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Highly sensitive lens culinaris agglutinin-reactive α-fetoprotein is useful for early detection of hepatocellular carcinoma in patients with chronic liver disease

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Abstract. The fucosylated fraction of α-fetoprotein (AFP-L3) is a specific marker for hepatocellular carcinoma (HCC). However, conventional AFP-L3% (c-AFP-L3%) has not always been reliable in cases with low serum α-fetoprotein (AFP) levels. In this study, we evaluated the clinical utility of a newly developed assay, highly sensitive AFP-L3% (hs-AFP-L3%). Subjects included 74 patients with benign liver disease (BLD), including chronic hepatitis and cirrhosis, and 94 with HCC. Serum hs-AFP-L3% was significantly higher than c-AFP-L3% in patients with early-stage HCC (solitary or <20 mm in diameter). Additionally, hs-AFP-L3% was significantly increased in patients with well-differentiated HCC. In patients with serum AFP <20 ng/ml, the sensitivities of c-AFP-L3% and hs-AFP-L3% were 12.5 and 44.6%, respectively, at a cut-off value of 5%. In 59 BLD patients with serum AFP <20 ng/ml, the HCC-positive rate in patients with hs-AFP-L3% ≥5% was significantly higher compared to those with hs-AFP-L3% <5% during the follow-up period (median, 35 months; range, 5-48 months). Importantly, none of the BLD patients with both serum AFP <20 ng/ml and hs-AFP-L3% <5% developed HCC. These results indicated that hs-AFP-L3% is useful for early detection of HCC in BLD patients, even for those with serum AFP <20 ng/ml. Furthermore, since hs-AFP-L3% increases before HCC is detectable by various advanced imaging modalities, this assay may help identify BLD patients with a higher risk of HCC.

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Key words: α-fetoprotein, α-fetoprotein fucosylated fraction L3, hepatocellular carcinoma, hepatocarcinogenesis

Introduction

Hepatocellular carcinoma (HCC) is the sixth most common cancer in the world, and the third most common cause of cancer-related death (1). Although it is more common in Asia and Africa, its incidence in the United States has increased over the past two decades, largely due to the spread of hepatitis C (HCV) infection, which is an underlying risk factor (2). Early detection of HCC increases the potential for curative treatment and improves prognosis. Several methods developed for the diagnosis of HCC, including evaluation of serum markers, ultrasonography (US), computed tomography (CT) and magnetic resonance imaging (MRI), have been tested clinically. α-fetoprotein (AFP) and des-γ carboxy prothrombin (DCP), serum proteins that are elevated in HCC, are the most widely used markers. Although routine screening offers the best chance for early tumor detection, the reported sensitivities and specificities of elevated serum AFP and DCP levels vary significantly (3-8). Furthermore, serum AFP levels increase in only 30-40% of patients with HCC, especially early in the disease process (5). Additionally, an increase in serum AFP is also seen in patients with non-cancerous conditions, including cirrhosis or exacerbation of chronic hepatitis (9). AFP-L3, the lectin lens culinaris agglutinin-bound fraction, is one of the three glycoforms of AFP, and is the major glycoform elevated in the serum of HCC patients. The reported sensitivities of AFP-L3 as a method of detecting HCC range from 75-97% with specificities of 90-92% (10,11). In cases of HCC, however, high percentage of AFP-L3 is closely associated with poor differentiation and biologically malignant characteristics, including portal vein invasion, of neoplastic cells (11,12). Therefore, it is not clear how useful this test is for the early detection of HCC. Additionally, measurement of AFP-L3 has not always been reliable for serum samples with low total AFP concentration, as determined by conventional lectin affinity system (LiBASys) (13).

Recently, a novel automated immunoassay for AFP-L3 has been developed. The new method uses on-chip electrokinetic reaction and separation by affinity electrophoresis (micro-total

analysis system; μ-TAS) (14). In patients with an AFP level of ≥20 μg/ml, μ-TAS AFP-L3% correlated well with LiBASys AFP-L3% (15). Furthermore, this system has enabled the accurate measurement of AFP-L3% at very low AFP concentrations. Therefore, in this retrospective study, we investigated the clinical utility of the new highly sensitive μ-TAS AFP-L3% assay for diagnosis of HCC in a population of patients with HCC or benign liver diseases (BLD), including chronic hepatitis or cirrhosis.

Patients and methods

Patients. Between December 2006 and September 2010, frozen serum samples were obtained from 94 patients with HCC, as well as from 74 patients with BLD, who had chronic hepatitis or liver cirrhosis, but not HCC (Table I). All patients met the eligibility criteria (availability of stored serum samples and written informed consent). Among the BLD patients, 20 were positive for hepatitis B surface antigen (HBsAg), 43 were positive for anti-hepatitis C virus (HCV) antibody, and 11 were negative for either HBsAg or anti-HCV antibody. The BLD patients were followed after serum sampling for 32.8±12.3 months (median, 35; range, 5-48); liver imaging was performed by US at 6- to 12-month intervals in most patients with chronic hepatitis, and CT, MRI, or US was performed at 3- to 6-month intervals in patients with liver cirrhosis.

HCC patients were diagnosed using imaging modalities such as US, MRI and CT during hepatic arteriography. Vascular invasion was evaluated by imaging modalities. In some cases that showed atypical features upon imaging, ultrasound-guided biopsies were performed. Based on imaging findings, tumor stage was ranked using the tumor-node-metastasis (TMN) staging system of the Liver Cancer Study Group of Japan (16,17): T1 (fulfilling the following three conditions: solitary, 2 cm, no vessel invasion), T2 (fulfilling two of the three conditions), T3 (fulfilling one of the three conditions), T4 (fulfilling none of the three conditions or showing presence of distant metastasis); N0 (no lymph node metastasis), N1 (metastasis to lymph nodes); M0 (no distant metastasis), M1 (distant metastasis); stage 1 (T1N0M0), stage II (T2N0M0), stage III (T3N0M0), and stage IV (T4N0M0 or any TN1M0, or any TN0-1M1).

Measurement of serum AFP and AFP-L3%. For the HCC group, AFP and AFP-L3% were measured in the same sample obtained at the time of HCC diagnosis, before any treatment. For the BLD without HCC group, measurements were made at the time of diagnosis of chronic liver disease. Highly sensitive AFP-L3% (hs-AFP-L3%) were measured by a microchip capillary electrophoresis and liquid-phase binding assay on a μ-TASWako i30 auto analyzer (Wako Pure Chemical Industries, Ltd., Osaka, Japan) (15). Conventional AFP-L3% (c-AFP-L3%) was examined using a column chromatography and liquid-phase binding assay on a LiBASys auto analyzer (Wako Pure Chemical Industries, Ltd.) (13). The analytical sensitivity of the μ-TASWako i30 auto analyzer is 0.3 μg/ml AFP; the AFP-L3% can be measured when AFP-L3 is over 0.3 μg/ml. Although the analytical sensitivity of the LiBASys is 0.8 μg/ml AFP, AFP-L3% cannot be measured at AFP <10 ng/ml. Therefore, the correlation between μ-TAS-L3% and LiBA-L3% was poor at AFP <20 ng/ml.

Statistical analysis. We used the Mann-Whitney U test, Z test and Chi-square test for evaluation of the statistical significance of each finding. SPSS version 17.0J (SPSS Inc., Chicago, IL, USA) was used to perform statistical analysis; $p<0.05$ was considered to indicate statistical significance.

Results

Clinical feature of patients. The demographics, etiology of liver disease, hepatic functional reserve ranked by Child-Pugh classification, tumor stage, tumor size and tumor number of the study patients are summarized in Table I. The HCC group included 94 patients: 35 patients with stage I, 35 with stage II, 14 with stage III, and 10 with stage IV; thus, ~75% of HCC cases were stage I or II. The incidence of cirrhosis in HCC patients (55.3%) was significantly higher than in BLD (25.7%), whereas the hepatic reserve expressed by Child-Pugh classification of HCC patients was significantly preserved compared with BLD patients.

Serum AFP levels in patients with HCC were significantly higher than those with BLD (Table I and Fig. 1A). hs-AFP-L3% was measurable in 47.3 and 78.7% of patients with BLD and HCC, respectively, whereas c-AFP-L3% was detected in 31.1 and 63.8% of patients. Thus, hs-AFP-L3% was significantly higher than c-AFP-L3% in both BLD and HCC patients (Table I and Fig. 1B). Since a cut-off value of 5% has been reported to be useful for diagnosis of HCC using hs-AFP-L3% (18), the cut-off value for AFP-L3% was set at 5% in the present study. The sensitivity and specificity of hs-AFP-L3% were 57.0 and 63.5%, respectively, whereas those of c-AFP-L3% were 40.4 and 81.1%.

hs-AFP-L3% significantly increases in HCC patients at early stage. Next, we analyzed serum AFP levels, c-AFP-L3% and hs-AFP-L3%, and compared early and advanced stages of HCC (Fig. 2). When compared with HCC patients with stage I or II cancer, serum AFP levels were significantly increased in patients with stage III and IV disease (Fig. 2A). Both c-AFP-L3% and hs-AFP-L3% in HCC patients with advanced stages were also significantly higher than in patients with early stages (Fig. 2B). Although 86% of HCC patients with stage I (n=35) exhibited serum AFP <20 ng/ml, c-AFP-L3% and hs-AFP-L3% were measurable in 46 and 69% of these patients, respectively; hs-AFP-L3% was significantly higher than c-AFP-L3%. Consequently, in HCC patients at stage I, the sensitivity of c-AFP-L3% or hs-AFP-L3% at a cut-off level of 5% were 17.1 or 48.6%, respectively.

