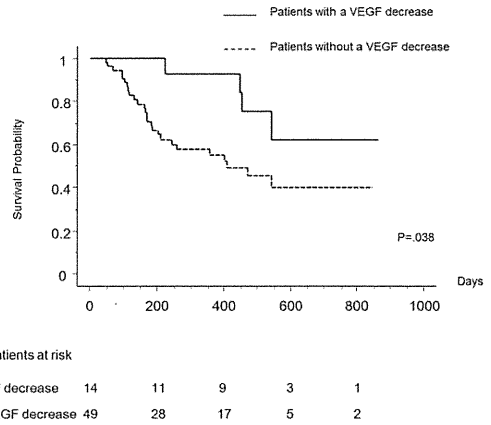

Figure 3. This Kaplan-Meier plot illustrates overall survival according to changes in vascular endothelial growth factor (VEGF) concentration.

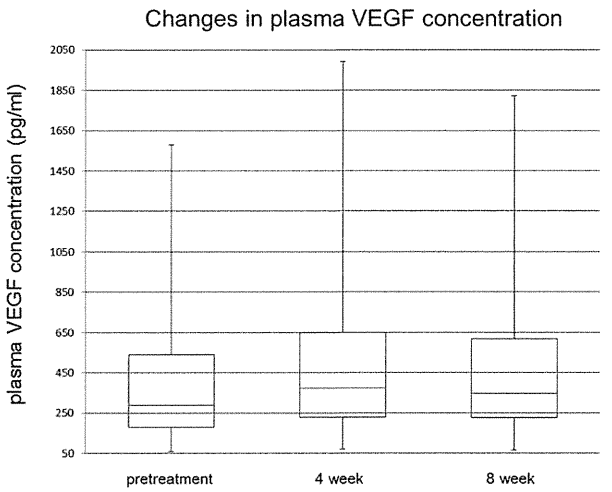

Figure 2. Changes in plasma vascular endothelial growth factor (VEGF) concentrations are illustrated.

(Fig. 1). Plasma VEGF concentrations at baseline, at 4 weeks, and at 8 weeks after the initiation of sorafenib treatment were 288 pg/mL (range, 60-1580 pg/mL), 372 pg/mL (range, 69-1990 pg/mL), and 347 pg/mL (range, 64-1840 pg/mL), respectively (Fig. 2). Plasma VEGF concentrations increased within 4 weeks after the administration of sorafenib in 47 of 63 patients (74.6%). The median survival of patients who had a decrease in their plasma VEGF concentration at week 4 (n = 16) and an increase in their plasma VEGF concentration at week 4 (n = 47) were 19.5 months and 16.8 months, respectively; and there was no significant difference in OS between changes in plasma VEGF at 4 weeks ($P = .645$). However, patients who had a VEGF decrease at week 8 (n = 14) had a longer median survival than those who did not have a VEGF decrease (n = 49; 30.9 months vs 14.4 months; $P = .038$) (Fig. 3), suggesting that a decrease in VEGF concentration 8 weeks after starting sorafenib treatment is closely associated with a favorable prognosis. The median percentage of decrease in the plasma VEGF concentration was 18.3% (range, 7%-41.7%). There were no differences in any pretreatment patient characteristics, including HCC stage and Child-Pugh score, between patients who did and did not have a VEGF decrease (Table 2).

Relation Between Radiologic Findings or Serum α-Fetoprotein Concentration and Overall Survival

The best radiologic responses to therapy assessed by modified RECIST were classified as a complete response (CR) (n = 4), a partial response (PR) (n = 16), stable disease (SD) (n = 34), and PD (n = 9). Fourteen patients had a VEGF decrease, and their best radiologic responses were a CR (n = 2), a PR (n = 2), SD (n = 9), and PD (n = 1). There was no significant difference in OS between the patients who had an objective response (CR + PR) and those with SD. The survival of patients who had PD was significantly worse than that of the patients without PD (median OS, 5.8 months and 19.4 months, respectively; $P = .0006$). There was no significant difference in OS between patients who had an AFP response and those who did not have an AFP response within the group that did not have PD (ie, those who attained a CR, a PR, or SD [the non-PD group]) (Fig. 4). There also was no significant difference ($P = .111$) between patients who did and did not have an AFP response among those in the non-PD group who had had an elevated AFP at baseline.

TABLE 2. Characteristics of Patients Categorized According to Variation in Vascular Endothelial Growth Factor Levels at 8 Weeks of Sorafenib Treatment

Characteristic	No. of Patients (%)		
	With VEGF Decrease, n = 14	Without VEGF Decrease, n = 49	*P*
Age, y	72	69	.325
Sex: Men	11 (78.6)	42 (85.7)	.679
Body weight, kg	58.3	62.3	.175
Cause of disease			.210
Hepatitis B	0 (0)	8 (16.3)	
Hepatitis C	9 (64.3)	24 (49)	
Other	5 (35.7)	17 (34.7)	
Prior treatment			.797
Yes	11 (78.6)	40 (81.6)	
No	3 (21.4)	9 (18.4)	
Baseline bilirubin, mg/dL	0.8	1.0	.375
Baseline albumin, g/dL	3.4	3.6	.190
Child-Pugh score			.178
5	7 (50)	30 (61.2)	
6	7 (50)	16 (32.7)	
7	0 (0)	3 (6.1)	
Maximum tumor size, cm			.892
≤5	8 (57.1)	22 (44.9)	
>5	6 (42.9)	27 (55.1)	
No. of tumors			.883
≤3	10 (71.4)	34 (69.4)	
>3	4 (28.6)	15 (30.6)	
Extrahepatic disease			.502
Yes	3 (21.4)	15 (30.6)	
No	11 (78.6)	34 (69.4)	
Site of metastatic disease			
Lung	1	7	
Bone	1	4	
Lymph node	1	3	
Lung and bone	0	1	
Major vascular invasion			.739
Yes	3 (21.4)	15 (30.6)	
No	11 (78.5)	34 (69.4)	

Abbreviations: VEGF: vascular endothelial growth factor.

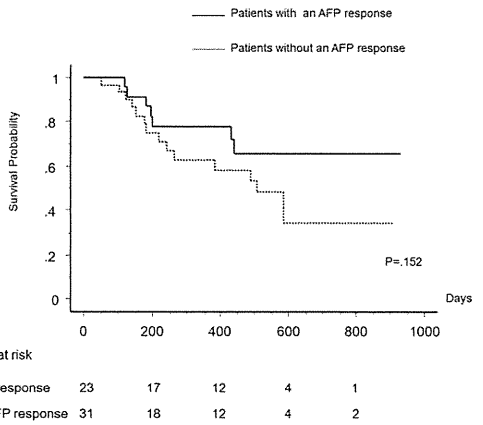

Figure 4. This Kaplan-Meier plot illustrates overall survival according to α-fetoprotein (AFP) response in patients without progressive disease (PD), classified as non-PD (ie, those who had a complete response, a partial response, or stable disease) according to modified Response Evaluation Criteria in Solid Tumors.

It is noteworthy that all patients who had a VEGF decrease and an AFP response survived during the observation period (median, 19.7 months; range, 6.5-31.0 months). In patients without a VEGF response (n = 49), there was no significant difference in OS between those who did and did not have an AFP response ($P = .147$). Of 49 patients who did not have a VEGF decrease at 8 weeks, 19 patients were able to survive beyond 1 year after starting sorafenib. Nine patients without a VEGF decrease at 8 weeks survived for >18 months.

Prognostic Factors After Sorafenib Administration

In univariate analysis, among all patients, a VEGF decease and an AFP response were associated significantly with OS after starting sorafenib. Major vascular invasion and PD, as evidenced by radiologic findings after sorafenib administration, also were significant prognostic factors. To predict which patients would have a highly favorable prognosis, the prognostic factors associated with 1-year survival after starting sorafenib were assessed in univariate and multivariate analyses. In the univariate analysis, a VEGF decrease, PD, and major vascular invasion were associated significantly with survival (Table 3). In the multivariate analysis, which was performed using those factors as covariates, a VEGF decrease was identified as an independent factor associated significantly with survival (Table 3). There was a significant difference in OS among the 3 groups (patients with a VEGF decrease and non-PD, patients without a VEGF decrease but non-PD, and patients without a VEGF decrease and PD; $P = .0013$) (Fig. 5). Only 1 patient who had a VEGF decrease was classified with PD. All 4 patients who had a VEGF decrease and an objective response (CR or PR) were able to survive during the observation period.

