

susceptibility to lamivudine *in vitro*. They also detected such mutations in virus from a patient with leukemia and speculated that truncated HBs gene might be related to the development of leukemia (7).

Analyzing nucleotide and amino acid sequences of HBV in patients who developed a breakthrough, we identified a novel mutant that showed nucleotide substitutions in the B domain of the reverse transcriptase. The G residues of nucleotides 669 and 670 were mutated to T and A, respectively, and associated with the amino acid substitution rtA181T. The substitutions also induced the amino acid substitution W172L in the overlapping HBs protein. Since the nucleotide substitution was associated with nucleotide and amino acid substitutions in the putative spacer region of the polymerase, we checked the importance of these substitutions for resistance to lamivudine *in vitro*. We also analyzed the resistance of this new strain *in vivo* using a human hepatocyte-chimeric mouse (27, 31). Furthermore, we analyzed the susceptibility of the mutant strain to adefovir and entecavir. When used alone or in combination with lamivudine, these drugs are known to be effective against wild-type as well as lamivudine-resistant HBV (2, 5, 14, 17, 32). Infrequent emergence of resistance compared with lamivudine resistance has been reported for both of these two drugs (2, 5). We also developed a detection system to identify the novel and previously reported (7, 34) nucleotide substitutions to study the incidence of such mutations.

MATERIALS AND METHODS

Antiviral compounds. Lamivudine [(−)-β-L-2',3'-dideoxy-3'-thiacytidine] was provided by GlaxoSmithKline (Stevenage, Herts, United Kingdom). Adefovir [9-[2-(phosphonomethoxyethyl)adenine] was provided by Gilead Sciences (Foster City, CA), and entecavir [2-amino-1,9-dihydro-9-[(1S,3R,4S)-4-hydroxy-3-(hydroxymethyl)-2-methylenecyclopentyl]-6H-purin-6-one, monohydrate] was provided by Bristol-Myers Squibb Pharmaceutical Research Institute (Wallingford, CT).

Analysis of virological markers. Hepatitis B surface antigen (HBsAg), hepatitis B envelope antigen (HBeAg), and antibody against HBeAg (anti-HBe) were quantified by enzyme immunoassay kits (Abbott Diagnostics, Chicago, IL). HBV-DNA was measured by real-time PCR using a Light Cycler (Roche, Mannheim, Germany). The primers used for amplification were 5'-TTTGGGCATGGACATTGAC-3' and 5'-GGTGAACAATGTTCCGGAGAC-3'. The amplification condition included initial denaturation at 95°C for 10 min, followed by 45 cycles of denaturation at 95°C for 15 s, annealing at 58°C for 5 s, and extension at 72°C for 6 s. The lower detection limit of this assay was 300 copies.

Cloning of HBV DNA and plasmid construction. HBV DNA was extracted from 100 µl of each serum sample by SMITEST (Genome Science Laboratories, Tokyo, Japan) and was dissolved in 20 µl H₂O. Full-length HBV DNA was amplified using the above HBV DNA samples by the method of Gunther et al. (13). Nucleotide sequence positions were numbered from the unique EcoRI site. The 1.4-genome-length HBV DNA amplified from the serum of a patient who showed lamivudine resistance was cloned into plasmid vector pTRE (Takara Bio, Tokyo, Japan) (patient strain). In brief, the PCR product amplified using serum from the patient was cleaved with BamHI and ApaI (HBV positions 1400 to 2600) and cloned into pcDNA3 (Invitrogen, San Diego, CA), and the resulting construct was named pcDNA3-1. Similarly, the PCR product was cleaved with ApaI and BamHI (HBV positions 2600 to 3215 and 1 to 1400) and cloned into pBlueScript SK+ (Stratagene, La Jolla, CA), and the resulting construct was named pB-1. The KpnI-BamHI fragment from pB-1 and the KpnI-ApaI fragment from pcDNA3-1 were cloned into pcDNA3-1. Finally, the plasmids were cleaved with HindIII and NotI within the multicloning site and cloned into plasmid vector pTRE. As a laboratory strain, we employed a plasmid containing a 1.4-genome-length wild-type genotype C HBV (wild-type strain; GenBank accession number AB206816) (31). To introduce the nucleotide substitutions into the S331C/rtA181T patient and wild-type strains, site-directed mutagenesis was performed with a QuikChange site-directed mutagenesis kit (Stratagene).

TABLE 1. *In vitro* susceptibility of the S331/rtA181 mutant to lamivudine*

Source	Strain Type	S331/rtA181 mutation	Lamivudine IC ₅₀ (µM)	Resistance (fold)
Patient	WT	-/-	0.19 ± 0.01	1
	S331C	C/-	0.23 ± 0.01	1.2*
	rtA181T	-/T	0.58 ± 0.08	3**
	S331C/rtA181T	C/T	0.57 ± 0.06	3**
Laboratory	WT	-/-	0.23 ± 0.04	1
	S331C	C/-	0.3 ± 0.05	1.3*
	rtA181T	-/T	0.88 ± 0.2	3.9**
	S331C/rtA181T	C/T	0.98 ± 0.12	4.3**

* Experiments were performed in triplicate. Values are expressed as means ± SD. WT, wild type. *, not significant; ** *P* < 0.001 compared to the wild type.

The eight plasmids with and without amino acid substitutions in the spacer and reverse transcriptase domain are listed in Table 1.

Cell culture, transfection, and determination of IC₅₀. HepG2 cells were grown in Dulbecco's modified Eagle's medium supplemented with 10% (vol/vol) fetal bovine serum at 37°C in 5% CO₂. Cells were seeded to semiconfluence in six-well tissue culture plates. Transfection of the plasmids into HepG2 cells was performed using TransIT-LT1 (Mirus, Madison, WI) according to the instructions provided by the supplier. To determine 50% inhibitory concentrations (IC₅₀) for each antiviral drug, various concentrations of lamivudine, adefovir, and entecavir were added after 24 h to the culture plate containing the cells, and cells were harvested after 5 days. The medium containing the drugs was changed on days 1, 3, and 4. A plasmid encoding β-galactosidase (β-Gal) was cotransfected to adjust the transfection efficiency. The β-Gal enzyme assay was performed with a β-Gal enzyme assay system (Promega, Madison, WI). All experiments were performed in triplicate. GraphPad Prism software (GraphPad Software, Inc.) was used to determine the best-fit values for individual dose-response equations.

Analysis of replicative intermediate of HBV by Southern blot hybridization and quantitation. The cells were harvested at 3 or 5 days after transfection and lysed with 250 µl of lysis buffer (10 mM Tris-HCl [pH 7.4], 140 mM NaCl, and 0.5% [vol/vol] NP-40) followed by centrifugation for 2 min at 15,000 × *g*. The core-associated HBV genome was immunoprecipitated by mouse anti-core monoclonal antibody 2A21 (Institute of Immunology, Tokyo, Japan) and subjected to Southern blot analysis after sodium dodecyl sulfate-proteinase K digestion followed by phenol extraction and ethanol precipitation. The DNA was detected with a full-length HBV-DNA probe labeled by the DIG DNA labeling and detection kit (Roche Diagnostics, Basel, Switzerland) according to the instructions provided by the manufacturer. Quantitative analysis was performed by real-time PCR with SYBR green using a Light Cycler. The HBV-specific primers used for amplification were 5'-TTTGGGCATGGACATTGAC-3' and 5'-GGTGAACAATGTTCCGGAGAC-3'. The amplification conditions included initial denaturation at 95°C for 10 min, followed by 45 cycles of denaturation at 95°C for 15 s, annealing at 58°C for 5 s and extension at 72°C for 6 s. The lower detection limit of this assay was 300 copies.

Evaluation of effects of antiviral drugs on mutant strains using human hepatocyte-chimeric mice. Human hepatocyte-chimeric mice were generated and used in the drug evaluation studies as described previously (27, 31). Briefly, human hepatocytes were transplanted into urokinase-type plasminogen activator-transgenic SCID mice, which are immunodeficient and develop liver failure. The transplanted cells were characterized in terms of *in vivo* growth potential and function. The human hepatocytes progressively repopulated the murine host liver and were susceptible to cultured-cell-line-produced HBV. All animal protocols were performed in accordance with the guidelines of the local committee for animal experimentation. The mice were inoculated with 50 µl of serum samples containing wild-type and newly identified drug-resistant strains. Serum samples obtained from mice were stored at -80°C before further analyses. After stable high-level HBV viremia was confirmed, the mice were administered food containing 30 mg of lamivudine/kg of body weight/day. The nucleotide sequences of wild-type and mutant strains were confirmed by sequencing analysis.

Detection of rtA181T mutants by PCR with restriction fragment length polymorphism (RFLP). HBV DNA extracted from serum samples were amplified by

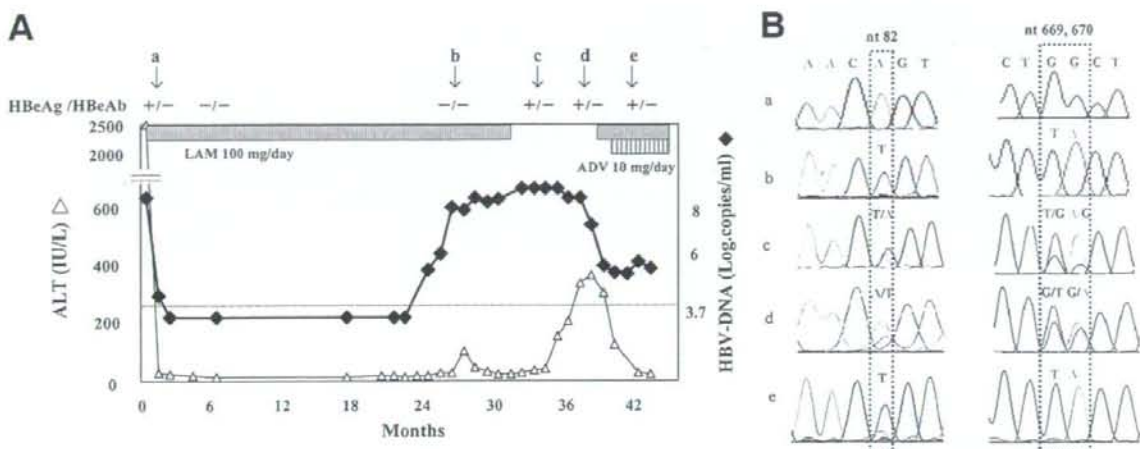


FIG. 1. (A) Clinical course of a patient who developed breakthrough without emergence of YMDD mutants during lamivudine therapy. Arrows a to e indicate time points of serum sampling for direct sequencing and RFLP PCR. (B) Nucleotide sequence analysis of the reverse transcriptase/polymerase gene of hepatitis B virus by direct sequencing. Time points of serum sampling (see panel A) were as follows: (a) just before lamivudine treatment, (b) after breakthrough, (c) after cessation of lamivudine treatment, (d) just before readministration of lamivudine, and (e) during readministration of the drug (e). Note that the wild type reappeared during the cessation of therapy (c and d), but it disappeared after readministration of the drug (e).

