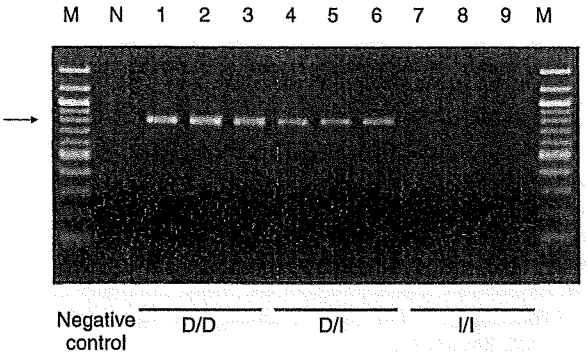

Figure 3 Detection of A3A-A3B fusion mRNA by PCR. A3A-A3B fusion mRNA was amplified by PCR using primers specific to A3A and A3B (see Materials and Methods) and detected by agarose gel electrophoresis. Lanes 1–3 are those from deletion homozygous patients, lanes 4–6 are from heterozygous patients and 7–9 are from insertion homozygous patients. M, molecular weight size marker (1 kb DNA Ladder; New England BioLabs, Ipswich, MA), N, negative control.

The deletion of APOBEC gene spans from 3′ end of the *A3A* gene to the 3′ portion of the *A3B* gene. This deletion results in the formation of a fusion gene that has *A3A* amino acid sequence and *A3B* 3′ untranslated region. The expression level of this protein may be different from the undeleted *A3A* due to different stability of RNA or different transcription levels. The results of context analysis also indicated that the effect of this alteration of expression levels of *A3A* is almost negligible compared with A3G. This is consistent with our results that showed lower levels of induction of hypermutation on HBV genome by *A3A* compared with *A3G*.

Our results indicated that the effect of both *A3A* and *A3B* is not significant in the development and progression of chronic hepatitis B. The two proteins also have only little influence on the hypermutation state of HBV in chronic HBV carriers. The results also showed higher induction levels of hypermutation by *A3G* than by *A3A*.

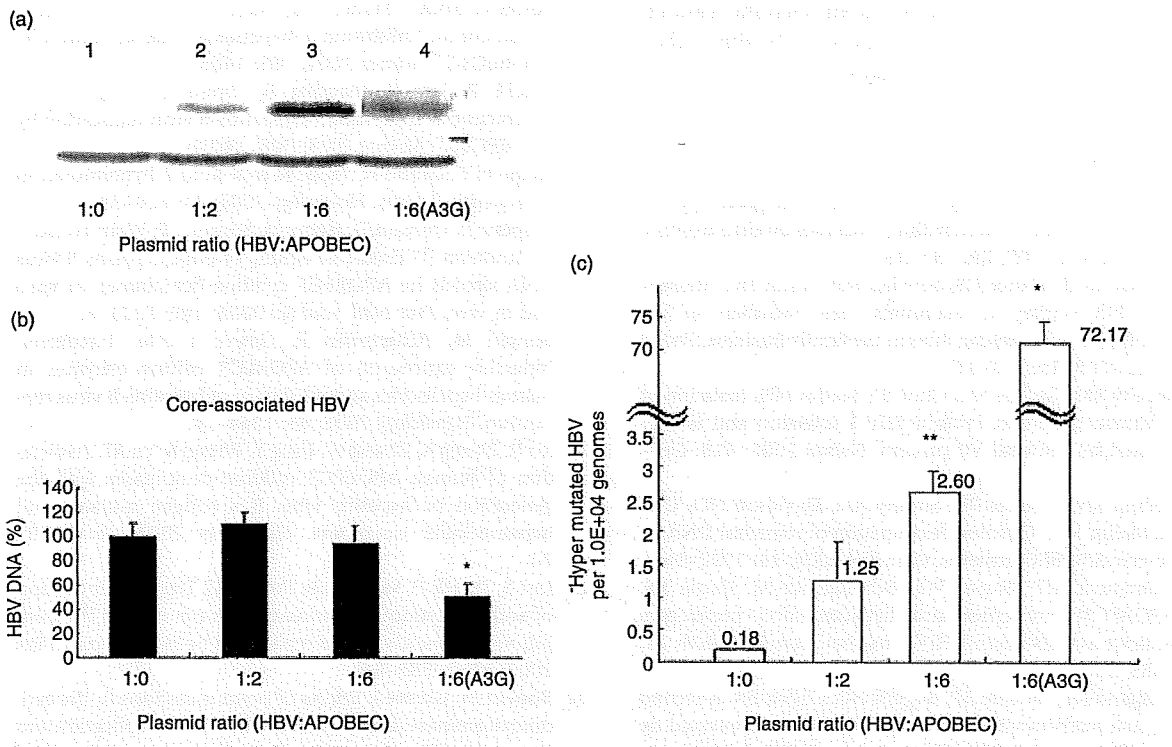

Figure 4 Analysis of inhibition of HBV replication and induction of hypermutation by A3A. HepG2 cells were transiently transfected with expression plasmid of A3A together with 1.4 genome length hepatitis B virus (HBV) expression vector. The indicated amounts of HBV and A3A (1:0, 1:2, 1:6) or A3G (1:6) expression plasmids were transfected into HepG2 cells. All experiments were performed more than twice with similar results. (a) APBEC3 gene expression levels were detected by western blot analysis. (b) The amounts of core associated replicative intermediates of HBV were measured by RT-PCR. (c) Quantitative measurement of hypermutated genomes by 3D real-time PCR. Data in (B) and (C) are mean ± SD. $*P < 0.05$; $**P < 0.01$

Sufficient evidence indicates that *A3G* has anti-viral effects on HBV,[14–17] suggesting that some but not all APOBEC3 proteins operate as part of the anti-viral immune system against HBV infection. Further study is needed to clarify the functional role of each APOBEC3 protein for innate anti-viral immunity in chronic HBV infection.

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G-to-A Hypermutation in Hepatitis B Virus (HBV) and Clinical Course of Patients with Chronic HBV Infection

Chiemi Noguchi,[1,2] Michio Imamura,[1,2] Masataka Tsuge,[1,2] Nobuhiko Hiraga,[1,2] Nami Mori,[1,2] Daiki Miki,[1,2] Takashi Kimura,[1,2] Shoichi Takahashi,[1,2] Yoshifumi Fujimoto,[1,2] Hidenori Ochi,[2,3] Hiromi Abe,[1,3] Toshiro Maekawa,[3] Chise Tateno,[2,4] Katsutoshi Yoshizato,[2,4] and Kazuaki Chayama[1,2,3]

[1]Department of Medicine and Molecular Science, Division of Frontier Medical Science, Programs for Biomedical Research, Graduate School of Biomedical Sciences, and [2]Liver Research Project Center, Hiroshima University, Hiroshima, [3]Laboratory for Liver Diseases, Single-Nucleotide Polymorphism Research Center, the Institute of Physical and Chemical Research, Yokohama, and [4]PhoenixBio, Higashihiroshima, Japan

Background. The apolipoprotein B messenger RNA editing enzyme, catalytic polypeptide–like family of cytidine deaminases induce G-to-A hypermutation in hepatitis B virus (HBV) genomes and play a role in innate antiviral immunity. The clinical relevance of this protein family is unknown.

Methods. We analyzed 33 instances in which 17 patients with chronic HBV infection experienced >2 increases of >100 IU/L in alanine aminotransferase (ALT) level; we used a quantitative differential DNA denaturation polymerase chain reaction assay to quantify the hypermutated HBV genomes observed during 21 of these 33 increases in ALT level.

Results. Of the 9 increases in ALT level that involved a >5-fold increase (relative to basal levels) in the number of hypermutated genomes observed, 8 were associated with a >2-log reduction in plasma HBV DNA level. In contrast, a corresponding decrease in plasma HBV DNA level was observed for only 1 of the 12 increases in ALT level that did not involve an increase in the number of hypermutated genomes ($P < .001$). Hepatitis B e antigen clearance was often observed in patients who experienced an increase in the number of hypermutated genomes. Interferon treatment induced hypermutation in HBV genomes in an animal model. However, there was no apparent increase in the number of hypermutated genomes among the majority of patients who received interferon therapy, probably because the number of hypermutated genomes had already increased prior to the initiation of therapy.

Conclusion. Our results suggest that a marked increase in the number of hypermutated genomes represents a strong immunological host response against the virus and is predictive of hepatitis B e antigen clearance and plasma HBV DNA level reduction.

Despite the availability of safe and effective vaccines for >2 decades, hepatitis B virus (HBV) infection is still a global health problem. Worldwide, >2 billion people are infected with HBV, and chronic HBV infection affects ~400 million people [1, 2]. It is estimated that >500,000 people die annually because of cirrhosis and/or hepatocellular carcinoma due to HBV infection [3].

Recent reports have shown that cellular cytosine deaminase (apolipoprotein B messenger RNA [mRNA] editing enzyme, catalytic polypeptide–like 3G [APOBEC3G]), packaged in human immunodeficiency virus type 1 (HIV-1), induces G-to-A hypermutation to a nascent reverse transcript of HIV-1 and reduces the infectivity of HIV, thus contributing in part to innate antiviral activity [4–8]. HIV-1 overcomes this innate defense barrier in T cells with HIV virion infectivity factor, a protein that specifically targets APOBEC3G to proteasomal degradation [9–12]. HIV-1 can infect resting CD4 T cells in lymphoid tissues but not those circulating in peripheral blood [13–16]. Resting CD4 T cells in peripheral blood are protected from HIV infection through the action of the deaminase-active

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Reprints or correspondence: Kazuaki Chayama, MD, Dept. of Medical and Molecular Science, Div. of Frontier Medical Science, Programs for Biomedical Research, Graduate School of Biomedical Science, Hiroshima University, 1-2-3 Kasumi, Minami-ku, Hiroshima 734-8551, Japan (chayama@hiroshima-u.ac.jp).

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Table 1. Clinical profiles of 17 patients with chronic hepatitis B virus (HBV) infection who experienced >2 increases of >100 IU/L in alanine aminotransferase (ALT) level.