Adverse Events During Sorafenib Treatment

The overall incidence of treatment-related adverse events was 100%. The rate of discontinuation of sorafenib as a result of adverse events was 22.2%. Adverse events that led to the discontinuation of sorafenib treatment were liver dysfunction (63.6%), hand-foot skin reaction (18.2%), interstitial pneumonia (9.1%), and rash (9.1%). Dose reductions because of adverse events occurred in 62 patients. The most frequent adverse event leading to dose reductions was liver dysfunction (33.9%). In addition,

TABLE 3. Prognostic Factors Associated With 1-Year Survival After Sorafenib Administration

Risk Factor	OR (95% CI)[a]	*P*
Univariate analysis		
Age, by every 10 y	1.47 (0.75-2.87)	.266
Sex		
Women	1.00	
Men	0.26 (0.50-1.39)	.116
HBV infection		
Negative	1.00	
Positive	0.33 (0.06-2.02)	.231
HCV infection		
Negative	1.00	
Positive	1.23 (0.41-3.74)	.714
Albumin, by every 1 g/dL,	1.34 (0.45-3.99)	.604
Total bilirubin, by every 1 mg/dL	0.79 (0.28-2.25)	.656
Pre-AFP, by every 10 ng/mL	1.00 (1.00-1.00)	.161
Tumor size, cm		
<5	1.00	
≥5	0.42 (0.14-1.32)	.147
No. of tumors		
≤3	1.00	
≥4	0.26 (0.06-1.08)	.064
Major vascular invasion		
Yes	1.00	
No	4.00 (1.12-14.4)	.034
Extrahepatic metastasis		
Yes	1	
No	1.82 (0.56-5.90)	.320
5% VEGF decrease at wk 8		
No	1.00	
Yes	11.1 (1.29-94.6)	.028
PD		
No	1.00	
Yes	0.16 (0.29-0.86)	.033
Objective response: CR + PR		
No	1.00	
Yes	1.63 (0.49-5.42)	.426
AFP response		
No	1.00	
Yes	2.76 (0.80-9.52)	.107
Multivariate analysis[b]		
5% VEGF decrease at wk 8		
No	1.00	
Yes	10.0 (1.02-91.3)	.041
PD		
No	1.00	
Yes	0.20 (0.29-1.39)	.104
Major vascular invasion		
Yes	1.00	
No	3.03 (0.71-12.9)	.134

Abbreviations: AFP, α-fetoprotein; CI, confidence interval; CR, complete response; HBV, hepatitis B virus; HCV, hepatitis C virus; PD, progressive disease; PR, partial response; VEGF, vascular endothelial growth factor.
[a] The ORs for 1-year survival were calculated using logistic regression analysis.
[b] In the multivariate logistic analysis, a 5% VEGF decrease, PD, and portal invasion were included as covariates.

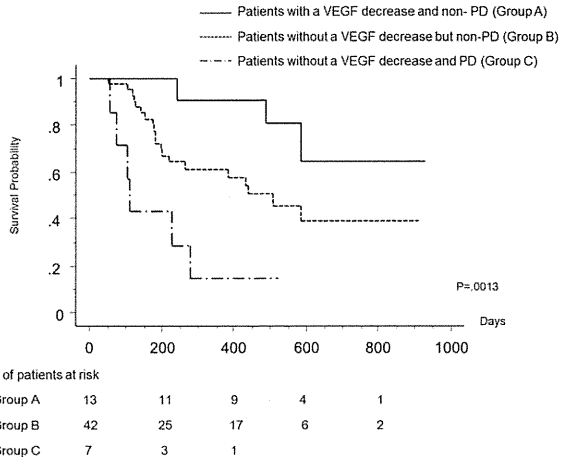

Figure 5. This Kaplan-Meier plot illustrates overall survival according to the combination of vascular endothelial growth factor (VEGF) changes and radiologic findings classified by modified Response Evaluation Criteria in Solid Tumors. Non-PD indicates patients who did not have progressive disease (PD) (ie, those who had a complete response, a partial response, or stable disease).

the incidence of adverse events was not related to plasma VEGF concentrations.

DISCUSSION

In the current study, we demonstrated that plasma VEGF concentrations change dynamically during sorafenib therapy, and changes in VEGF concentration are closely associated with OS in patients who receive treatment with sorafenib. VEGF is the major mediator of angiogenesis in HCC, and several studies have correlated VEGF concentrations with the prognosis of patients who have advanced HCC.[5,14-21]

Recently, a new staging system was proposed that includes the plasma VEGF concentration along with the Cancer of the Liver Italian Program (CLIP) score; this new system—known as the V-CLIP score—classifies patients with advanced HCC more appropriately into a homogeneous prognostic group.[22] Therefore, the concentration of circulating VEGF is included as a candidate prognostic marker for HCC, especially in patients with advanced disease. The objective of our study was to elucidate the important question of whether an on-treatment change in VEGF is a potentially useful new biomarker for predicting prognosis in patients who survive beyond 8 weeks, because such an on-treatment predictor among patients who have relatively longer survival has not yet been elucidated. In this study, plasma VEGF concentrations increased from pretreatment levels within 4 weeks of starting sorafenib in 47 of 63 patients (74.6%). This was followed by a decrease in plasma VEGF levels at 8 weeks in 68.1% of patients. A possible mechanism of this transient increase in VEGF after starting sorafenib may be related to a reactive increase against the inhibition of VEGF activity or hypoxia induced by sorafenib. This

hypothesis is supported by the demonstration that plasma VEGF concentrations increased shortly after treatment with TACE.[24-26] It is believed that these increases in plasma VEGF concentration are related to the induction of tissue hypoxia.[27] However, the peak time point of VEGF elevation during sorafenib administration was different from that previously reported in TACE, in which a transient elevation of VEGF was observed within 7 days after TACE.[24-26] This observed difference may be related to the continuous induction of hypoxia by sorafenib administration.

It is noteworthy that, in our study, decreases in plasma VEGF observed within 8 weeks of sorafenib administration were associated with better OS. One possible reason for this association may be that the decrease in VEGF concentrations reflects a decrease in the number of tumor cells secreting VEGF. An association between changes in VEGF concentrations and disease progression was observed in a previous study of an anti-VEGF antibody, bevacizumab, in patients with advanced HCC.[23] In that study, plasma VEGF-A concentrations decreased from baseline in all patients after 8 weeks of bevacizumab therapy and increased to near baseline levels in 5 of 6 patients at the time of disease progression. Unfortunately, plasma VEGF-A levels after 8 weeks of bevacizumab in that study were available for only 8 of 46 patients who were enrolled the study, and plasma VEGF-A levels after 4 weeks were not evaluated. In our study, all patients were evaluated before and every 4 weeks after starting sorafenib. Moreover, we demonstrated the usefulness of plasma VEGF concentrations at 8 weeks and not at 4 weeks. Zhu et al[28] reported that plasma levels of VEGF and placental growth factor increased after cediranib, a pan-VEGFR tyrosine kinase inhibitor monotherapy for advanced HCC. In that study, progression-free survival was correlated inversely with baseline levels of VEGF, soluble VEGFR2 (sVEGFR2), and basic fibroblast growth factor and with on-treatment levels of basic fibroblast growth factor and insulin-like growth factor-1; and progression-free survival was directly associated with on-treatment levels of interferon-γ. Because changes of VEGF concentrations during therapy were not identified as a prognostic factor in the study by Zhu et al, biomarkers that predict prognosis may be different among different types of tyrosine kinase inhibitors. Jayson et al[29] reported that plasma VEGF-A in patients who received bevacizumab was potentially predictive and prognostic in metastatic breast, gastric, and pancreatic cancers; however, it was only prognostic (and not predictive) in metastatic colorectal cancer, nonsmall cell lung cancer, and renal cell carcinoma. In our study, we measured plasma VEGF concentrations and not plasma VEGF-A concentrations. Sorafenib is a multikinase inhibitor, whereas bevacizumab is a humanized monoclonal antibody that recognizes and blocks VEGF-A expression. Further studies to evaluate the clinical usefulness of determining VEGF and VEGF-A concentrations during sorafenib therapy are necessary in various cancers. Although the precise mechanism underlying the association between serial changes in VEGF and disease progression is unclear, the findings of the current study are extremely valuable for clinical practice in predicting the prognosis of patients who receive treatment with sorafenib.

Llovet et al[5] studied plasma biomarkers as predictors of outcome in patients with advanced HCC. They measured plasma biomarkers in 491 patients at baseline and in 305 patients after 12 weeks in a phase 3, randomized, controlled trial (the SHARP trial). Those authors concluded that angiopoietin-2 and VEGF were independent predictors of survival in patients with advanced HCC and that none of the tested biomarkers significantly predicted response to sorafenib. In our study, by measuring plasma VEGF monthly, we demonstrated that the changes 8 weeks after starting sorafenib were important for predicting OS.

It has been reported that modified RECIST guidelines are useful for predicting efficacy and prognosis after patients with advanced HCC receive treatment with sorafenib.[30] However, modified RECIST can only be used for typical hypervascular HCC, and not for atypical HCC, including poorly differentiated HCC and diffuse-type HCC. Moreover, the percentage of patients in our study who had PD was only 11.1% (9 of 63 patients), and the objective response rate (CR + PR vs SD) could not predict OS, suggesting that using only modified RECIST guidelines was insufficient for predicting OS in most patients who received sorafenib (non-PD patients). Therefore, it is important to identify a predictive biomarker for those patients who can expect long survival during sorafenib therapy, although their radiologic findings may not be categorized as objective responses.

