intrahepatic cccDNA levels is slower than that of serum HBV DNA levels during NA administration (15, 16). We found that suppression of cccDNA by NAs could prevent the development of recurrent primary HCC. Because cccDNA provides the template for pregenomic and viral messenger RNA-encoded viral proteins (33–35), the transcriptional activity of cccDNA may induce carcinogenesis. Further research is required to validate this hypothesis. Serum HBcrAg can be a surrogate marker of the intrahepatic cccDNA pool because of the viral proteins transcribed through messenger RNA from cccDNA (20, 21). Therefore, we consider that serum HBcrAg reflects the intrahepatic viral status more accurately than serum HBV DNA. Recently, Chan *et al.* (36) showed that serum HBsAg quantification could reflect intrahepatic cccDNA in patients treated with peginterferon and LAM combination therapy. They also indicated that reduction in HBsAg had good correlation with reduction in cccDNA. We tried to measure HBsAg levels at the start of NA therapy and the time of HCC diagnosis using a commercial assay (chemiluminescent immunoassay). However, HBsAg levels declined very slowly during NAs monotherapy in this study (data not shown). Brunetto *et al.* (37) showed that mean reduction for 48 weeks in HBsAg was 0.02log IU/ml in patients treated with LAM monotherapy, different from peginterferon therapy. Meanwhile, the median reduction from the start of NA to the diagnosis of HCC in HBcrAg was 1.4logU/ml in this study (Table 1). It seems that HBcrAg is a superior on-treatment risk predictor (e.g. tumour recurrence) to HBsAg during NAs monotherapy in terms of reduction of titres in each assay. HBcrAg is also more useful in terms of needless to serum sample dilution. As HBcrAg levels can be measured from serum samples, they are clinically useful, compared with the measurement of cccDNA, which requires liver specimens. It is not practical to carry out liver biopsy and the measurement of cccDNA for patients who have normal AST/ALT levels and viral suppression during antiviral therapy. Liver specimens cannot be also taken from patients who undergo ablation therapy for HCC. The measurement of serum HBcrAg levels in these patients is helpful to indirectly estimate the status of intrahepatic cccDNA. In the future, it is necessary to investigate whether HBcrAg in patients receiving NAs can be a predictor of primary carcinogenesis.

Previous studies have indicated that the rates of intrahepatic cccDNA loss and serum HBcrAg loss differ from serum HBV DNA loss under NA therapy, with the former two being much slower (15, 16, 19). In this study, the period of serum HBV DNA loss was longer, with lower intrahepatic cccDNA and serum HBcrAg levels (Fig. 2B). Therefore, these findings suggest that a long period of time is required to prevent the development of recurrent primary HCC by viral suppression under antiviral therapy. In contrast, the serum HBcrAg levels at the time of HCC diagnosis were higher in patients with emergent LAM-resistant mutants and subsequent VBT

than in patients without mutants and VBT (Fig. 6). This result suggests that it is important to administer a potent NA early for drug-resistant strains and suppress viral replication to prevent subsequent carcinogenesis. Although we evaluated the relationship between the development of primary HCC and serum HBcrAg levels by a case–control study, the serum HBcrAg levels at the commencement of NA therapy and 1 year later were not associated with the development of primary HCC (unpublished data). This finding is attributable to the slow decline of the serum HBcrAg levels during antiviral therapy. The measurement of HBcrAg at intervals of 3–6 months may be helpful to predict the development of HCC. However, further studies are needed to confirm the finding.

In summary, HBcrAg is a predictor of the post-treatment recurrence of HCC during antiviral therapy. Measurement of the serum HBcrAg level is simple and useful because it reflects the intrahepatic viral status. Further, intrahepatic cccDNA and serum HBcrAg suppression by NAs is important to prevent HCC recurrence.

Acknowledgements

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CLINICAL STUDIES

HBcrAg is a predictor of post-treatment recurrence of hepatocellular carcinoma during antiviral therapy

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Abstract

Background/Aims: The recurrence rate of hepatitis B virus (HBV)-related hepatocellular carcinoma (HCC) is high even in patients receiving curative therapy. In this study, we analysed the risk factors for tumour recurrence after curative therapy for HBV-related HCC while under treatment with nucleot-(s)ide analogues (NAs) by measuring serum HBcrAg and intrahepatic covalently closed circular DNA (cccDNA) levels to elucidate the viral status associated with HCC recurrence. *Methods:* We enrolled 55 patients who developed HCC during NA therapy and underwent either curative resection or percutaneous ablation for HCC. *Results:* Hepatocellular carcinoma recurred in 21 (38%) of the patients over a period of 2.2 (range, 0.2–7.4) years. In multivariate analysis, serum HBcrAg levels ≥ 4.8log U/ml at the time of HCC diagnosis (hazard ratio, 8.96; 95% confidential interval, 1.94–41.4) and portal vein invasion (3.94, 1.25–12.4) were independent factors for HCC recurrence. The recurrence-free survival rates of the high cccDNA group were significantly lower than those of the low cccDNA group only in patients who underwent resection ($P = 0.0438$). A positive correlation ($P = 0.028$; $r = 0.479$) was observed between the intrahepatic cccDNA and the serum HBcrAg levels at the incidence of HCC. *Conclusion:* HBcrAg is a predictor of the post-treatment recurrence of HCC during antiviral therapy. Serum HBcrAg and intrahepatic cccDNA suppression by NAs may be important to prevent HCC recurrence.