Patient	Sex	Age, years	ALT level, IU/L		Plasma HBV DNA level, log copies/mL	HBV serum marker status[a]		HBV subtype	Histologic result[b]	Receipt of IFN treatment
			Minimum	Maximum		HBeAg	HBeAb			
1	M	50	26	2000	8.1	+	−	C	F2, A2	Yes
2	M	31	22	230	8.2	+	−	C	F3, A2	Yes
3	F	23	14	313	8.7	+	−	C	F2, A2	Yes
4	M	22	16	846	6.9	+	−	C	F2, A1	Yes
5	F	42	10	100	7.8	+	−	C	L	No
6	F	33	21	748	8.8	+	−	C	F2, A3	Yes
7	M	23	22	339	8.4	+	−	C	L	Yes
8	F	54	22	108	6.7	−	+	C	F2, A2	No
9	M	44	17	512	9.5	+	−	C	F2, A3	No
10	M	27	39	115	8.8	+	−	C	F1, A1	Yes
11	M	36	16	452	3.8	+	−	C	F4, A3	Yes
12	M	20	21	1295	7.2	+	−	C	F2, A2	No
13	M	36	24	481	5.7	−	+	C	F2, A2	Yes
14	M	22	20	696	5.9	+	−	C	F1, A1	Yes
15	F	24	14	1544	7.7	+	−	C	F2, A2	Yes
16	M	35	10	1618	4.7	+	−	C	F2, A1	Yes
17	M	30	21	1655	6.7	+	−	C	L	Yes

NOTE. HBeAg, HBV e antigen; HBeAb, antibody against HBV e antigen; IFN, interferon; L, liver cirrhosis.

[a] Before increase in ALT level.

[b] Histologic evaluation of chronic hepatitis by use of the scoring system of Desmet et al. [29].

APOBEC3G [17]. Recent reports have shown that interferon (IFN)–α is a potent inducer of APOBEC3G [18–21]. It has also been reported that some of the HIV restriction exerted by APOBEC3G may be independent of its cytidine deaminase activity [17, 22–24].

We and others have reported the presence of small numbers of hypermutated genomes in serum samples obtained from HBV-infected patients [25–27]. Studies using HepG2 cell lines and primary human hepatocytes showed that such hypermutation is induced by the cytidine deaminase activity of the APOBEC family of proteins [27]. In our previous study, IFN induced little hypermutation in the HBV genome [27]. However, after extensive investigation supported by development of a quantitative analysis of hypermutation, we showed that both IFN-α and IFN-γ actually increase transcription of APOBEC3G mRNA in HepG2 cell lines and induce an increase in the number of hypermutated genomes [28]. We also showed that APOBEC3G induces hypermutation in HBV and reduces HBV replication levels in the absence of the deaminase activity. Thus, APOBEC3G has dual antiviral actions against HBV and is thought to be part of the host defense mechanisms, as has been shown for HIV infection. Although it is assumed that APOBEC3G is important in the host anti-HBV defense system, little is known about the clinical importance of this enzyme, because there are no methods available for the precise quantification of small amounts of hypermutated genomes.

Using a method that can measure small amounts of hypermutated genomes (differential DNA denaturation polymerase chain reaction [3D-PCR] combined with TaqMan PCR [28]), we analyzed fluctuations in the number of hypermutated genomes observed in patients with chronic HBV infection who experienced increased alanine aminotransferase (ALT) levels. The study group included patients who received IFN treatment and patients who did not.

METHODS

Patients. From 2002 through 2006 at Hiroshima University Hospital (Hiroshima, Japan), there were 17 consecutive patients with chronic hepatitis B who experienced >2 increases of >100 IU/L in ALT level and for whom stored serum samples were available. These 17 patients were enrolled in this study, among whom 33 such increases in ALT level were observed. Thirteen of 17 patients received IFN treatment, usually during an increase in ALT level. The clinical profiles of these 17 patients are shown in table 1. Written informed consent was obtained from all patients, and the study was approved by the Hiroshima University Ethics Committee.

HBV markers. Hepatitis B e antigen and antibody against e antigen were quantified by use of enzyme immunoassay kits (Abbott Diagnostics). HBV DNA was measured by use of real-time PCR performed with the 7300 Real-Time PCR System (Applied Biosystems), in accordance with the manufacturer's instructions. The primers used for amplification were 5'-TT-

TGGGCATGGACATTGAC-3' (nt 1893–1912; nucleotide numbers are those of HBV subtype C as reported by Norder et al. [30]) and 5'-GGTGAACAATGTTCCGGAGAC-3' (nt 2029–2049). For real-time PCR, we used 25 μL of SYBR Green PCR Master Mix (Applied Biosystems) with 1 μL of the DNA solution and 200 nmol/L of each primer. The amplification conditions were as follows: 2 min at 50°C, 10 min at 95°C, followed by 40 cycles of amplification (denaturation at 95°C for 15 s and annealing and extension at 60°C for 1 min). The lower detection limit of this assay was 10^3 copies/mL.

Extraction of HBV DNA and quantitative analysis of hypermutated genomes. HBV DNA was extracted from 100-μL serum samples by use of the SMITEST DNA Extraction Kit (Genome Science Laboratories) and dissolved in 20 μL of water. Hypermutated genomes were quantified by use of TaqMan 3D-PCR performed with the 7300 Real-Time PCR System (Applied Biosystems); we used a procedure described elsewhere [28], with slight modifications. In brief, the HBV DNA fragments were amplified by use of 3D-PCR in which the denaturation temperature was set lower than usual so that only G-to-A hypermutated genomes would be amplified. The amplification conditions were as follows: activation at 95°C for 10 min; followed by initial denaturation at 89°C for 20 min, to allow nonhypermutated genomes reanneal; and 45 cycles of amplification (denaturation at 89°C for 20 s, annealing at 50°C for 30 s, and extension at 62°C for 90 s). TaqMan PCR was performed using the following primers: 5'-ACTTCAACCCCAACAMRRATCA-3' (nt 2978–2999) and 5'-AGAGYTTGKTGGAATGTKGTGGA-3' (nt 24–1), where M is A or C, R is G or A, Y is T or C, and K is G or T. The probe was a 6-carboxyfluorescein (FAM)–labeled MGB probe, 5'-(FAM)-TTAGAGGTGGAGAGATGG-(MGB)-3' (nt 3184–3167). The detection limit of hypermutated genomes was 10^2 copies/mL, and nonhypermutated genomes were not amplified by 3D-PCR [28]. The reproducibility of the assay was quite high (as indicated by the small standard deviation relative to the results of the quantitative PCR control reaction), as reported in our previous study [28].

Cell culture and transfection. HepG2 cell lines were grown in Dulbecco's modified Eagle medium supplemented with 10% (vol/vol) fetal calf serum at 37°C in 5% CO_2. Cells were seeded to semiconfluence in 6-well tissue culture plates and transfected with the plasmid pTRE-HB-wt, which contained 1.4–genome length wild-type HBV genomes [31], by calcium phosphate precipitation. Seventy-two hours after transfection, the supernatant was collected for HBV DNA quantification by real-time PCR and for quantitative analysis of G-to-A hypermutated genomes [28]. The remaining supernatant was stored at −80°C for infection experiments using human hepatocyte–chimeric mice.

Quantitative analysis of G-to-A hypermutated genomes with human hepatocyte–chimeric mice. A human hepatocyte–chimeric mouse model was developed, as described previously [32], and used in infection and IFN-treatment experiments. The human hepatocytes progressively repopulated the murine host liver and were susceptible to HBV produced in cultured cell lines [31]. All animal protocols were in accordance with the guidelines of the local animal experimentation committee. The experimental protocol was approved by the Ethics Review Committee for Animal Experimentation of the Graduate School of Biomedical Sciences, Hiroshima University. Hepatocyte-chimeric mice were inoculated with 500 μL of the supernatant produced by transiently transfected cell lines. After confirmation of high-level HBV viremia, the mice were treated with 7000 IU/g/day of IFN-α, injected intramuscularly, for 14 days (the IFN-α was a gift from Hayashibara Biochemical Labs in Okayama, Japan). Human serum albumin in mouse serum was measured with the Human Albumin ELISA Quantitation Kit (Bethyl Laboratories), used in accordance with the manufacturer's instructions.

Statistical analysis. Differences between clinical groups with respect to HBV DNA and e antigen levels were examined for statistical significance, using the Mann-Whitney *U* test. A *P* value $<.05$ was considered to indicate a statistically significant difference. All statistical analyses were performed with StatView (version 5.0; SAS Institute).

RESULTS

Clinical course of disease in patients with increased ALT levels and fluctuations in the number of hypermutated genomes. Figure 1*A*–1*D* shows clinical courses for 4 representative patients (patients 1–4 in Table 1) with chronic HBV infection who experienced increases in ALT level. We observed marked decreases in HBV DNA level in association with marked increases in hypermutated genomes (figure 1*A*–1*C*, black arrows). In contrast, there was no apparent reduction in HBV level in the absence of an increase in hypermutated genomes (1*A*–1*D*, white arrows). We also analyzed the effect of IFN therapy on the number of hypermutated genomes. In some patients, we observed an increase in the number of hypermutated genomes during IFN therapy (figure 1*B* and 1*C*) as well as a marked increase in the number of hypermutated genomes and a reduction of the virus accompanied by an increase in ALT level just after cessation of IFN therapy (1*A*–1*C*, black arrows). However, in some patients, such as patient 1 (figure 1*A*), we observed no apparent increase in the number of hypermutated genomes in response to IFN therapy. However, the number of hypermutated genomes observed in samples from this patient obtained just before the initiation of IFN therapy (996/10^6 genomes) was already higher than the baseline level (157/10^6 genomes). Samples from patient 4 (figure 1*D*) showed an increase in the number of hypermutated genomes during IFN therapy (1907/10^6 genomes), though this is less than the increase observed during natural exacerbation (12,404/10^6 genomes). In fact, there was no significant difference between IFN-treated patients and untreated patients with respect to the number of hypermutated genomes observed (data not shown). These results suggest that the host's antiviral immunity level was higher at baseline than it was after