Next, we evaluated the relationship between AFP-L3% and tumor number or size (Fig. 3). hs-AFP-L3% was significantly higher than c-AFP-L3%, even in patients with single or small HCC (<20 mm in diameter) (Fig. 3). Conversely, when compared to HCC patients with solitary or small HCC, both c-AFP-L3% and hs-AFP-L3% were increased in cases with multiple or ≥20 mm HCC, and there was no statistical difference between c-AFP-L3% and hs-AFP-L3%. These results indicate that hs-AFP-L3% is a useful biomarker for detecting early-stage HCC.

An increase in hs-AFP-L3% is observed in both BLD and HCC patients with AFP <20 ng/ml. We analyzed c-AFP-L3%

Table I. Clinical features of patients with BLD and HCC.

	BLD (n=74)	HCC (n=94)	p-value
Age	56.23±13.88	65.76±12.98[a]	<0.001
Gender (male/female)	30/44	56/38[a]	0.015
CH/LC	55/19	42/52[a]	<0.001
HBV/HCV/NBNC	20/43/11	5/61/28[a]	<0.001
Child-Pugh class (A/B/C/unknown)	39/5/4/26	75/19/0/0[a]	<0.001
TNM stage (I/II/III/IV)		35/35/14/10	
Tumor size (mean ± SD)		22.35±16.42	
<20 mm/≥20 mm		58/36	
Tumor number (single/multiple)		50/44	
AFP (ng/ml)	46.17±163.6	2871.5±9882.7[a]	<0.001
c-AFP-L3%	2.96±6.45	18.19±26.95[a]	<0.001
hs-AFP-L3%	3.84±5.59	21.12±29.01[a]	<0.001
Platelet count (x10^4/μl)	14.98±6.82	11.39±4.73[a]	0.001
AST (IU/l)	70.55±95.87	55.78±22.92	0.099
ALT (IU/l)	85.38±144.71	48.28±24.13	0.783

BLD, benign liver disease; HCC, hepatocellular carcinoma; CH, chronic hepatitis; LC, liver cirrhosis; HBV, hepatitis B virus; HCV, hepatitis C virus; hs-AFP-L3%, hypersensitive-AFP-L3%; c-AFP-L3%, conventional-AFP-L3%.

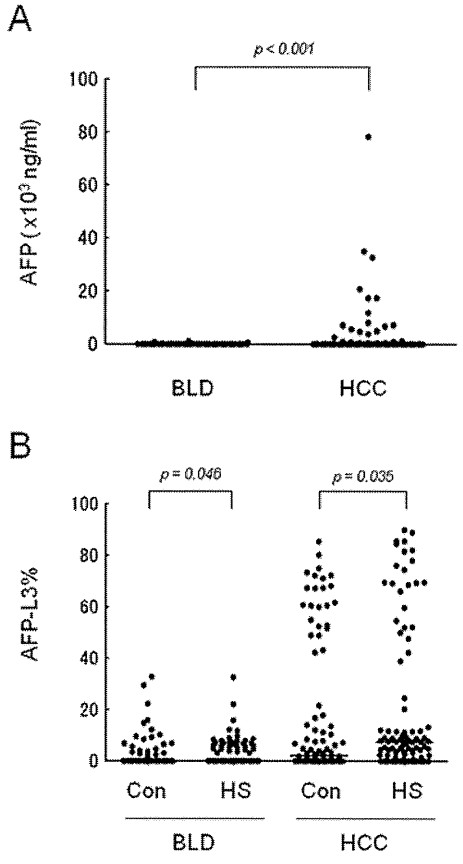

Figure 1. Serum levels of AFP, c-AFP-L3% and hs-AFP-L3% in patients with BLD or HCC. (A) Serum AFP concentrations in HCC patients (n=94) were significantly higher than those in BLD (n=74). (B) hs-AFP-L3% (HS) significantly increased in comparison with c-AFP-L3% (Con) in both BLD and HCC patients.

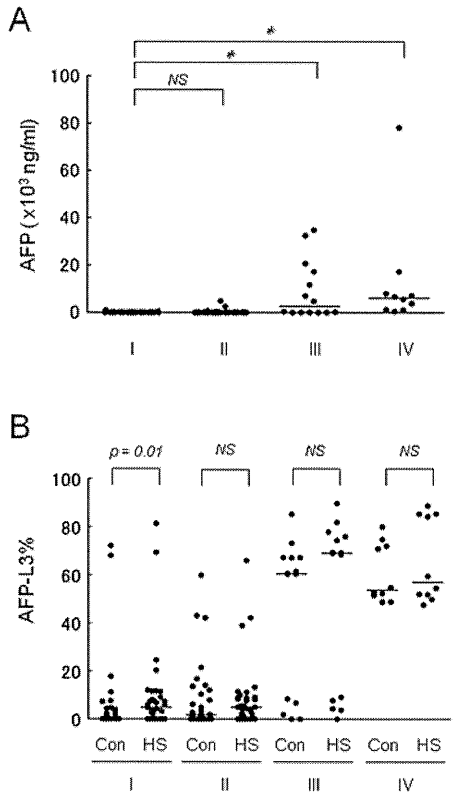

Figure 2. Serum levels of AFP, c-AFP-L3% and hs-AFP-L3% in patients with early or advanced HCC. (A) Serum AFP levels in HCC patients at stage III (n=14) or IV (n=10) were significantly higher than those at stage I (n=35) or II (n=35). *p<0.05. (B) hs-AFP-L3% (HS) was significantly higher than c-AFP-L3% (Con) in patients with HCC at stage I, whereas there was no significant difference between c- and hs-AFP-L3% in HCC patients at stages II, III and IV.

Table II. Clinical features of BLD and HCC patients with AFP <20 ng/ml.

	BLD (n=59)	HCC (n=56)	p-value
Age	56.78±13.51	68.88±12.05[a]	<0.001
Gender (male/female)	23/36	26/30	0.422
CH/LC	45/14	25/31[a]	0.001
HBV/HCV/NBNC	14/35/10	5/32/19[a]	0.008
Child-Pugh class (A/B/C/unknown)	31/4/1/23	50/6/0/0[a]	<0.001
TNM stage (I/II/III/IV)		30/21/5/0	
Tumor size (mean ± SD)		16.16±11.59	
<20 mm/≥ 20 mm		47/9	
Tumor number (single/multiple)		35/21	
AFP (ng/ml)	4.68±3.6	8.92±5.23[a]	<0.001
c-AFP-L3%	0.83±3.92	1.86±3.16[a]	0.002
hs-AFP-L3%	2.7±5.15	4.86±5.19[a]	0.003
Platelet count (x10^4/μl)	15.93±6.67	11.93±4.49[a]	0.001
AST (IU/l)	43.91±25.72	54.32±21.61[a]	0.003
ALT (IU/l)	49.21±51.7	48.66±24.41	0.184

BLD, benign liver disease; HCC, hepatocellular carcinoma; CH, chronic hepatitis; LC, liver cirrhosis; HBV, hepatitis B virus; HCV, hepatitis C virus; hs-AFP-L3%, hypersensitive-AFP-L3%; c-AFP-L3%, conventional-AFP-L3%.

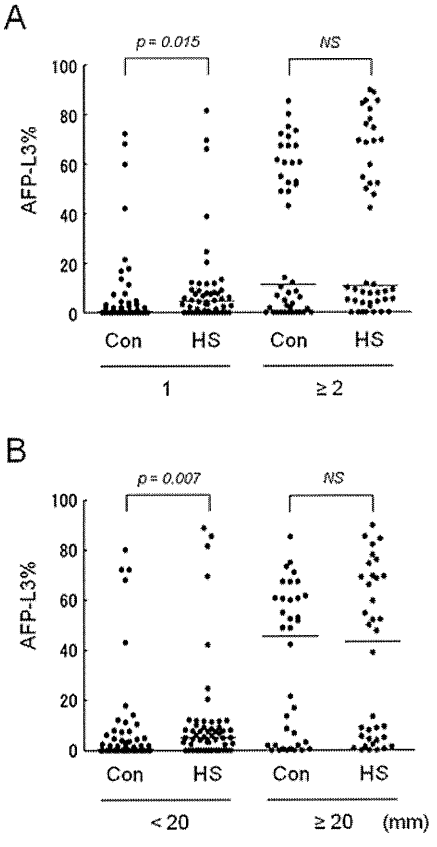

Figure 3. hs-AFP-L3% significantly increased in patients with solitary or small HCC, but not multiple or HCC ≥20 mm in diameter. (A) hs-AFP-L3% (HS) was significantly higher than c-AFP-L3% (Con) in patients with solitary HCC (n=50), but not in patients with multiple HCC (n=44). (B) hs-AFP-L3% significantly increased in comparison with c-AFP-L3% in patients with small HCC (<20 mm in diameter) (n=58), but not in patients with large HCC (≥20 mm) (n=36).