Worldwide, an estimated 400 million people are infected with hepatitis B virus (HBV) persistently, and one million people die of decompensated cirrhosis and/or hepatocellular carcinoma (HCC) annually (1, 2). Recently, oral nucleot(s)ide analogues (NAs) have been used as the mainstay therapeutic strategy against chronic hepatitis B. Five such antiviral agents have been approved, and range in the profundity and rapidity of HBV DNA suppression, barrier to resistance and side-effect profile (3–10). Lamivudine (LAM) was the first NA to be approved for treating chronic hepatitis B, followed by adefovir dipivoxil (ADV) and entecavir (ETV), in Japan. However, a major problem with long-term LAM treatment is the potential development of drug resistance, mainly caused by mutation of the thyrosine–methionine–aspartic acid–aspartic acid (YMDD) motif of reverse transcriptase (11, 12). For preventing breakthrough hepatitis induced by LAM-resistant mutants, additional ADV administration has been recommended (13, 14).

The methods for monitoring the treatment response include measurements of the serum alanine transaminase (ALT) levels, HBV DNA levels, HBeAg and antibody levels, HBsAg and antibody levels and liver histology. Other serum markers have been reported to be useful for monitoring the effect of antiviral therapy (15, 16). Recently, a new assay was developed for detecting the HBcrAg, consisting of HBcAg, HBeAg and a 22 kDa precore protein coded with the precore/core gene (17, 18). Because NAs have no inhibiting action on the transcription and translation activities of viral mRNA, HBcAg- and HBeAg-related proteins continue to be produced for a certain period of time in spite of the achievement of adequate suppression of the viral DNA synthesis. Therefore, HBcrAg is a viral marker independent of HBV DNA for monitoring the antiviral effect of NAs (19). In addition, recent reports have indicated another interesting aspect of serum HBcrAg levels: these levels were found to be correlated with intrahepatic covalently closed circular DNA (cccDNA) levels and could be a surrogate marker of the intrahepatic cccDNA pool (20, 21). This phenomenon may be explained by the fact that the production of HBcrAg depends on the

the treatment for HCC and stored in $-80\,°C$. Liver tissue from patients who underwent resection was collected, rapidly frozen and stored in $-80\,°C$. Written informed consent was obtained from each patient. The study protocol conformed to the ethical guidelines of the 1975 Declaration of Helsinki, as reflected in *a priori* approval by the institution's human research committee.

Antiviral therapy

Forty-seven patients received 100 mg LAM daily, and drug-resistant YMDD mutants developed in 26 (55%) of these patients, accompanied by an increase in HBV DNA $\geq 1\log$ copies/ml. Seventeen of the 26 patients received 10 mg ADV in addition to LAM (100 mg) daily. The remaining nine continued to receive LAM monotherapy because of the lack of approval for ADV administration in Japan at the time, but received ADV with LAM after approval was obtained during the HCC post-treatment period. Eight NA-naïve patients received 0.5 mg ETV daily. These antiviral therapies were continued after the resection or percutaneous ablation.

Follow-up and HCC recurrence

The patients were followed for liver function and virological markers of HBV infection monthly, as well as blood counts and tumour makers including α-fetoprotein and des-γ-carboxylprothrombin. They also underwent ultrasonography or helical dynamic computed tomography every 3 months. Cirrhosis was diagnosed by laparoscopy or liver biopsy or by the clinical data, imaging modalities and portal hypertension. The median observation period after HCC treatment for the entire cohort was 2.7 years (range, 0.3–8.4 years). HCC recurrence was diagnosed by the typical hypervascular characteristics on angiography and/or histological examination with fine needle biopsy specimens, in addition to certain features on computed tomography and ultrasonography.

Markers of HBV infection

HBeAg was determined by enzyme-linked immunosorbent assay using a commercial kit (HBeAg EIA; Institute of Immunology, Tokyo, Japan). HBV DNA was quantitated using the Amplicor monitor assay (Roche Diagnostics, Tokyo, Japan) with a dynamic range over 2.6–7.6log copies/ml or COBAS TaqMan HBV v.2.0 (Roche Diagnostics) with a dynamic range over 2.1–9.0log copies/ml. Serum HBV DNA levels were measured using the Amplicor assay at both the start of NA therapy and the diagnosis of HCC and using the TaqMan assay at the diagnosis of HCC. For statistical analysis, the value of that HBV DNA was tentatively set at 2.1 if HBV DNA levels were under 2.1log copies/ml. HBV genotypes were determined serologically by the combination of epitopes expressed on the pre-S2 region product, which is specific for each of the seven major genotypes (A–G), using a commercial kit (HBV Genotype EIA; Institute of

Immunology). YMDD mutants were determined by polymerase chain reaction-based enzyme-linked mini-sequence assay using a commercial kit (Genome Science Laboratories, Tokyo, Japan).