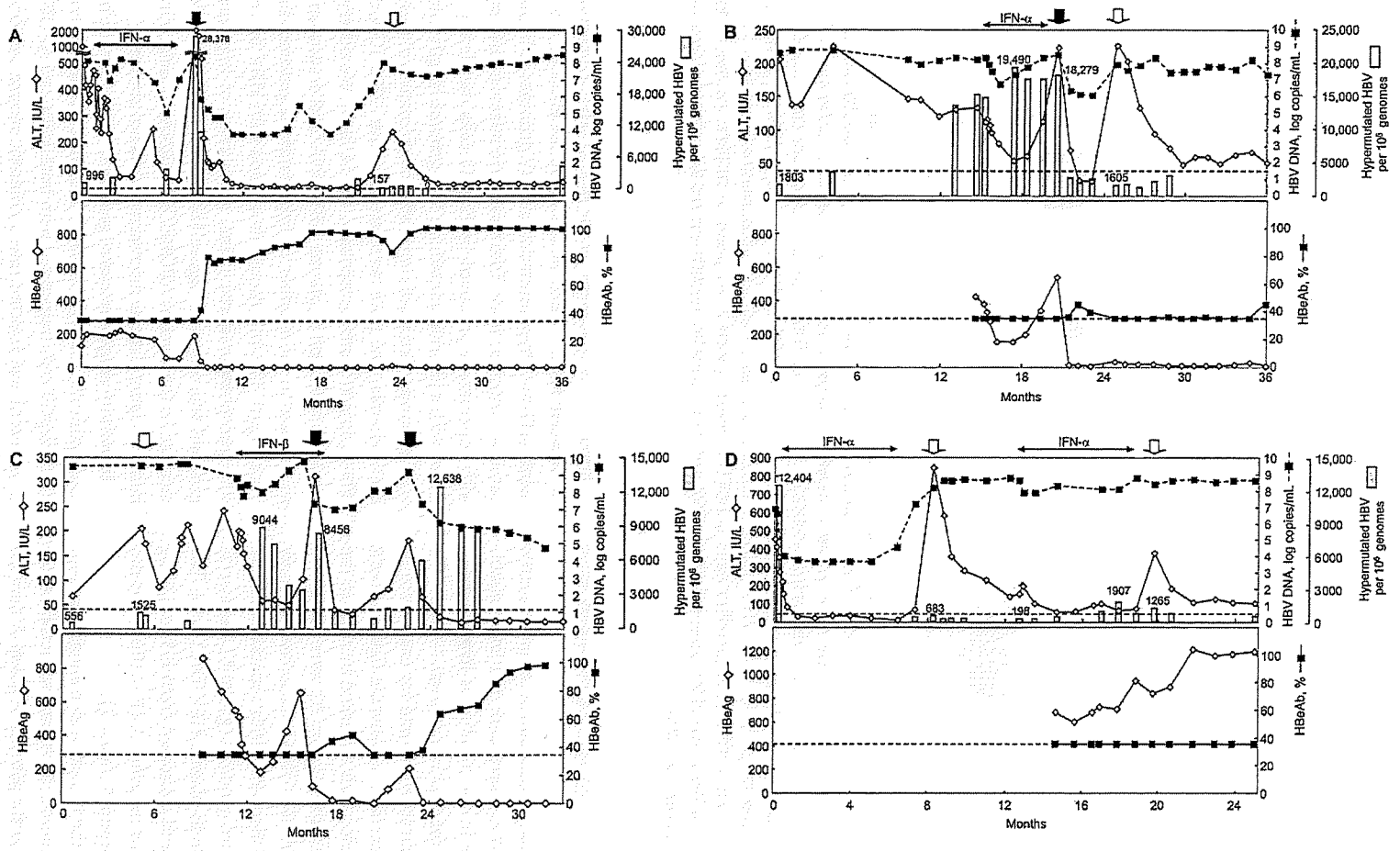

Figure 1. Clinical courses for 4 patients *(A–D)* with chronic hepatitis B virus (HBV) infection who experienced exacerbation of infection. *Black arrows,* exacerbation associated with an increase in the number of hypermutated genomes (>5 times basal levels); *white arrows,* exacerbation not associated with an increase in the number of hypermutated genomes; *horizontal dotted lines,* upper normal limit of alanine aminotransferase (ALT) (40 IU/mL; *upper panel, A–D*) and the detection limit for antibody against e antigen (HBeAb) (35%; *lower panel, A–D*). HBeAb, antibody against HBV e antigen; HBeAg, HBV e antigen; IFN, interferon.

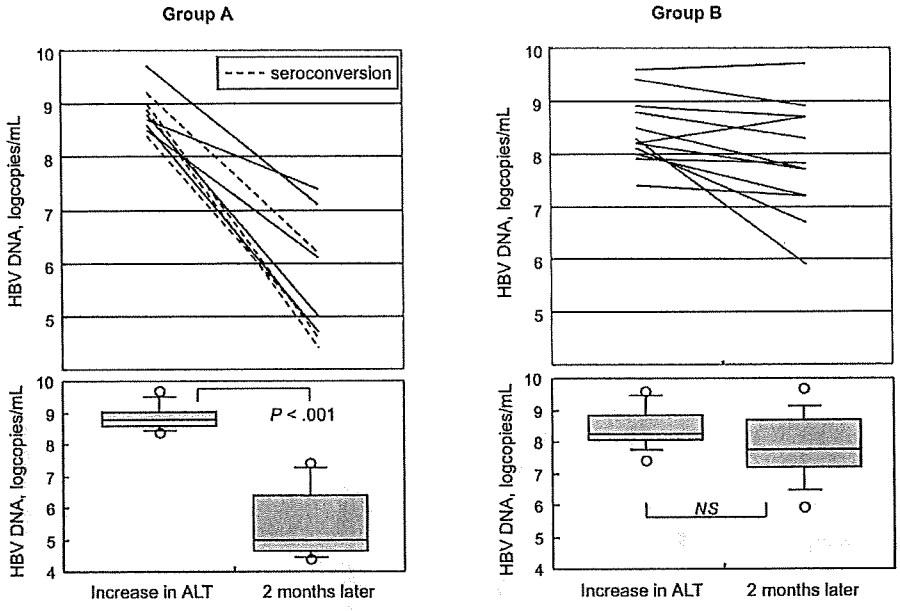

Figure 2. Relationship between increase in the number of hypermutated genomes and plasma levels of hepatitis B virus (HBV) DNA in 17 patients with chronic HBV infection who experienced >2 increases of >100 IU/L in alanine aminotransferase (ALT) level. Patients' exacerbations were divided into 2 groups, A and B, according to the extent of increase in the number of hypermutated genomes, relative to the basal number (group A included 9 exacerbations that involved a >5-fold increase in the number of hypermutated genomes; group B included 12 exacerbations that involved a ≤5-fold increase in the number of hypermutated genomes). *Upper panel* for groups A and B, individual HBV DNA levels at the time the ALT level increased and 2 months later; in the upper panel for group A, *dashed lines* indicate 4 exacerbations associated with seroconversion to positivity for antibody against e antigen. *Lower panel* for groups A and B, box-and-whisker plots for HBV DNA levels at same 2 time points. In the plots, the lines in the boxes indicate median values; the upper and lower lines of the boxes indicate the 25th and 75th percentiles, respectively; and the upper and lower whiskers represent the 90th and 10th percentiles, respectively.

IFN or that the feedback system for IFN signaling was already active before initiation of therapy.

We also compared the degree of reduction in the plasma HBV DNA level for exacerbations (i.e., increases in ALT level) associated with a marked increase in the number of hypermutated genomes (i.e., those in which the peak number was >5 times the number observed prior to exacerbation) and for exacerbations not associated with such an increase. As shown in figure 2, 8 of 9 exacerbations that were coupled with a marked increase in the number of hypermutated genomes (group A) were associated with a >2-log reduction in the HBV DNA level. In contrast, only 1 of the 12 exacerbations not associated with a marked increase in the number of hypermutated genomes (group B) was associated with a >2-log reduction in plasma HBV DNA level. The median serum HBV DNA level decreased from 8.8 to 5.0 log copies/mL among the patients in group A ($P < .001$) but did not decrease for patients in group B (figure 2).

In addition, we compared the reduction in e antigen level for these 2 groups. Levels were reduced in both groups, but the median reduction was more prominent for patients in group A than for those in group B (figure 3). All 4 exacerbations coupled with e antigen seroconversion (from positive to negative) were associated with marked increase in hypermutated genomes (figure 3).

Effect of IFN treatment on the rate of HBV hypermutation in chimeric mice. Next, we examined the effect of IFN treatment on G-to-A hypermutation in HBV genomes in human hepatocyte–chimeric mice. Two mice were intravenously injected with supernatant produced by HepG2 cells transiently transfected with a plasmid containing 1.4–genome length wild-type HBV genomes. Ten weeks later, after confirmation of high-level HBV viremia, the mice were treated with 7000 IU/g/day of IFN-α, injected intramuscularly, for 14 days. We observed an ~1.5-log reduction in plasma HBV DNA level accompanied by an increase in the number of hypermutated genomes in both mice (figure 4*A*). In a mouse inoculated with HBV but treated with phosphate-buffered saline, no increase of hypermutated genomes was observed (figure 4*B*). We also observed a 36-fold increase in the level of APOBEC3G mRNA, as determined by human oligonucleotide microarray (data not shown).

Infectivity of hypermutated genomes. To study the biological significance of hypermutated genomes, culture supernatant from HepG2 cells transfected with both HBV and APOBEC3G (5 μg each) was injected into a chimeric mouse. As shown in figure 5, the culture supernatant contained a large number of hypermutated genomes. In contrast, we could not detect hypermutated genomes in the chimeric mouse inoculated with this