PCR using the primers 5'-GCCCGTTTGCCTCTACTTCCA-3' and 5'-ACCACTGAACAAATGGCACTAGTAAGCTGA-3'. The reverse primer was designed to introduce an *EspI* site (GCTCAGC) into only wild-type sequences. The PCR was performed in a total volume of 25 μ l, consisting of a reaction buffer (100 mmol/liter Tris-HCl [pH 8.3], 50 mmol/liter KCl, and 15 mmol/liter MgCl₂), 0.2 mmol/liter of each deoxynucleoside triphosphate, 1 μ l of the DNA solution, 10 pmol of each primer and 1 U of *Taq* DNA polymerase (Gene Taq; Wako Pure Chemicals, Tokyo, Japan) with 0.2 μ g of anti-*Taq* high (Toyobo Co., Osaka,

Japan). The amplification conditions included an initial denaturation at 94°C for 2 min, 35 cycles of amplification (denaturation at 94°C for 1 min, annealing of primer at 58°C for 1 min, extension at 72°C for 2 min), and final extension at 72°C for 7 min. Two μ l of PCR products was digested with 5 U of *EspI* and subjected to electrophoresis in a 3.5% agarose gel.

Statistical analysis. Data are expressed as means \pm standard deviations (SD). Group comparisons were performed using the Student *t* test. A *P* value of less than 0.05 was considered statistically significant.

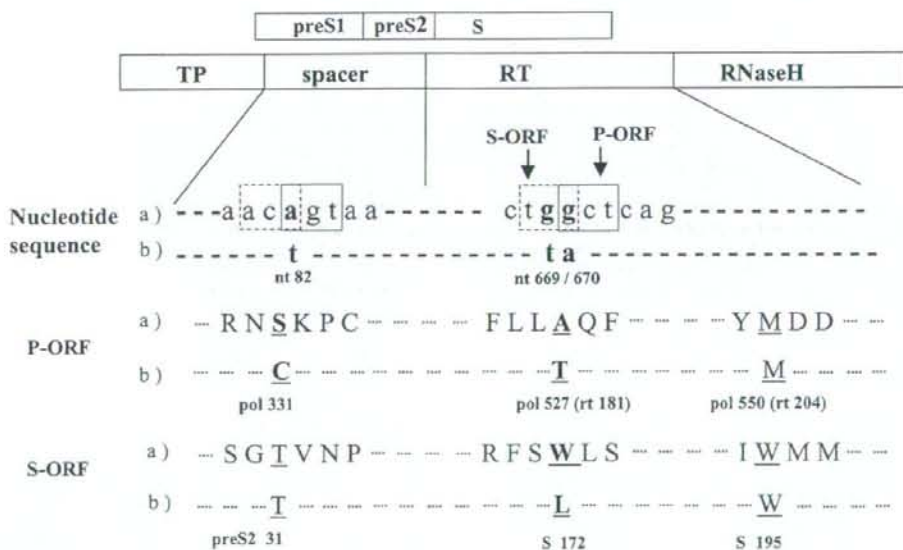


FIG. 2. Comparison of nucleotide sequences and amino acid sequences of two overlapping open reading frames, reverse transcriptase/polymerase and the HBs gene of the hepatitis B virus, before and after viral breakthrough. Sequences obtained from serum samples before (a) and after (b) breakthrough were compared. See Fig. 1A for time points of serum sampling. Nucleotide sequence numbers are those of typical HBV (e.g., accession no. AB206816 [31]), which starts from a unique *EcoRI* site.

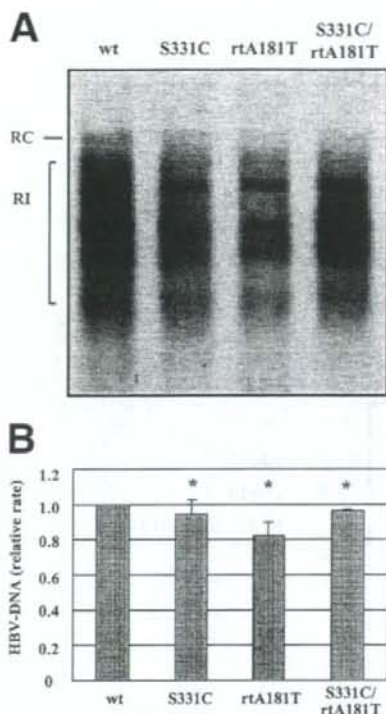


FIG. 3. Replication ability of wild-type HBV and three mutants (S331C, rtA181T, and S331C/rtA181T). Plasmids containing 1.4-genome-length HBV were transiently transfected into HepG2 cells. (A) The replicative intermediates were analyzed by Southern blot hybridization. Core-associated replicative intermediates of HBV DNA were isolated from HepG2 cells at 3 days after transfection. The positions of relaxed circular DNA (RC) and replication intermediates (RI) are indicated. (B) Quantitative analyses of core-associated intermediates of HBV. Experiments were performed in triplicate. Values are relative to those of the wild type and are expressed as means \pm SD. *, not significant compared to the wild type.

RESULTS

Isolation of a novel lamivudine-resistant strain with an intact YMDD motif. The novel lamivudine-resistant strain of HBV was isolated from a 44-year-old Japanese man with chronic HBV infection (Fig. 1A). In this patient, lamivudine successfully reduced the HBV level at the initial stage of treatment, but viral breakthrough was observed at 24 months after the beginning of therapy. The patient was very punctual and confirmed that he took lamivudine with perfect compliance. The HBV viral load reached up to 8.5 log copies/ml, but nucleotide sequence analysis showed no YMDD mutation. The YIDD and YVDD mutants were not detected even with a peptide nucleic acid-mediated PCR clamping method sensitive for detection of YMDD mutants (6). The analysis also showed that this isolate belonged to genotype C of HBV. Comparison by the direct sequence method of nucleotide sequences obtained before and after the viral breakthrough showed three nucleotide substitutions that induced two amino acid substitutions in both spacer (polS331C) and reverse transcriptase

(polA527T or rtA181T) domains of the polymerase (Fig. 1B and 2). The latter nucleotide substitutions induced an amino acid change in the overlapping HBs protein (W172L) (Fig. 2). Twelve HBV genomes were cloned from the serum of this patient after viral breakthrough, and eleven of them showed the above amino acid substitutions. Only one clone showed the wild-type sequence. The new strain of HBV became undetectable when lamivudine therapy was discontinued, and this strain outcompeted the wild-type strain upon administration of the drug (Fig. 1B). These results prompted us to study the significance of each of these mutations.

Effect of substitutions on HBV replication. To assess the effect of nucleotide substitutions on HBV replication, four plasmids containing 1.4-genome-length patient-specific HBV genome (Table 1) were generated and transfected into HepG2 cells. In comparison with the patient's wild-type strain, the replication capacities of the S331C, rtA181T, and S331C/rtA181T mutants were not different (94%, 82%, and 96%, respectively), suggesting that these mutants can replicate at almost the same rate as the wild-type strain (Fig. 3).

Susceptibility of mutants to lamivudine in vitro. To analyze the role of the polS331C and rtA181T mutations in lamivudine resistance, four patient-specific strains and four laboratory strains were transfected into HepG2 cells (Fig. 4; Table 1). A single amino acid substitution in the spacer region did not contribute to resistance in either patient or laboratory strains. In contrast, an amino acid substitution in the polymerase (rtA181T) induced resistance that was 3.0 and 3.9 times greater than that of patient and laboratory strains ($P < 0.001$), respectively. The presence of both of these amino acid changes induced 3.0 and 4.3 times greater resistance in each of the above strains. Thus, the spacer mutation had little effect on the susceptibility to lamivudine (Table 1).

We also compared the rtA181T mutant identified in this study with the rtA181T mutant reported previously, which had premature termination in the HBs protein (7, 34), for replication ability and susceptibility to lamivudine. Although the HBs antigen produced to culture supernatant was different between the two strains (52.5 ± 8.2 and 4.4 ± 0.6 IU/ml, respectively), there was no noticeable difference in replication ability and lamivudine sensitivity between the two mutants (data not shown).

Assessment of drug resistance of novel mutations in vivo using human hepatocyte-chimeric mice. To confirm the lamivudine resistance of the novel mutant strain, two human hepatocyte-chimeric mice were each inoculated with a serum sample obtained from the patient who developed breakthrough without mutations in the YMDD motif (Fig. 1A). The serum was obtained during breakthrough while the patient was still taking the drug. Twelve weeks after the inoculation of the serum samples, both mice developed high-level viremia (7.8 and 6.6 log copies/ml, respectively). Direct sequence analysis showed that the nucleotide sequence of the virus that replicated in the chimeric mice was in accordance with the mutant strain. Cloning and sequencing analysis showed that only 1 of 12 clones obtained from the inoculum was wild type, while the remaining 11 clones were rtA181T mutants with an intact YMDD motif. We also analyzed the serum of the two infected mice before and after lamivudine therapy. All 11 and 15 clones before and all 11 and 12 clones during therapy had the

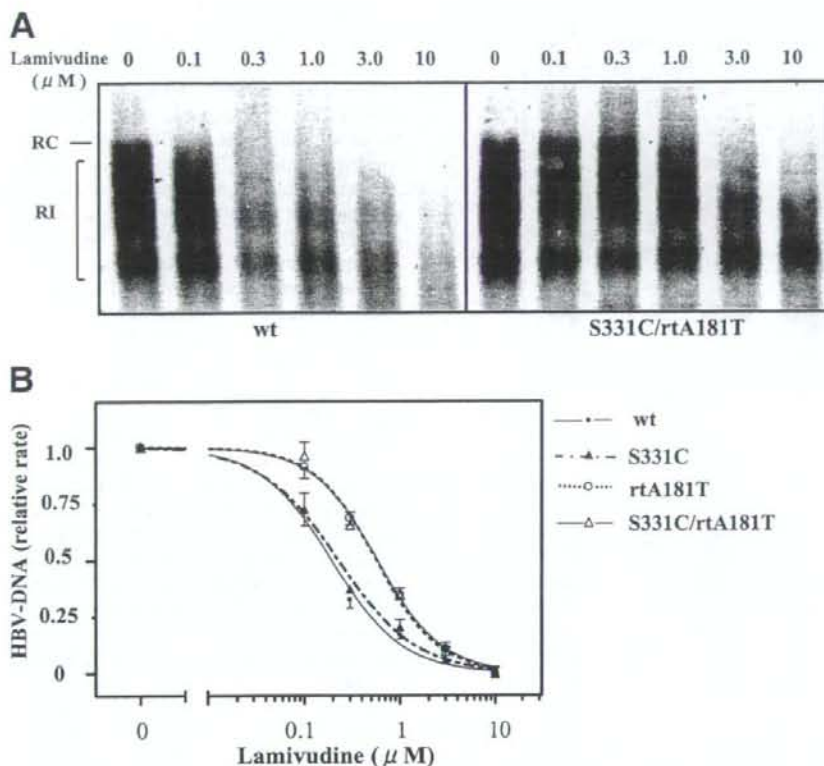


FIG. 4. In vitro analyses of susceptibility of wild-type HBV and three mutants (S331C, rtA181T, S331C/rtA181T) to lamivudine after transient transfection into HepG2 cells. Cells were transiently transfected with plasmids containing 1.4-genome-length HBV and treated with the indicated amount of lamivudine. (A) Southern blot analysis of replicative intermediate. Representative results for the wild type (wt) and the S331C/rtA181T mutant are shown. The positions of relaxed circular (RC) and replication intermediate (RI) forms of HBV DNA are indicated. (B) Dose-response curves of the four HBV strains against lamivudine. The curves were used to estimate the lamivudine IC_{50} s for each HBV strains. Values are relative to no-lamivudine controls for each strain. Experiments were performed in triplicate. Values are expressed as means \pm SD.

rtA181T mutation (data not shown). Two other mice were inoculated with wild-type HBV obtained from a patient not treated with lamivudine as a control, and both mice also developed high-level viremia (8.3 and 9.3 log copies/ml, respec-

tively). Thirteen weeks later, the viremia reached plateau and the mice were fed food containing lamivudine. After 6 weeks of treatment, the mean viral load decreased by 2.8 log copies/ml in the wild type, whereas it decreased by only 0.39 log copy/ml in the mutant ($P < 0.001$) (Fig. 5).