From this point of view, decreases in VEGF observed in non-PD patients at week 8 may identify patients who have a favorable prognosis. According to our results, the median survival of patients who had a VEGF decrease was extremely good at 31.0 months, and we demonstrated that a VEGF decrease, but not modified RECIST or AFP, was the only significant post-therapeutic factor associated with favorable survival after sorafenib administration (Table 3). In our study, all

patients who had both a VEGF decrease and an AFP response survived during the observation period (median, 19.7 months). Taken together, the combination of a plasma VEGF decrease, an AFP response, and modified RECIST is useful for predicting an extremely favorable prognosis.

This study had a few limitations. The first was our subanalysis of consecutive patients. However, the median survival for the 23 excluded patients who were available for estimation was equivalent to that of the included patients (16.8 months); therefore, it is unlikely that selection bias affected our results. The second limitation is that we measured only plasma VEGF concentrations. In previous studies, many factors, including VEGF-A, short VEGF-A isoform, sVEGFR1, sVEGFR2, sVEGFR3, angiopoietin-2, and insulin-like growth factor-2, were evaluated as biomarkers. However, to our knowledge, this is the first clinical study to demonstrate the early dynamic changes in plasma VEGF concentrations in patients who received sorafenib. Finally, the number of patients in this study was relatively small to make recommendations to physicians. Our results indicated that patients who have decreased VEGF concentrations at 8 weeks have a favorable prognosis, regardless of their radiologic findings. However, further studies with a larger number of patients will be necessary to propose new recommendations.

In conclusion, changes in plasma VEGF concentrations during sorafenib treatment are dynamic in patients with advanced HCC, and an observed decrease in the plasma VEGF concentration 8 weeks after starting sorafenib is associated significantly with favorable OS. Today, because many clinical trials of new molecular-targeted agents for HCC are being conducted, it is necessary for hepatologists and oncologists to determine the time when alternative agents should be started as a second or third line of treatment. Our results have potentially important clinical implications for physicians and may influence their decisions regarding a treatment strategy for advanced HCC in individual patients.

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CONFLICT OF INTEREST DISCLOSURES

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Deep-Sequencing Analysis of the Association between the Quasispecies Nature of the Hepatitis C Virus Core Region and Disease Progression

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Variation of core amino acid (aa) 70 of hepatitis C virus (HCV) has been shown recently to be closely correlated with liver disease progression, suggesting that the core region might be present as a quasispecies during persistent infection and that this quasispecies nature might have an influence on the progression of disease. In our investigation, the subjects were 79 patients infected with HCV genotype 1b (25 with chronic hepatitis [CH], 29 with liver cirrhosis [LC], and 25 with hepatocellular carcinoma [HCC]). Deep sequencing of the HCV core region was carried out on their sera by using a Roche 454 GS Junior pyrosequencer. Based on a plasmid containing a cloned HCV sequence (pCV-J4L6S), the background error rate associated with pyrosequencing, including the PCR procedure, was calculated as 0.092 ± 0.005/base. Deep sequencing of the core region in the clinical samples showed a mixture of "mutant-type" Q/H and "wild-type" R at the core aa 70 position in most cases (71/79 [89.9%]), and the ratio of mutant residues to R in the mixture increased as liver disease advanced to LC and HCC. Meanwhile, phylogenetic analysis of the almost-complete core region revealed that the HCV isolates differed genetically depending on the mutation status at core aa 70. We conclude that the core aa 70 mixture ratio, determined by deep sequencing, reflected the status of liver disease, demonstrating a significant association between core aa 70 and disease progression in CH patients infected with HCV genotype 1b.

Hepatitis C virus (HCV)-related liver disease gradually advances from chronic hepatitis (CH) to liver cirrhosis (LC) and to hepatocellular carcinoma (HCC) over 20 to 30 years (1). However, the rates of disease progression differ: some patients develop HCC over several years, while others show persistently normal alanine aminotransferase (PNALT) levels for decades, and the cause of the difference remains poorly understood.

The involvement of viral and host factors in the progression of liver disease and hepatocarcinogenesis is complex (2). With regard to viral factors, the relationship between the viral core region and disease progression in HCV genotype 1b infection has attracted clinical attention. Specifically, it has been reported that the core amino acid (aa) 70 residue, identified as a variable related to the outcome of interferon (IFN) therapy (3), is closely associated with the progression of hepatitis and hepatocarcinogenesis in Japan and North America (4–7). Those previous studies and our own have reported that core aa 70 variation is strongly linked to carcinogenesis and that substitutions in the core aa 70 region aggravate hepatitis and heighten the risk of hepatocarcinogenesis during the clinical course, corroborating the relationship between the status of the core region and disease progression (8, 9).

With regard to host factors, a genomewide association study (GWAS) has recently shown that single nucleotide polymorphisms (SNPs) around the interleukin 28B (IL28B) gene (rs12979860 and rs8099917), encoding the type III IFN IFN-λ3, are strongly correlated with the outcomes of therapy with pegylated IFN-α plus ribavirin for chronic hepatitis C (CH-C) (10–13). Interestingly, in contrast to the core region, consensus has not been reached as to the relationship between disease progression and the IL28B SNP, which is associated with IFN resistance (14–17). Previously, we reported that there was no correlation between the onset of HCC and the IL28B SNP (9). However, it was reported that the IL28B rs8099917 TG/GG allele was markedly correlated with the presence of Q (glutamine) or H (histidine) instead of the R (arginine) residue at core aa 70, while the IL28B rs8099917 TT allele was correlated with core aa 70R (8). Moreover, the core amino acid R70Q/H change occurs more often in patients with IL28B rs8099917 TG/GG than in those with IL28B rs8099917 TT (9). In this manner, the contributions of the core aa 70 residue and the IL28B SNP, which were found to be IFN sensitivity factors, to the progression of liver disease have gradually been elucidated.

HCV exists in a host as a swarm of variants, known as a "quasispecies," and this quasispecies nature has been considered to play a critical role in pathogenesis (18). However, detailed analysis has been technically difficult, and the clinical significance has not been clarified in detail thus far. Considering the observation of core aa 70 gene changes over time, it is assumed that a variety of core aa 70 isolates may exist as a quasispecies, and this could be related to pathogenesis as described above.

Recently, deep-sequencing technology has advanced rapidly and has enabled us to analyze viral quasispecies in association with the status of the disease (19–22). In this study, we investigated how the quasispecies of the HCV core gene, either at the hot spot of the core aa 70 residue or in the almost-entire core gene, is created and is involved in disease progression in patients with CH-C.

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TABLE 1 Patient characteristics classified by disease progression

Characteristic[a]	Value for patients with:			P
	CH (n = 25)	LC (n = 29)	HCC (n = 25)	
No. male/female	14/11	10/19	12/13	0.278
Age (yr) (mean ± SD)	63.4 ± 14.6	66.5 ± 9.2	68.4 ± 8.2	0.539
Platelets (10^{-4}/mm^3) (mean ± SD)	16.1 ± 4.7	9.8 ± 3.9	11.1 ± 5.1	<0.001
Albumin (g/dl) (mean ± SD)	4.4 ± 0.3	3.9 ± 0.6	3.5 ± 0.5	<0.001
γ-GTP (IU/liter) (median [range])	53.5 (12–230)	38.0 (12–108)	40.8 (15–110)	0.845
T. chol. (mg/dl) (mean ± SD)	161 ± 28	148 ± 30	140 ± 28	0.053
HCV RNA (kIU/ml) (median [range])	7,047 (501–19,953)	5,369 (126–25,119)	8,421 (110–25,119)	0.288
Alpha-fetoprotein (ng/ml) (median [range])	5.0 (1.1–16.5)	32.2 (1.0–252.6)	614.8 (1.9–13,418)	<0.001
AST (IU/liter) (mean ± SD)	42.4 ± 17.8	51.1 ± 23.5	59.1 ± 28.2	0.046
ALT (IU/liter) (mean ± SD)	46.6 ± 23.1	43.9 ± 29.3	60.7 ± 52.7	0.263
No. with R/(Q/H) at core aa 70[b]	19/6	12/17	8/17	0.005
No. with L/(M/C) at core aa 91[b]	17/8	19/10	15/10	0.834
No. of ISDR mutations (median [range])[b]	0.8 (0–6)	1.2 (0–7)	0.9 (0–8)	0.799
No. of IRRDR mutations (median [range])[b]	4.9 (1–10)	4.7 (2–9)	5.2 (1–12)	0.962
No. with TT/non-TT at IL28B SNP (rs8099917)	18/7	17/12	14/11	0.458
No. without/with a history of interferon therapy	14/11	16/13	15/10	0.933

[a] T. chol., total cholesterol; AST, aspartate transaminase; ALT, alanine aminotransferase.
[b] Core aa 70, core aa 91, the interferon sensitivity-determining region (ISDR), and the interferon-ribavirin resistance-determining region (IRRDR) were dominant viral sequences determined by direct sequencing.