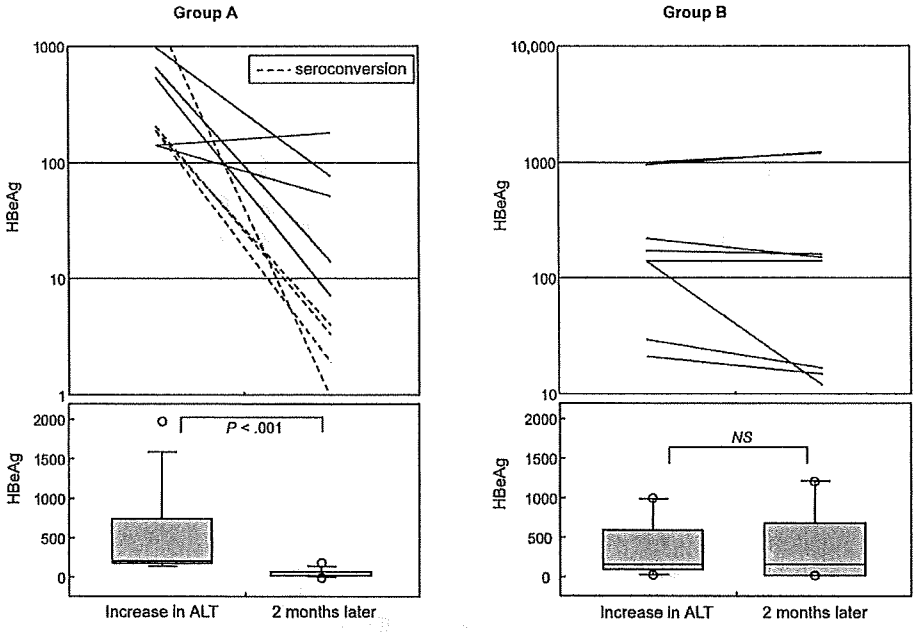

Figure 3. Relationship between increase in the number of hypermutated genomes and hepatitis B virus (HBV) e antigen (HBeAg) levels in 15 HBeAg-positive patients with chronic HBV infection who experienced >2 increases of >100 IU/L in alanine aminotransferase (ALT) level. Patients' exacerbations were divided into 2 groups, A and B, according to the extent of increase in the number of hypermutated genomes, relative to the basal number (group A included 9 exacerbations that involved a >5-fold increase in the number of hypermutated genomes; group B included 8 exacerbations that involved a ≤5-fold increase in the number of hypermutated genomes). *Upper panel* for groups A and B, individual e antigen levels at the time the ALT level increased and 2 months later; in the upper panel for group A, *dashed lines* indicate 4 exacerbations associated with seroconversion to positivity for antibody against e antigen. *Lower panel* for groups A and B, box-and-whisker plots for e antigen levels at these same 2 time points. In the plots, the lines in the boxes indicate median values; the upper and lower lines of the boxes indicate the 25th and 75th percentiles, respectively; and the upper and lower whiskers represent the 90th and 10th percentiles, respectively.

supernatant (figure 5*A* and 5*B*). These results suggest that the infectivity (or replication ability) of HBV with hypermutated genomes is very poor. It is possible that the inoculum contained less abundantly mutated genomes. To test this, we cloned and sequenced 72 clones of 217-bp DNA fragments amplified at a denaturation temperature of 95°C. Of 72 clones obtained from the inoculum, we found 1 clone with 8 G-to-A substitutions, 1 clone with 5 substitutions, 2 clones with 3 substitutions, and 1 clone with 1 substitution (figure 5*C*). In contrast, 1 of the 72 clones obtained from the mouse serum had 1 G-to-A substitution. If G-to-A substitutions were excluded, the only other nucleotide substitution observed in the 144 clones sequenced was a single C-to-T substitution.

DISCUSSION

In a previous study, we found that the majority of serum samples obtained from HBV-infected patients contained a small number of hypermutated genomes [27]. Recently, we developed a method (TaqMan 3D-PCR) to measure small numbers of hypermutated genomes [28]. Using this method, we reported dual antiviral effects for APOBEC3G, namely induction of hypermutation and reduction of viral replication. We also reported that IFN increased the transcription of APOBEC3G and enhanced the effect of the protein in vitro [28]. Other investigators also showed that IFN enhances the action of APOBEC proteins against HIV [18–21]. It is thus assumed that the antiviral effect of APOBEC proteins should be enhanced by IFN and other cytokines in vivo.

In the present study, we showed that an increase in ALT level accompanied by an increase in the number of hypermutated genomes was associated with reduction in the plasma HBV DNA level. In contrast, no decrease in HBV DNA level was observed if the increase in ALT level occurred in the absence of an increase in the number of hypermutated genomes. It is difficult to know which of the dual antiviral effects of APOBEC3G (or other APOBEC proteins) reduced the viral level. It is also impossible to estimate the importance of APOBEC proteins in this reduction. However, it is clear that the increase in the number of hypermutated genomes of HBV correlates with activation of the host antiviral defense against HBV.

We also demonstrated that exacerbations of HBV infection associated with a marked increase in the number of hypermutated genomes were associated not only with a decrease in the plasma HBV DNA level but also with clearance of e antigen.

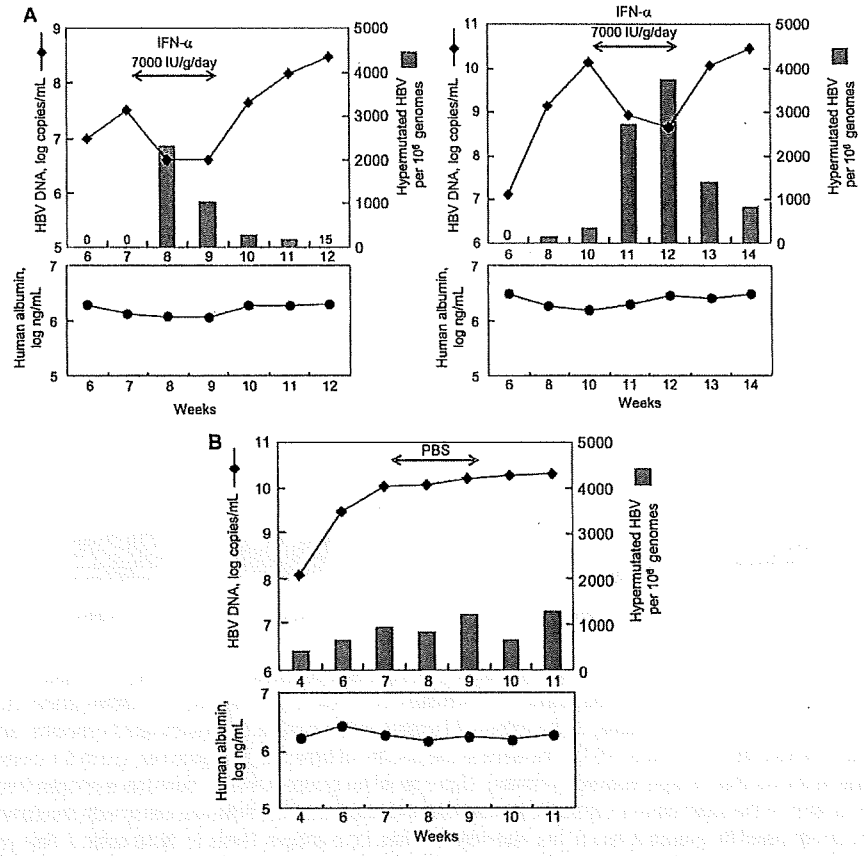

Figure 4. Effect of interferon (IFN)–α therapy on hepatitis B virus (HBV) hypermutation in HBV-infected, human hepatocyte–chimeric mice. Two chimeric mice *(A)* were inoculated with recombinant wild-type HBV produced by transfected HepG2 cells; 10 weeks later, after confirmation of high-level HBV viremia, they were treated with IFN-α at 7000 IU/g/day for 14 days, by intramuscular injection. *Upper panels* in both parts of *A*, serum HBV DNA levels and the number of hypermutated genomes; *lower panels* in both parts of *A*, human serum albumin concentrations. Note that the albumin levels are stable during IFN-α therapy. A control mouse *(B)* was inoculated with recombinant wild-type HBV produced by transfected HepG2 cells and treated with phosphate-buffered saline (PBS). Upper and lower panels of *B* show the same information as in *A*.

Furthermore, all exacerbations followed by seroconversion to positivity for antibody against e antigen were associated with a marked increase in the number of hypermutated genomes. Clearance of e antigen often results from a G-to-A nucleotide substitution at the first position of a 5'-GGGG stretch in the precore coding sequence (the G1896A mutation). Because this substitution (changing TGGGG to TAGGG) is in agreement with the dinucleotide pattern preferentially edited by APOBEC3G, one might assume that G-to-A substitution in this region could be caused by this enzyme and is related to the clearance of e antigen. However, we observed that hypermutation was induced in only some genomes, whereas the majority of genomes were unaffected. Thus, it seems unlikely that APOBEC proteins play a role in seroconversion to positivity for antibody against e antigen, although it is still possible that the 5'-GGGG stretch in the precore region is the preferred editing site for the enzyme. Importantly, such substitution of the 5'-GGGG stretch should result in the occurrence of multiple stop codons (TAG, TGA, and TAA) in HBV genomes, as we observed and reported in our previous study [28], which makes the replication of mutated genomes impossible.

In the present study, we did not observe any increase in the number of hypermutated genomes during IFN therapy in some patients. This finding is discrepant from the results of previous in vitro experiments that showed increased numbers of hypermutated genomes after the application of IFN [28]. Interestingly, our experimental results also showed the induction of APOBEC3G gene expression, an increase in the number of hypermutated genomes, and a reduction of plasma HBV DNA level in 2 human hepatocyte–chimeric mice treated with IFN (figure 4). What is the reason for the lack of increase in hypermutation in some IFN-treated patients? We usually administer IFN to patients who have high ALT levels. The patients in this study had abnormal ALT levels prior to treatment with IFN—that is, their livers were inflamed, and the levels of many cytokines produced by the immune cells in the liver were already high. We presume that the effect of these elevated cytokine levels masked the effect of the IFN we administered. It could also be argued that the effect