HBcrAg measurement

Serum HBcrAg levels were measured using a CLEIA HBcrAg assay kit (Fujirebio Inc., Tokyo, Japan) with a fully automated analyser system (Lumipulse System; Fujirebio Inc.) as described previously (21). In brief, 150 µl of serum was incubated with 150 µl of pretreatment solution containing 15% sodium dodecyl sulphate at $60\,°C$ for 30 min. After heat treatment, 120 µl of pretreated specimen was added to a ferrite microparticle suspension in an assay cartridge. Ferrite particles were coated with monoclonal antibody mixture (HB44, HB61 and HB114) against denatured HBcAg, HBeAg and the 22 kDa precore protein. After 10 min of incubation at $37\,°C$ and washing, further incubation was carried out for 10 min at $37\,°C$ with alkaline phosphatase conjugated with two kinds of monoclonal antibodies (HB91 and HB110) against denatured HBcAg, HBeAg and the 22 kDa precore protein. After washing, 200 µl of substrate solution [3-(2'-spiroada-mantan)-4-methoxy-4-(3'-phosphoryloxy)phenyl-1,2-dioxetane disodium salt] (Applied Biosystems, Bedford, MA, USA) was added to the test cartridge, which was then incubated for 5 min at $37\,°C$. The relative chemiluminescence intensity was measured, and the HBcrAg concentration was calculated by a standard curve generated using a recombinant pro-HBeAg (amino acids -10 to 183 of the precore/core gene product). The HBcrAg concentration was expressed in U/ml, which is defined as the immunoreactivity of 10 fg/ml of recombinant pro-HBeAg. In this study, the HBcrAg values were expressed as log U/ml, and the cut-off value was set at 3.0 log U/ml. For the statistical analyses, HBcrAg-negative cases were calculated as 3.0log U/ml.

Intrahepatic cccDNA measurement

Intrahepatic cccDNA levels were analysed as described previously (21). In brief, liver specimens surrounding the tumour tissue were obtained and stored at $-80\,°C$ before DNA extraction. HBV DNA was extracted using a QIAamp DNA Mini Kit (Qiagen KK, Tokyo, Japan). The concentration of purified DNA was based on the absorbance at 260 nm. For this study, two oligonucleotide primers cccF2 (5'-cgtctgtgccttctcatctga-3', nucleotides 1424–1444) and cccR4 (5'-gcacagcttggaggcttgaa-3', nucleotides 1755–1737) and probe cccP2 (5'-VIC-accaatttat gcctacag-MGB-3', nucleotides 1672–1655) were designed using PRIMER EXPRESS software (Applied Biosystems, Foster City, CA, USA) to flank the direct repeat region between the hepatitis B core and the polymerase gene. The use of cccF2 and cccR4, oligonucleotide primers spanning the direct repeat region of the HBV genome, allows the polymerase chain reaction of native viral DNA in the

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was detected in the NA-naïve patients receiving ETV monotherapy.

Correlation between serum HBcrAg and serum HBV DNA levels at the incidence of HCC

The median serum HBcrAg value was 6.6log U/ml (range, 3.3 to > 6.8) at the start of NA therapy and 5.0log U/ml (range, < 3.0 to > 6.8) at the time of HCC diagnosis. We observed a positive correlation ($P < 0.001$; $r = 0.610$) between the levels of HBcrAg and HBV DNA in serum at the time of HCC diagnosis (Fig. 2A).

HBcrAg was detectable in 23 (82%) of 28 patients with undetectable HBV DNA levels using TaqMan assay and was > 4.8log U/ml in eight (29%) of 28 patients. In contrast, serum HBV DNA was detectable in spite of undetected HBcrAg in only two patients. Then, we examined the correlation between the serum HBcrAg levels at the time of HCC diagnosis and the antiviral effect. The median duration of on-treatment undetected serum HBV DNA was 1.1 years (range, 0.1–4.8) before the first diagnosis of HCC. As shown in Figure 2B, we observed a significant negative correlation between the levels of HBcrAg in serum at the time of HCC diagnosis and the duration of undetected HBV DNA in

serum just before the first diagnosis of HCC ($P < 0.001$; $r = -0.568$).

Factors associated with HCC recurrence

Hepatocellular carcinoma recurred in 21 (38%) of the 55 patients, 17 (46%) of 37 patients who had undergone resection and four (22%) of 18 patients who had undergone ablation. Because a proportion of patients who had undergone resection with TNM Stage II or over (24 of 37 patients) was greater than ablation (six of 18), there were more patients who had HCC recurrence after resection than ablation. Eight factors were associated with the recurrence in univariate analysis: HBeAg positivity at the start of NA therapy, HBV DNA ≥ 2.1log copies/ml, HBcrAg level ≥ 4.8log U/ml, AST level ≥ 50 IU/L, ALT level ≥ 40 IU/L, tumour multiplicity, portal vein invasion at the time of HCC diagnosis and HCC treatment. In the multivariate analysis, HBcrAg level ≥ 4.8log U/ml and portal vein invasion were independent risk factors for the recurrence of HCC (Table 2). The cumulative recurrence-free survival rates in patients with ≥ 4.8log U/ml HBcrAg levels at the time of HCC diagnosis were 70% at 1 year, 35% at 3 years and 28% at 5 years. In contrast, the rates in patients with < 4.8log U/ml HBcrAg levels were 96% at 1 year, 89% at 3 years and 89% at 5 years. The recurrence-free survival rates of the high HBcrAg group (≥ 4.8log U/ml) were significantly lower than those of the low HBcrAg group (< 4.8log U/ml; $P < 0.001$), as shown in Figure 3A. Then, the cumulative recurrence-free survival rates in patients with ≥ 2.1log copies/ml HBV DNA levels at the time of HCC diagnosis were 70% at 1 year, 44% at 3 years and 39% at 5 years. In contrast, the rates in patients with < 2.1log copies/ml HBV DNA levels were 93% at 1 year, 76% at 3 years and 76% at 5 years. The recurrence-free survival rates of the positive HBV DNA group (≥ 2.1log copies/ml) were significantly lower than those of the negative HBV DNA group (< 2.1log copies/ml; $P = 0.007$), as shown in Figure 3B. The cumulative recurrence-free survival rates were 33% at 1 year and 33% at 2 years with portal vein invasion, and 87% at 1 year, 73% at 2 years and 64% at 3 years without invasion. Three of the six patients with portal vein invasion died of recurrent HCC.