PATIENTS AND METHODS

Patients. The subjects were 79 patients persistently infected with HCV genotype 1b who were followed up at Yamanashi University Hospital. The patients all fulfilled the following criteria: (i) they were negative for hepatitis B surface antigen; (ii) they had no other forms of hepatitis, such as primary biliary cirrhosis, autoimmune liver disease, or alcoholic liver disease; (iii) they were free of coinfection with human immunodeficiency virus; and (iv) signed consent was obtained for the study protocol. The study protocol had been approved by the Human Ethics Review Committee of Yamanashi University Hospital and conformed to the ethical guidelines of the Declaration of Helsinki.

The breakdown was as follows: 25 patients with CH, 29 with LC, and 25 with HCC. The patients' clinical backgrounds, including histories of interferon-based antiviral therapy, are shown in Table 1. Deep-sequencing analysis was performed using serum samples taken at the most recent visit from patients with chronic hepatitis or liver cirrhosis and at the first diagnosis of HCC from patients with HCC. A direct-sequencing method, which determines the dominant viral sequence, was performed as described previously (9) to determine the dominant viral sequences of the core region, the interferon sensitivity-determining region (ISDR), and the interferon-ribavirin resistance-determining region (IRRDR) from the serum of each patient.

Deep sequencing. Deep sequencing of the viral core region was performed for each of 79 patients. Briefly, RNA was extracted from the stored sera of these patients and was reverse transcribed to cDNA. Then two-step nested PCR was carried out with primers specific for the core region of the HCV genome (23). The primers for the second-round PCR had barcodes attached, were 10 nucleotides (nt) long, and differed for each sample, so that PCR products from each sample were identifiable (see Table S1 in the supplemental material). After the band densities of the PCR products were quantified using a Bioanalyzer (Agilent Technologies, Palo Alto, CA), the concentrations of the samples were adjusted to a common value, and pooled samples were prepared. Libraries were then subjected to emulsion PCR, the enriched DNA beads loaded onto a picotiter plate, and pyrosequencing carried out with a Roche GS Junior/454 sequencing system using titanium chemistry (Roche, Branford, CT). In order to determine the error rate of the procedure, deep sequencing was carried out under similar conditions with a plasmid containing a cloned HCV sequence (pCV-J4L6S) (24). Amplicon Variant Analyzer software, version 2.5p1 (Roche), was used for analysis.

A dominant sequence of the core region for each patient was deposited in GenBank. Although the study amplified 499 nucleotides, from the 25th to the 523rd nucleotide of the core region, by PCR (Fig. 1), information for only 459 of the 499 nucleotides was uploaded for each patient, since some minor PCR amplicons obtained by deep sequencing did not include the full 499 nucleotides.

Phylogenetic tree analysis. Phylogenetic trees were constructed from the sequences by using the neighbor-joining method with BioEdit and MEGA5.05, and bootstrapping was performed with 1,000 replicates (25). In constructing phylogenetic trees, the three bases of the core codon 70 were removed in the analysis of all trees, since the mutation rate of other parts of the core region is known to be rather low, and it was possible that the influence of the core aa 70 mutations might be overestimated in the phylogenetic trees. In addition, using genetic distance data obtained from the phylogenetic analysis, the genetic distances between every two HCVs with core aa 70R, between every two HCVs with a residue other than R at core aa 70 (core aa 70non-R), and between every two HCVs with different residues at core aa 70 (one HCV with R and one with a non-R residue) were also compared statistically in order to reveal the genetic associations among those HCV core subgroups.

Statistical analysis. Statistical differences in the parameters, including all available patients' demographic, biochemical, hematological, virological, and SNP data in the three groups (CH, LC, and HCC), were determined using the Kruskal-Wallis test. The Mann-Whitney U test was used for statistical differences in numerical variables between two groups. Trends for categorical data

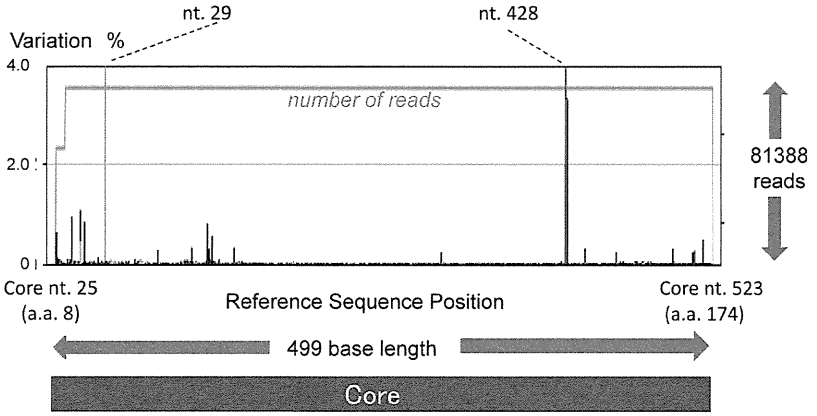

FIG 1 The core region of pCV-J4L6S (genotype 1b) from the 25th to the 523rd nucleotide, and from the 9th to the 174th codon, was subjected to deep sequencing, and the background error rate of pyrosequencing was calculated. In order to show rare background errors, those errors with low percentages are magnified.

were evaluated using the Cochran-Armitage trend test. All *P* values of <0.05 by the two-tailed test were considered significant in comparisons of genetic distances.

Nucleotide sequence accession numbers. The dominant sequences of the core regions from the patient samples have been deposited in GenBank under accession numbers AB822372.1 to AB822459.1.

RESULTS

Calculation of background errors in deep sequencing. First, the background error rate of pyrosequencing was calculated with a plasmid containing a cloned HCV sequence (pCV-J4L6S). Figure 1 shows the results of deep sequencing from the 25th to the 523rd nucleotide of the core region (499 nt) in pCV-J4L6S. Among 81,388 reads, each 499 nt long, the maximum error rate was 99.14% at the 428th base, and the next highest error rate was 64.17% at the 29th base. A six-C homopolymer region ending at the 428th base was read as a five-C homopolymer and a five-A homopolymer region ending at the 29th base was read as a four-A homopolymer in most of the obtained sequences; these homopolymer sequences are a weak point of pyrosequencing (26, 27).

A base appearing six times consecutively was the longest sequence of identical repeated nucleotides and was found only at the 428th nt position in the core region of pCV-J4L6S. Five consecutive bases were found at two sites (the 336th and 436th nt) in addition to the 29th nt position, but this error (i.e., the miscounting of homopolymer length) occurred only at the 29th base closest to the end of the sequence. Excluding the 428th and 29th nt positions, the error rate was ~1% or lower, as shown in Fig. 1. There was no single nucleotide error in the codons for aa 70 and aa 91in the repeated control experiments. From repeated deep sequencing of the plasmid, the overall nucleotide error rate was calculated as 0.092 ± 0.005 (mean ± standard deviation [SD])/base. Based on this analysis, a mixture of bases detectable above the background error of 0.102% (mean background error rate + 2 SDs) was defined as a real mixture.

Baseline characteristics. The baseline characteristics of the 79 patients are shown in Table 1. The values for viral factors core aa 70 and aa 91, NS5A-ISDR, and NS5A-IRRDR are the results of the direct-sequencing study. As shown in Table 1, the results for the variables platelets, albumin, alpha-fetoprotein, and core aa 70 differed significantly according to disease progression. On the other hand, no difference was observed in core aa 91 and IL28B SNP (rs8099917) according to disease progression.

Quasispecies nature of core amino acid 70 and disease progression. Deep sequencing of the core region was carried out with a variety of clinical samples. Simultaneous analysis was carried out using the barcoded primers, and approximately 950 reads were obtained per sample (Table 2). When the analysis was focused on core aa 70, the proportion of non-R (Q/H) sequences increased as disease severity advanced from CH to LC to HCC, as shown in Fig. 2A and Table 3 ($P = 0.018$). When a mixture of 0.102% or more was defined as a real mixture, deep sequencing showed the presence of a mixture at core aa 70 in 71 of the 79 patients (89.9%).

The relationship between disease progression and the occurrence of a quasispecies was also analyzed at the codon for core aa 91, which has also been reported to be associated with the outcomes of IFN therapy and the occurrence of HCC. As with core aa 70, a quasispecies was recognized at this site, and mixtures were observed in most patients. However, in contrast to the core aa 70 codon, there was no clear relationship with disease progression (Fig. 2B and Table 3).

Figure 2C and D show the correlation between mixtures in the core aa 70 and 91 regions and IL28B SNPs. As shown in Fig. 2C and Table 4, the proportion of mutations in the core aa 70 codon was highly dependent on the IL28B SNP (*P*, <0.005 [Table 4]). Such a relationship was also found between the proportion of mutations in core aa 91 and IL28B SNPs (Fig. 2D and Table 4), although its significance was rather weaker (*P*, 0.010).