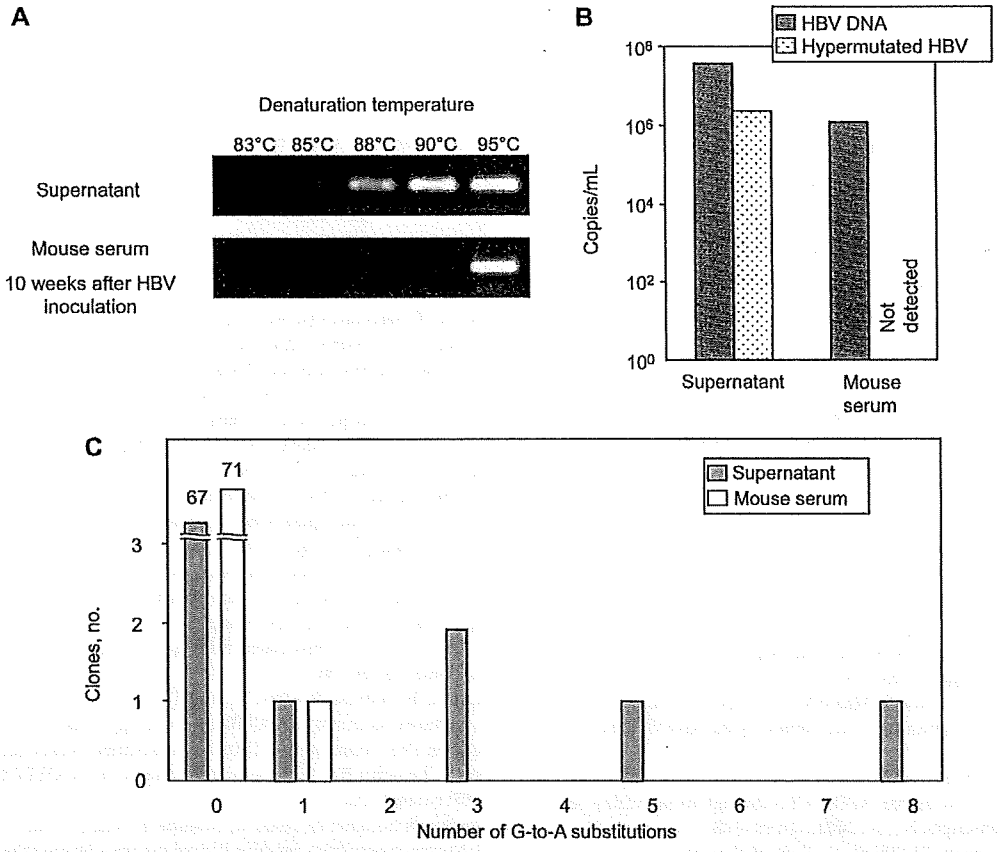

Figure 5. Results for a human hepatocyte–chimeric mouse inoculated with hepatitis B virus (HBV) produced by HepG2 cells transfected with an equal amount (5 μg each) of HBV and apolipoprotein B messenger RNA editing enzyme, catalytic polypeptide–like 3G plasmids. The inoculum contained ~6.25% hypermutated genomes. A serum sample was obtained 10 weeks after the inoculation. *A*, HBV DNA was amplified by polymerase chain reaction (PCR) that used different denaturation temperatures and run on 2% agarose gel. *B*, Quantitative measurement of HBV DNA and hypermutated DNA in the inoculum and mouse serum. *C*, Number of G-to-A substitutions found in each of 72 clones obtained from products of PCR of culture supernatant or mouse serum.

observed in mice represents the absence of the immune response in mice, whereas the lack of a clear response to IFN in the study patients was the result of the complex immune response in human beings. Alternatively, the concentrations of IFN in treated patients might be lower than those used for the cell culture or the chimeric mice. Although we did not perform this analysis in the present study, it would be interesting to determine the expression levels of APOBEC proteins and IFN-stimulated genes in the liver of IFN-treated patients.

The present study showed that the number of hypermutated genomes increased during some increases in ALT level, probably as a result of IFN-activated APOBEC proteins and other cytokines in patients with chronic hepatitis B. However, the number of hypermutated genomes was very small, only 28,378 in 10^6 HBV genomes at most (figure 1*A*). Because it was possible that the less abundantly hypermutated genomes were not detected (i.e., that genomes with only 1 or 2 G-to-A substitutions were not amplified by 3D-PCR), cloning and sequencing were performed to detect such genomes. However, the number of genomes containing G-to-A substitutions was still low (5 [6.9%] of 72 clones), even in the culture medium of HepG2 cells cotransfected with APOBEC3G and HBV (figure 5*C*). This means that the number of genomes with only a small number of G-to-A substitution was not high, suggesting that only selected DNA molecules were heavily mutated while the remaining DNA was not. Does this mean that the effect of APOBEC proteins in antiviral defense is trivial in patients with chronic HBV infection? It is a possible that the heavily deaminated genomes are an easy target for uracil DNA glycocylase. Although the dual antiviral effects of APOBEC proteins are currently known to reduce the amount of HBV, the importance and magnitude of APOBEC proteins with respect to in vivo virus reduction should be investigated further.

Treatment of patients with chronic HBV infection has improved with the advent of new nucleoside and nucleotide analogues. However, reactivation of HBV and flare-ups of hepatitis are often seen in patients who stop such therapy. Furthermore, hepatitis B surface antigen clearance is rare in patients treated

with these antiviral drugs. On the other hand, most patients with chronic HBV infection achieve sufficient viral suppression and disease quiescence through immunological suppression of the virus. As we showed in this study, the immunological suppression of HBV is much stronger than that achieved with IFN therapy, but it is often transient. It is thus necessary to clarify the mechanism of transient immune response and to develop treatment that produces persistent suppression of HBV. Quantitative measurement of hypermutated genomes should be useful in monitoring the immune response in this context.

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Research Article

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Association between mutations in the core region of hepatitis C virus genotype 1 and hepatocellular carcinoma development

Shingo Nakamoto, Fumio Imazeki*, Kenichi Fukai, Keiichi Fujiwara, Makoto Arai, Tatsuo Kanda, Yutaka Yonemitsu, Osamu Yokosuka

Department of Medicine and Clinical Oncology, Graduate School of Medicine, Chiba University, 1-8-1 Inohana, Chuo-Ward, Chiba City, Chiba 260-8670, Japan

Background & Aims: To determine whether amino acid mutations in the core region of hepatitis C virus (HCV) genotype 1 are associated with response to interferon (IFN) therapy and development of hepatocellular carcinoma (HCC).

Methods: We followed up 361 patients (median duration, 121 months), and IFN monotherapy was administered to 275 (76%) [sustained virological response (SVR) rate, 26.5%]. Using pretreatment sera, mutations at core residues 70 and 91 were analyzed [double wild (DW)-type amino acid pattern: arginine, residue 70; leucine, residue 91].

Results: A low aspartate aminotransferase (AST)/alanine aminotransferase (ALT) ratio and low HCV load were independently associated with SVR, but core mutations were not. During follow-up, 12 of 81 (14.8%) patients with the DW-type pattern and 52 of 216 (24.1%) patients with non-DW-type pattern developed HCC ($p = 0.06$, Breslow–Gehan–Wilcoxon test). Multivariate analysis with the Cox proportional-hazards model revealed the following independent risk factors for HCC: male gender [$p < 0.0001$; risk ratio (RR), 3.97], older age ($p < 0.05$; RR, 2.08), advanced fibrosis ($p < 0.0001$; RR, 5.75), absence of SVR ($p < 0.01$; RR, 10.0), high AST level ($p < 0.01$; RR, 2.08), high AST/ALT ratio ($p < 0.01$; RR, 2.21), and non-DW-type pattern ($p < 0.05$; RR, 1.96). In patients with F0–F2 fibrosis at entry, non-DW-type was likely to lead to cirrhosis ($p = 0.051$).

Conclusions: In HCV genotype 1 patients, HCC risk could be predicted by studying core mutations, response to IFN, and host factors like age, gender, and liver fibrosis.

Keywords: Hepatitis C virus; Core region; Hepatocellular carcinoma; Interferon; Sustained virological response.

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* Corresponding author. Tel.: +81 43 226 2083; fax: +81 43 226 2088.

E-mail address: imazekif@faculty.chiba-u.jp (F. Imazeki).

Abbreviations: HCV, hepatitis C virus; IFN, interferon; HCC, hepatocellular carcinoma; SVR, sustained virological response; DW-type, double wild-type; RR, risk ratio; AST, aspartate aminotransferase; ALT, alanine aminotransferase; US, ultrasonography; CT, computed tomography; MRI, magnetic resonance imaging; PCR, polymerase chain reaction; OR, odds ratio.

Introduction

Hepatitis C virus (HCV) infection is a global health problem and the number of chronic carriers worldwide is estimated at 170 million [1]. HCV causes chronic hepatitis, which may progress to liver cirrhosis and hepatocellular carcinoma (HCC); the speed of disease progression, though, varies among patients [2,3]. Age, gender, steatosis, liver fibrosis, and response to interferon (IFN) therapy are reported to be associated with disease progression and HCC development [4–7]. HCV has six major genotypes, of which genotype 1 is most common in Japan and reported to be associated with increased severity and progression of chronic liver disease [8,9]. HCV contributes to HCC by directly modulating the pathways promoting the malignant transformation of hepatocytes [10–13]. Studies on transgenic mice revealed that the HCV core protein has oncogenic potential [14], but other studies yielded conflicting results [15,16]. Recently, mutations at amino acids 70 and 91 in the core region were shown to predict virological response to therapy with IFN plus ribavirin and also HCC development [17–19]. However, few studies support these results, and hence, the clinical impact of core mutations on HCC development is still unclear. In order to determine the viral factors associated with HCC development, we performed a retrospective cohort study on 361 patients with chronic liver disease caused by HCV genotype 1 infection and analyzed the amino acids present at core residues 70 and 91. Additionally, we evaluated whether these mutations were associated with IFN treatment, cirrhosis development, or host factors like age and gender.

Patients and methods

Study population

We enrolled 361 consecutive HCV genotype 1-infected patients who had undergone liver biopsy between August 1986 and June 1998 at Chiba University Hospital. At the enrollment time, the absence of HCC was proven by abdominal ultrasonography (US), computed tomography (CT), or magnetic resonance imaging (MRI). All the patients tested positive for anti-HCV antibody, determined by second-generation enzyme-linked immunosorbent assay. Patients with chronic hepatitis B, autoimmune hepatitis, primary biliary cirrhosis, hemochromatosis, Wilson disease, or alcoholic liver disease were excluded, as were patients with a history of alcoholism, drug abuse, or IFN therapy. Written informed consent was obtained from all patients before performing liver biopsy.

Table 1. Baseline characteristics of 361 hepatitis C (HCV) genotype 1-infected patients according to hepatocellular carcinoma (HCC) development.

Patients	$n = 361$	HCC development		
		(+), $n = 82$	(−), $n = 279$	p value
Gender (male/female)	219/142	56/26	163/116	0.1
Age (years)	50.5 ± 12.2	56.8 ± 7.1	48.6 ± 12.7	<0.0001
BMI (kg/m^2)	23.1 ± 2.9	23.1 ± 2.8	23.1 ± 3.3	0.82
Staging of fibrosis (F0–1/F2/F3/F4)	197/59/52/53	13/18/23/28	184/41/29/25	<0.0001
IFN treatment and response				
SVR/non-SVR/non-IFN	73/202/86	4/55/23	69/147/63	0.0004
Laboratory data				
AST (IU/L)	87 ± 62	109 ± 59	80 ± 61	0.0001
ALT (IU/L)	125 ± 93	139 ± 80	121 ± 96	0.13
AST/ALT	0.75 ± 0.26	0.84 ± 0.28	0.73 ± 0.25	0.0003
Platelets (10^4/mm^3)	17.7 ± 6.7	13.0 ± 3.3	18.2 ± 6.9	<0.0001
Albumin (g/dL)	4.2 ± 0.36	4.1 ± 0.39	4.3 ± 0.35	<0.0001
Total bilirubin (mg/dL)	0.8 ± 0.6	0.9 ± 0.3	0.8 ± 0.6	0.39
Core protein (pg/mL)	201 ± 245	283 ± 273	177 ± 231	0.001
Amino acid pattern				
70 Wild/non-wild/ND	168/129/64	32/32/18	136/97/46	0.23*
91 Wild/non-wild/ND	139/158/64	28/36/18	111/122/46	0.58*
DW/non-DW/ND	81/216/64	12/52/18	69/164/46	0.08*

BMI, body mass index; DW, double wild (arginine at residue 70 and leucine at residue 91 in the core region); ND, not detected; ND cases were excluded.