Correlation between intrahepatic cccDNA and serum HBV DNA levels at the incidence of HCC

We measured intrahepatic cccDNA using liver specimens from 22 of 37 patients who underwent resection. The median intrahepatic cccDNA value was 4.2log copies/μg (range, 3.0–5.0). As shown in Figure 4A and B, we observed significant positive correlations between the levels of intrahepatic cccDNA and HBV DNA in serum ($P = 0.019$; $r = 0.486$) and between the levels of intrahepatic cccDNA and HBcrAg in serum at the time of HCC diagnosis ($P = 0.028$; $r = 0.479$). Twenty-eight patients who underwent resection had early- or intermediate-stage

(A)

$y = 0.530x + 3.139$
$r = 0.665$
$P < 0.001$

(B)
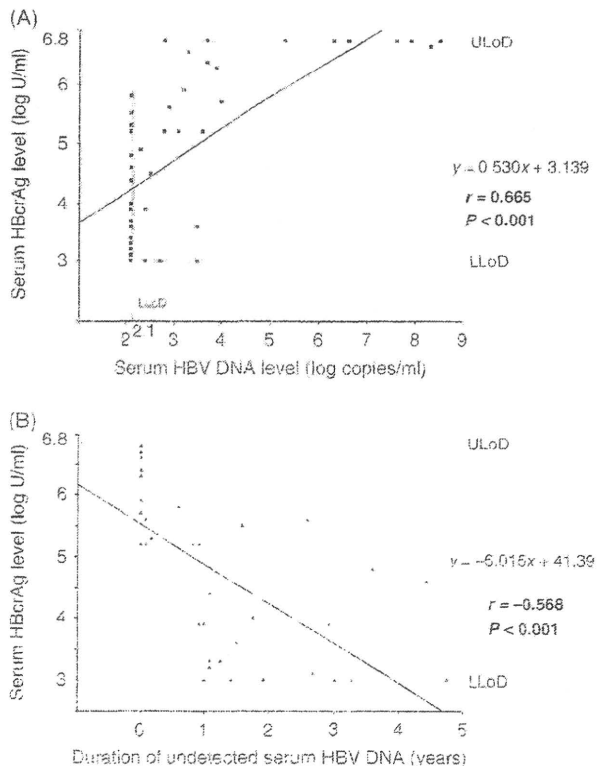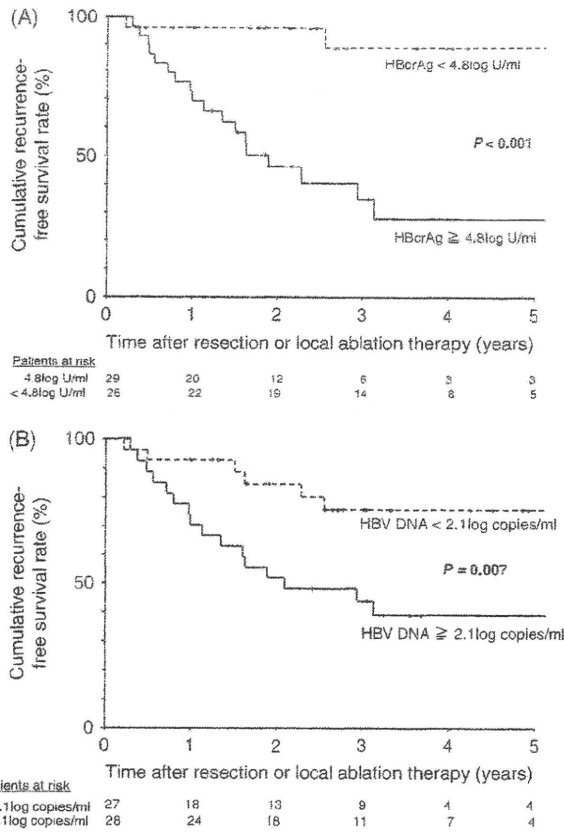
$y = -6.015x + 41.39$
$r = -0.568$
$P < 0.001$

Fig. 2. (A) Correlation between serum HBcrAg and hepatitis B virus DNA (HBV DNA) levels at the time of hepatocellular carcinoma (HCC) diagnosis for each patient. (B) Correlation between serum HBcrAg levels at the time of HCC diagnosis and the duration of undetected serum HBV DNA (< 2.6log copies/ml).