Susceptibility of mutants to adefovir and entecavir in vitro. We also analyzed the effects of adefovir and entecavir against the S331C/rtA181T mutant using a transient-transfection assay with HepG2 cells. The IC_{50} s of these drugs for the mutant strain and wild type were almost the same (Table 2).

Detection of rtA181T mutant in patients treated with lamivudine. In this study, we developed a RFLP PCR method to detect the rtA181T mutants, by which we were able to detect mutant strains even when they were mixed with the wild type (Fig. 6). The system also detected the rtA181T (HBs stop) mutant reported by Chien et al. (7) and Yeh et al. (34). Using this method, we analyzed 40 patients who showed viral breakthrough (increase in viral load equal to or more than 1 log) during lamivudine therapy. We found that only one of these patients was positive (Fig. 6A). Nucleotide sequence analysis of serum samples obtained from this patient showed that the

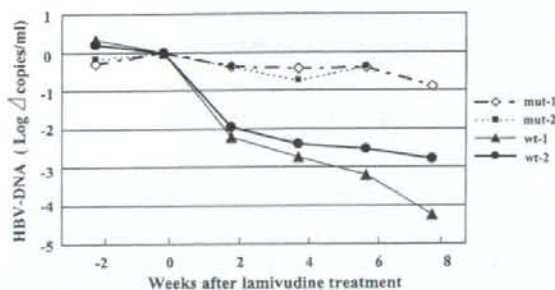


FIG. 5. In vivo analyses of the effect of lamivudine on wild-type and S331C/rtA181T mutant HBV. Four human hepatocyte-chimeric mice were inoculated with serum samples containing wild-type or mutant HBV. One of the animals fed with lamivudine died 6 weeks after the beginning of therapy.

TABLE 2. In vitro susceptibility of the S331/rtA181 mutant to lamivudine, adefovir, and entecavir^a

Patient strain	S331/rtA181	Lamivudine		Adefovir		Entecavir	
		IC ₅₀ (μM)	Resistance (fold)	IC ₅₀ (μM)	Resistance (fold)	IC ₅₀ (nM)	Resistance (fold)
WT	-/-	0.19 ± 0.01	1	0.37 ± 0.1	1	0.19 ± 0.02	1
S331C/rtA181T	C/T	0.57 ± 0.06	3**	0.36 ± 0.08	0.98*	0.23 ± 0.05	1.2*

^a Experiments were performed in triplicate. Values are expressed as means ± SD. WT, wild type. *, not significant; ** *P* < 0.001 compared to the wild type.

mutant strain had the rtA181T mutation with a truncated HBs antigen, as reported previously (7, 34). The YMDD motif of HBV detected in this patient was of the wild type. All 39 remaining patients with viral breakthrough were positive for YIDD and/or YVDD mutants. The RFLP PCR analysis of these 39 samples showed that four contained a small amount of rtA181T mutants (Fig. 6B). Nucleotide sequence analyses of these samples showed that they contained only a small amount of rtA181T mutants with a truncated HBs antigen (Fig. 6C).

Finally, we examined the presence of YMDD or rtA181T mutants in eight patients who showed a poor response with lamivudine treatment (HBV viral load above 6.0 log copies/ml after 6 months of treatment). None of these patients tested positive for both of these mutations (data not shown).

DISCUSSION

In this study, we identified a novel lamivudine-resistant strain of HBV with an intact YMDD motif in a patient who received long-term lamivudine therapy. YMDD mutants were

not detected even by a sensitivity-enhanced detection method, which was reported previously by our group (6). The double nucleotide substitutions (GG to TA) induced amino acid substitutions in both polymerase (rtA181T) and HBs antigen (HBs W172L). One might assume that the compliance of the patient was poor. However, the patient was very punctual and confirmed that he took lamivudine with perfect compliance.

Our study demonstrated that the rtA181T mutation reduced the susceptibility to lamivudine 3.0- to 3.9-fold in vitro (Table 1). Furthermore, we also confirmed lamivudine resistance of this mutant strain in vivo using human hepatocyte-chimeric mice. The amino acid substitution in the reverse transcriptase (RT) domain is similar to that reported previously (7, 34). However, in contrast to our results, the mutant strains in the latter reports emerged with or after those with the mutation in the YMDD motif (YIDD or YVDD) and took over them (34). There are two additional differences between the substitutions we identified and those described by Yeh et al. (34), as detailed below.

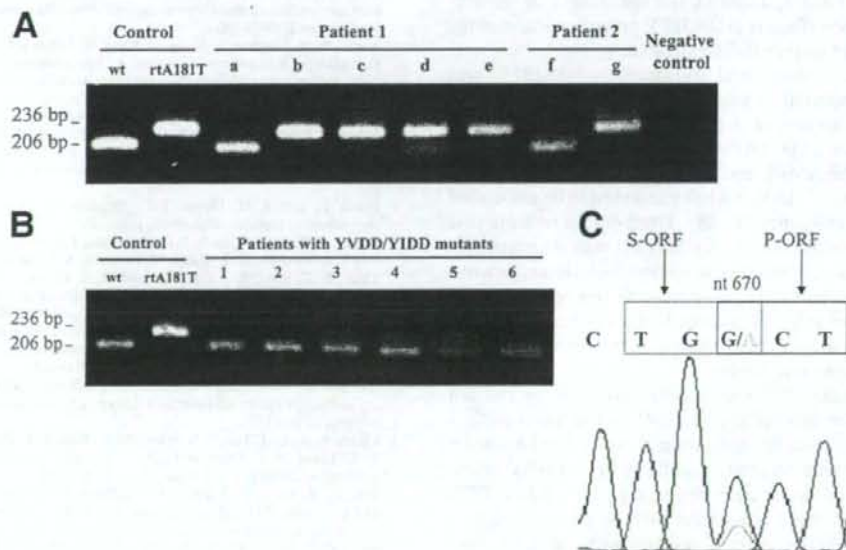


FIG. 6. Detection of the rtA181T mutant by RFLP PCR assay. PCR-amplified DNA fragments were treated with *EspI*, which digests only wild-type sequences, and separated in a 3.5% agarose gel. (A) Agarose gel electrophoresis of RFLP PCR products. Wild-type and rtA181T mutant plasmids were used as controls. See Fig. 1A for the time points of serum sampling (a to e) for patient 1 and see Fig. 1B for a comparison with nucleotide sequence analyses. f and g indicate the time points before and after viral breakthrough for patient 2. (B) Agarose gel electrophoresis of RFLP PCR products using HBV DNA samples obtained from 39 patients who showed lamivudine breakthrough. Of the 39 samples, 35 were wild type (lanes 1 and 2). The remaining four samples (lanes 3 to 7) showed partial digestion, suggesting a mixture of wild-type and mutant strains. (C) Nucleotide sequence analysis of a sample by RFLP PCR suggested the presence of a wild-type-mutant mixture (lane 5 of panel B).

Firstly, the HBs antigen was prematurely terminated in the mutant strain reported by Yeh et al. (34). In this regard, a similar amino acid substitution of the B domain of the polymerase FLA motif in woodchuck hepatitis virus (WHV) treated with lamivudine was reported (15, 28). The HBs antigen in these WHV mutant strains also had premature stop codons. These findings suggest that the mutant strains of HBV and WHV cannot replicate and spread by themselves because of the lack of HBs antigen. Such strains are thought to replicate by using in vivo-supplied HBs antigen from wild-type strains as helper antigens. In contrast, the novel strain identified in this study had no premature termination of the HBs gene. The in vitro study suggested that the strain had a replication ability similar to that of the wild type. Furthermore, we also showed that the strain infected and reached a high viral load in human hepatocyte-chimeric mice. Although the inoculum contained only a small amount of wild-type strain (one of 12 clones), all clones obtained from mouse serum were mutant strains (rtA181T). Considering these results and the fact that the index patient showed high viral titers after breakthrough (more than 7.6 log copies/ml), this mutant strain can spread and replicate by itself and has strong replicative ability.

Secondly, the substitutions identified in this study appeared with nucleotide and amino acid substitutions in the spacer region of the polymerase (S331C). There are only a few studies that reported the function of the spacer domain (19–21, 28), leaving the biological significance of this region unknown. The substitution in the spacer region reappeared with the A181T mutation in the RT domain in the index patient after the patient restarted lamivudine therapy. Although our study showed no significant contribution of this mutation to drug resistance (Fig. 3 and 4; Table 1), the significance of the mutation in this region (fingers in the HBV polymerase homology model [8]) should further be investigated.

Recently, the amino acid substitutions rtA181T and rtA181V were reported to emerge with resistance against adefovir (11, 32). Tillmann et al. (29) reported one case in which the virus developed the rtA181T mutation during famciclovir breakthrough. The A556T mutation of WHV, analogous to the rtA181T mutation of HBV, has been reported to be associated with lamivudine resistance (15, 28). These results indicate that the amino acid substitutions at position 181 may associate with resistance against many nucleoside analogues, including lamivudine, famciclovir, and adefovir. Although our in vitro study indicated that the rtA181T mutant had no resistance against adefovir and the animal study showed that combination therapy with lamivudine and adefovir effectively reduced the virus load in woodchucks (15), such combination therapy did not produce sufficient suppression of HBV in the index patient (Fig. 1A). The amino acid substitution at position 181 has to be further analyzed with regard to resistance to anti-HBV drugs.

The rtA181T mutation detection system using RFLP PCR developed in this study is a useful tool, as we were able to distinguish the wild type from all mutants with nucleotide substitutions in a given region. The system also enabled us to monitor the fluctuation of the wild-type/mutant ratio during therapy against HBV (Fig. 1 and 6). The incidence of rtA181T mutants with an intact YMDD motif is rare in Japanese patients with chronic HBV infection treated with lamivudine. Interestingly, 4 of the 39 (10%) patients who developed lamivudine breakthrough and were positive for YMDD mutants were found to have small amounts of rtA181T mutant strains. Different from the previous report (34), the mutants did not take over another strain and were not preceded by exacerbation. We have to monitor these patients carefully for further population change of mutants and for exacerbation of hepatitis.