The clinical backgrounds of the patients are shown in Table 1. The study population was predominantly male (59% men), and the mean age of the patients was 50.5 ± 12.2 years, with 15% patients having liver cirrhosis.

Laboratory examination

Serum samples were obtained and stored at −30 °C until analysis. We assumed that genotype 1 corresponds to group 1 when determining the HCV RNA genotypes by serologic grouping of serum antibodies [20]. The serum HCV load of the patients was determined at the time of liver biopsy, using the HCV core protein detection kit (Eiken Chemical, Tokyo, Japan; detection limit, 8 pg/mL) [21].

Histopathological examination

Percutaneous liver biopsy was performed, and specimens were histopathologically assessed as described previously [22]. According to the criteria of Desmet et al. [23], the staging of fibrosis was defined as F0 (no fibrosis), F1 (mild fibrosis), F2 (moderate fibrosis), F3 (severe fibrosis), and F4 (cirrhosis).

Core nucleotide sequences

HCV RNA was extracted from the serum samples obtained at the time of liver biopsy, and it was reverse-transcribed using SuperScript III reverse transcriptase (Invitrogen, Carlsbad, CA, USA). Nucleic acids were amplified by PCR with the

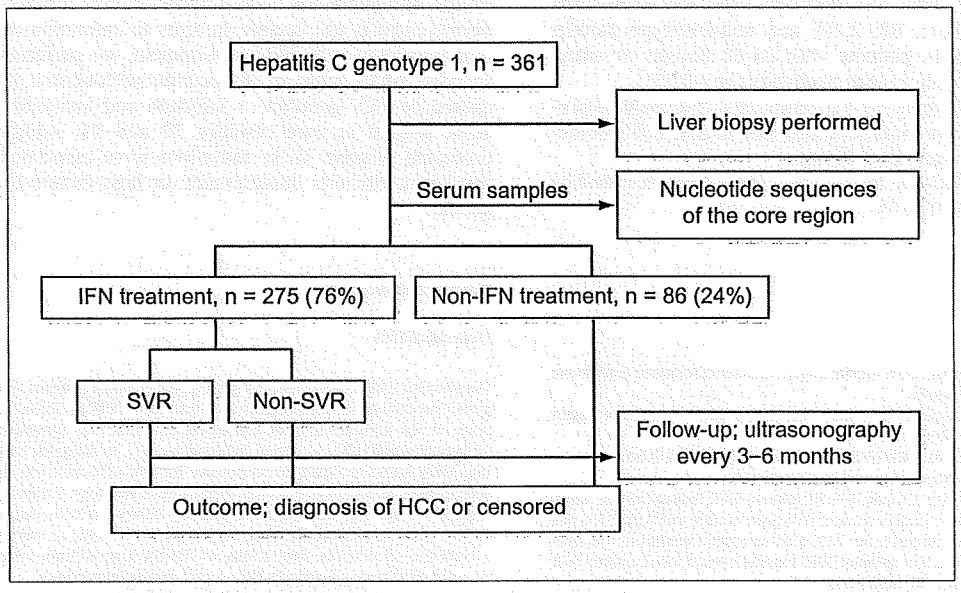

Fig. 1. Clinical courses after enrollment and the evaluation methods. IFN, interferon; SVR, sustained virological response; HCC, hepatocellular carcinoma. [This figure appears in colour on the web.]

HotStart Taq Master Mix kit (Qiagen, Hilden, Germany) and primers that have been previously described [24]. Polymerase chain reaction (PCR) was initiated with a denaturation step at 95 °C for 15 min, followed by 45 cycles at 94 °C for 1 min, 45 °C for 1 min, and 72 °C for 3 min, and subsequent extension for 7 min. PCR products were resolved by agarose gel electrophoresis, purified using the QIA quick PCR purification kit (Qiagen), and directly sequenced using a Big Dye Terminator v3.1 Cycle Sequencing kit (Applied Biosystems, Tokyo, Japan). The sequences were determined using an ABI PRISM 310 Genetic Analyzer (Applied Biosystems).

As described previously, the double wild-type (DW-type) amino acid pattern was defined as the presence of arginine at residue 70 (wild-type) and leucine at residue 91 (wild-type) [19].

IFN treatment

Depending on whether IFN was administered, the patients were divided into the IFN (76%) and non-IFN groups (24%) (Fig. 1). Patients who received IFN monotherapy during follow-up were divided into two subgroups: the sustained virological response (SVR) group, including patients who tested negative for HCV RNA at 24 weeks after completion of therapy, and non-SVR group (Fig. 1). Of the 275 patients in the IFN group, 73 (26.5%) achieved SVR.

Follow-up and diagnosis of cirrhosis and HCC

Clinical assessments were performed at least once every month during IFN treatment and every 3–6 months after the treatment. During follow-up, abdominal US was performed every 3–6 months to determine whether HCC had developed (Fig. 1). If necessary, additional procedures like CT, MRI, abdominal angiography, and US-guided tumor biopsy were performed to confirm HCC development. We also evaluated whether cirrhosis had developed in non-cirrhotic patients (F0–F2 stage). Cirrhosis was diagnosed according to the criteria of cirrhosis as described previously [25,26]. The follow-up period was the duration from the initial liver biopsy to HCC diagnosis or the last follow-up visit. For non-cirrhotic patients, this was the duration from the start point to cirrhosis diagnosis.

Statistical analysis

The χ^2 test was used to compare categorical variables, and Student's t test to compare continuous variables related to background characteristics among groups. Continuous variables were expressed as mean ± standard deviation. The cumulative incidence of HCC and cirrhosis was calculated using the Kaplan–Meier method and evaluated using the Breslow–Gehan–Wilcoxon test. Multivariate analysis was performed using the Cox proportional-hazards model or multiple logistic regression analysis. The Cochran–Armitage trend test was used for analyzing the association between the prevalence of mutation and subject age. Statistical significance was defined as $p < 0.05$.

Results

Cumulative HCC incidence

During follow-up (median duration, 121 months; range, 8–257 months), 82 (22.7%) patients developed HCC [HCC group; 13 of 197 (6.6%) from F0–F1, 18 of 59 (30.5%) from F2, 23 of 52 (44.2%) from F3, and 28 of 53 (52.8%) from F4 stage at entry] and 279 (77.3%) did not (non-HCC group). The cumulative HCC incidence at 5, 10, and 15 years of follow-up was 9.5%, 22.9%, and 30.9%, respectively.

Core nucleotide sequences

The core nucleotide sequence was determined for 297 of 361 (82.3%) patients. In the entire patient group, the proportions of DW-type and non-DW-type patterns were 22% and 60%, respectively (Table 1).

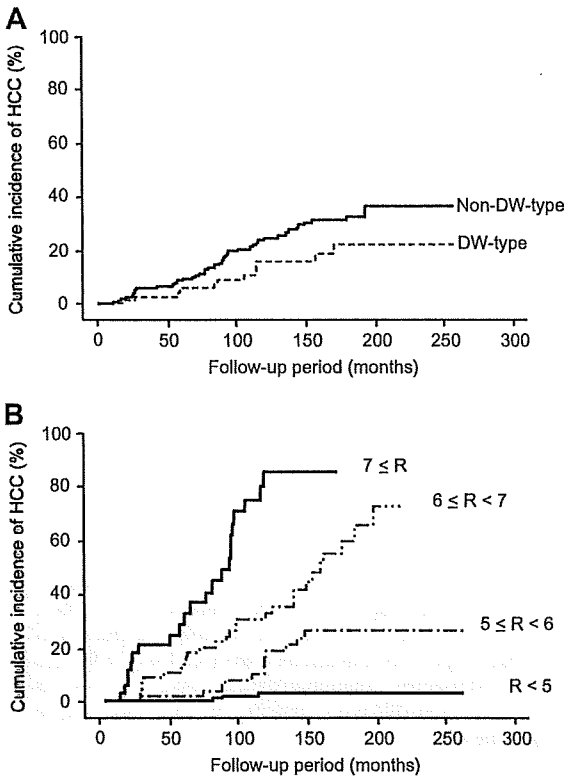

Fig. 2. Cumulative incidence of hepatocellular carcinoma (HCC) in hepatitis C genotype 1-infected patients. (A) Comparison between patients with double wild-type (DW-type: arginine, residue 70; leucine, residue 91) ($n = 81$) and non-DW-type ($n = 216$) amino acids in the core region ($p = 0.06$). (B) Comparison based on risk score (R) calculated using independent variables for HCC risk ($p < 0.0001$).

The core nucleotide sequence could not be determined for 64 patients because their samples showed significantly lower levels of the HCV core protein than those obtained from the 297 patients in whom the core sequence could be detected (119 vs. 217 pg/mL; $p = 0.0083$). There was no significant difference between the other variables shown in Table 1.

Cumulative HCC incidence according to core amino acid mutations

During follow-up, 12 of 81 (14.8%) patients with the DW-type pattern and 52 of 216 (24.1%) patients with the non-DW-type pattern developed HCC. Cumulative HCC incidence was 6.8% and 11% at 5 years, 19.1% and 27.7% at 10 years, and 26.6% and 38% at 15 years in the DW-type and non-DW-type groups, respectively. Cumulative HCC incidence in the DW-type group tended to be lower than that in the non-DW-type group ($p = 0.06$; Fig. 2A).

Predictive factors associated with HCC development

Potential predictive factors associated with HCC development are shown in Table 1. Univariate analysis revealed 10 parameters correlating with HCC development (Table 1). Multivariate analy-

Table 2. Factors associated with hepatocellular carcinoma development in hepatitis C genotype 1-infected patients, identified by multivariate analysis using the Cox proportional-hazards model.