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Fig. 3. (A) Kaplan–Meier life table for the cumulative recurrence-free survival rates by the serum HBcrAg levels and comparison by the log-rank test. (B) Kaplan–Meier life table for the cumulative recurrence-free survival rates by the serum hepatitis B virus DNA (HBV DNA) levels at the time of hepatocellular carcinoma (HCC) diagnosis for each patient and comparison by the log-rank test.

Fig. 4. (A) Correlation between intrahepatic covalently closed circular DNA (cccDNA) and serum hepatitis B virus DNA (HBV DNA) levels at the time of hepatocellular carcinoma (HCC) diagnosis for each patient who underwent resection ($n = 22$). (B) Correlation between intrahepatic cccDNA and serum HBcrAg levels at the time of HCC diagnosis. (C) Kaplan–Meier life table for the cumulative recurrence-free survival rates by the intrahepatic cccDNA levels in patients with early- or intermediate-stage HCC ($n = 17$).

developed HCC after the commencement of NA therapy and underwent radical therapy for HCC. The recurrence rates of HCC were high in patients with high levels of intrahepatic cccDNA and serum HBcrAg. In particular, HBcrAg levels were measurable by using serum samples and clinically useful.

Nucleot(s)ide analogues, including LAM, ADV and ETV, are widely used for the treatment of chronic hepatitis B, and reportedly reduce the development of HCC in such patients (22, 23). Although few events of HCC development occur during NA therapy (24–26), analysis of a large number of patients is needed to examine the risk factors for HCC. We could clarify the risk factors associated with the development of primary HCC after radical therapy by enrolling patients who underwent radical therapy for HCC in spite of their small number. High HBV loads in serum have been reported to be associated with HCC recurrence after resection or radical therapy in NA-naïve patients (27–31), but no study has demonstrated the viral risk factors of recurrence in patients receiving NAs. The novel finding of this study is that serum HBcrAg and
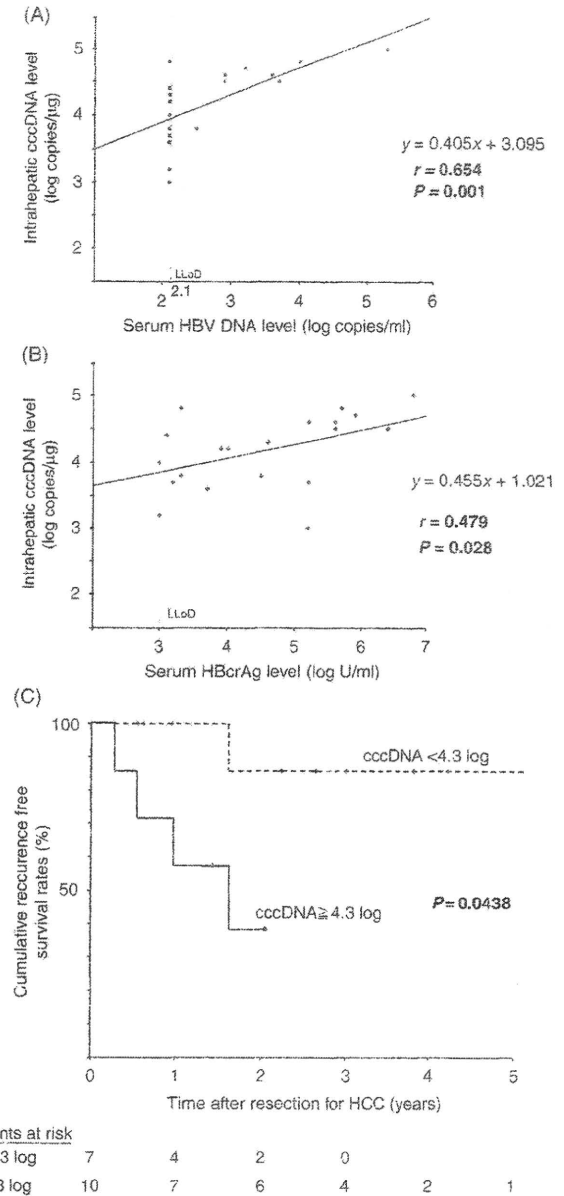
intrahepatic cccDNA levels are predictors of HCC recurrence in patients radically treated for HCC during NA therapy.

In this study, the serum HBV DNA levels at the time of HCC diagnosis were associated with recurrence by univariate analysis. However, the serum HBcrAg level was the only viral factor associated with recurrence in multivariate analysis. There are two possible reasons for the