A recent study reported that the prevalence of genotype A HBV infection is increasing in Japan and that the incidence of disease chronicity is higher than for other genotypes (26). It is thus expected that an increasing number of the sexually active population will receive nucleoside analogue therapy against HBV and multiple mutant strains can potentially emerge and spread along with long-term treatment. There is an increasing possibility of emergence of novel mutants resistant to multiple anti-HBV drugs. The importance and significance of the rtA181 mutations, including the novel mutant strain identified in this study, should be investigated further to develop more useful treatment strategies.

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CLINICAL RESEARCH STUDY

AJM Theme Issue: Infectious Disease

Long-term Outcome of HBV Carriers with Negative HBe Antigen and Normal Aminotransferase

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ABSTRACT

PURPOSES: To elucidate the incidence of hepatitis activation and hepatocellular carcinogenesis in patients with negative HBe antigen and normal aminotransferase, long-term observation was performed in a retrospective cohort.

METHODS: Among 116 consecutive patients with normal aminotransferase and negative HBe antigen at the time of liver biopsy, sequential frozen sera for initial 5 years were available for 95 patients. Hepatitis B virus (HBV) DNA assay (sensitivity >400 copy/mL) and aminotransferase were annually examined in the initial 5 years after biopsy.

RESULTS: Liver biopsy showed minimal hepatitis (F0) in 9, F1 in 53, F2 in 21, F3 in 6, and F4 or cirrhosis in 6. Initial HBV DNA concentration was low (less than 10^4 copies/mL) in 33, intermediate (10^4 - 10^6) in 53, and high (10^6 or more) in 9. Hepatitis activation rates with twice as high as normal aminotransferase at the end of the third year were 12.1% in the low DNA group, 43.4% in the intermediate group, and 66.7% in the high DNA group. Initial HBV DNA values were significantly associated with future increase in aminotransferase ($P < .0001$). Initial DNA, history of aminotransferase elevation, and histological staging independently affected future hepatitis activation. Carcinogenesis rate in patients with and without high DNA of 10^6 copies/mL during the initial 3 years were 6.9% and 0%, respectively, at the end of the 5th year, and 11.5% and 1.8%, respectively, at the 10th year, ($P = .021$).

CONCLUSION: Advanced stages of hepatitis were sometimes found in HBe antigen-negative, aminotransferase-normal HBV carriers. Serial HBV DNA assessment in early 3 years predicted future hepatitis activation and carcinogenesis. © 2006 Elsevier Inc. All rights reserved.

KEYWORDS: Hepatitis B virus; DNA; HBe-antigen; Carcinogenesis; Prognosis; Chronic hepatitis

HBe antigen loss and appearance of anti-HBe antibody are usually associated with normalization of aminotransferase in patients with chronic hepatitis,¹⁻³ and these changes have long been considered as a reliable clinical indicator of inactive and innocent state of chronic hepatitis B. However, the level of aminotransferase sometimes fluctuates under the state of negative HBe antigen in chronic hepatitis B, and there is occasional histological evidence of disease progression.⁴⁻⁶ Because hepatitis B virus (HBV) DNA is usually

detected in the sera of these patients, mutant HBV has been confirmed to cause the hepatitis activity.^{7,8} Moreover, hepatocellular carcinoma (HCC) sometimes occurs in patients with mild hepatitis and normal aminotransferase levels.^{9,10} It is an important problem from the viewpoint of early detection of HCC that general practitioners and even hepatologists are sometimes unaware of those patients with negative HBe antigen and normal aminotransferase as high-risk subjects for HCC.

There is little information about how many patients with both normal alanine aminotransferase (ALT) and negative HBe antigen have active or advanced histologically confirmed hepatitis,^{11,12} and how many patients in

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whom ALT level increases over long-term follow-up. Recently, for evaluation of the activity of chronic hepatitis B, simple and sensitive HBV DNA assays using polymerase chain reaction (PCR) have replaced serologic examination of HBe antigen-antibody. The high sensitivity of DNA assays has contributed to our understanding of the pathogenetic role of the virus and provided useful information about hepatitis activity in individual patients.¹²⁻¹⁸ An arbitrary serum DNA level of 10^5 copies/mL was proposed by the National Institute of Health Workshop for the differentiation of chronic hepatitis B from an inactive carrier state (HBe antigen-negative, persistently normal ALT).¹⁹ Martinot-Peignoux et al²⁰ also reported that a cutoff

DNA value of 10^5 copies/mL effectively discriminated inactive hepatitis in a follow-up study of 1 to 6 years. On the other hand, Manesis et al²¹ suggested that a cutoff DNA level of 3×10^4 copies/mL was more appropriate for differentiating inactive carriers from patients with HBeAg-negative chronic hepatitis B. Furthermore, Chu et al²² concluded that a single cutoff DNA value could not differentiate inactive carriers from patients with HBeAg-negative chronic hepatitis after retrospective analysis of 165 Chinese patients. Previous studies indicated that the above data still did not provide sufficient information as to the longitudinal outcome of hepatitis activation and carcinogenesis, considering the fluctuating course of HBeAg-negative chronic hepatitis.^{19,22} Here we report the results of our long-term study (median follow-up of 10.2 years) in patients with negative HBe antigen and normal alanine aminotransferase (ALT).

The purposes of this retrospective study were to elucidate the incidence of advanced liver disease in patients with negative HBe antigen and normal ALT value, and to estimate the future activation of hepatitis and carcinogenesis rate in those patients, using life-table method with multivariate analysis. We also analyzed whether the initial few years of biochemical and virological observation (annual measurements of ALT and HBV DNA concentration) could predict future outcome of the patients.

PATIENTS AND METHODS

Patients

Among 1048 patients who were diagnosed with HBV-related chronic hepatitis by peritoneoscopy and/or biopsy from 1974 to 2002 in our hospital, 116 patients were negative HBe antigen and had normal aminotransferase at the time of liver biopsy. Of these, 95 (81.9%) were thoroughly observed for 5 years or longer, and their data were available for analysis of HBV DNA concentration.

The initial sera of all these 95 patients were positive for HBs antigen, negative HBe antigen, and negative anti-HCV antibody. ALT concentration was also normal for 2 months or longer before admission to the hospital for examination of liver biopsy. The enrolled patients included 75 men and 20 women

aged 21 to 67 years, with a median of 39 years. None of the patients received antiviral therapy before liver biopsy. All the clinical practices were performed in accordance with the ethical committee of the hospital and with general agreement of domestic medical insurance.

Table 1 shows demographic and laboratory data of the 95 patients. Family history of liver disease or HBV infection has been closely investigated and assessed to a relative in the fourth degree using each family

line. Because all the patients had been negative for HBe antigen and normal ALT since the initial visit to our hospital, the time of seroconversion from HBe antigen to HBe antibody was not clear in most of the patients. HBV subtyping showed that genotype C was the most prevalent type (74.7%) in the cohort, the rate of which was slightly lower than that of Japanese patients with chronic hepatitis type B.^{23,24} Two authors (K.I. and H.K.) assessed the pathology and translated the biopsy findings to the classification of Desmet et al.²⁵

CLINICAL SIGNIFICANCE

- Advanced stages of hepatitis should not be overlooked in patients with HBe antigen-negative, aminotransferase-normal HBV carriers.
- Serial DNA assessment in the early few years predicted future hepatitis activation and the risk of carcinogenesis.

Table 1 Demography and Laboratory Data of 95 Patients with Positive HBs Antigen who Showed Normal Aminotransferase and Negative HBe Antigen at the Time of Biopsy

Data	
Demographic data	
Men:Women	75:20
Age (years - median, range)	39 (18-67)
HBe antigen positive	0 (0%)
HBV genotype A	3 (3.2%)
B	18 (18.9%)
C	71 (74.7%)
Others/undetectable	3 (3.3%)
Anti-HCV antibody positive	0 (0%)
Past alcohol intake of 500 kg or more	15 (15.8%)
History of blood transfusion	4 (4.2%)
Laboratory data*	
Aspartic aminotransferase (normal 6-38 IU)	26 (10-37)
Alanine aminotransferase (normal 6-50 IU)	28 (6-50)
Platelet count (normal $149-315 \times 10^3/\text{mm}^3$)	185 (86-311)
ICG _{R15} ** (normal, $\leq 10\%$)	11 (3-33)
Albumin (normal, 3.9-5.2 g/dL)	4.3 (3.6-5.4)
Bilirubin (normal, ≤ 1.1 mg/dL)	0.9 (0.2-1.9)
Prothrombin time (normal, $\geq 70\%$)	97.5 (67-111)

*Data are median (range).

**ICG_{R15}: Indocyanine green retention rate at 15 minutes.

Follow-up Studies

After liver biopsy, follow-up examinations were conducted on a monthly to tri-monthly basis by monitoring biochemical and virological data. Although 27 (28.4%) patients started to receive interferon (IFN) therapy because of ALT elevation, none underwent lamivudine therapy during the course of the study. "Activation of hepatitis" or "flare-up of ALT" was defined as an increase of ALT value of twice or more of the upper limit of normal.

Imaging studies were performed annually in each patient and included computed tomography (CT) or ultrasound (US) after 1985. At least 2 imaging procedures were performed in those patients with cirrhosis. HCC was diagnosed by typical hypervascular characteristics on angiography in addition to certain features of CT and US. Pathological confirmation of surgically resected specimens or autopsy was made in 3 (60.0%) of 5 patients who developed HCC during the study.

A total of 17 patients were lost to follow-up after 5 years. The observation period ranged from 5.1 to 24.7 years, with a median of 10.2 years.

Assays of HBV Markers

Serum HBsAg was measured by radioimmunoassay (Dainabot, Tokyo, Japan), and HBeAg and anti-HBe were determined by enzyme-linked immunosorbent assay (ELISA, Institute of Immunology) using commercially available kits. Anti-HCV antibody was analyzed using second-generation anti-HCV kits (enzyme-linked immunosorbent assay, Dainabot). HBV DNA was assayed using frozen sera stored at -80°C and measured with Amplicor HBV Monitor kits (Roche Diagnostics Japan Co., Tokyo). The effective measurement of the concentration ranged from $10^{2.6}$ (400) copies/mL to $10^{7.6}$ (40,000,000) copies/mL. All measurements of HBV DNA were performed at the same time using the same assay kits. Quantitative HBV DNA was conducted at the time of liver biopsy, at the end of 6 months, and at the end of the 1st, 2nd, 3rd, and 5th years.