Factor*	Category	Risk ratio (95% CI)	p value
Gender	Male	3.97 (2.05–7.63)	<0.0001
	Female	1.0	
Age (years)	⩾50	2.08 (1.01–4.33)	0.049
	<50	1.0	
Staging of fibrosis	⩾2	5.75 (2.68–12.35)	<0.0001
	<2	1.0	
IFN treatment and response	Absence of SVR	10.0 (2.29–43.48)	0.002
	SVR	1.0	
AST (IU/L)	>90	2.08 (1.20–3.62)	0.009
	⩽90	1.0	
AST/ALT	⩾0.8	2.21 (1.24–3.97)	0.007
	<0.8	1.0	
Amino acid pattern	Non-DW	1.96 (1.02–3.76)	0.04
	DW	1.0	

CI, confidence intervals; DW, double wild (arginine at residue 70 and leucine at residue 91 in the core region).
*Significant factors are shown.

sis with the Cox proportional-hazards model showed that the following seven independent parameters were significantly associated with HCC development: male gender ($p < 0.0001$), age ⩾ 50 years ($p = 0.049$), fibrosis ⩾ F2 ($p < 0.0001$), absence of SVR ($p = 0.002$), aspartate aminotransferase (AST) level > 90 IU/L ($p = 0.009$), AST/alanine aminotransferase (ALT) ratio ⩾ 0.8 ($p < 0.007$), and non-DW-type pattern in the core region ($p = 0.04$) (Table 2).

Prediction of HCC development based on risk score

Using the predictive variables from the previous step (Table 2), the risk score (R) for HCC development was calculated from the beta coefficients derived from the Cox proportional-hazards model as follows: $R = 0.671 \times$ (non-DW-type) + $2.307 \times$ (absence of SVR) + $0.733 \times$ (AST > 90 IU/L) + $0.733 \times$ (age ⩾ 50 years) + $1.752 \times$ (staging of fibrosis ⩾ 2) + $1.378 \times$ (male) + $0.795 \times$ (AST/ALT ⩾ 0.8) (each variable: yes = 1, no = 0). Fig. 2B shows the cumulative HCC incidence of four subgroups categorized by risk score, and the RR of each group is shown in Table 3. The cumulative HCC incidence increased with the risk score: from highest to lowest it was 84.7%, 35.1%, 18.5%, and 3.0% at 10 years.

Cumulative HCC incidence according to IFN treatment and response

During follow-up, 4 (5.5%) patients in the SVR, 55 (27.2%) in the non-SVR, and 23 (26.7%) in the non-IFN groups developed HCC; cumulative HCC incidence was 0%, 11.3%, and 13.2%, respectively, at 5 years; 7.8%, 25.6%, and 27.3%, respectively, at 10 years; and 7.8%, 36.5%, and 35.5%, respectively, at 15 years. Moreover, cumulative HCC incidence was significantly lower in the SVR group than other groups ($p < 0.001$; Fig. 3).

Table 3. Relative risk of HCC development based on risk score, using the Cox proportional-hazards model.

Score (R)	Risk ratio (95% CI)	p value
$R < 5$	1	
$5 \leqslant R < 6$	9.22 (2.60–32.7)	0.0006
$6 \leqslant R < 7$	26.9 (8.15–89.0)	<0.0001
$7 \leqslant R$	88.3 (25.8–302)	<0.0001

CI, confidence intervals.

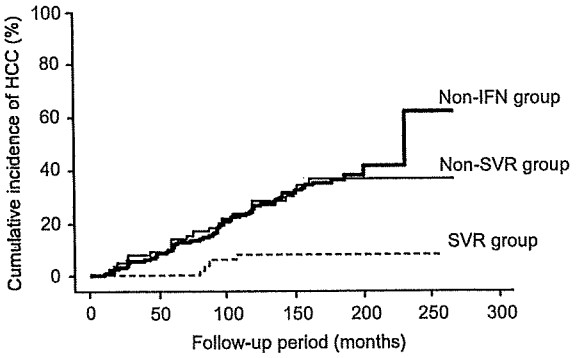

Fig. 3. Cumulative incidence of hepatocellular carcinoma (HCC). Comparison between the sustained virological response (SVR) ($n = 73$), non-SVR ($n = 202$), and non-interferon (IFN) ($n = 86$) groups ($p = 0.002$).

Analysis of SVR-associated factors

Compared to those in the non-IFN group, patients in the IFN group were younger (49 years vs. 54 years, $p = 0.003$), had higher aminotransferase levels (AST, 93 vs. 68 IU/L, $p = 0.001$; ALT, 137 vs. 87 IU/L, $p < 0.0001$) and lower core protein levels (183 vs. 263 pg/mL, $p = 0.01$). Table 4 shows baseline characteristics of patients according to interferon response. Univariate analysis revealed six SVR-associated parameters, whereas multiple logistic regression analysis revealed two independent significant predictors of SVR: AST/ALT ratio of <0.8 [$p = 0.005$; odds ratio (OR), 3.09; 95% confidence interval (CI), 1.40–6.82] and core protein level of <200 pg/mL [$p < 0.0001$; OR, 70.94; 95% CI, 9.56–526.2]. However, both univariate ($p = 0.64$) and multivariate analyses (data not shown) showed that the DW-type pattern in the core region was not associated with SVR.

Table 4. Baseline characteristics of patients according to interferon response.

Nature of the Regime	SVR $n = 73$	Non-SVR $n = 202$	p value
Gender (Male/Female)	47/26	126/76	0.76
Age (years)	46.6 ± 13.3	50.5 ± 11.5	0.02
BMI (kg/m^2)	22.7 ± 2.8	23.2 ± 3.0	0.24
Staging of fibrosis: (F0-1/F2/F3/F4)	45/12/9/7	104/34/34/30	0.42
Laboratory data			
AST (IU/L)	79 ± 56	97 ± 69	0.048
ALT (IU/L)	132 ± 92	139±100	0.60
AST/ALT	0.65 ± 0.22	0.75 ± 0.27	0.003
Platelets (10^4/mm^3)	18.6 ± 6.7	16.7 ± 6.1	0.03
Albumin (g/dL)	4.3 ± 0.3	4.2 ± 0.4	0.06
Total bilirubin (mg/dL)	0.7 ± 0.4	0.8 ± 0.4	0.02
Core protein (pg/mL)	31 ± 50	234 ± 226	<0.0001
Amino acid pattern			
70 Wild/Non-wild/ND	35/21/17	89/74/39	0.30
91 Wild/Non-wild/ND	24/32/17	76/87/39	0.62
DW/Non-DW/ND	14/42/17	46/117/39	0.64

BMI, body mass index; DW, double wild (arginine at residue 70 and leucine at residue 91 in the core region); ND, not detected.

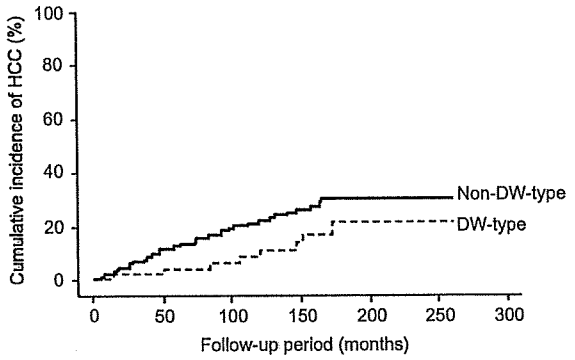

Fig. 4. Cumulative incidence of cirrhosis in non-cirrhotic patients (F0–F2). Comparison between patients with double wild-type (DW-type: arginine, residue 70; leucine, residue 91) ($n = 81$) and non-DW-type ($n = 216$) amino acids in the core region ($p = 0.051$).

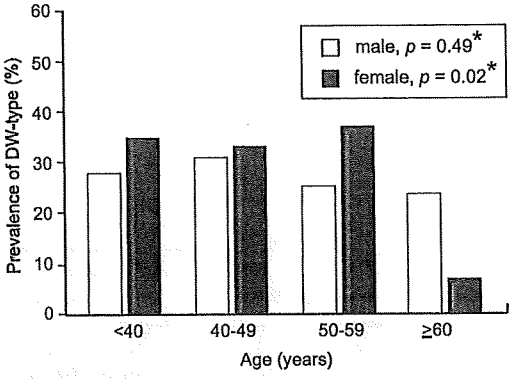

Fig. 5. Prevalence of double wild-type (DW-type: arginine, residue 70; leucine, residue 91) amino acids in the hepatitis C core region according to age and gender. *By the Cochran-Armitage trend test.

Cumulative cirrhosis incidence for non-cirrhotic patients (F0–F2)

Of the 256 non-cirrhotic patients (197 from F0–F1, 59 from F2), 50 (19.5%) developed cirrhosis (cirrhosis group) and 206 (80.5%) did not (non-cirrhosis group). The cumulative cirrhosis incidence at 5, 10, and 15 years of follow-up was 9.7%, 18.2%, and 26.4%, respectively. The HCC incidence was higher in the cirrhosis group [23/50 (46%)] than the non-cirrhosis group [8/206 (3.9%); $p < 0.0001$]. In the entire population, 71 of 82 (86.6%) patients who developed HCC had underlying cirrhosis and 11 (13.4%) did not, when HCC was detected ($p < 0.0001$).

Cumulative cirrhosis incidence according to the amino acid pattern in the core region for F0–F2 patients

The cumulative cirrhosis incidence tended to be higher in the non-DW-type group than the DW-type group (11.9% and 3.6% at 5 years, 21.5% and 10.4% at 10 years, and 29.7% and 20.7% at 15 years of follow-up, respectively; $p = 0.051$; Fig. 4).

Analysis of factors associated with cirrhosis development in F0–F2 patients

We analyzed the factors associated with cirrhosis development in patients with F0–F2 fibrosis at enrollment. Univariate analysis revealed nine parameters correlating with cirrhosis development: male gender ($p = 0.04$), older age ($p < 0.0001$), advanced fibrosis ($p < 0.0001$), absence of SVR ($p < 0.0001$), high AST level ($p < 0.0001$), high ALT level ($p = 0.01$), high AST/ALT ratio ($p = 0.001$), low platelet count ($p = 0.0009$), and high core protein level ($p = 0.02$). Multivariate analysis, including analysis of the amino acid pattern in the core region with the Cox proportional-hazards model, showed that the following three independent parameters were significantly associated with cirrhosis development: male gender ($p = 0.004$), fibrosis = F2 ($p = 0.004$), and absence of SVR ($p = 0.02$). Meanwhile, the presence of the non-DW-type pattern in the core region tended to lead to cirrhosis development (RR, 2.13; 95% CI, 0.93–4.91; $p = 0.07$).