intrahepatic cccDNA levels is slower than that of serum HBV DNA levels during NA administration (15, 16). We found that suppression of cccDNA by NAs could prevent the development of recurrent primary HCC. Because cccDNA provides the template for pregenomic and viral messenger RNA-encoded viral proteins (33–35), the transcriptional activity of cccDNA may induce carcinogenesis. Further research is required to validate this hypothesis. Serum HBcrAg can be a surrogate marker of the intrahepatic cccDNA pool because of the viral proteins transcribed through messenger RNA from cccDNA (20, 21). Therefore, we consider that serum HBcrAg reflects the intrahepatic viral status more accurately than serum HBV DNA. Recently, Chan *et al.* (36) showed that serum HBsAg quantification could reflect intrahepatic cccDNA in patients treated with peginterferon and LAM combination therapy. They also indicated that reduction in HBsAg had good correlation with reduction in cccDNA. We tried to measure HBsAg levels at the start of NA therapy and the time of HCC diagnosis using a commercial assay (chemiluminescent immunoassay). However, HBsAg levels declined very slowly during NAs monotherapy in this study (data not shown). Brunetto *et al.* (37) showed that mean reduction for 48 weeks in HBsAg was 0.02logIU/ml in patients treated with LAM monotherapy, different from peginterferon therapy. Meanwhile, the median reduction from the start of NA to the diagnosis of HCC in HBcrAg was 1.4logU/ml in this study (Table 1). It seems that HBcrAg is a superior on-treatment risk predictor (e.g. tumour recurrence) to HBsAg during NAs monotherapy in terms of reduction of titres in each assay. HBcrAg is also more useful in terms of needless to serum sample dilution. As HBcrAg levels can be measured from serum samples, they are clinically useful, compared with the measurement of cccDNA, which requires liver specimens. It is not practical to carry out liver biopsy and the measurement of cccDNA for patients who have normal AST/ALT levels and viral suppression during antiviral therapy. Liver specimens cannot be also taken from patients who undergo ablation therapy for HCC. The measurement of serum HBcrAg levels in these patients is helpful to indirectly estimate the status of intrahepatic cccDNA. In the future, it is necessary to investigate whether HBcrAg in patients receiving NAs can be a predictor of primary carcinogenesis.

Previous studies have indicated that the rates of intrahepatic cccDNA loss and serum HBcrAg loss differ from serum HBV DNA loss under NA therapy, with the former two being much slower (15, 16, 19). In this study, the period of serum HBV DNA loss was longer, with lower intrahepatic cccDNA and serum HBcrAg levels (Fig. 2B). Therefore, these findings suggest that a long period of time is required to prevent the development of recurrent primary HCC by viral suppression under antiviral therapy. In contrast, the serum HBcrAg levels at the time of HCC diagnosis were higher in patients with emergent LAM-resistant mutants and subsequent VBT

than in patients without mutants and VBT (Fig. 6). This result suggests that it is important to administer a potent NA early for drug-resistant strains and suppress viral replication to prevent subsequent carcinogenesis. Although we evaluated the relationship between the development of primary HCC and serum HBcrAg levels by a case–control study, the serum HBcrAg levels at the commencement of NA therapy and 1 year later were not associated with the development of primary HCC (unpublished data). This finding is attributable to the slow decline of the serum HBcrAg levels during antiviral therapy. The measurement of HBcrAg at intervals of 3–6 months may be helpful to predict the development of HCC. However, further studies are needed to confirm the finding.

In summary, HBcrAg is a predictor of the post-treatment recurrence of HCC during antiviral therapy. Measurement of the serum HBcrAg level is simple and useful because it reflects the intrahepatic viral status. Further, intrahepatic cccDNA and serum HBcrAg suppression by NAs is important to prevent HCC recurrence.

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Clinical and Virological Effects of Long-Term (Over 5 Years) Lamivudine Therapy

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Ideally, long-term lamivudine therapy should not induce tyrosine–methionine–aspartate–aspartate (YMDD) mutants (reverse transcription [rt]; rt M204I/V) in patients with chronic hepatitis B. There is little or no information on the clinical features of patients who do not develop such mutants. We analyzed 368 patients who received lamivudine therapy for more than 6 months between 1995 and 2003. Among them, 98 patients were negative for YMDD mutants during 5-year lamivudine therapy. Multivariate analysis identified hepatitis B e antigen (HBeAg) negativity, lack of cirrhosis, and high gamma glutamyltranspeptidase (GGTP) level as independent factors associated with lack of emergence of YMDD mutants during 5-year treatment. In these 98 patients, 21 patients developed YMDD mutants in the 5-year posttreatment follow-up. Old age was identified as the only factor associated with the emergence of YMDD mutants during that period. For all patients, 53 showed no elevation of alanine aminotransferase (ALT) or viral load after emergence of YMDD mutants during 5 years. Short latency to emergence of YMDD mutants, mixed (tyrosine–isoleucine–aspartate–aspartate (YIDD) [rtM204I]+tyrosine–valine–aspartate–aspartate (YVDD) [rtM204V]) type, and low ALT level were identified as independent factors associated with elevation ALT or viral load. HBeAg negativity, lack of cirrhosis, and high GGTP level were associated with lack of emergence of YMDD mutants during 5-year period. Young age protected against emergence of YMDD mutants over the 5-year period. Moreover, after the emergence of YMDD mutants, short latency to the emergence of YMDD mutant, mixed type mutants, and low baseline ALT level were associated with elevation of ALT or viral load. *J. Med. Virol. 82:684–691, 2010.*
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KEY WORDS: YMDD mutant; HBV; lamivudine; GGTP; ALT; long-term

INTRODUCTION

Approximately 400 million people worldwide have chronic hepatitis B (CHB) infection, and 25–40% of these will develop hepatocellular carcinoma (HCC) and/or cirrhosis [Lee, 1997]. Prevention of disease progression is the primary target of treatment. To date, the nucleoside analogs, lamivudine, adefovir, dipivoxil, and entecavir, have been approved for the treatment of CHB [Zoulim and Perrillo, 2008]. Lamivudine markedly reduces viral load and hepatic necroinflammatory activity [Lai et al., 1998; Dienstag et al., 1999], and improves liver fibrosis [Dienstag et al., 2003a], and function. Unfortunately, failure of antiviral therapy is associated with the appearance of new viral variants, allowing hepatitis B virus (HBV) to become resistant. Lamivudine has the highest rate of drug resistance emergence. The number of patients with tyrosine–methionine–aspartate–aspartate (YMDD) mutation is higher with prolonged use of lamivudine. The cumulative rate of YMDD mutant reaches 60–70% after 4–5 years of treatment [Nafa et al., 2003; Suzuki et al., 2003]. On the other hand, 20–30% of patients continue long-term lamivudine therapy without YMDD mutations. There is little information at this stage about the

clinical differences between patients with and without YMDD mutants on long-term lamivudine therapy.