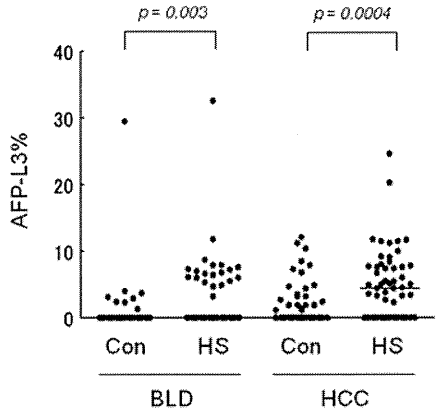

Figure 4. Higher levels of hs-AFP-L3% were observed in both BLD and HCC patients with serum AFP <20 ng/ml. c-AFP-L3% (Con) and hs-AFP-L3% (HS) in BLD and HCC patients with AFP <20 ng/ml (n=59 and 56, respectively) were analyzed. c-AFP-L3% was detectable in 13.6 and 39.3% of BLD and HCC patients, respectively, whereas hs-AFP-L3% was measurable in 33.9 and 64.3% of BLD and HCC patients, respectively; hs-AFP-L3% was significantly higher than c-AFP-L3%.

and hs-AFP-L3% in BLD and HCC patients with AFP <20 ng/ml (Table II). Forty-seven of 56 (83.4%) HCC patients exhibited small HCCs (<20 mm in diameter); 35 patients (62.5%) exhibited solitary tumors. c-AFP-L3% was detectable in 13.6 and 39.3% of BLD and HCC patients, respectively. Conversely, hs-AFP-L3% was measurable in 33.9 and 64.3% of BLD and HCC patients, respectively, and the levels of hs-AFP-L3% were significantly higher than those of c-AFP-L3% [BLD: mean ± SD (range) 0.83±3.92 (1.3-29.5) vs. 2.70±5.15%, p=0.003, and HCC: 1.86±3.16 (1.1-12.1) vs. 4.86±5.19% (2.3-24.6), p=0.004] (Fig. 4). The sensitivity and specificity of hs-AFP-L3%

Table III. Characterization of seven BLD patients, who developed HCC.

Case no.	1	2	3	4	5	6	7
Age	58	70	63	70	53	60	59
Gender	M	F	F	F	M	M	F
CH/LC	LC	CH	LC	LC	LC	LC	CH
HCV/NBNC	HCV	HCV	HCV	NBNC	HCV	HCV	HCV
AFP (ng/ml)	5.3	8.3	10.7	10.9	27.8	28.5	32.0
c-AFP-L3%	ND	ND	29.5	4.9	15.9	12.2	3.4
hs-AFP-L3%	6.0	7.0	32.6	8.4	12.2	9.6	3.7
ALT (IU/l)	31	48	23	39	41	65	116
Months until HCC detection	13	31	5	13	18	8	31

F, female; M, male; ND, not detectable.

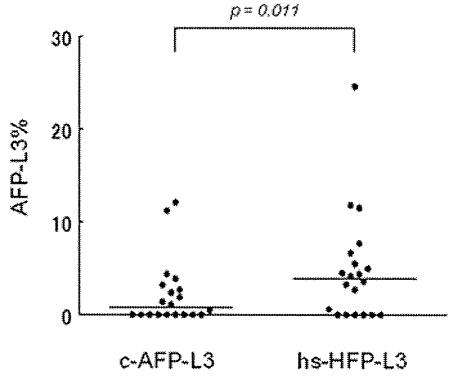

Figure 5. Patients with well-differentiated HCC showed an increase in hs-AFP-L3%. hs-AFP-L3% (HS) was significantly higher than c-AFP-L3% in patients with well-differentiated HCC; this was confirmed by histological examination.

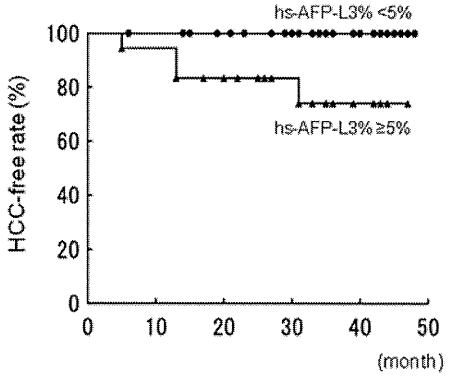

Figure 6. No patients with both serum AFP <20 ng/ml and hs-AFP-L3% <5% developed HCC. Patients with BLD (n=74) were periodically followed by US, CT, or MRI during the follow-up period (median, 35 months; range, 5-48 months). In cases of BLD with AFP <20 ng/ml (n=59), HCC was newly detected in 4 patients with hs-AFP-L3% ≥5%. The HCC-free rate in patients with hs-AFP-L3% ≥5% (▲) was significantly higher than in patients with hs-AFP-L3% <5% (●) (log-rank test and Wilcoxon test; p=0.0012 and p=0.0017, respectively). Importantly, no patients with hs-AFP-L3% <5% developed HCC.

at a cut-off level of 5% were 44.6 and 71.2%, whereas those of c-AFP-L3% were 12.5 and 98.3%, respectively. These results suggest that hs-AFP-L3% is useful for early detection of HCC, even when serum AFP is <20 ng/ml.

Serum hs-AFP-L3% increases in patients with well-differentiated HCC. Most HCC, initially present as well-differentiated HCC, develops in patients with chronic liver disease. Therefore, we evaluated c-AFP-L3% and hs-AFP-L3% in 20 patients with well-differentiated HCC, which was confirmed by histological examination. Fifteen patients (75.0%) exhibited small HCCs (<20 mm), and 9 (45.0%) suffered from liver cirrhosis. Serum AFP was 14.2±12.4 ng/ml (1.4-54.1), and 18 patients (90%) exhibited serum AFP levels <20 ng/ml. hs-AFP-L3% was measurable in 14 patients (70%), while 11 patients (55%) exhibited detectable levels of c-AFP-L3% (Fig. 5). Consequently, hs-AFP-L3% was significantly higher than c-AFP-L3% [4.81±5.91 (0.6-24.6) vs. 2.24±3.53% (0.5-12.1), p=0.011]. These results support the possible utility of hs-AFP-L3% for detection of early-stage HCC.

hs-AFP-L3% increases prior to detection of HCC in patients with BLD. Seven of 74 patients with BLD developed HCC during the follow-up period (median, 35 months; range, 5-48) (Table III). Five patients suffered from liver cirrhosis, and 6 exhibited hepatitis C virus infection. Two of the patients with chronic hepatitis required a longer period (31 months) for appearance of HCC than did the 5 patients with cirrhosis (5-18 months). Five patients exhibited measurable c-AFP-L3%, and an increase in c-AFP-L3% (≥5%) was observed in 3 patients. In contrast, hs-AFP-L3% was measurable in all 7 patients prior to detection of HCC, and 6 patients (85.7%) exhibited hs-AFP-L3% ≥5%. In 59 BLD patients with serum AFP <20 ng/ml, 4 patients developed HCC (Table III). An increase in c-AFP-L3% (≥5%) was observed only in 1 patient, who developed HCC during the follow-up period, whereas the other three patients exhibited undetectable levels or <5% of c-AFP-L3%. Conversely, all 4 patients with serum AFP <20 ng/ml exhibited an increase in hs-AFP-L3% (≥5%) prior to detection of HCC.

Next, we analyzed the HCC-free rate in BLD patients with serum AFP <20 ng/ml during the follow-up period (Fig. 6). The HCC-free rate in patients with hs-AFP-L3% ≥5% was

significantly higher than those with hs-AFP-L3% <5%. Of importance, HCC was not detected in BLD patients with both serum AFP <20 ng/ml and hs-AFP-L3% <5%, whereas 3 out of 58 patients with both serum AFP <20 ng/ml and <5% of c-AFP-L3% developed HCC. These results suggest that an increased hs-AFP-L3% allows prediction of HCC development; measurement of hs-AFP-L3% is useful for selecting BLD patients with higher risk of HCC.

Discussion

Most HCC occurs in patients with chronic liver diseases, especially cirrhosis. Therefore, periodical measurement of tumor markers for HCC, such as AFP and DCP, is recommended in patients who are at high risk for HCC. However, recent advances in diagnostic imaging techniques, including US, CT and MRI, facilitate the detection of small and early-stage HCC (19-21), resulting in an increase in the number of HCC patients diagnosed without an observed increase in serum AFP. Indeed, the 18th survey and follow-up study of primary liver cancer in Japan has reported that most patients with HCC exhibited low levels of serum AFP, <15 ng/ml. Additionally, although AFP-L3% status is known to be a specific marker for HCC, measurement of c-AFP-L3% has not always been reliable in patients with AFP <20 ng/ml.