Statistical Analysis

The chi-square test, Fisher's exact test, and Kruskal-Wallis test were used to analyze the relationship between HBV markers and the clinical course. Cumulative flare-up rate of hepatitis and carcinogenesis rate were calculated with the Kaplan-Meier method,²⁶ and differences in the rates were analyzed by the log-rank test. Multivariate Cox proportional hazard model²⁷ was adopted to analyze the prediction of future hepatitis activation and carcinogenesis. A *P*-value of less than .05 with 2-tailed test was considered significant. Data analysis was performed using the SPSS software version 11.²⁸

RESULTS

Histological Findings

According to the classification of Desmet et al,²⁵ liver biopsy showed minimal hepatitis (F0) in 9 (9.5%), F1 in 53 (55.8%), F2 in 21 (22.1%), F3 in 6 (6.3%), and F4 or cirrhosis in 6 (6.3%). Occult cirrhosis with normal ALT and negative HBe antigen was found in 6.3%. Inflammatory activity was minimal (A0) in 18 (18.9%), A1 in 72 (75.8%), and A2 in 5 (5.3%).

Reasons for Liver Biopsy

The reasons for liver biopsy in spite of "stable hepatitis" included a history of ALT elevation in the past (group A, $n = 41$), patient's apprehension based on family history of advanced liver diseases (group B, $n = 25$), possible advanced liver disease on ultrasonography (US) or liver function tests (group C, $n = 8$), or simple desire for thorough examination including biopsy (group D, $n = 21$). We also assessed the relationship between background features and reasons for undergoing liver biopsy (Table 2).

Advanced liver disease of F3 or F4 was present in 4 of 41 (9.8%) patients in group A, 4 of 25 (16.0%) in group B, 3 of 8 (37.5%) in group C, and 1 of 18 (5.6%) in group D. The median platelet count was the lowest in group C, which suggested that the group included more numbers of patients with advanced stages of the disease. The median HBV DNA concentration at the beginning was the highest in group A. HBV genotype A was exclusively found in group D and the incidence of genotype B was higher in groups A and D.

Initial and Serial Assays of HBV DNA Concentration

The median DNA concentration at the time of liver biopsy was $10^{4.4}$ copies/mL, with 25th percentile of $10^{3.2}$, and 75th percentile of $10^{5.2}$ (range, $<10^{2.6}$ to $>10^{7.6}$).

The relationship between the initial HBV DNA values and serial measurements of DNA during the observation were assessed, classifying the initial DNA concentration into 4 groups: low DNA group ($<10^4$ copies/mL), DNA concentration of 10^4 - $10^{4.9}$ copies/mL, DNA concentration of 10^5 - $10^{5.9}$ copies/mL, and high DNA of $\geq 10^6$ copies (Figure 1). Among 33 patients with initial HBV DNA concentration of $<10^4$ copies/mL, 29 (87.9%) showed a continuously low DNA of less than 10^6 copies/mL, and 4 (12.1%) showed an intermittent rise of the DNA to $>10^6$ copies/mL. Among 34 patients with initial HBV DNA of 10^4 to $10^{4.9}$ copies/mL, 25 (73.5%) showed persistently low DNA, and 9 (26.5%) an intermittent rise of the DNA. Of 18 patients with initial DNA of 10^5 to $10^{5.9}$ copies/mL, 10 (55.5%) showed persistently low DNA course, and 8 (44.4%) an intermittent elevation of the DNA. Among 10 patients with initial DNA of $\geq 10^6$ copies/mL, an intermittent rise of the DNA was found in 9 patients (90.0%) and persistently high DNA in one (10.0%). The initial HBV DNA concentration was significantly associated with the subsequent serial HBV DNA course ($P < .0001$).

Table 2 Demographic, Histological, Biochemical and Virological Findings According to the Reasons for Examination Including Liver Biopsy

	Reasons for Liver Biopsy			
	Group A	Group B	Group C	Group D
Number of patients	41	25	8	21
Male/Female	36/5	15/10	5/3	19/2
Age (years - median, range)	39 (18-61)	38 (30-67)	41 (30-57)	41 (21-58)
Family history of liver disease or HBV infection	18 (37.5%)	38 (100%)	5 (62.5%)	6 (28.6%)
Liver histology				
F0 (minimal)	1	5	0	3
F1	21	15	2	15
F2	15	1	3	2
F3	2	2	1	1
F4 (cirrhosis)	2	2	2	0
AST (IU/L) (median, range)	27 (17-37)	22 (10-37)	24 (16-28)	21 (14-34)
ALT (IU/L)	34 (18-50)	20 (6-48)	21 (12-48)	20 (8-50)
Platelet ($\times 1000/\text{mm}^3$)	169 (94-274)	185 (96-311)	156 (86-216)	196 (128-296)
ICG _{R15} (%)	12 (6-24)	9.5 (3-33)	9 (7-13)	12 (5-72)
Albumin (g/dL)	4.3 (3.6-5.1)	4.4 (3.9-5.4)	4.15 (3.9-5.4)	4.4 (3.7-4.9)
Bilirubin (mg/dL)	1.0 (0.2-1.5)	1.1 (0.4-1.8)	0.75 (0.3-1.1)	0.8 (0.3-1.9)
Prothrombin (%)	89 (67-111)	100 (70-108)	100 (76-101)	100 (73-101)
HBV DNA (Log ₁₀ copy/ml) (median, 25-75 percentiles)	4.6 (4.2-5.3)	4.2 (3.1-5.4)	3.45 (<2.6-4.8)	3.9 (<2.6-4.8)
HBV genotype				
A	0	0	0	3
B	11	0	0	7
C	29	25	7	10
Others/unidentified	1	0	1	1

Group A: History of ALT elevation in the past.

Group B: Advanced liver disease in family members.

Group C: Possible advanced disease on ultrasonography or blood examination.

Group D: Simple desire for thorough examination

Activation of Hepatitis and Its Prediction

Twenty-five patients showed twice as high as normal ALT concentration, and the other 27 patients showed activation of hepatitis with ALT elevation followed by IFN therapy. Consequently, a total of 52 patients (54.7%) showed an abnormal ALT concentration during a median observation period of 10.2 years. The cumulative rate of hepatitis activation was 34.7% at the end of the 3rd year, 45.4% at the 5th year, and 55.7% at the 10th year.

The incidence of hepatitis activation was assessed in the following 4 groups according to the initial HBV DNA concentration: $<10^4$ copies/mL ($n = 33$), 10^4 to $10^{4.9}$ ($n = 34$), 10^5 to $10^{5.9}$ ($n = 18$), and $\geq 10^6$ ($n = 10$). Cumulative hepatitis flare-up rates in each group were 12.0%, 41.2%, 44.4%, and 70.0%, respectively, at the end of the 3rd year; 12.0%, 61.8%, 55.5%, and 80.0%, respectively, at the 5th year; and 18.6%, 70.3%, 80.0%, and 80.0%, respectively, at the 10th year (Figure 2). The initial DNA load correlated significantly with future hepatitis activation rate ($P < .0001$). Average DNA concentration during the initial 5 years was closely associated with hepatitis activation for the period: 52 patients with ALT elevation had a high average DNA value of $10^{3.3}$ (median, range: $<10^{2.6}$ - $10^{5.3}$), and 43 patients without ALT elevation showed $10^{4.8}$ (median, range: $10^{2.9}$ - $>10^{7.6}$).

The hepatitis activation rates in groups A, B, C, and D were 70.7%, 36.0%, 25.0%, and 14.3%, respectively, at the end of the 5th year; and 81.7%, 45.1%, 25.0%, and 26.7%, respectively, at the end of the 10th year (Figure 3). The ALT flare-up rate in patients of group A was the highest ($P < .0001$).

Multivariate proportional hazard analysis disclosed that initial HBV DNA concentration, a past history of ALT elevation, and histological staging were significantly associated with reactivation of hepatitis in the follow-up (Table 3). Patients with HBV DNA of 10^4 to $10^{5.9}$ copy/mL had a high hazard ratio of 5.73, and those with 10^6 copy/mL or higher showed a hazard ratio of 10.43, compared with those with lower DNA concentration $<10^4$. Past history of ALT elevation also was associated with hepatitis activation with a hazard ratio of 3.62. Histological staging of F2 or higher also showed a high risk for carcinogenesis with a hazard ratio of 3.06.

Relationship between HBV DNA in First 2 Years and Hepatitis Activation

The prediction of hepatitis activation was analyzed using HBV DNA level in the first 2 years (DNA measurements at the time of observation, 6th, 12, and 24th month). Using various cutoff values of DNA, patients were classified into

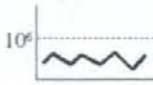
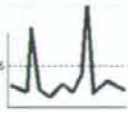
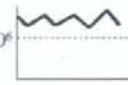
		Patterns of serial of HBV DNA for 5 years		
Initial HBV DNA (copies/ml)		lower than 10^6 persistently	10^6 or higher intermittently	10^6 or higher persistently
				
< 10^4	(N=33)	29 (87.9%)	4 (12.1%)	0
10^4 - $10^{4.9}$	(N=34)	25 (73.5%)	9 (26.5%)	0
10^5 - $10^{5.9}$	(N=18)	10 (55.6%)	8 (44.4%)	0
$\geq 10^6$	(N=10)	0	9 (90%)	1 (10%)

Figure 1 Relationship between initial HBV DNA values and serial DNA during the initial 5 years.

low DNA group (persistently low) and high DNA group (a high value at least once during the observation period).

When patients were divided using a cutoff value of 10^6 copies/mL (Figure 4a), hepatitis activation rates in low DNA group ($n = 69$) and high DNA group ($n = 26$) were 27.5% and 53.8%, respectively, at the end of the 3rd year; 37.7% and 65.4%, respectively, at the 5th year; and 46.0% and 79.2%, respectively, at the 10th year. The hepatitis activation rate in the high DNA group was significantly higher than that of the low DNA group ($P = .0014$). If DNA

concentration remained $< 10^6$ copies/mL for 2 years, 53.6% (37/69) of the patients did not show flare-up of ALT during the observation period.

Next, when patients were divided using a cutoff value of 10^5 copies/mL (Figure 4b), hepatitis activation rates in the low DNA group ($n = 47$) and high DNA group ($n = 48$) were 14.9% and 54.2%, respectively, at the end of the 3rd year; 23.4% and 66.7%, respectively, at the 5th year; and 30.8% and 79.4%, respectively, at the 10th year. Hepatitis activation rate in the high DNA group was significantly

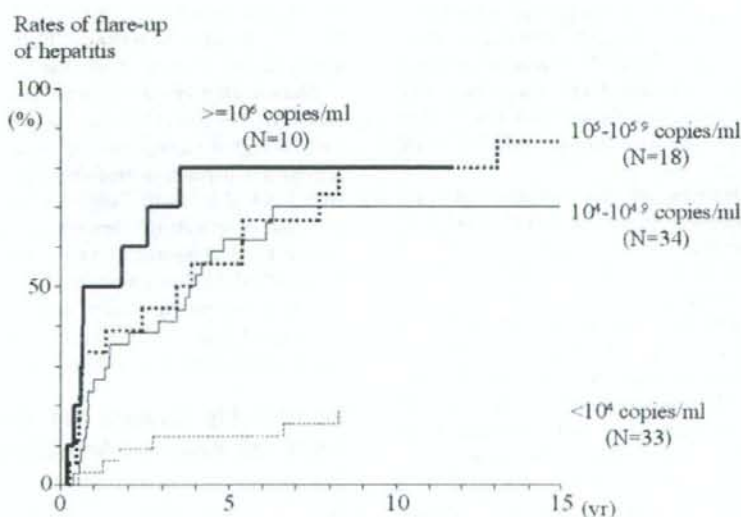


Figure 2 Cumulative hepatitis activation rates in the 4 patient groups according to initial HBV DNA values: Log₁₀ HBV DNA of <4.0, 4.0-4.9, 5.0-5.9, and ≥ 6 .