TABLE 2 Amplicon read numbers obtained by deep sequencing of samples from 79 patients

Group	No. of patients	Total no. of reads	Avg no. of reads ± SD (range)/sample
CH	25	22,365	894.6 ± 222.8 (367–1,486)
LC	29	28,537	982.5 ± 258.1 (660–1,528)
HCC	25	24,284	971.4 ± 242.5 (405–1,749)
Total	79	75,186	951.7 ± 240.9 (367–1,749)

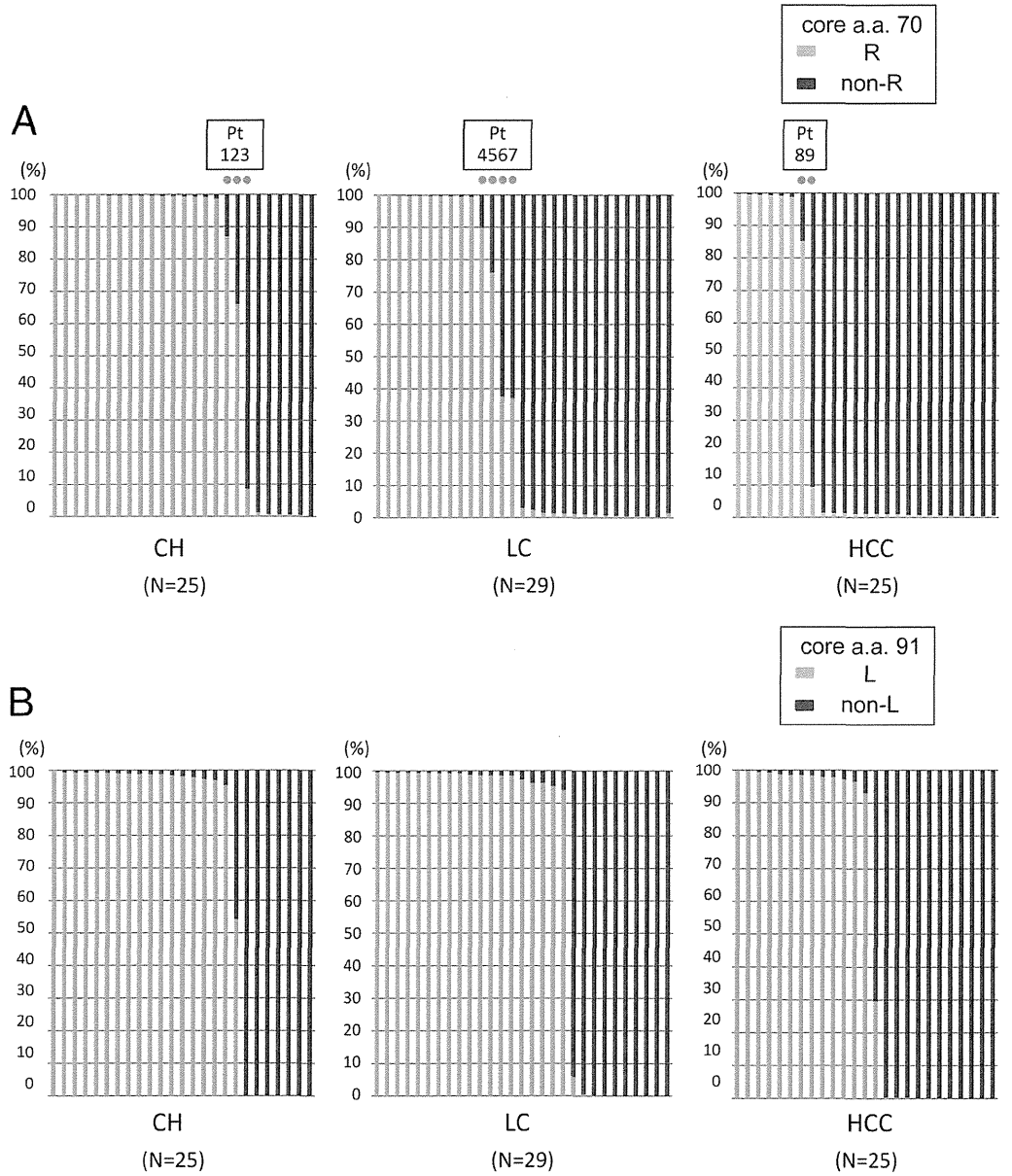

FIG 2 The core regions of the HCV genomes from 79 patients persistently infected with HCV genotype 1b (25 patients with chronic hepatitis [CH], 29 with liver cirrhosis [LC], and 25 with hepatocellular carcinoma [HCC]) were subjected to deep sequencing. Each bar represents the result for a single patient. At the specific locations of core aa 70 and aa 91, no single nucleotide mutation was observed in the previous control plasmid experiment. (A) Disease stages and percentages of mutations at core aa 70. Nine dots indicate the nine patients with a high mixture rate (between 5% and 95%) at core aa 70 (R and non-R). (B) Disease stages and percentages of mutations at core aa 91. (C) IL28B SNP and percentages of mutations at core aa 70. (D) IL28B SNP and percentages of mutations at core aa 91.

Since direct sequencing has also shown an association of several sites other than core aa 70 and 91 with the occurrence of HCC (6), those sites were also investigated for such an association. However, there was no clear relationship between these sites and disease progression, except for G209A (core aa R70Q) (see Fig. S1 and Table S2 in the supplemental material).

Phylogenetic tree analysis of HCV core region focusing on the core aa 70 residue. Because it was clear that the core aa 70 quasispecies state was significantly associated with disease progression, our next interest was to determine how this single hot spot is correlated with the remainder of the (almost-entire) core region. Therefore, phylogenetic tree analysis was performed, and genetic distances among aa 70-associated core sequences were also compared statistically. In constructing all phylogenetic trees, the three bases of the core 70 codon were removed, since the mutation rate of other parts of the core region is known to be rather low, and it was possible that the influence of the core aa 70 mutations might be overestimated in the phylogenetic trees.

At first, to determine the associations among the remainder of the core sequences across different patients, a phylogenetic tree was constructed for all 79 patients using dominant core sequences obtained from each patient. In constructing the tree, two domi-

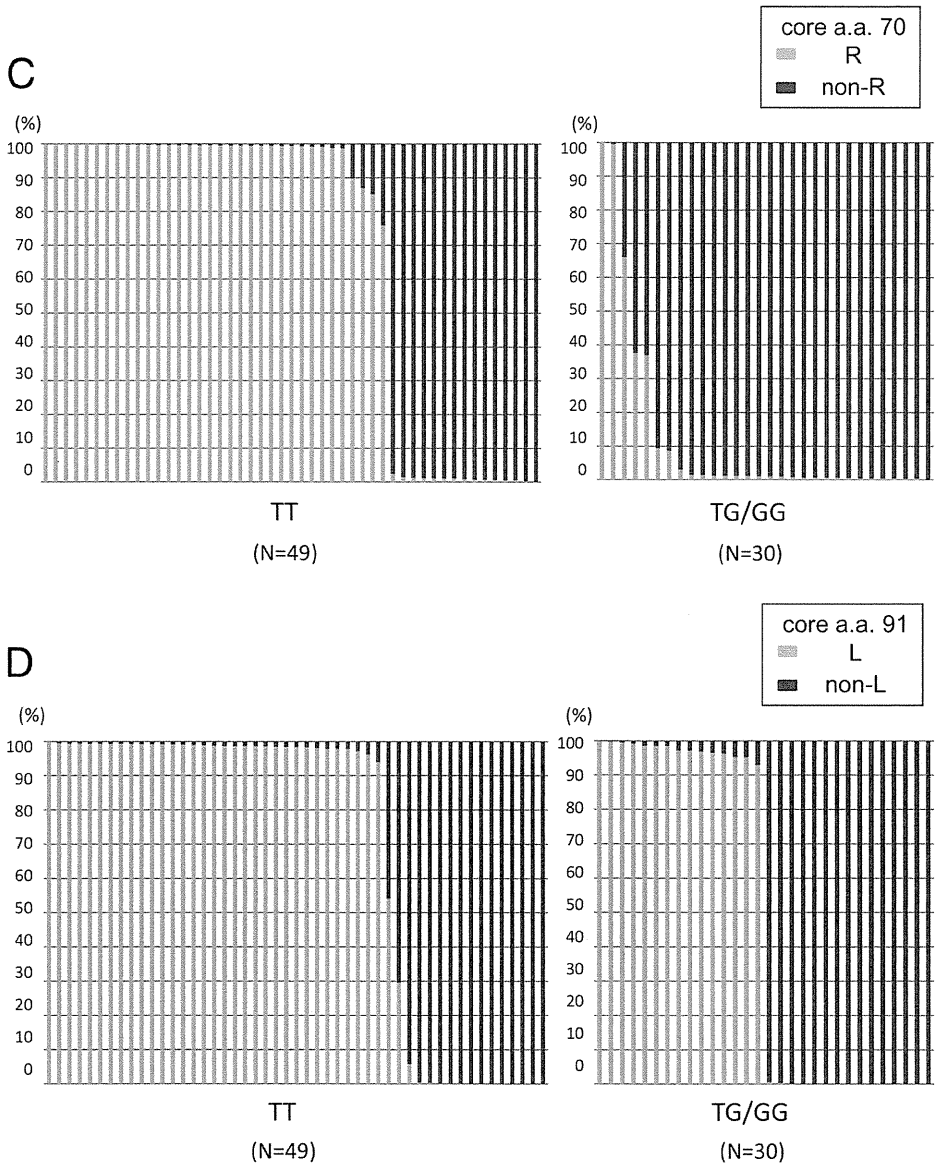

FIG 2 continued

nant sequences (the dominant core sequence in isolates with aa 70R and the dominant core sequence in isolates with aa 70non-R) were included in the analysis for each of the nine patients with high mixture rates (5% or more) of R and non-R at core aa 70 (Fig. 2A), while one dominant sequence each was included for other patients. As shown in Fig. 3A and Table 5, genetic distances calculated between every two core sequences with aa 70R (R-R) were significantly larger than those between two core sequences with aa 70non-R (non-R–non-R) or those between a