In this study, we investigated the clinical utility of hs-AFP-L3%, which was measured by a newly developed and highly sensitive method, μ-TAS, in patients with BLD and HCC. Here, we showed that although most HCC patients with stage I cancer did not exhibit an increase in serum AFP levels (≥20 ng/ml), hs-AFP-L3% was measurable in ~70% of the patients, and was significantly increased in comparison with c-AFP-L3% (Fig. 2). Since hs-AFP-L3% is reliable even when serum AFP is <20 ng/ml, it is possible to set the cut-off value for hs-AFP-L3% at 5-7% (18,22,23). We show here that at a cut-off level of 5%, the sensitivity and specificity of hs-AFP-L3% were 44.6 and 71.2%, respectively, in HCC patients with serum AFP <20 ng/ml (Fig. 4). Recent investigations have shown that diagnostic sensitivity of hs-AFP-L3% at a cut-off level of 5 or 7% was 41.5 or 41.1%, respectively, in HCC patients with serum AFP <20 ng/ml (18,22). Therefore, our findings in this study support the specificity of hs-AFP-L3% in patients with serum AFP <20 ng/ml, as previously reported.

The sensitivity of c-AFP-L3% is relatively low (22.2-38.6%) in early-stage HCCs <20 mm in diameter (24,25). In this study, although the sensitivity of c-AFP-L3% was <20% in patients with HCC at stage I, hs-AFP-L3% was significantly higher than c-AFP-L3% in patients with solitary or small (<20 mm) HCC or with stage I HCC (Figs. 2 and 3); consequently, ~50% of HCC patients at stage I exhibited hs-AFP-L3% ≥5%. Additionally, in patients with well-differentiated HCC, hs-AFP-L3% was also significantly higher than c-AFP-L3%. Conversely, patients with stage III or IV HCC (multiple or larger (≥20 mm) tumors) exhibited an increase in both hs- and c-AFP-L3%, with no statistical difference. HCC initially develops as well-differentiated HCC, and then progresses to moderately- to poorly-differentiated HCC via a process of dedifferentiation. Thus, an increase in hs-AFP-L3% in patients with well-differentiated HCC and early-stage HCC supports the conclusion that measurement of hs-AFP-L3% is useful for early detection of HCC.

HCC often develops in patients with chronic infection of hepatitis B or C virus; especially in patients with chronic HCV infection, the annual incidence of HCC increases as a function of the stage of liver fibrosis, from 0.5% at stages F0 to F1 to 7.9% at stage F4 (cirrhosis) (26). Recently, Tateyama *et al* demonstrated that elevated AFP levels are a risk factor for the development of HCC in patients with HCV infection; the 10-year cumulative incidence rates of HCC in the patients with AFP levels of <6, 6-20 and ≥20 ng/ml at entry were 6.0, 24.6 and 47.3%, respectively, and that AFP levels may be used as a non-invasive and predictive marker in place of stage of fibrosis (27). In this study, all 7 BLD patients who developed HCC during the follow-up period exhibited measurable hs-AFP-L3% prior to detection of HCC, and 6 patients exhibited hs-AFP-L3% ≥5%. Of particular note, even when serum AFP levels increased to up to 20 ng/ml, HCC was not detected in patients with hs-AFP-L3% <5% (Fig. 6).

Although prolonged observation will be required in order to clarify whether hs-AFP-L3% is useful for prediction of HCC, the findings presented here indicated that hs-AFP-L3% is useful for early detection of HCC in BLD patients even with serum AFP <20 ng/ml, and also that an increase in hs-AFP-L3% prior to detection of HCC by various advanced imaging modalities may contribute to more precisely identifying BLD patients with a higher risk of HCC.

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ORIGINAL ARTICLE

Analysis of viral amino acids sequences and the IL28B SNP influencing the development of hepatocellular carcinoma in chronic hepatitis C

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Abstract
Background and aims The association between hepatitis C virus (HCV) sequences with interleukin 28B (IL28B) single-nucleotide polymorphism (SNP) in the development of hepatocellular carcinoma (HCC) has not been well clarified.
Methods Complete HCV open-reading frame sequences were determined in 20 patients developing HCC and 23 non-HCC patients with HCV-1b infection in two distant time points. An additional 230 patients were studied cross-sectionally for core and NS5A sequences with HCC development. Among them, 98 patients with available samples were investigated for changes in viral core sequences over time. Finally, IL28B SNPs and HCC development were investigated in 228 patients.
Results During observation period (HCC for 10.8 years, and non-HCC for 11.1 years), changes in core a.a. 70 and three amino acid positions in NS5A were characteristics of the patients developing HCC. In 230 patients, Q (glutamine) or H (histidine) to R (arginine) ratio at core a.a. 70 was significantly higher in the HCC group (HCC group 43:22 vs. non-HCC group 66:99, $p = 0.001$). A change in core R70Q was observed over time in 11 patients associated with a decrease in platelets ($p = 0.005$) and albumin ($p = 0.005$), while a Q70R change was observed in 4 patients without associated changes in platelets (nonsignificant) and albumin (nonsignificant). IL28B SNP showed significant correlation with the core a.a. 70 residue. There was no evident link between IL28B SNPs and the occurrence of HCC.
Conclusions Hepatitis C virus core a.a. 70 residue is associated with liver disease progression and is independent factor for HCC development in genotype-1b infection. IL28B SNPs are related to core a.a. 70 residue, but not to HCC. The functional relevance of core a.a. 70 residue in hepatitis C pathogenesis should be further investigated.

Keywords HCV · HCC · Core · IL28B

Introduction

Hepatitis C virus (HCV) infection is a major risk factor for hepatocellular carcinoma (HCC). Chronic HCV infection can result in liver cirrhosis (LC) and HCC over the course of 20–30 years [1]. However, the rate of progression is variable; some patients remain for a long time with persistently normal ALT values, while others progress rapidly to LC and HCC.

Viral factors, host factors, and their interplay appear to play an important role in determining the progression of chronic hepatitis C to LC and HCC. In terms of viral factors, most previous clinical studies have focused on searching for HCV regions correlated with the response to interferon (IFN)-based therapy. In those analyses, correlation between amino acid substitutions and treatment response have been reported for the IFN sensitivity

M. Miura and S. Maekawa have contributed equally to this study.

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determining region in nonstructural (NS)5A [2], a.a. 70 and 91 in core [3], the PKR/eIF-2alpha phosphorylation homology domain (PePHD) in envelope (E)2 [4], and the IFN–ribavirin resistance determining region (IRRDR) in NS5A [5].

Regarding the viral factors related to disease progression, among the various HCV proteins, the core protein has been thought widely to contribute because it has been shown experimentally to affect multiple cellular functions, in addition to the evidence from clinical studies [6–10]. Core protein modifies cellular apoptosis, oncogenic signaling, reactive oxygen species formation, lipid metabolism, transcriptional activation, transformation, and immune reactivity. Core protein has oncogenic potential in transgenic mice [11]. In contrast, fewer clinical studies to date have systematically investigated the correlation between the variability of HCV regions and disease progression. However, some of those limited clinical studies reported a correlation between amino acid substitutions in core or NS5A with disease progression [12–15]. Despite those reports, few studies to date support the correlation. Moreover, it is unclear whether those viral sequences change during disease progression or how the disease activity is modified by those viral sequences in the long course of chronic hepatitis.

On the other hand, regarding host factors, recent reports disclosed a significant correlation between polymorphisms in the IL28B gene and responses to pegylated-IFN plus ribavirin therapy for HCV patients [16–19]. This single-nucleotide polymorphism (SNP) also showed significant correlation with natural HCV clearance [20]. However, it remains unknown whether the IL28B SNP is related to disease progression or the development of HCC.

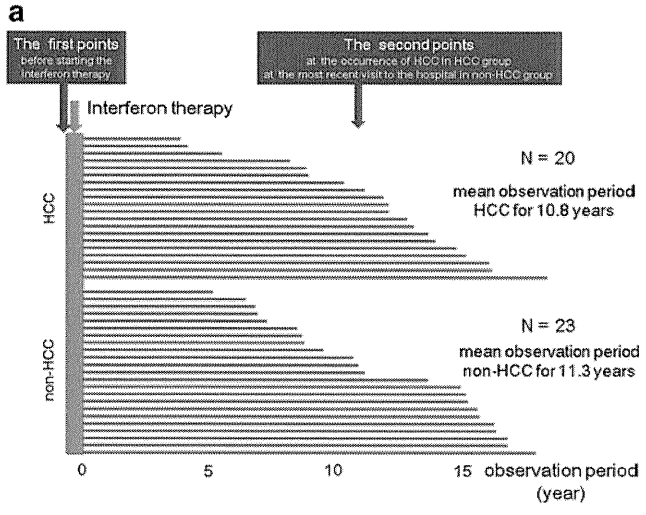
In this study, we first undertook the analysis to identify the viral regions related to disease progression and HCC development through the analysis of complete HCV open-reading frame (ORF) sequences. Because some regions in HCV core and NS5A showed characteristic changes over time in patients developing HCC during the observation period, we proceeded further to analyze the contribution of those regions to disease progression, in association with time and with the IL28B SNP.

Patients and methods

Patients

This study is based on the analysis of two groups of patients, 43 in Group 1 and 230 patients in Group 2.