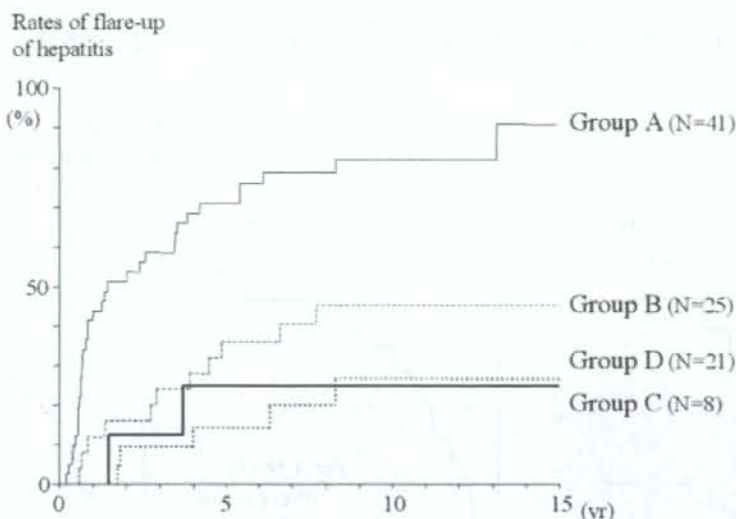


Figure 3 Cumulative hepatitis activation rates in subgroup A, B, C, and D: Patients in group A had a history of aminotransferase elevation in the past, those in group B had apprehension of their own diseases based on a significant family history, those in group C were suspected of having an advanced liver disease on ultrasonography or liver function tests, and those in group D had a simple desire for thorough examination with biopsy.

higher than that of the low DNA group ($P < .0001$). If DNA concentration remained $< 10^5$ copies/mL for 2 years, 70.2% (33/47) of the patients did not show flare-up of ALT during the observation period.

Similarly, when patients were divided using a cutoff value of 10^4 copies/mL (Figure 4c), hepatitis activation rates in the low DNA group ($n = 24$) and high DNA group ($n = 71$) were 4.2% and 45.1%, respectively, at the end of the 3rd year; 4.2% and 59.1%, respectively, at the 5th year; and 8.3% and 72.1%, respectively, at the 10th year. Hepatitis activation rate in the high DNA group was significantly higher than that of the low DNA group ($P < .0001$). If DNA concentration remained $< 10^4$ copies/mL for 2 years, 91.7%

(22/24) of the patients did not show flare-up of ALT during the observation period.

A receiver-operating characteristic (ROC) curve was generated to assess the best cutoff value of HBV DNA for the prediction of future hepatitis activation (Figure 5). Cutoff value of $10^{6.0}$ or higher predicted 86.0% of future hepatitis activation, but persistently lower value than $10^{6.0}$ predicted only 36.5% of stable disease. On the contrary, cutoff value of $10^{4.0}$ or higher predicted only 51.2% of future ALT elevation, but constantly lower value than $10^{4.0}$ predicted 96.2% of stable hepatitis.

Hepatocellular Carcinogenesis and Its Prediction

During a median observation period of 10.2 years, 5 patients (5.3%) developed HCC. Among the 5 patients who developed HCC, one had low HBV DNA concentration of $\leq 10^4$ copies/mL, 3 had intermediate value of 10^4 to 10^6 , and one had high DNA concentration of $\geq 10^6$ copies/mL. Among 90 patients who did not develop HCC, 32 had low DNA, 50 had intermediate viral load, and 8 had high concentration ($P = .62$). The cumulative carcinogenesis rates in patients with and without high DNA concentration of $\geq 10^6$ copies/mL during the initial 3 years were 6.9% and 0%, respectively, at the end of the 5th year, and 11.5% and 1.8%, respectively, at the 10th year (Figure 6).

Those patients with high DNA concentration of $\geq 10^6$ copies/mL at least once during the initial 3 years had a significantly higher carcinogenesis rate than those without DNA elevation ($P = .021$). Average DNA concentration during the initial 5 years also was associated with hepatitis

Table 3 Factors Associated with Future Hepatitis Activation in Patients with Positive HBs Antigen who Showed Normal Aminotransferase and Negative HBe Antigen at the Time of Biopsy

Factor	Category	Hazard Ratio	(95% CI)	P Value
Initial HBV DNA	0: $-10^{3.9}$	1		
	1: 10^4 - $10^{5.9}$	5.73	(2.36-13.9)	<.0001
	2: $10^{6.0}$ -	10.43	(3.44-31.60)	<.0001
History of ALT elevation	0: no	1		
	1: yes	3.62	(1.97-6.67)	<.0001
Histological staging	0: F0-F1	1		
	1: F2-F4	3.06	(1.73-5.42)	<.0001

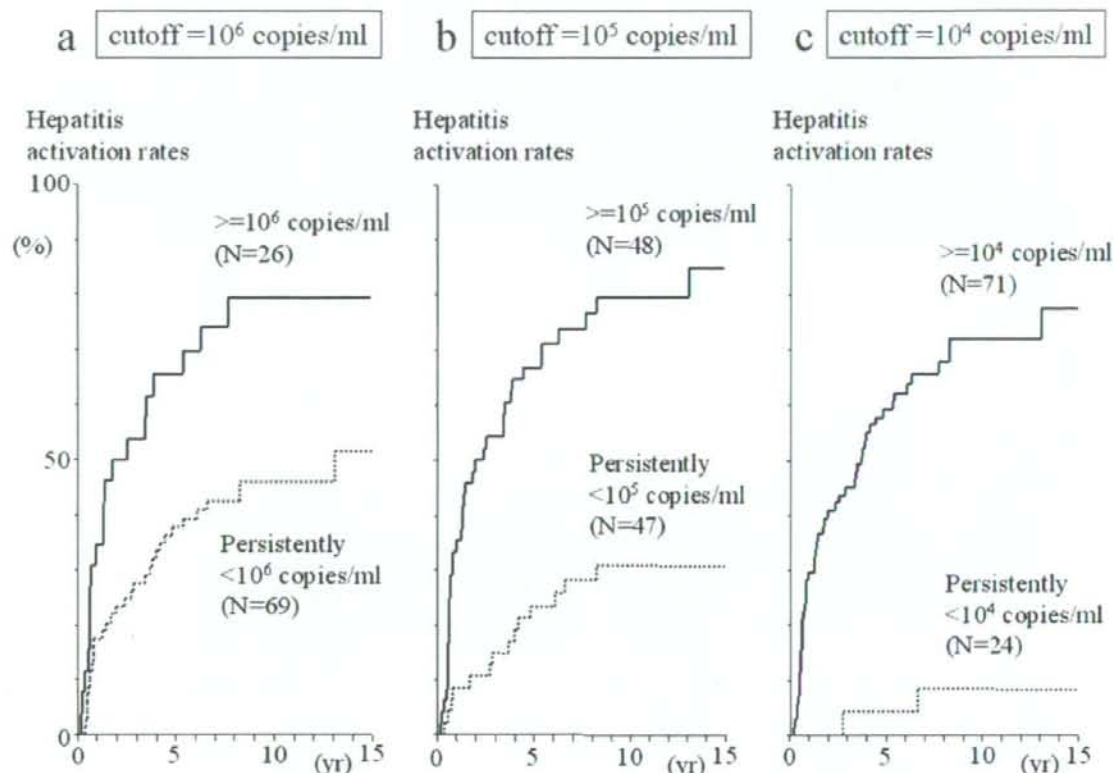


Figure 4 Cumulative hepatitis activation rates in patients with high HBV DNA and those with low DNA. The cutoff values of HBV DNA during the initial 2 years were set at 10^6 copies/mL (a), 10^5 copies/mL (b), and 10^4 copies/mL (c).

activation: 5 patients with HCC development had a high average DNA value of $10^{4.5}$ (median, range: $10^{3.0}$ - $10^{6.6}$), and 90 patients without HCC showed $10^{4.1}$ (median, range: $<10^{2.6}$ - $>10^{7.6}$). Multivariate proportional hazard analysis disclosed that only serial HBV DNA concentration was significantly associated with hepatocarcinogenesis in the observation period. Hepatitis staging, age, platelet count, and gender did not affect carcinogenesis rate in this study.

DISCUSSION

The present study showed that 90% of the patients with negative HBe antigen and normal ALT concentration had pathologically confirmed chronic hepatitis or occult cirrhosis. Although the analyzed patients in our study might not be considered as average representatives of such patients in this country, general practitioners should recognize the incidence of the activity and staging.

The development of sensitive HBV DNA assays greatly helped our understanding of the pathogenesis and variable clinical meanings of hepatitis B virus infection.^{12-18,29-31} There is a general agreement among various research groups that hepatitis activity in chronic hepatitis B correlates well with serum DNA concentration.^{14,18-22} Because

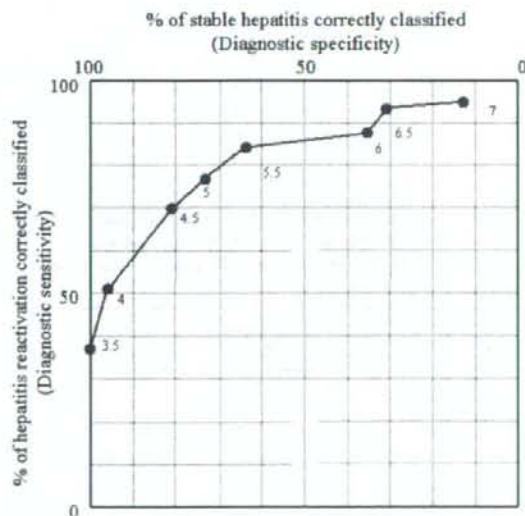


Figure 5 A receiver-operating characteristic (ROC) curve for prediction of future hepatitis activation according to cutoff value of HBV DNA. HBV DNA was expressed as common logarithm of the concentration.