TABLE 3 Correlation between quasispecies composition and disease progression

Patient group (*n*)	Median % (range) with:	
	R at core aa 70[a]	L at core aa 91[b]
CH (25)	70.35 (0.00–100.00)	69.12 (0.00–99.40)
LC (29)	43.22 (0.24–100.00)	64.54 (0.00–99.50)
HCC (25)	28.20 (0.00–99.80)	52.23 (0.00–100.00)

[a] *P*, 0.018.
[b] *P*, 0.630.

TABLE 4 Correlation between quasispecies composition and IL28B SNP rs8099917

Group (sequence at IL28B SNP rs8099917)	Median % (range) with:	
	R at core aa 70[a]	L at core aa 91[b]
TT (n = 49)	68.15 (0.00–100.00)	68.24 (0.00–100.00)
TG/GG (n = 30)	12.64 (0.00–100.00)	48.76 (0.00–100.00)

[a] *P*, <0.005.
[b] *P*, 0.010.

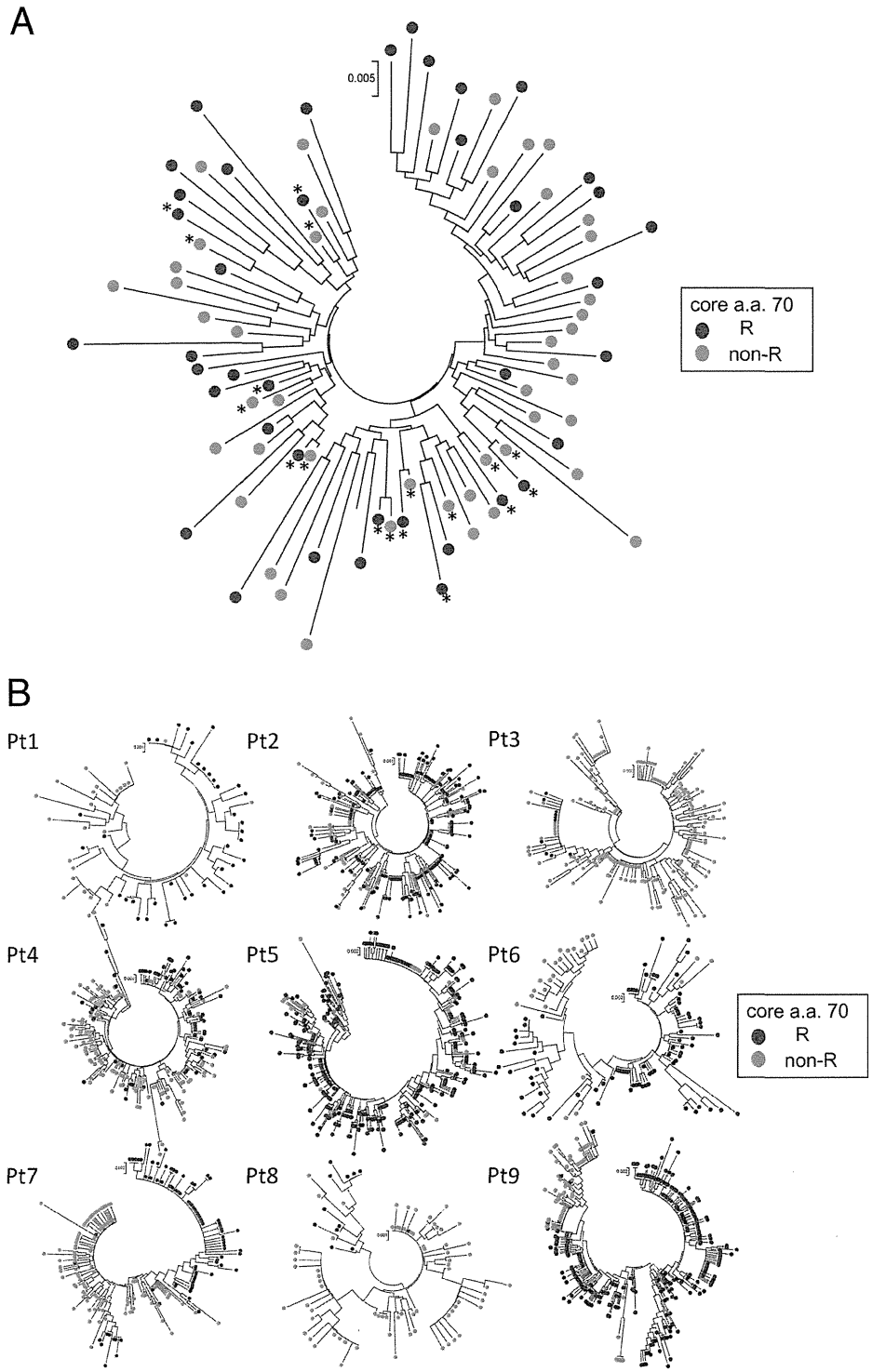

FIG 3 Phylogenetic trees were constructed using core sequences covering almost the entire core region. In the construction of those trees, the three bases of the core 70 codon were removed in the analysis of all 79 patients. Branches with core aa 70R are indicated by blue circles, while those with core aa 70non-R are indicated by pink circles. (A) Phylogenetic trees were constructed for all 79 patients by using dominant core sequences obtained from each patient. In the construction of the tree, two dominant sequences (a dominant core sequence in isolates with aa 70R and a dominant core sequence in isolates with aa 70non-R) were included in the analysis for each of the nine patients with high mixture rates (5% or more) of R and non-R at core aa 70 (Fig. 2A), while one dominant sequence each was included for other patients. (B) A phylogenetic tree of the core region was constructed for each patient with a high mixture rate (5% or more) of core aa 70R and core aa 70non-R. A total of nine patients were included in this analysis (patients 1 to 3 had CH; patients 4 to 7 had LC; and patients 9 and 10 had HCC). Pt, patient.

TABLE 5 Comparison of genetic distances among core subgroups related to aa 70 residues

Patient(s)[a]	Genetic distance (mean ± SD) between two core sequences[b]			Comparison of genetic distance measurements					
				Non-R–R vs non-R–non-R		Non-R–R vs R-R		Non-R–non-R vs R-R	
	Non-R–non-R	Non-R–R	R-R	Larger genetic distance	*P*	Larger genetic distance	*P*	Larger genetic distance	*P*
All (n = 79)	0.0349 ± 0.0101	0.0379 ± 0.0109	0.0401 ± 0.0113	Non-R–R	<0.001	R-R	<0.001	R-R	<0.001
CH									
Pt 1	0.0086 ± 0.0042	0.0098 ± 0.0037	0.0064 ± 0.0042	Non-R–R	<0.001	Non-R–R	<0.001	Non-R–non-R	<0.001
Pt 2	0.0097 ± 0.0048	0.0104 ± 0.0041	0.0087 ± 0.0038	Non-R–R	<0.001	Non-R–R	<0.001	Non-R–non-R	0.009
Pt 3	0.0107 ± 0.0058	0.0137 ± 0.0050	0.0034 ± 0.0022	Non-R–R	<0.001	Non-R–R	<0.001	Non-R–non-R	<0.001
LC									
Pt 4	0.0078 ± 0.0036	0.0103 ± 0.0038	0.0053 ± 0.0029	Non-R–R	<0.001	Non-R–R	<0.001	Non-R–non-R	<0.001
Pt 5	0.0118 ± 0.0090	0.0232 ± 0.0085	0.0159 ± 0.0170	Non-R–R	<0.001	Non-R–R	<0.001	No difference	0.991
Pt 6	0.0115 ± 0.0057	0.0121 ± 0.0055	0.0108 ± 0.0056	Non-R–R	<0.001	Non-R–R	<0.001	Non-R–non-R	<0.001
Pt 7	0.0141 ± 0.0085	0.0146 ± 0.0070	0.0136 ± 0.0067	Non-R–R	0.002	Non-R–R	<0.001	Non-R–non-R	<0.001
HCC									
Pt 8	0.0124 ± 0.0063	0.0225 ± 0.0060	0.0181 ± 0.0094	Non-R–R	<0.001	Non-R–R	<0.001	R-R	<0.001
Pt 9	0.0082 ± 0.0042	0.0162 ± 0.0047	0.0078 ± 0.0050	Non-R–R	<0.001	Non-R–R	<0.001	Non-R–non-R	<0.001

[a] Pt, patient.