In the first part, we tried to characterize and extract viral sequences specific to disease progression through the analysis of complete HCV ORFs (Fig. 1a). In particular, we focused our investigation on the changes in viral sequences over time in association with disease progression by comparing HCV sequences of two sufficiently distant time points. With this aim, we determined to investigate patients with a history of IFN therapy, because those patients often were followed long-term with preservation of old and recent sera. However, we excluded sustained



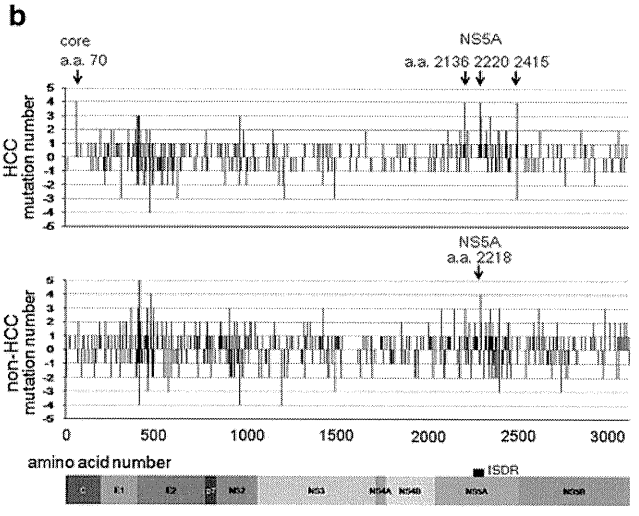


Fig. 1 **a** A total of 43 patients were analyzed for complete HCV ORF sequences. They were all non-responders to the previous IFN therapy. Twenty patients developed HCC during the observation period, while the 23 patients did not. HCV ORF sequences were determined for the paired samples and the predicted amino acid changes were compared in each patient. **b** Specific HCV amino acid changes associated with disease progression was evaluated by the analysis of the full-length viral ORF during the observation period for each patient according to the following rules: *1* +1 point for consensus to non-consensus, *2* −1 point for non-consensus to consensus, *3* 0 point for non-consensus to non-consensus. These points were added together and are shown for HCC and non-HCC patients. Patient with later HCC development (*upper panel*). Non-HCC patients (*lower panel*)

virologic response (SVR) patients because we thought that the viral clearance leads to improvement of the liver disease and, therefore, viral regions influencing the IFN response would be extracted as affecting the course of disease. Between March 1992 and April 2004, 273 consecutive patients with HCV-1b infection were given IFN monotherapy at Yamanashi University Hospital, and 133 were followed long-term. A total of 65 patients showed SVR, while 68 showed non-SVR. Among these 68 non-SVRs, 43 patients were included in the study because laboratory data and sera were available from the two distant time points (Group 1). Twenty patients developed HCC during the observation period, while the remaining 23 did not. Regarding the sera, the first time point for both groups was before starting IFN therapy, while the second points were at the occurrence of HCC for the HCC group and at the most recent visit to the hospital for the non-HCC group (Fig. 1a).

An additional 230 HCV-1b patients were recruited (Group 2) as the second study group. They were mainly outpatients at Yamanashi University Hospital and were selected randomly from those with stored sera at the time of disease diagnosis. Sixty-five had HCC, while the remaining 165 did not. They all were positive for HCV RNA at the time of study, although 74 patients had a history of IFN therapy. Parts of the core and NS5A sequences were determined at HCC onset in 65 HCC patients and at the most recent visit to the hospital in 165 non-HCC patients. Because historical sera around 10 years before were also available for 55 of these 230 patients, HCV sequence analysis was also performed for core and NS5A at those previous time points in those patients.

From these two study groups, 228 patients (68 HCCs and 160 non-HCCs) with available genomic DNAs were examined to determine the IL28B SNP.

All the patients studied all fulfilled following criteria: (1) Negative for hepatitis B surface antigen. (2) No other forms of hepatitis, such as primary biliary cirrhosis, autoimmune liver disease, or alcoholic liver disease. (3) Free of coinfection with human immunodeficiency virus. (4) A signed consent was obtained for the study protocol that had been approved by Human Ethics Review Committee of Yamanashi University Hospital.

Complete and partial HCV ORF sequence determination by direct sequencing from sera

HCV RNA extraction, complementary DNA synthesis and amplification by two-step nested PCR from serum samples were done using the specific primers for full HCV ORF or partial viral regions as described previously [15]. PCR amplicons were sequenced directly by Big Dye Terminator Version 3.1 (ABI, Tokyo, Japan) with universal M13 forward and reverse primers using an ABI prism 3130 sequencer (ABI). Generated sequence files were assembled using Vector NTI software (Invitrogen, Tokyo, Japan) and base-calling errors were corrected following inspection of the chromatogram.

IL28B SNP analysis

Human genomic DNA was extracted from peripheral blood using a blood DNA extraction kit (QIAGEN, Tokyo, Japan) according to the manufacturer's protocol. The allele typing of each DNA sample was performed by real-time PCR with a model 7500 (ABI) using FAM-labeled SNP primer for the locus rs8099917 (ABI).

Statistical analysis

Statistical differences in the parameters, including all available patients' demographic, biochemic, hematologic, and virologic data, were determined between different groups of patients by Student's t test for numerical variables and Fisher's exact probability test for categorical variables. Odds ratios and their 95% confidence intervals were used to quantify the level of association. All p values of <0.05 by the two-tailed test were considered significant throughout. Multiple logistic regression analyses were used to identify the independent variables influencing core a.a. 70 residue and HCC development. Because most variables used for the analyses were generally considered to correlate with the disease progression, we entered all the variables into the multiple logistic regression analysis even if some of them did not reach significant differences in individual univariate analysis.

Results

Comparing complete HCV amino acid sequences between patients with and without HCC

The clinical characteristics of the 43 patients (Group 1) analyzed for HCV ORF changes over time are shown in Table 1. At the start of observation, clinical characteristics did not differ significantly between the HCC group and the non-HCC group. The mean observation period was comparable between the two groups and was 10.8 years for the HCC group and 11.3 years for non-HCC group ($p = 0.745$). On the other hand, platelets ($p < 0.001$), albumin ($p < 0.001$), and AFP ($p = 0.001$) became significantly lower or higher in the HCC group at the end of observation (Table 1).

We proceeded to investigate viral amino acid changes during the course of disease in each patient to determine

Table 1 Patient characteristics in Group 1

	At the start of observation			At the end of observation		
	HCC ($N = 20$)	Non-HCC ($N = 23$)	p value	HCC ($N = 20$)	Non-HCC ($N = 23$)	p value
Observation period (years)				10.8 ± 3.6	11.3 ± 3.8	0.745
Sex (male/female)	11/9	12/11	0.999	11/9	12/11	0.999
Age (years)	51.5 ± 8.0	50.0 ± 9.9	0.604	61.7 ± 10.0*	61.0 ± 10.9*	0.818
Stage of fibrosis (F1/2/3/4)	1/7/6/6	5/11/4/3	0.190	N/A	N/A	–
AST (IU/L)	102 ± 114	74 ± 40	0.695	71 ± 36*	51 ± 30	0.048
ALT (IU/L)	124 ± 86	104 ± 71	0.411	69 ± 47*	52 ± 31*	0.159
Platelets (10^{-4}/mm^3)	16.2 ± 4.8	18.3 ± 6.2	0.217	9.7 ± 3.9*	15.3 ± 5.1	<0.001
Albumin (g/dL)	4.1 ± 0.4	4.1 ± 0.2	0.639	3.6 ± 0.4	4.1 ± 0.5	<0.001
γGTP (IU/L)	90 ± 60	71 ± 46	0.275	69 ± 59	45 ± 38*	0.114
T.Chol (mg/dL)	169 ± 28	156 ± 22	0.110	146 ± 21	164 ± 5,108	0.086
Alpha-fetoprotein (ng/mL)	10.5 ± 6.8	9.3 ± 10.8	0.695	42.4 ± 41.1	4.7 ± 2.7	0.001
HCV RNA concentration (kIU/mL)	706 ± 696	614 ± 1,181	0.760	3,325 ± 415*	4,508 ± 5,108*	0.426

* Factors with significant changes over time (<0.05)

whether specific amino acid changes related to disease progression could be identified. First, the consensus amino acid was determined at each amino acid position in the HCV ORF after determination of all sequences in these 43 patients. Amino acid changes were determined according to the following rules to highlight directional changes according to disease progression: When an amino acid changed from the consensus to the non-consensus during the observation period, we scored +1 point. Conversely, a change from the non-consensus to the consensus scored −1 point. We scored 0 point for a change from one non-consensus amino acid to another. As shown in Fig. 1b, directional amino acid changes were observed throughout the HCV genome to some degree both in patients with and without HCC development during the clinical course of almost 10 years, and frequent substitutions in E2 hypervariable region were common in both groups. On the other hand, in patients with HCC development, as many as four directional changes were observed at core a.a. 70 and at three amino acid positions of NS5A (Fig. 1b, upper panel). In contrast, in patients without HCC, the significant change ($n = 4$) was observed at a.a. 2,218 of NS5A when E2 hypervariable region was excluded (Fig. 1b, lower panel).

Core and NS5A sequences in patients with and without HCC

Because the first analysis suggested that the patients with later HCC development might accumulate specific mutations in core and NS5A at the time of HCC occurrence, additional sequences were analyzed from 230 HCV-1b patients to confirm the result. The clinical backgrounds of the additional 230 patients are shown in Table 2 (Group 2).