After the emergence of YMDD mutant, breakthrough hepatitis occurs at a high frequency. This is important because breakthrough hepatitis can occasionally cause liver decompensation [Liaw et al., 2000]. However, alanine aminotransferase (ALT) and viral load are not elevated at least in some patients with YMDD mutant. The difference between these groups remains poorly defined. The aims of the present investigation were the following: (1) characterize the clinical and virological features of patients who do not show emergence of YMDD mutants during 5 years of lamivudine therapy. (2) Identify the factor(s) associated with the emergence of YMDD mutants in patients on >5 years of lamivudine therapy. (3) Determine the factors associated with elevation of ALT (>50 IU/L) and viral load (>5.0 log copies/ml) after the emergence of YMDD mutant.

PATIENTS AND METHODS

Patients

The study subjects were 368 patients (66 females and 302 males, median age 43 years [range 19–76]) who commenced treatment with lamivudine at the Department of Hepatology, Toranomon Hospital, Tokyo, between September 1995 and June 2003 and adhered to treatment for more than 6 months (Table I). All patients were followed from commencement of therapy at our hospital. Some of these patients have been reported previously [Chayama et al., 1998; Suzuki et al., 2003]. All patients were negative for hepatitis C serologic markers, but all had detectable hepatitis B virus surface antigen (HBsAg) for at least 6 months prior to commencement of lamivudine therapy. Lamivudine was administered orally at 100 mg/day. Chronic hepatitis or cirrhosis was confirmed by needle biopsy, peritoneoscopy, or clinically before treatment. The

clinical criteria for chronic hepatitis included elevated ALT levels over 6 months and absence of clinical evidence of portal hypertension, such as esophageal varices, ascites, hepatic encephalopathy, and imaging features suggestive of cirrhosis on ultrasonography. Chronic hepatitis and cirrhosis were diagnosed in 309 and 57, respectively. Informed consent was obtained from each patient enrolled in the study; and the study protocol conformed to the ethical guidelines of Declaration of Helsinki and was approved by the human research committee of our institution.

Blood Tests, Serum Viral Markers, and Assessment of Response to Therapy

Routine biochemical tests were performed before and during therapy at least once every 2 months, using standard procedures. Serial blood samples were taken before and during therapy and stored at −80°C until used for HBV molecular analysis. Viral load was measured by polymerase chain reaction (PCR)-based method (Amplicor HBV monitor; Roche Diagnostics, Tokyo, Japan). Mutation of the HBV deoxyribonucleic acid (DNA) polymerase gene (rtM204I/V) was determined using PCR and restriction fragment length polymorphism, as described previously [Chayama et al., 1998] or PCR-ELMA method [Kobayashi et al., 2000]. The presence of YMDD mutation was determined at baseline and at yearly intervals. Resistance to lamivudine was determined annually before the development of mutations, and, if a mutation appeared, the time of appearance of resistance was confirmed by monthly measurement.

Statistical Analysis

Differences between groups were examined for statistical significance using the χ^2 test for categorical variables and Mann–Whitney U-test for continuous variables. The association of mutations with specific

TABLE I. Characteristics of Patients at Commencement of Lamivudine Therapy

Demography	
Total patients	368
Sex: female/male	302/66
Age (years)	43 (19–76)
Family history of HBV	245 (66.6%)
Cirrhosis	57 (15.5%)
Median duration of treatment, years (range)	5 (0.5–12.8)
Laboratory data	
Aspartate aminotransferase (IU/L)	80 (19–2,593)
Alanine aminotransferase (IU/L)	120.5 (12–2,274)
Bilirubin (mg/dl)	0.7 (0.2–16.5)
Gamma glutamyltranspeptidase (IU/L)	64 (13–475)
Albumin (g/dl)	3.9 (2.1–4.8)
Viral load (log copies/ml)	7.1 (<2.7 to >7.6)
HBeAg positive	187 (50.8%)
HBV genotypes: A/B/C/D/F/unknown	12/25/317/1/2/11

HBV, hepatitis B virus; HBeAg, hepatitis B envelope antigen.
The family history of six patients was not clear. Viral load was measured by PCR. All viral load values below the lower limit of detection (<2.7 log copies) were set to 2 while those over the upper limit of detection (>7.6) ware set to 8 for calculation purposes.
Data are median and range values except for the last two parameters.

predictive variables was assessed by Cox proportional hazard model. To determine the factors that affect YMDD mutation, multiple logistic regression analysis was carried out. Spearman correlation coefficient (two-tailed) was used to evaluate the correlation between gamma-glutamyltranspeptidase (GGTP) and other factors. Two-tailed P-value <0.05 was considered statistically significant. All data were analyzed using the statistical package SPSS (version 11.0, SPSS, Inc., Chicago, IL).