[b] Non-R–non-R, comparison of two core sequences with residues other than R at aa 70; Non-R–R, comparison of a core sequence with a residue other than R at aa 70 and a core sequence with aa 70R; R-R, comparison of two core sequences with aa 70R. Genetic distances were calculated for all patients by using dominant sequences and for a single patient by using quasispecies sequences.

core sequence with aa 70R and a core sequence with aa 70non-R (non-R–R), demonstrating that core sequences with aa 70R were heterogeneous, while core sequences with aa 70non-R were homogeneous.

Next, to determine the association of the remainder of the core sequences in a single patient, phylogenetic trees were also constructed for each of the nine patients with high mixture rates (5% or more) of R and non-R residues at core aa 70 (Fig. 3B). As shown in Fig. 3B, HCV isolates with core aa 70R and those with core aa 70non-R formed distinctly clustered subgroups on the phylogenetic tree, according to the mutation status at core aa 70. Comparison of genetic distances also proved the finding that HCV isolates with core aa 70R and those with core aa 70non-R form distinctly clustered subgroups on the phylogenetic tree in a single patient, since genetic distances calculated between every two core sequences with aa 70R (R-R) or between every two core sequences with aa 70non-R (non-R–non-R) were significantly smaller than those between a core sequence with aa 70R and a core sequence with aa 70non-R (non-R–R). On the other hand, no significant difference was found when the genetic distance between two core sequences with aa 70non-R (non-R–non-R) and that between two core sequences with aa 70R (R-R) were compared in a single patient (Table 5).

Since the genetic relationships of the remainder of the core sequences were found to differ significantly according to the core aa 70 residue, we then investigated whether there are any common haplotypic sequences specific to each residue. In the comparison of dominant sequences in all 79 patients, most amino acid substitutions clustered in three amino acids (aa 70, aa 75, and aa 91) both in core sequences with aa 70R and in those with aa 70nonR, but no other substitutions specific to each core aa 70 residue were found (Fig. 4).

Quasispecies at core aa 70 and clinical characteristics. To clarify the association of the core aa 70 quasispecies with the clinical picture, levels of gamma-glutamyl transpeptidase (γ-GTP), albumin, platelets, and alpha-fetoprotein, as well as disease progression in the liver, were investigated for correlation with the core aa 70R/non-R mixture ratio. As shown in Fig. 5A and B, the values for these clinical parameters became significantly more abnormal as the proportion of non-R residues increased, showing that a high proportion of non-R residues at core aa 70 was significantly associated with disease severity and hepatocarcinogenesis.

DISCUSSION

This study examined, for the first time, the relationship between the progression of liver disease and the quasispecies nature of the HCV core region (already known to be associated with liver disease progression) by deep sequencing, with the focus on the core aa 70 residue. The analysis revealed that core aa 70 existed as a mixture of "mutant" Q/H (non-R) and "wild-type" R residues in most of the patients and that the proportion of mutant residues increased as liver disease advanced to LC and HCC. Meanwhile, phylogenetic analysis showed that the viral sequences of the almost-entire core region differed genetically depending on the status of core aa 70.

Before starting the analysis, we verified the rate of background error associated with the process of pyrosequencing by analyzing the control plasmid pCV-J4L6S (Fig. 1). Homopolymers of repeated bases, a weak point of pyrosequencing, were generated at two sites, with the same base appearing five and six times. The overall mutation rate at other sites was 0.092% ± 0.005%, and a mutation rate of 0.102% (mean + 2 SDs) or higher was defined as significant in the analysis, in order to avoid detecting background errors.

We focused our analysis on the quasispecies state of core aa 70,

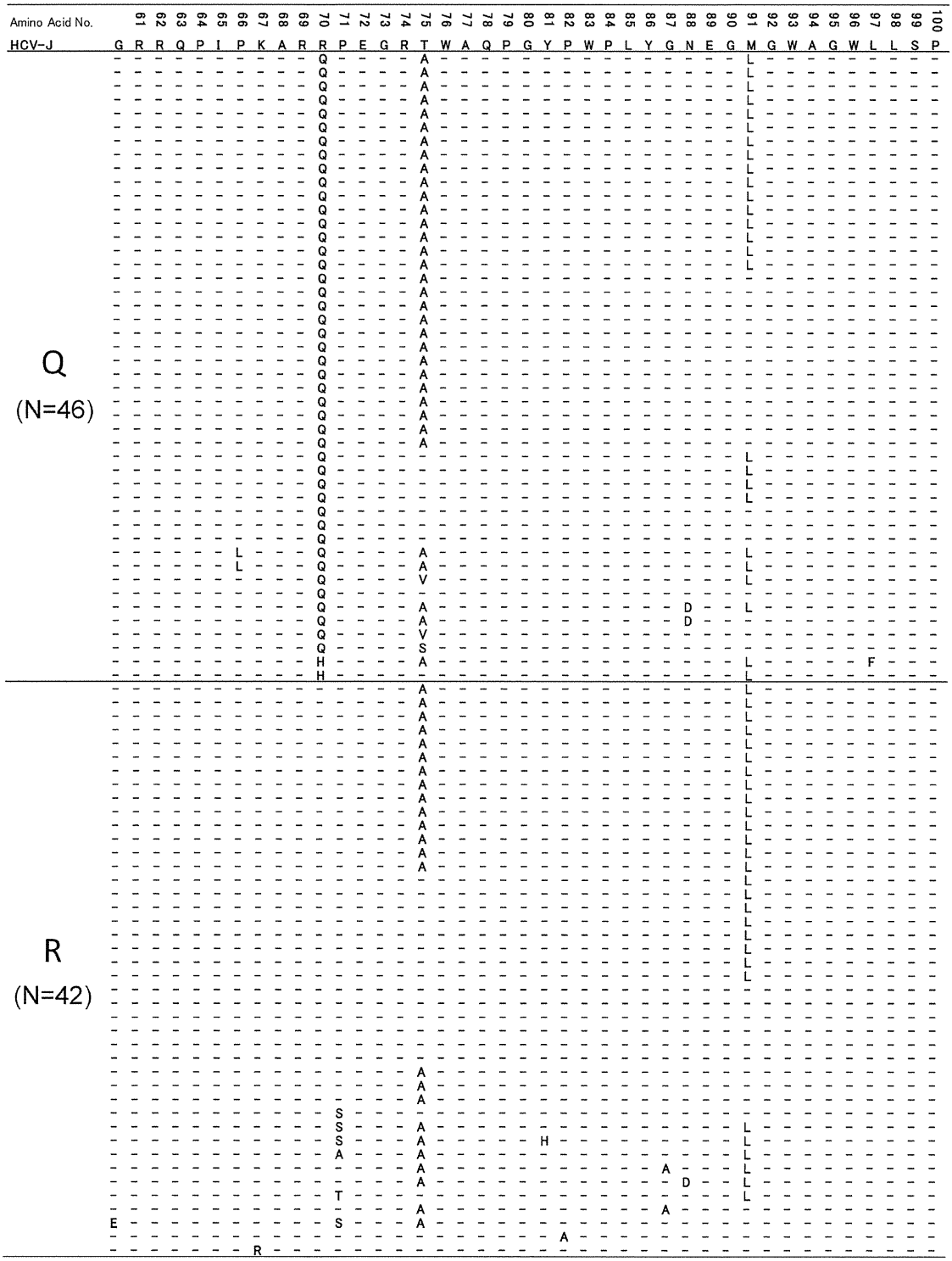

FIG 4 Dominant core amino acid haplotypic sequences dependent on the core aa 70 residues are given for all 79 patients. Two dominant sequences (a dominant core sequence in isolates with aa 70R and a dominant core sequence in isolates with aa 70non-R) were included for each of nine patients with high mixture rates (5% or more) of R and non-R at core aa 70, while one dominant sequence each was included for other patients. Therefore, a total of 88 haplotypic sequences are shown here. Since most amino acid mutations were observed in the limited core region, only that part of the core sequence is shown. The HCV-J isolate is used as the reference sequence for the core region.