Table 2 Patient characteristics in Group 2

	HCC ($N = 65$)	Non-HCC ($N = 165$)	p value
Observation period (years)			
Sex (male/female)	42/23	76/89	0.018
Age (years)	68.2 ± 9.2	62.4 ± 11.7	<0.001
AST (IU/L)	66 ± 35	41 ± 21	<0.001
ALT (IU/L)	67 ± 47	44 ± 47	<0.001
Platelets (10^{-4}/mm^3)	11.3 ± 5.8	15.3 ± 6.2	<0.001
Albumin (g/dL)	3.6 ± 0.5	4.4 ± 2.9	0.025
γGTP (IU/L)	59 ± 53	38 ± 40	0.001
T.Chol (mg/dL)	153 ± 30	165 ± 31	0.004
Alpha-fetoprotein (ng/mL)	302 ± 1,670	10 ± 25	0.025
HCV RNA concentration (kIU/mL)	5,400 ± 13,574	7,990 ± 8,512	0.104

All patients were positive for HCV RNA. Between the HCC (65 patients) and non-HCC (165 patients) groups, HCC patients were older ($p < 0.001$) and more frequently tended to be males ($p = 0.018$). Moreover, AST, ALT, γGTP, and AFP were significantly higher, and platelets, albumin, and cholesterol were significantly lower in the HCC group. Different predicted amino acids in the core and NS5A regions, between the two groups, are demonstrated in Fig. 2a. The ratio of the core a.a. 70Q (glutamine) or H (histidine) to R (arginine) was significantly higher with the existence of HCC as demonstrated in Fig. 2a (left panel). On the other hand, evident correlations were not confirmed between mutations in NS5A and disease progression (Fig. 2a, right panel). The ratio of Q or H

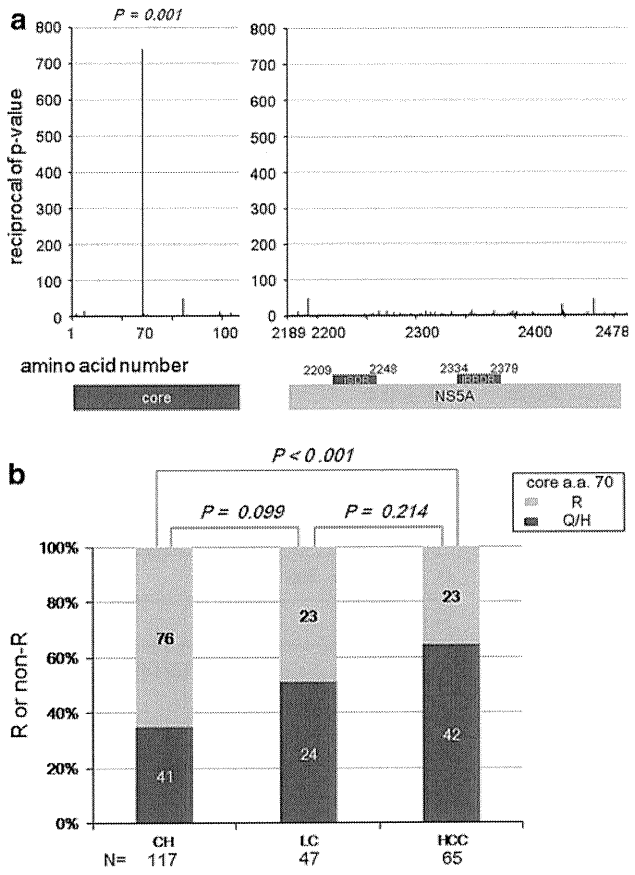


Fig. 2 Core and NS5A sequences in additional patients were studied. **a** Using sera from 230 additional patients at the time of diagnosis, amino acid usage was compared between HCC and non-HCC patients for the part of core and the NS5A region, and this difference is shown as the *bar height* expressed as reciprocal *p* values. **b** In 230 patients, the association between polymorphisms of core a.a. 70 and the state of liver disease (chronic hepatitis, LC, or HCC) is shown

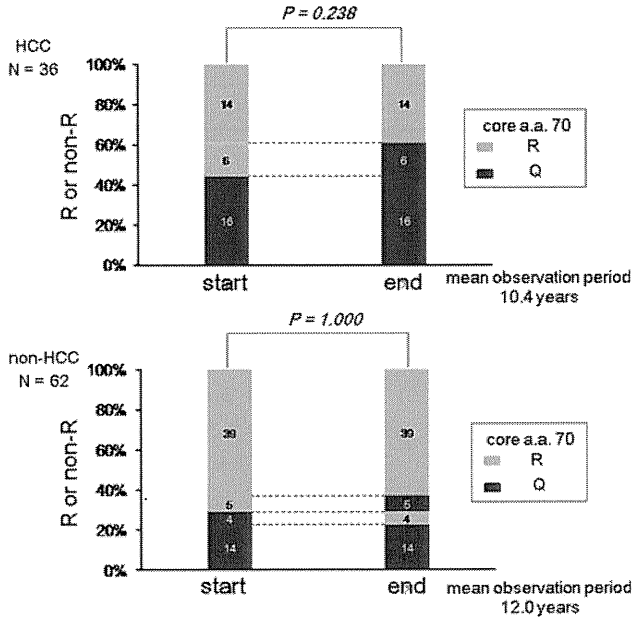


Fig. 3 Changes in core a.a. 70 over time were studied. In 98 patients available for the analysis of 2, sufficiently distant time points, amino acid changes of core a.a. 70 were investigated over time in each patient group. Patients with later HCC development (*upper panel*). Non-HCC patients (*lower panel*)

to R progressively increased in patients in the three major groups of disease activity: chronic hepatitis, cirrhosis, and HCC (Fig. 2b). The association between the disease progression and core a.a. 70 polymorphism also was observed irrespective of IFN-based therapy (data not shown).

Changes in core a.a. 70 over time in patients with and without HCC

We then examined changes in core a.a. 70 over time in association with disease progression (Fig. 3). For this analysis, 55 patients from Group 2, for whom sera from two distant time points were available, were added to the 43 patients in Group 1 and a total of 98 patients were enrolled. When they were classified into two groups according to later HCC onset, the mean observation period was comparable between the groups, 10.4 years for the HCC group and 12 years for the non-HCC group. The occurrence of core a.a. 70Q was 61% (22/36) at the time of HCC onset in the HCC group (Fig. 3, upper panel), but 31% (19/62) for the non-HCC group (Fig. 3, lower panel). In contrast, it was 44% (16/36) at the start of observation in the HCC group (Fig. 3, upper panel) and 29% (18/62) for the non-HCC group (Fig. 3, lower panel). Regarding the core a.a. 70 changes over time, R was dominant throughout the observation period in the non-HCC group (71% at the start and 69% at the end), while the dominant amino acid changed from R (56%) to Q (61%) in the HCC group, so that the core a.a. 70 residues of 17% of the HCC patients changed from R to Q during the course of HCC development. In other words, 6 of 22 patients with 70Q at the onset of HCC had 70R originally (6/22, 27%), while 0 of 14 (0%) with 70R at the most recent observation time had 70Q at the beginning. There were no patients with core a.a. 70H throughout the observation period in this population. The result demonstrates that the relationship between 70Q and HCC development is significant at the time of HCC development. At the start of observation, there was also a tendency that the patients with 70Q compared with 70R develop HCC. However, this difference did not reach statistical significance as shown in Supplementary Fig. 1.

Core a.a. 70 changes over time and their association with disease progression

These 98 patients were classified into four groups according to the pattern of core a.a. 70 change (Table 3) and their

Table 3 Progression of liver disease in 98 patients categorized by core a.a. 70 changes over time