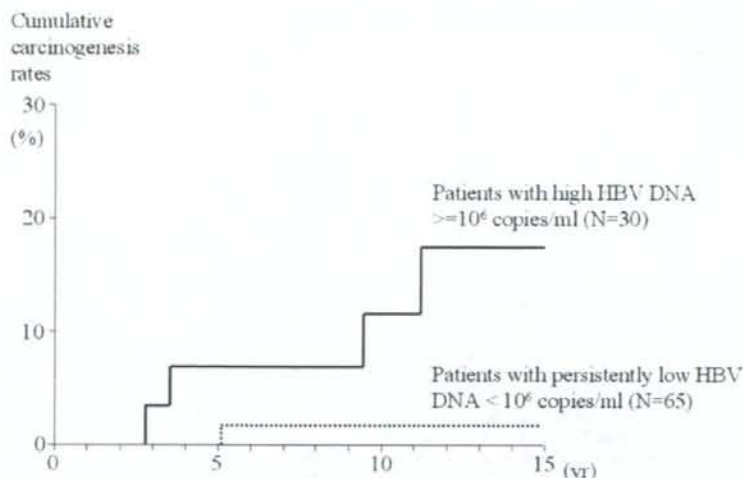


Figure 6 Cumulative hepatocellular carcinogenesis rates in patients with and without high HBV DNA concentration during the initial 3 years.

hepatitis activity often fluctuates with significant changes of DNA concentration in the patients, even sensitive DNA assays demonstrate an obvious limitation from a single time measurement.²² Our retrospective study, therefore, analyzed the chronological changes in DNA and biochemistry in a patient cohort over a period of more than 5 years (median, 10.2 years).

We found all patients with negative HBeAg and normal ALT had a detectable value of serum HBV DNA by PCR assay, and that the DNA value correlated well with high ALT concentration and the incidence of future ALT elevation, in agreement with other reports.^{19-22,32-35} A few studies^{19,20,36} reported that a cutoff value of 10^5 copies/mL was practical in discriminating chronic hepatitis from asymptomatic carrier state, whereas Manesis et al²¹ reported that a cutoff DNA level of 3×10^4 copies/mL was more appropriate for the same purpose. In forecasting future ALT elevation in a narrower patient cohort with negative HBe antigen and normal ALT concentrations, however, a cutoff value of 10^4 copies/mL effectively predicted reactivation of hepatitis. The efficacy of the cutoff value of 10^4 copies/mL was true in using both the initial DNA value at a single-time assay and multiple assays during 2-year follow-up. From the longitudinal data, only 8.3% of patients with persistently low DNA of $<10^4$ copies/mL in the initial 2 years showed ALT elevation during a median of 10.2 years of observation.

The fate of patients regarding future DNA elevation and ALT fluctuation also depends on the reason for undergoing invasive diagnostic procedures including liver biopsy. Patients of group A (patients with history of ALT elevation) showed the highest initial DNA concentration and future ALT elevation rate. Those of group B (patients with family history of advanced disease) showed the second highest value of initial DNA and high incidence of ALT elevation.

Although we analyzed more than 80% of consecutive patients in our hospital, the background features of patients should be taken into account in the study of HBV-related disease, when a tertiary medical center performs a retrospective cohort study using a selected patient group.

Among the stable patients with negative HBe antigen and normal ALT, HCC occurred in 5 patients (5.3%) during a median of 10.2 years. As was reported previously,^{33,37,38} hepatocarcinogenesis was significantly associated with persistently high HBV DNA. In this cohort study, patients with DNA of $\geq 10^6$ copies/mL had a significantly higher carcinogenesis rate than those with low DNA. The cutoff concentration of DNA of 10^6 copies/mL was consistent with other cohorts with cirrhosis^{33,37,38} in the prediction of carcinogenesis. The reason for the higher cutoff value for carcinogenesis than that for hepatitis reactivation might be explained by differences in the pathogenetic processes. Although hepatocarcinogenesis in these patients may well be associated with DNA concentration severity of the liver disease, or merely persistence of high ALT concentration, general practitioners or physicians should be aware of the risk of HCC development in these stable patients.

The precise role of HBV in oncogenesis is still unknown, but increasing evidence indicates that the virus plays an important role in the development of HCC. Because the disease activity and carcinogenic potency can change significantly during the course of HBV-related liver disease, a longitudinal analysis is desirable for the study of carcinogenesis from HBV-related cirrhosis. Future studies should be aimed, therefore, at defining the basic oncogenic mechanisms and roles of serum DNA concentration in carcinogenesis in patients with HBV infection.

In conclusion, advanced stages of hepatitis should not be overlooked in patients with HBe antigen-negative, aminotransferase-normal HBV carriers. Serial DNA assessment

in the early few years predicted future hepatitis activation and the risk of carcinogenesis.

ACKNOWLEDGMENT

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Anticarcinogenic Impact of Interferon on Patients with Chronic Hepatitis C: A Large-Scale Long-Term Study in a Single Center

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Key Words

Cirrhosis · Fibrosis · Hepatitis C virus · Hepatocellular carcinoma · Interferon

Abstract

Background: The anticarcinogenic capacity of interferon (IFN) was assessed in a cohort of Japanese patients with chronic hepatitis C en masse. **Patients and Methods:** The rate of hepatocarcinogenesis was analyzed in 2,166 patients with chronic hepatitis C, of whom 1,654 had received IFN therapy while 512 had not. **Results:** Crude rates of hepatocarcinogenesis in treated and untreated patients were 2.6 and 4.6% at the end of the 5th year, 5.8 and 12.7% at the 10th year and 13.9 and 23.9% at the 15th year (after completion of IFN therapy for those treated) ($p < 0.001$). IFN decreased the hazard ratio of carcinogenesis to 0.42 ($p < 0.001$) in multivariate analysis with adjustments for significant covariates including fibrotic stage, γ -glutamyl transpeptidase level, gender, platelet count and age. Among the 1,654 patients treated with IFN, 606 (36.6%) achieved persistent loss of hepatitis C virus (HCV) RNA and an additional 266 (16.1%) gained normal levels of alanine aminotransferase without loss of HCV RNA for 6 months or longer after the completion of IFN therapy. Cumulative rates of hepatocarcinogenesis in sustained virological responders and biochemical responders were 1.4 and 2.0% at the end of the 5th year,

1.9 and 3.6% at the 10th year and 1.9 and 7.5% at the 15th year, respectively. The hazard ratio of sustained virological response was 0.10 ($p < 0.001$), and that of biochemical response was 0.12 ($p < 0.001$). Normalization of aminotransferase levels after IFN therapy without loss of serum HCV RNA decreased hepatocarcinogenesis. **Conclusion:** IFN significantly decreased the rate of hepatocarcinogenesis in patients with chronic hepatitis C as a whole in Japan, even in those who fail to clear HCV RNA from serum.

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Introduction

In most developed countries, hepatitis B virus (HBV) and hepatitis C virus (HCV) infections account for the great majority of hepatocellular carcinoma (HCC), with incidence rates dependent on the regional prevalence of these hepatitis viruses. HCV-associated HCC typically develops through a sequence of events that progress from chronic inflammation through fibrosis and cirrhosis accompanying dysplasia and ultimately to HCC. In our previous cohort study on Japanese patients with HCV-related cirrhosis [1], cumulative rates of developing HCC at 5, 10 and 15 years were 21.5, 53.2 and 75.2%, respectively. According to our observations of untreated patients with chronic hepatitis C [2], rates of hepatocarcino-

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genesis at 5, 10 and 15 years were estimated to be 4.8, 13.6 and 26.0%, respectively. The life expectancy of patients with HCV-related cirrhosis is largely influenced by the development of HCC in the clinical course. As the efficacy of radically curative therapies for HCC remains limited at best, and since a severe organ shortage does not provide with sufficient chances for liver transplantation, the prevention of HCC in patients with chronic liver disease is of great importance at the present.

Interferon (IFN) is effective in eliminating HCV and reducing serum levels of alanine aminotransferase (ALT) in some patients with chronic hepatitis C [3-6]. Reduced incidence of HCC in HCV-associated cirrhosis by IFN has been reported by many investigators including ourselves [7-14]; only a few studies have failed to find its benefit [15, 16]. However, many published studies had shortcomings in the study design, in terms of pooling patients who received IFN in diverse regimens, relatively short periods of follow-up despite a long incubation period of HCC, large numbers of dropouts and retrospective studies with historical controls. Moreover, almost all studies evaluated the activity of IFN to prevent HCC by comparing responders and nonresponders to the treatment. Due to difficulties in studying patients with chronic hepatitis C, a number of nonrandomized studies examined the effect of IFN on the incidence of hepatocarcinogenesis [17-20]. With invariable limitations in study design and interpretation of the results, these studies have disclosed useful information as regards the treatment of patients with chronic HCV infection.

In order to evaluate whether IFN can reduce the rate of carcinogenesis in patients with chronic hepatitis C, we compared 1,654 patients with IFN therapy with 512 patients without treatment in a single clinical center, who were adjusted for background features by the multivariate analysis. Therefore, the principal aims of our study were to show the role of IFN in preventing HCC in chronic hepatitis type C en masse and to establish the extent to which IFN decreases the rate of carcinogenesis as a sequel to chronic hepatitis C in a society.

Patients and Methods

Study Population

A total of 2,166 patients with chronic hepatitis were examined, whose initial sera tested negative for hepatitis B surface antigen by radioimmunoassay (Ausria, Dainabot, Tokyo, Japan) and positive for anti-HCV by the second-generation enzyme-linked immunosorbent assay (Dainabot); anti-HCV was tested in sera that had been stored frozen at -80°C . They included 1,421 men and 745

women aged 14-78 with a median of 50 years. They were all diagnosed with chronic hepatitis by liver biopsy with or without peritoneoscopy between 1970 and 2000 at the Department of Gastroenterology in Toranomon Hospital, Tokyo, Japan. Patients who had possibly developed HCC already at the time of diagnosis of hepatitis were strictly excluded from the study. In order to exclusively investigate hepatocarcinogenesis in HCV-related cirrhosis, patients coinfecting with HBV were excluded.

Among the 2,166 patients with HCV-related hepatitis, 1,654 (76.4%) received IFN therapy, mostly since 1987 when IFN was available in Japan; new antivirals or anticarcinogenic treatments of viral cirrhosis, except for IFN, were not introduced in 1987 or thereafter in Japan. The remaining 512 patients did not receive IFN or any other antiviral therapies. This is a retrospective cohort study with historical controls composed of patients before 1987 and those who refused or could not receive IFN for various reasons since 1987.

Background and Laboratory Findings

Table 1 shows demographic profiles and laboratory data for the 1,654 patients treated with IFN and the 512 without receiving IFN since they were diagnosed with chronic hepatitis. There were more males, with a median age 3 years lower in treated than in nontreated patients. There were 299 treated patients (18.1%) with a history of alcohol intake ≥ 500 g until the diagnosis of chronic hepatitis (corresponding to daily consumption of 3,000 ml of beer or 300 ml of whiskey for 20 years) and 113 (22.1%) untreated patients ($p < 0.001$). Because IFN was introduced to our hospital in 1987, the observation period was significantly shorter in the treated than in untreated patients (median 10.4 vs. 12.3 years; $p < 0.0001$).