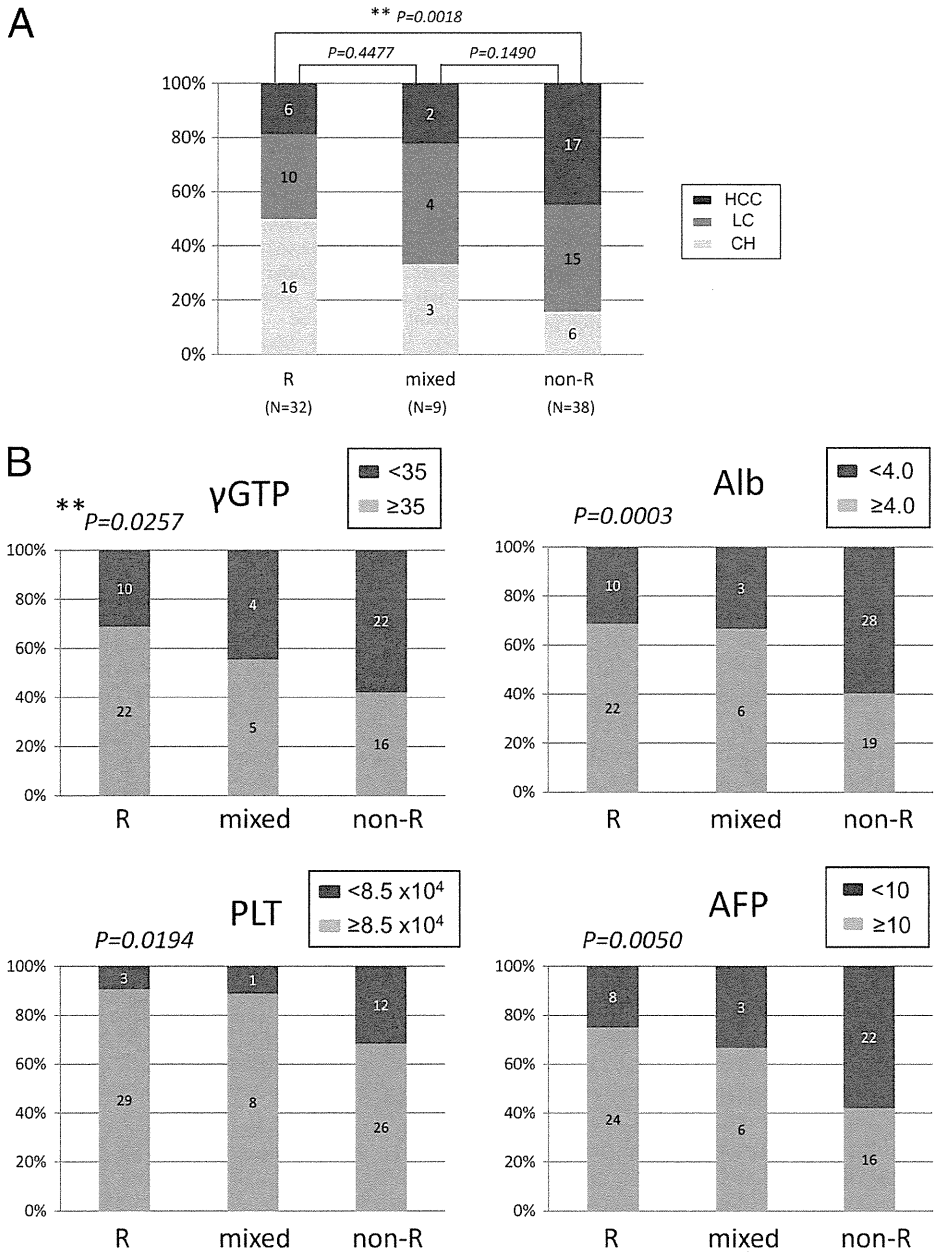

FIG 5 The advance of liver disease (A) and the levels of γ-GTP, albumin (Alb), platelets (PLT), and alpha-fetoprotein (AFP) (B) were investigated for correlation with the ratio of R to non-R at core aa 70. Results for R/R + non-R ratios of ≥95% (R), ≥5% and <95% (mixed), and <5% (non-R) are shown. **, Cochran-Armitage analysis.

because the presence of a quasispecies was expected at this position, considering reports by previous studies of its association with liver disease progression and the frequent observation of time-dependent changes (8, 9). R and non-R residues were mixed in 89.9% of the 79 patients examined in this study, indicating that the absence of a mixture was rare. Furthermore, the percentage of total isolates encoding non-R residues at this position showed a relationship with the advance of chronic liver disease, as shown in Fig. 2A and Table 3. Therefore, with regard to the relationship between the advance of liver disease and core aa 70, it may be accurate to say that a change in the ratio of amino acids at core aa 70, rather than mutation of core aa 70, was related to the advance of liver disease.

Because information for almost the entire core region was obtained from each patient, our next interest was to determine whether core aa 70 is associated with other viral regions. In other words, we sought to determine whether HCVs with core aa 70R and HCVs with core aa 70non-R are phylogenetically distinct variants. To clarify the issue, phylogenetic tree analysis using dominant sequences for the (almost-entire) core regions from all 79 patients was performed at first. This analysis disclosed, after the calculation of genetic distances, that core sequences with aa

70non-R were significantly more homogeneous than those with aa 70R, demonstrating that the hot spot core aa 70 residue is significantly associated with the remainder of the core sequence. Although the underlying mechanism is unclear, we speculated that the close correlation between core aa 70 residues and IL28B SNPs might have contributed to the result. That is, since endogenous IFN levels are known to be upregulated in patients with IL28B minor types (TG/GG) relative to those in patients with the IL28B major type (TT) in its natural state (28), it is possible that HCVs with core aa 70non-R, which are closely linked to IL28B TG/GG, are under strong antiviral pressure induced by IFN, resulting in the selection of more-homogeneous HCVs, which can survive in such an environment.

Considering this possibility, we proceeded to perform phylogenetic analyses of core sequences in single patients with high-percentage mixtures (5% or more) of R and non-R residues at core aa 70 by using deep-sequencing data, since the influence of endogenous IFNs was considered equal for all HCV isolates in a single patient. The deep-sequencing data showed that the genetic heterogeneity of core sequences in a single patient did not differ according to the core aa 70 residue but that core sequences formed distinct subgroups on the phylogenetic tree according to the core aa 70 residue (Fig. 3B), and this result was also proved by the calculation of genetic distances (Table 5). However, since no common haplotypic sequences specific to each residue at core aa 70 were found across the patients (Fig. 4), we cannot determine whether core aa 70R and aa 70non-R HCVs are phylogenetically distinct variants. It is possible that the result simply reflects a major evolutional event of core aa 70 mutations followed by derivative variants; however, extension of the investigation and analysis to viral regions beyond the core region might reveal such associations. However, due to the technical limitations of second-generation sequencers, deep-sequencing analysis of the long amplicon is difficult, and new technology is needed.

With regard to the mechanism underlying the relationship between the core protein and disease progression and hepatocarcinogenesis, a study using transgenic mice showed that the core protein induces HCC (29). Fat metabolism was accelerated in the liver, leading to inflammation, iron metabolism, oxidative stress, and insulin resistance, which were considered to be the carcinogenic factors (30–32). Clinically, mutation of the core and the concentration of γ-GTP in serum, a marker of steatosis, are related, and the relationship between IL28B SNP and liver steatosis or γ-GTP has been elucidated (33). In this study, moreover, we have confirmed the correlation between the core aa 70 mixture ratio, determined by deep-sequencing analysis, and clinical parameters reflecting disease progression, illustrating the significant association of core aa 70 with disease progression (Fig. 5A and B).

In conclusion, the quasispecies state of the core region was analyzed by deep sequencing. It was found that the status of the quasispecies was closely related to the advance of HCV-associated liver disease. In order to understand the mechanism of hepatocarcinogenesis, it is desirable to elucidate pathogenesis further by detailed examination of the quasispecies of the HCV core gene.

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ORIGINAL ARTICLE—Liver, Pancreas, and Biliary Tract

Genetic variation near interleukin 28B and the risk of hepatocellular carcinoma in patients with chronic hepatitis C

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Abstract
Background We aimed to clarify the association between single nucleotide polymorphism (SNP) located near *interleukin 28B* and hepatocellular carcinoma (HCC).
Methods A cohort comprising 792 patients treated with interferon for chronic hepatitis C was investigated. SNPs at rs8099917 and rs12979860 were determined. Cumulative incidence and HCC risk were analyzed by Kaplan–Meier and Cox proportional hazard analyses for a mean follow-up period of 4.9 years. Fibrosis progression rate (FPR) was determined in these patients with a known time of infection ($n = 294$).
Results Cumulative HCC incidence was significantly higher in rs8099917 nonTT (minor homozygote or heterozygote) patients than in rs8099917 TT (major homozygote) patients (20.8 vs. 10.5 % over 10 years, logrank test, $p = 0.002$). This difference was notable in patients infected with genotype 1 and those treated with pegylated interferon and ribavirin. Among nonSVRs, interferon had a limited effect in suppressing alanine aminotransferase (ALT) and/or α-fetoprotein (AFP) levels in nonTT patients. The suppression of these values after interferon therapy was associated with a lower incidence of HCC. FPR were similar in TT and nonTT patients.
Conclusions rs8099917 nonTT is related to higher HCC development in patients with HCV genotype 1 and those treated with pegylated interferon and ribavirin. Higher HCC incidence observed in nonTT patients partly results from the limited suppression of ALT and/or AFP by interferon in these patients.

Keywords Hepatocarcinogenesis · Fibrosis · Interferon · Alanine aminotransferase · α-Fetoprotein

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