	R → R ($N = 53$)			Q → R ($N = 4$)		
	Start	End	p value	Start	End	p value
HCC rate (HCC/non-HCC)	–	26.4% (14/39)	–	–	0% (0/4)	–
Sex (male/female)	–	25/28	–	–	4/0	–
Observation period (years)	–	11.1 ± 3.4	–	–	12.9 ± 3.5	–
Age (years)	51.3 ± 11.7	62.4 ± 12.1	<0.001	48.0 ± 11.6	61.0 ± 9.1	0.128
AST (IU/L)	68 ± 73	48 ± 26	0.066	56 ± 32	83 ± 61	0.456
ALT (IU/L)	80 ± 71	48 ± 35	0.003	114 ± 71	96 ± 42	0.678
Platelets (10^{-4}/mm^3)	17.0 ± 5.8	15.0 ± 6.7	0.104	21.3 ± 3.9	17.2 ± 5.2	0.251
Albumin (g/dL)	4.1 ± 0.4	3.9 ± 0.6	0.225	4.4 ± 0.4	4.3 ± 0.4	0.647
γGTP (IU/L)	56 ± 51	38 ± 40	0.052	95 ± 51	61 ± 46	0.371
T.Chol (mg/dL)	172 ± 36	158 ± 33	0.032	152 ± 14	175 ± 32	0.222
Alpha-fetoprotein (ng/mL)	8.3 ± 9.5	12.5 ± 22.1	0.202	6.0 ± 6.0	5.2 ± 2.2	0.816
HCV RNA concentration (kIU/mL)	4,634 ± 8,509	7,070 ± 14,159	0.291	5,798 ± 7,970	13,676 ± 1,881	0.162
	R → Q ($N = 11$)			Q → Q ($N = 30$)		
	Start	End	p value	Start	End	p value
HCC rate (HCC/non-HCC)		54.5% (6/5)			53.3% (16/14)	
Sex (male/female)		6/5			13/17	
Observation period (years)		13.7 ± 1.65			10.8 ± 3.5	
Age (years)	56.4 ± 7.5	69.3 ± 9.3	0.002	54.6 ± 8.5	64.9 ± 9.9	<0.001
AST (IU/L)	62 ± 47	46 ± 12	0.285	79 ± 51	60 ± 31	0.087
ALT (IU/L)	100 ± 69	37 ± 15	0.008	95 ± 58	59 ± 36	0.006
Platelets (10^{-4}/mm^3)	17.7 ± 3.9	11.8 ± 4.8	0.005	16.3 ± 6.5	11.9 ± 5.6	0.007
Albumin (g/dL)	4.2 ± 0.2	3.8 ± 0.4	0.005	4.1 ± 0.3	3.8 ± 0.5	0.009
γGTP (IU/L)	73 ± 53	33 ± 16	0.025	101 ± 55	71 ± 65	0.065
T.Chol (mg/dL)	157 ± 21	144 ± 27	0.245	163 ± 28	150 ± 32	0.100
Alpha-fetoprotein (ng/mL)	7.1 ± 4.3	97.8 ± 63.6	0.267	20.8 ± 50.0	35.1 ± 54.7	0.295
HCV RNA concentration (kIU/mL)	2,415 ± 3,163	2,349 ± 1,851	0.957	2,869 ± 3,984	3,229 ± 4,026	0.731

clinical characteristics were investigated. Significant decreases of platelets ($p = 0.007$) and albumin ($p = 0.009$) were observed in the Q unchanged group during the observation period, but not in the R unchanged group ($p = 0.104$ and 0.225, respectively). Because platelets and albumin are markers of liver disease progression, it was considered that the Q unchanged group progressed rapidly with frequent HCC occurrence (53%, 16/30) while the R unchanged group showed stable disease with less frequent HCC occurrence (26%, 14/53). In contrast, the R to Q group showed progressive disease ($p = 0.005$ and 0.005, respectively) similar to the Q unchanged group, while the Q to R group showed stable disease similar to the R unchanged group ($p = 0.251$ and 0.647, respectively), demonstrating that amino acid changes of core a.a. 70 were significantly associated with disease progression.

The IL28B SNP and its association with core a.a. 70 and disease progression

Next, the association between the state of liver disease and IL28B SNP was analyzed for a total of 228 patients through the analysis of the rs8099917 locus. Among them, 162 patients (71%) had the major homozygous TT alleles, while 66 patients (29%) had the minor homozygous or heterozygous alleles (GG/TG). Although some patients had a history of IFN therapy, all patients were positive for HCV RNA at the time of study. The clinical characteristics related to disease progression were compared, as shown in Table 4. Each group consisted of patients with similar distributions of age and sex. Though most clinical factors showed no evident differences in these groups, γGTP was high ($p = 0.020$) and HCV RNA concentration was apt to be low ($p = 0.085$) in TG/GG group. Moreover, the ratio

Table 4 Patient characteristics classified by IL28B SNPs at the time of diagnosis

	TT ($N = 162$)	TG/GG ($N = 66$)	p value
Sex (male/female)	81/81	32/34	0.951
Age (years)	63.3 ± 10.7	63.8 ± 11.9	0.735
Platelets (10^{-4}/mm^3)	13.8 ± 5.8	14.3 ± 6.6	0.632
Albumin (g/dL)	4.2 ± 3.0	4.0 ± 0.5	0.528
γGTP (IU/L)	41 ± 39	55 ± 49	0.020
T.Chol (mg/dl)	162 ± 31	157 ± 31	0.237
HCV RNA concentration (kIU/ml)	7,576 ± 10,292	5,069 ± 6,701	0.085
Alpha-fetoprotein (ng/ml)	39.0 ± 152.2	27.3 ± 48.3	0.555
AST (IU/L)	49.6 ± 29.6	51.9 ± 30.5	0.607
ALT (IU/lL)	54.5 ± 53.9	51.6 ± 37.7	0.689
Core a.a. 70R/(Q/H)	106/56	17/49	<0.001
Core a.a. 91L/(M/C)	108/54	38/28	0.253
ISDR	1.2 ± 2.0	0.9 ± 1.5	0.164
IRRDR	5.1 ± 2.4	4.7 ± 2.2	0.207
HCC −/+	115/47	45/21	0.788
IFN −/+	95/67	34/32	0.402

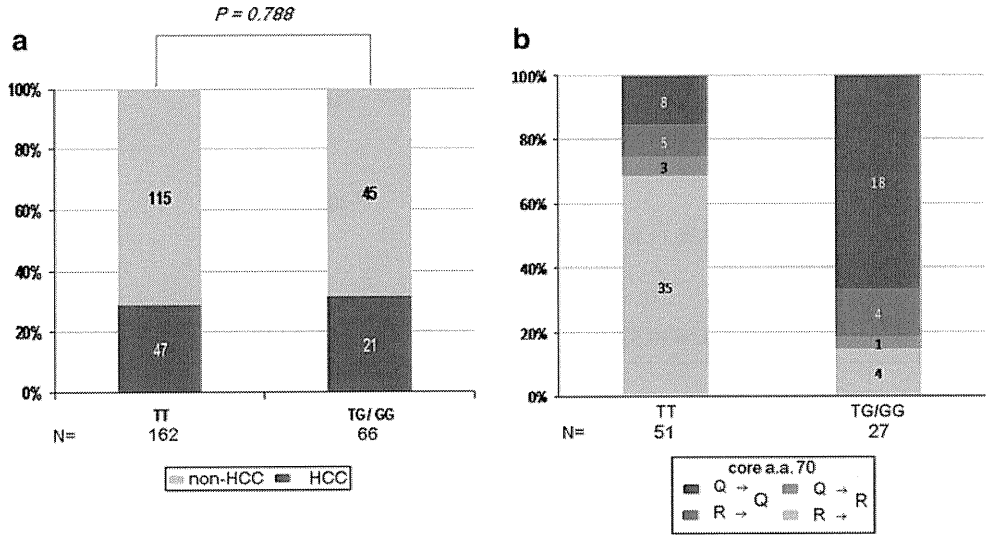


Fig. 4 **a** Association between the state of liver disease and IL28B SNP. **b** Time-dependent core a.a. 70 changes and its relation to IL28B SNP was investigated in 78 patients

of R/(Q/H) at core a.a. 70 was significantly higher in those with the TT alleles than in those with TG/GG ($p < 0.001$). In association of IL28B SNP with HCC development, there was no evident relationship as demonstrated in Fig. 4.

IL28B SNP and time-dependent core a.a. 70 changes

In Fig. 4b, it is demonstrated that the direction of time-dependent core a.a. 70 change was influenced by IL28B SNPs. In IL28B TG/GG patients, 4 (50%) out of 8 patients with the initial core a.a. 70R changed into 70Q, while only 1 (5%) out of 19 patients with the initial core a.a. 70Q changed into 70R, demonstrating that core a.a. 70 tended to change into Q over time in IL28B TG/GG patients ($p = 0.034$). On the other hand, there was no evident changing direction in IL28B TT patients; 5 (13%) out of 40 patients with the initial core a.a. 70R changed into 70Q, while 3 (27%) out of 11 patients with the initial core a.a. 70Q changed into 70R ($p = 0.45$).

Multivariate analysis for independent factors influencing core a.a. 70

To investigate further the relationship between core a.a. 70, the IL28B SNP, and HCC development, we divided the patients according to the specification of core a.a. 70 and

Table 5 Factors related to polymorphism of core a.a. 70

Variables	Univariate analysis ($N = 228$)		Multivariate analysis ($N = 228$)	
	Odds ratio (95% CI)	p value	Odds ratio (95% CI)	p value
Sex				
Female	1	0.415	1	0.812
Male	1.23 (0.74–2.01)		1.08 (0.58–1.99)	
Age (years)				
<65	1	0.216	1	0.855
≥65	1.39 (0.82–2.35)		1.06 (0.57–1.96)	
Platelets (10^{-4}/mm^3)				
>12	1	0.004	1	0.844
≤12	1.76 (1.03–2.99)		1.07 (0.53–2.16)	
Albumin (g/dL)				
>4	1	0.002	1	0.300
≤4	2.28 (1.33–3.91)		1.46 (0.71–3.00)	
γGTP (IU/L)				
<41	1	0.003	1	0.299
≥41	2.32 (1.32–4.09)		1.42 (0.73–2.79)	
ALT (IU/L)				
<41	1	0.040	1	0.573
≥41	1.74 (1.03–2.94)		1.22 (0.62–2.39)	
IL28B				
TT	1	<0.001	1	<0.001
TG or GG	5.46 (2.88–10.30)		5.74 (2.91–11.31)	
HCC				
−	1	<0.001	1	0.046
+	2.98 (1.65–5.37)		2.21 (1.01–4.83)	
Previous IFN therapy				
−	1	0.874	1	0.644
+	0.96 (0.57–1.62)		0.87 (0.47–1.59)	

those factors, as well as clinical factors, were compared in univariate and multivariate analyses. In Table 5, it may be seen that platelets, albumin, γGTP, ALT, the IL28B SNP, and number of patients with HCC development differed significantly between the two groups in univariate analysis. In contrast, successive multivariate analysis demonstrated that the number of patients with HCC development ($p = 0.046$) and the IL28B SNP ($p < 0.001$) were extracted as independent variables correlated with the core a.a. 70 residue (Table 5).