Although all patients tested positive for HCV RNA during their clinical courses, tests for the concentration of HCV RNA in the initial serum was possible in 1,863 (86.5%) patients. HCV genotypes were analyzed by the serological typing method with a commercial kit (Kokusai Diagnostic Corporation, Kobe, Japan) in which the serological group 1 represented genotypes 1a and 1b, and group 2 stood for 2a and 2b genotypes. HCV in the serological group 2 was significantly more frequent in patients with IFN treatment than in those without. Concentration of HCV RNA was determined in the initial sera from 1,873 (86.5%) patients by the competitive polymerase chain reaction (PCR) method with the HCV probe assay (Chiron Corp., Emeryville, Calif., USA) or by PCR with Amplicor HCV Monitor kits (Roche Diagnostics Japan Co., Tokyo, Japan). High concentration of HCV ($\geq 10^6$ copies/ml by the competitive PCR or $\geq 10^6$ equivalents/ml by the HCV probe assay) was significantly more frequent in untreated than in treated patients ($p < 0.0001$). The stage of hepatic fibrosis was not different between the two groups.

Interferon Treatment and Judgment of the Effect

A total of 1,654 patients underwent IFN therapy in one or more treatment courses: 1,358 patients (82.1%) received IFN once, 240 patients (14.5%) twice, and the remaining 56 patients (3.4%) three times or more. Initial treatment was performed with natural or recombinant IFN- α ($n = 1,238$), natural IFN- β ($n = 386$) or both ($n = 30$). Regimens of IFN were variable: 926 (56.0%) patients received IFN 6-9 million units (MU) daily for 8 weeks, followed by 2 or 3 times per week for 16 weeks; 329 (20.0%) received IFN 6-9 MU daily for 2-4 weeks, followed by 3 times per week for 20-22 weeks; 185 (11.2%) underwent a short-course therapy with IFN

Table 1. Patient profiles and laboratory data at the diagnosis of chronic hepatitis

Factors	Interferon therapy		p value
	yes (n = 1,654)	no (n = 512)	
Male	1,110 (67.1%)	311 (60.7%)	0.024
Age, years	50 (16-72)	53 (21-78)	<0.001
History of transfusion	607 (36.7%)	229 (44.7%)	0.001
Family member with liver disease	426 (25.8%)	140 (27.3%)	0.47
Alcohol intake \geq 500 kg	299 (18.1%)	113 (22.1%)	0.044
Observation period, year	10.4 (0.1-33.6)	12.3 (0.1-33.6)	<0.001
Laboratory data			
ALT, IU/l	63 (4-1,266)	67 (4-704)	0.098
AST, IU/l	106 (9-1,660)	96 (12-832)	0.0001
γ -GTP, IU/ml	62 (6-1,118)	70 (3-850)	0.39
Platelet counts, $\times 1,000/\text{mm}^3$	169 (27-433)	165 (35-560)	0.091
ICG R ₁₅ , %	14 (1-90)	16 (1-95)	0.003
AFP, ng/ml	4 (1-90)	5 (1-1,180)	0.42
HCV serological group			
Group 1, genotypes 1a/1b	1,021 (66.1%)	259 (81.4%)	<0.0001
Group 2, genotypes 2a/2b	488 (31.6%)	48 (15.1%)	
Undetermined	36 (2.3%)	11 (3.5%)	
HCV RNA concentration			
High ^a	937 (58.4%)	191 (71.3%)	<0.0001
Low ^b	668 (41.6%)	77 (28.7%)	
Histological stage of hepatitis			
F1, slight fibrosis	1,029 (62.2%)	298 (58.2%)	0.10
F2/F3, moderate/severe fibrosis	625 (37.8%)	214 (41.6%)	

AST = Aspartate aminotransferase; AFP = α -fetoprotein; ICG R₁₅ = retention of indocyanine green at 15 min.

^a HCV RNA concentration $\geq 10^6$ copies/ml by the competitive PCR or $\geq 10^6$ equivalents/ml by the HCV probe assay.

^b HCV RNA concentrations less than high concentrations.

daily for 4-8 weeks; 128 (7.7%) were administered with intermittent IFN 3 times per week for 24 weeks; 72 (4.4%) had a prolonged course of IFN for 8-36 months; 8 (0.5%) received IFN- β 6 MU daily for 6-18 months, and the remaining 6 (0.4%) were given IFN- α combined with IFN- β for 4 months. The median dose of 624 MU was administered during the median period of 24 weeks. IFN for 24 weeks or longer was given to 83.2% of the patients. IFN therapy was usually initiated within a few months after the diagnosis of chronic hepatitis, and all patients were started on it within 12 months. The median interval between liver biopsy and initiation of IFN was 9 days.

Almost all the patients given IFN showed varied degrees of fever, chills, myalgia, headache and general malaise after the first injection. Most patients developed leukocytopenia and thrombocytopenia in various degrees. A significant thrombocytopenia $\leq 40,000/\text{mm}^3$ required a reduction of the IFN dose in 39 patients. IFN therapy was discontinued due to psychosis in 35 patients and ophthalmological symptoms in 12 patients. None of the patients developed decompensated liver disease with ascites, encephalopathy, jaundice or variceal bleeding. Although only 88 (5.3%) patients could not continue injection with IFN, studies for carcinogenesis were analyzed on the intention-to-treat basis.

The efficacy of IFN was judged by the clearance of HCV RNA from serum and ALT levels 12 months after the completion of treatment. Sustained virological response (SVR) was defined as persistent disappearance of HCV RNA after therapy, biochemical response (BR) as normal ALT levels without elimination of HCV RNA for at least 6 months after therapy, and no response (NR) as persistently elevated or transiently normalized ALT levels without loss of HCV RNA lasting for less than 6 months.

Follow-Up of Patients and Diagnosis of HCC

Patients were followed up monthly after diagnosis of chronic hepatitis in our outpatient clinic and monitored for hematological, biochemical and virological parameters. With their admission, during and after the treatment with IFN, weekly or biweekly follow-up was performed in almost all patients who received IFN. Imaging diagnosis was made once or twice per year in the majority of patients with ultrasonography or computed tomography. Angiography was performed only when HCC was highly suspected on imaging by ultrasonography or computed tomography.

When angiography pictured a characteristic hypervascular nodular specific for HCC in patients, histological confirmation was not required in the majority of them. Microscopic examinations of liv-

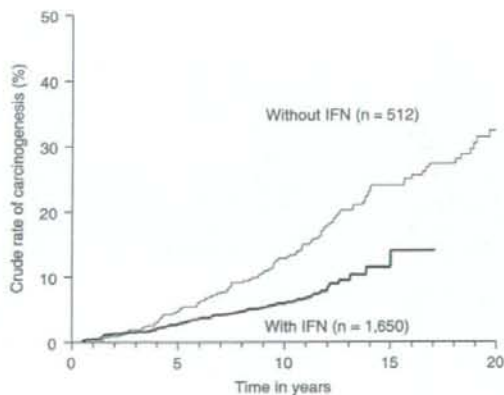


Fig. 1. Crude rates of hepatocarcinogenesis in patients treated with IFN and those untreated. The carcinogenesis rate was significantly lower in treated than in untreated patients (log-rank test, $p < 0.0001$).

er tissues obtained by a fine-needle biopsy were performed in 14 patients whose angiogram could not portray a typical image of HCC. There were 89 patients in whom HCC was confirmed histologically on liver specimens obtained at surgery or autopsy. Detection of serological tumor markers and increase with time were also taken into account in the diagnosis of HCC.

There were 223 (10.3%) patients lost to follow-up, including 164 (9.9%) treated and 59 (11.5%) untreated. Rates of annual dropouts in treated and untreated patients were 0.95 and 0.93%, respectively. In 9 patients, the response to IFN was judged by information on aminotransferase levels determined in other clinics and by persistent HCV RNA, as well as aminotransferase levels at 6 months after the completion of therapy in an additional 3 patients. Therefore, the response to IFN could be judged in all patients including the 12 who were lost to our follow-up early. Since the eventual outcome with respect to the development of HCC was not confirmed in these patients, their data were censored in statistical analyses [21]. Deaths unrelated to liver disease were censored and withdrawn from the analysis. The date of the last follow-up in this study was May 1, 2004, and the median observation period of studied patients was 10.7 years, with a range of 0.1–33.6 years.

Statistical Analysis

Nonparametric Mann-Whitney U test and χ^2 test were used for analysis of background characteristics of patients. The rate of HCC development was calculated by the Kaplan-Meier method [22]; it was based on the duration between diagnosis of chronic hepatitis by liver biopsy and detection of HCC. Differences in slopes of carcinogenesis curves were evaluated by the log-rank test. To gain a robust statistical power for the anticarcinogenic activity of IFN, observation of treated patients was initiated at the commencement of IFN therapy, in lieu of the diagnosis of chronic hepatitis. Independent factors associated with the development of HCC were studied using the stepwise Cox regression analysis [23]. The follow-

ing 18 variables were analyzed for potential covariates in hepatocarcinogenesis at the time when hepatitis was diagnosed: age, sex, total alcohol intake, family history of liver disease, history of blood transfusion, stage of hepatic fibrosis, aspartic aminotransferase, ALT, albumin, bilirubin, globulin, γ -glutamyl transpeptidase (γ -GTP), platelet count, retention of indocyanine green at 15 min, serological grouping of HCV, HCV RNA level and IFN treatment.

Although continuous variables without conversion of data were evaluated in multivariate analyses, several variables were transformed into categorical data consisting of two or three ordinal numbers in calculating hazard ratios. All factors found to be marginally associated with hepatocarcinogenesis with p values < 0.15 were tested by the multivariate Cox proportional hazard model. All analyses of data were performed with the computer program SPSS version 11 [24], and a p value < 0.05 was considered significant.

Results

Response to IFN

Response to IFN was judged 12 months after the completion of therapy by both HCV RNA and serial ALT readings. Among the 1,654 patients with IFN treatment, SVR (elimination of HCV RNA) was achieved by 606 (36.6%), BR (ALT normalized for at least 6 months without clearance of HCV RNA from serum) in 266 (16.1%) and NR (elevated or transiently decreased ALT levels without loss of serum HCV RNA) in 782 (47.3%).

Crude Rates of Hepatocarcinogenesis

During the median observation period of 10.7 years, HCC developed in 199 of the 2,166 (9.2%) patients, including 96 of the 1,654 (5.8%) patients treated with IFN and 103 of the 512 (20.1%) patients without IFN (fig. 1). Among the 199 patients with HCC, 140 (70.4%) imaged a typical hypervascular stain on angiography and dynamic computed tomography, while 59 failed to exhibit tumor stains on angiography. HCC in these 59 patients was confirmed histologically on liver specimens obtained at surgery or by fine-needle biopsy.

Crude rates of hepatocarcinogenesis in patients treated with IFN and those untreated were 1.3 and 1.8% at the end of the 3rd year (after the completion of therapy), 2.6 and 4.6% at the end of the 5th year, 5.8 and 12.7% at the 10th year and 13.9 and 23.9% at the 15th year, respectively (fig. 1). The carcinogenesis rate was significantly lower in patients treated with IFN than in untreated patients (log-rank test, $p < 0.0001$).

Impact of IFN on Hepatocarcinogenesis

During the observation period, HCC developed in 96 of the 1,654 (5.8%) patients treated with IFN, including