Analysis of factors associated with mutations at core residues 70 and 91

Eighty-one patients with the DW-type pattern at core residues 70 and 91, who were at low risk for HCC, tended to be younger than the 216 patients with the non-DW-type pattern, who were at high risk for HCC (48.4 ± 11.8 years vs. 51.1 ± 11.8 years, respectively; $p = 0.08$). Separate analysis of men and women (Fig. 5) showed that the DW-type pattern was rare in women aged 60 years or above ($p = 0.02$).

Consistent with these results, HCC incidence was the same in men and women aged 60 or above (19% vs. 10% at 5 years and 32% vs. 38% at 10 years of follow-up, respectively; $p = 0.89$); however, in patients aged less than 60 years, HCC incidence was lower in women than in men (4% vs. 11% at 5 years and 15% vs. 22% at 10 years of follow-up, respectively; $p = 0.03$).

Discussion

Male gender, older age, advanced-stage fibrosis, and no IFN treatment are reported as important predictors of HCC development in chronic hepatitis C patients [4–7]. Viral factors associated with HCC development were also reported [27–29]. Several studies showed that mutations in the core protein are associated with HCC among HCV genotype 1b-infected patients, but the results varied between studies [18,30,31]. Consistent with a report by Akuta et al. [18], we showed that the presence of the non-DW-type pattern at core residues 70 and 91 is an independent risk factor for HCC development. Akuta et al. [18] studied 313 chronic hepatitis C patients who received IFN therapy (101 were excluded), and found that non-DW-type was an independent risk factor for HCC development (RR, 5.92; 95% CI, 1.58–22.2; $p = 0.008$) by using the Cox proportional-hazards model, and its correlation with HCC risk was stronger than that found in our study (RR, 1.96; 95% CI, 1.02–3.76; $p = 0.04$). We analyzed cirrhotic patients (14.7% of total population), most of whom developed HCC, and also non-cirrhotic patients, and found that the non-DW-type was still an independent risk factor for HCC development (RR, 2.90; 95% CI, 1.11–7.61; $p = 0.03$). Furthermore, we

found that the non-DW-type in patients with F0–F2 fibrosis was likely to lead to cirrhosis, diagnosed by US ($p = 0.051$). Moreover, the non-DW-type in patients with F0–F3 fibrosis was significantly associated with cirrhosis development ($p = 0.007$, data not shown). These results suggest that the non-DW-type may affect HCC development by accelerating cirrhosis development; however, prospective studies of histological findings are needed to confirm this.

It is unclear why the amino acids at residues 70 and 91 affect HCC development. The core protein cooperates with the Ras oncogene and transforms primary rat embryo fibroblasts into the tumorigenic phenotype [10]. The HCV core protein (residues 25–91) also interacts with the heterogeneous nuclear ribonucleoprotein K, which stimulates the c-myc promoter, downstream of the Wnt/beta-catenin signal [11]. Pavio et al. reported that the HCV core (residues 59–126, residues at 70 and 91 were non-wild-type) interacts with Smad3 and inhibits the TGF-beta pathway, important in apoptosis [12]. Mutations in the clustering variable regions (residues 39–76) are often seen in HCC patients [30], and mutations in the *N*-myristoylation sites (e.g., residue 91) in the core region, are associated with growth control and virus replication [31]. Delhem et al. have shown that the core protein with non-wild-type amino acids at residues 70 and 91 obtained from a HCC patient binds and activates PKR, which might cause carcinogenesis [13]. It was reported that the presence of a non-wild-type amino acid at residue 91 enhances internal initiation of HCV protein synthesis, leading to the expression of a core isoform, which may interact with viral and cellular components [32]. These results suggest that residues 70 and 91 themselves or via interactions with adjacent amino acids may be involved in HCC development; however, further studies are needed to evaluate the effect of core mutations on HCC development.

The presence of the DW-type pattern in the core region is also reportedly a predictor of the virological response to therapy with peginterferon and ribavirin [19]. With this therapy, an SVR of approximately 50% could be achieved by HCV genotype 1-infected patients having high viral load. We found the absence of an SVR and the non-DW-type pattern to be predictors of HCC development; however, the non-DW-type pattern was not a predictor of the absence of an SVR. This may be partly because we used IFN monotherapy without ribavirin, with which the SVR rate (26.5% in our study) was lower than that with peginterferon plus ribavirin [33,34]. Therefore, we believe that combination therapy, rather than IFN monotherapy, would more efficiently eradicate HCV with the DW-type pattern in the core region; however, further studies are required to test this hypothesis. Our current focus is on a prospective study to examine the association between core mutations and the outcome of combination treatment with peginterferon plus ribavirin.

Our study revealed that the DW-type pattern, associated with a low HCC risk, was rare in women aged 60 years or above. This may explain why HCC incidence in women was as high as that in men. The underlying mechanisms by which age or gender influence core-region mutations are unknown. In previous studies, a mutation at residue 70 was correlated with virological response to therapy with IFN plus ribavirin [17] and with AFP levels [35] in HCV genotype 1b-infected patients without HCC. Further follow-up studies must examine whether a mutation occurs in the wild-type amino acid.

We investigated two specific amino acid mutations in the HCV core region by direct sequencing. The HCV core sequence can be easily amplified using PCR because of its conservative nature and analysis of only two amino acid positions is timesaving; therefore, this method might be feasible for identifying predictive markers for HCC. A specific PCR method for detecting these mutations was reported [36]. Furthermore, we developed a rapid and sensitive real-time PCR method for quantitatively detecting these mutations [37]. We hope this method can be used to detect HCV sequences in case of a low viral load, and believe that it will be more useful for predicting HCC.

In conclusion, HCC risk could be predicted by studying mutations in the HCV core region, response to IFN, and host factors like age, gender, and liver fibrosis in HCV genotype 1-infected patients. These mutations might be involved in an oncogenic mechanism leading to HCC development in chronic HCV patients.

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Hepatitis A virus (HAV) proteinase 3C inhibits HAV IRES-dependent translation and cleaves the polypyrimidine tract-binding protein

T. Kanda,[1] V. Gauss-Müller,[2] S. Cordes,[2] R. Tamura,[1] K. Okitsu,[1] W. Shuang,[1] S. Nakamoto,[1] K. Fujiwara,[1] F. Imazeki[1] and O. Yokosuka[1] [1]*Department of Medicine and Clinical Oncology, Graduate School of Medicine, Chiba University, Inohana, Chuo-ku, Chiba, Japan; and* [2]*Institute of Medical Molecular Biology, University of Lübeck, Lübeck, Germany*

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SUMMARY. Hepatitis A virus (HAV) infection is still an important issue worldwide. A distinct set of viruses encode proteins that enhance viral cap-independent translation initiation driven by an internal ribosome entry site (IRES) and suppress cap-dependent host translation. Unlike cytolytic picornaviruses, replication of HAV does not cause host cell shut off, and it has been questioned whether HAV proteins interfere with its own and/or host translation. HAV proteins were coexpressed in Huh-7 cells with reporter genes whose translation was initiated by either cap-dependent or cap-independent mechanisms. Among the proteins tested, HAV proteinase 3C suppressed viral IRES-dependent translation. Furthermore, 3C cleaved the polypyrimidine tract-binding protein (PTB) whose interaction with the HAV IRES had been demonstrated previously. The combined results suggest that 3C-mediated cleavage of PTB might be involved in down-regulation of viral translation to give way to subsequent viral genome replication.

Keywords: 3C protease, hepatitis A virus, IRES, PTB, translation.

INTRODUCTION

The messenger-sense RNA genome of hepatitis A virus (HAV) is about 7500 nucleotides in length and contains a single large open-reading frame (ORF) encoding a polyprotein with the capsid proteins representing the amino-terminal third and the remainder comprising a series of nonstructural proteins required for viral RNA replication: 2B, 2C, 3A, 3B, $3C^{pro}$ (cysteine proteinase responsible for most post-translational cleavage events within the polyprotein) and $3D^{pol}$ (RNA-dependent RNA polymerase, see Fig. 1a, top panel) [1]. In a regulated cascade, the viral polyprotein is cleaved by $3C^{pro}$ into intermediate and mature products that fulfill distinct functions in the viral life cycle. At both ends of the picornaviral genome, the ORF is flanked by highly structured nontranslated regions (5′NTR and 3′NTR). The down-stream part of the 5′NTR presents an internal ribosome entry site (IRES) that allows translation by a cap-independent mechanism [1–3]. Several IRES trans-acting factors (ITAF) have been identified as mediating IRES binding to the ribosome [4]. Whereas glyceraldehyde-3-phosphate-dehydrogenase (GAPDH) and La autoantigen suppress HAV IRES activity, the poly(C)-binding protein (PCBP) and the polypyrimidine tract-binding protein (PTB) were found to enhance HAV translation [3,5–9]. PTB, a 57-kDa protein, is a member of the heterogeneous nuclear ribonucleoprotein family that shuttles between the nucleus and cytoplasm [10]. While experimental data have demonstrated PTB binding to polypyrimidine tracts (UCUUU or UCUUC) in picornaviral IRES, the exact cellular functions of PTB are as yet incompletely defined [3,10,11].

Proteolytic cleavage of host proteins is a common mechanism executed by picornaviruses to shut off host cell protein synthesis and to regulate viral protein and RNA synthesis. These two synthetic processes are central in the viral life cycle and mutually exclusive on the same RNA template. As HAV does not shut off host protein synthesis, it seems that HAV cap-independent translation constantly

Abbreviations: GAPDH, glyceraldehyde-3-phosphate-dehydrogenase; HAV, Hepatitis A virus; IRES, internal ribosome entry site; ITAF, IRES trans-acting factors; ORF, open-reading frame; PABP, poly(A)-binding protein; PCBP, poly(C)-binding protein; PTB, polypyrimidine tract-binding protein.

Correspondence: Dr Tatsuo Kanda, Department of Medicine and Clinical Oncology, Graduate School of Medicine, Chiba University, 1-8-1 Inohana, Chuo-ku, Chiba 260-8677, Japan. E-mail: kandat-cib@umin.ac.jp