Multivariate analysis for independent factors influencing HCC development

To disclose factors influencing HCC development, multivariate analysis was performed. As shown in Table 6, age, albumin, and core a.a. 70 residue were extracted as independent factors. On the other hand, IL28B SNP was not extracted as one of those factors.

Discussion

In this study, we have documented several important findings. Through the investigation of HCV sequences, including complete HCV ORFs analysis, we have shown that the core a.a. 70 residue and its changes over time are associated with the disease progression as well as HCC development in genotype-1b HCV infection. Specifically, core a.a. 70Q/H was associated with HCC development and disease progression; core a.a. 70 often changed with time and R70Q substitutions were associated with progressive disease, while Q70R substitutions were associated with the stable disease. Moreover, we have shown that the IL28B SNP and core a.a. 70 showed significant linkage. In contrast, we have also shown that HCC development and disease progression were not apparently correlated with the IL28B SNP.

Recently, core amino acids have been reported in several studies to be associated with HCC [12, 21–25]. In

Table 6 Factors related to influencing HCC development

Variables	Univariate analysis ($N = 228$)		Multivariate analysis ($N = 228$)	
	Odds ratio (95% CI)	p value	Odds ratio (95% CI)	p value
Sex				
Female	1	0.161	1	0.190
Male	1.50 (0.85–2.67)		1.69 (0.77–3.71)	
Age (years)				
<65	1	0.006	1	0.004
≥65	2.30 (1.28–4.16)		3.26 (1.46–7.25)	
Platelets (10^{-4}/mm^3)				
>12	1	<0.001	1	0.021
≤12	5.82 (3.11–10.88)		2.59 (1.16–5.82)	
Albumin (g/dL)				
>4	1	<0.001	1	<0.001
≤4	13.75 (6.69–28.24)		7.73 (3.53–16.94)	
γGTP (IU/L)				
<41	1	<0.001	1	0.122
≥41	3.09 (1.70–5.62)		1.87 (0.85–4.13)	
ALT (IU/L)				
<41	1	<0.001	1	0.109
≥41	3.88 (2.06–7.31)		1.98 (0.86–4.56)	
IL28B				
TT	1	0.626	1	0.290
TG or GG	1.17 (0.13–2.17)		0.63 (0.27–1.49)	
Core a.a. 70				
R	1	<0.001	1	0.029
Q/H	2.91 (1.61–5.26)		2.44 (1.09–5.44)	
Previous IFN therapy				
−	1	0.949	1	0.331
+	0.98 (0.55–1.74)		1.46 (0.68–3.16)	

these studies, patients with core a.a. 70Q/H frequently developed HCC with exacerbation of liver damage. In this analysis, we confirmed the previous findings. However, because this association might be a reflection of the core-dependent IFN sensitivity differences often reported in recent studies [12, 22, 25], we restricted the analysis to patients, who were unable to clear HCV RNA previously through IFN-based therapy. Moreover, we also confirmed the relationship of the core sequences and disease development among the populations without a previous history of IFN therapy (data not shown). These findings strongly confirmed the role of core a.a. 70 in disease progression, independent of any IFN response.

It is a focus of interest how the core sequence evolves with time or with the course of disease. If the core sequences were fixed throughout the course of disease, HCV with core 70Q might be an "oncogenic" virus, while HCV with core 70R might be "non-oncogenic", and the initial viral sequence might forecast future liver disease. In this study, we have demonstrated that core sequences changed in 15% (15/98) of patients during the observation period of around 10 years. Among these changes, R70Q ($N = 11$) was more common than Q70R ($N = 4$). Interestingly, changes in this region were significantly associated with disease activity or HCC development, although patients with R70Q substitutions were significantly more likely to have exacerbation of the disease and Q70R substitutions were associated with the stable disease. These results demonstrate that the core a.a. 70 residue is not fixed, but often changes with time during the course of disease in close association with disease progression and HCC development. Although the molecular mechanism of their interaction needs further exploration, this result highlights the important clinical and basic implications for the association between host and virus.

The importance of the IL28B SNP has been demonstrated recently in HCV infection in terms of a correlation with treatment outcome of pegylated-IFN plus ribavirin

therapy [16–19]. The contribution of the IL28B SNP to the outcome of therapy was confirmed in successive studies, although the mechanism remains under investigation. On this basis, we sought to investigate the impact of the IL28B SNP on disease progression and HCC development, separate from the IFN-based treatment response. As shown in Table 4, we compared the clinical features between the two groups (IL28B GG/TG vs. IL28B TT). Importantly, this comparison disclosed a significant correlation between the core a.a. 70 polymorphisms and the IL28B SNP ($p < 0.001$) and confirmed the existence of a complex interaction between the host and the virus in chronic HCV infection. According to the result, patients with IL28B TG/GG were more likely to be infected with HCV with core a.a. 70Q/H than with core a.a. 70R and vice versa. Although the molecular mechanisms of their relationship remain unknown, it could be speculated that the IL28B SNP has an influence on the viral core sequences, because the host IL28B SNP remains fixed and cannot be influenced by the viral core sequence.

On the other hand, we observed no evident association between the IL28B SNP and HCC development. This was rather unexpected because it is considered that the IL28B SNP has a significant influence on the core a.a. 70 residue. Therefore, to clarify the correlation among core a.a. 70, IL28B, and HCC development, we undertook multivariate analysis to extract the independent variables affecting the core 70 residue. As demonstrated in Table 5, the IL28B SNP and the development of HCC were extracted as variables independently correlated with the core a.a. 70 residue. The result indicates that the core a.a. 70 residue was not only influenced by the IL28B SNP, but also by factors strongly related to HCC development, independent of the IL28B SNP. When considering the result, it is not strange if there is no direct relationship between IL28B SNP and HCC development. In contrast, multivariate analysis undertaken for disclosing factors influencing HCC development revealed that core a.a. 70 residue was a variable independently associated with HCC development other than age, albumin, or platelets even though the IL28B SNP was not extracted (Table 6). However, further comprehensive studies are warranted to disclose the molecular mechanisms for the complicated relationships among core a.a. 70, IL28B, and HCC development.

In conclusion, we have shown that core a.a. 70 was closely associated with disease progression and, often, changes of that residue were accompanied by temporal changes in liver damage, in close relationship with the IL28B SNP.

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ORIGINAL ARTICLE

Characterization of naturally occurring protease inhibitor-resistance mutations in genotype 1b hepatitis C virus patients

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Abstract
Background and aims Protease inhibitor (PI)-resistant hepatitis C virus (HCV) variants may be present in substantial numbers in PI-untreated patients according to recent reports. However, influence of these viruses in the clinical course of chronic hepatitis C has not been well characterized.
Methods The dominant HCV nonstructural 3 (NS3) amino acid sequences were determined in 261 HCV genotype 1b-infected Japanese patients before pegylated interferon plus ribavirin (PEG-IFN/RBV) therapy, and investigated the patients' clinical characteristics as well as treatment responses including sustained virological response (SVR) rate. HCV-NS3 sequences were also determined in 39 non-SVR patients after completion of the therapy.
Results Four single mutations (T54S, Q80K, I153V, and D168E) known to confer PI resistance were found in 35 of 261 patients (13.4%), and double mutations (I153V plus T54S/D168E) were found in 6 patients (2.3%). Responses to PEG-IFN/RBV therapy did not differ between patients with and without PI-resistance mutations (mutation group, SVR 48%; wild-type group, SVR 40%; $P = 0.38$). On the other hand, two mutations appeared in two non-SVR patients after PEG-IFN/RBV therapy (I153V and E168D, 5.1%).
Conclusions PI-resistance-associated NS3 mutations exist in a substantial proportion of untreated HCV-1b-infected patients. The impact of these mutations in the treatment of PIs is unclear, but clinicians should pay attention to avoid further development of PI resistance.

Keywords HCV · Protease inhibitor · Naturally occurring viral resistance mutations

Introduction

Hepatitis C virus (HCV) infects more than 170 million persons worldwide and thus represents a global health problem. At least 130 million infected individuals are chronic carriers of HCV and are at significant risk of developing liver cirrhosis and hepatocellular carcinoma [1]. The current standard treatment with pegylated interferon plus ribavirin (PEG-IFN/RBV) is complicated by frequent adverse reactions, and a sustained virologic response (SVR) can be achieved only in 50% of patients infected with the most prevalent genotype 1 [2]. In Japan, since 70% of patients are infected with intractable genotype 1b HCV, more effective treatments are urgently required.

A promising approach is the development of specifically targeted antiviral therapies for hepatitis C (STAT-C). HCV-specific protease inhibitors (PIs) target an essential step in HCV replication by blocking the nonstructural 3/4A (NS3/4A) protease-dependent cleavage of the HCV polyprotein

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