RESULTS

Clinical and Virological Features of Patients Free of YMDD Mutations

Lamivudine therapy was provided for a median duration of 5 years [range 0.5–12.8 years]. Forty patients discontinued lamivudine therapy due to pregnancy, expectation of a change to another therapy, or loss to follow-up. Among the remaining 328 patients, YMDD mutants were identified in 230 patients during the 5-year treatment. Table II summarizes the characteristics of patients without and with YMDD mutant during the 5-year treatment. There were more patients with genotype B, and fewer patients with genotype A in the former than in the latter group (P < 0.001). Furthermore, a high proportion of hepatitis B e antigen (HBeAg)-negative patients were noted in the former group than in the latter group (P = 0.001). In the latter group, the emergence of YMDD mutant was associated with elevated ALT and/or viral load in 177 patients while it was not in 53 patients. On the other hand, 98 patients showed no emergence of YMDD mutants during the 5-year treatment (Fig. 1).

Figure 2 shows the cumulative rate of patients who showed emergence of YMDD mutations duringlamivudine therapy [129, 74, and 48 patients developed tyrosine–isoleucine–aspartate–aspartate (YIDD), tyrosine–valine–aspartate–aspartate (YVDD), and mixed (YIDD + YVDD) mutants, respectively]. YMDD mutants were registered in 11 (92%) of 12 patients with genotype A, 13 (52%) of 25 patients with genotype B,

219 (69%) of 317 patients with genotype C, 0 (100%) of 1 patients with genotype D, 2 (100%) of 2 patients with genotype F, and 6 (55%) of 11 patients with unidentified genotype.

We then explored the factors associated without emergence of YMDD mutants. Patients free of YMDD mutants were considered to have ideal response to lamivudine therapy. The following significant independent factors for the lack of YMDD mutations during the 5-year treatment were identified in univariate analysis: HBV genotype B, lack of cirrhosis, HBeAg negativity, free family history of liver disease, high aspartate aminotransferase (AST) level (>75 IU/L), high ALT level (>180 IU/L), high GGTP level (>110 IU/L), high albumin level (3.7 g/dl), and low viral load (<5.9 log copies/ml). Multivariate analysis identified HBeAg negativity, high GGTP level (>110 IU/L), and lack of liver cirrhosis (LC) as significant determinants for the lack of YMDD mutations during the 5-year treatment (Table III).

GGTP is regarded as a marker of fatty liver and alcoholic liver disease [Patton et al., 2008]. Fatty liver disease correlates with liver fibrosis and carcinogenesis [Yuan et al., 2004; Yu et al., 2008]. However, the influence of treatment with nucleos(t)ide analog is not clear. Next, we investigated the correlation between GGTP and other factors (Table IV). GGTP correlated significantly with ALT (r = 0.562, n = 355, P < 0.001), AST (r = 0.562, n = 355, P < 0.001), α-fetoprotein (AFP) (r = 0.430, n = 319, P < 0.001), total bilirubin (r = 0.264, n = 354, P < 0.001), and platelet count (r = −0.129, n = 330, P = 0.019). GGTP did not correlate with liver fibrosis (r = −0.28, n = 276, P = 0.641), total cholesterol (r = −0.77, n = 132, P = 0.379), or blood glucose (r = 0.118, n = 115, P = 0.355) was. Based on the above results, GGTP correlated with ALT, AST, and other liver function-related parameters and does not seem to be related to other metabolic factors.

Among 163 patients who were positive for HBeAg at the commencement of lamivudine therapy, 35 (21%) did not show emergence of YMDD mutants during the 5-year treatment. Of these, 31 (89%) achieved HBeAg

TABLE II. Comparison of Patients With and Without YMDD Mutants During 5-Year Lamivudine Therapy

Category	Without YMDD mutation (n = 98)	With YMDD mutation (n = 230)	P-value
Age (years)[a]	43 (24–76)	44 (23–71)	0.783
Sex: male/female	77/21	194/36	0.206
Genotype: A/B/C/others	1/12/81/4	11/9/203/7	<0.001
Histology: chronic hepatitis/cirrhosis	88/10	185/43	0.052
Bilirubin (mg/dl)[a]	0.7 (0.2–12.2)	0.7 (0.2–16.5)	0.898
Alanine aminotransferase (IU/L)[a]	136 (16–2,077)	118.5 (14–2,274)	0.237
Gamma glutamyltranspeptidase (IU/L)[a]	72 (13–442)	58 (16–402)	0.197
Viral load (log copies/ml)[a]	7.1 (<2.7 to >7.6)	7.2 (<2.7 to >7.6)	0.136
HBeAg: positive/negative	35/63	128/102	0.001
Latency to emergence of YMDD mutation		2 (0–4.9)	

YMDD, tyrosine–methionine–aspartate–aspartate; HBV, hepatitis B virus; HBeAg, hepatitis B e antigen.
Viral load was measured by PCR. All viral load values below the lower limit of detection (<2.7 log copies) were set to 2 and those over the upper limit of detection (>7.6) ware set to 8 for calculation purposes.
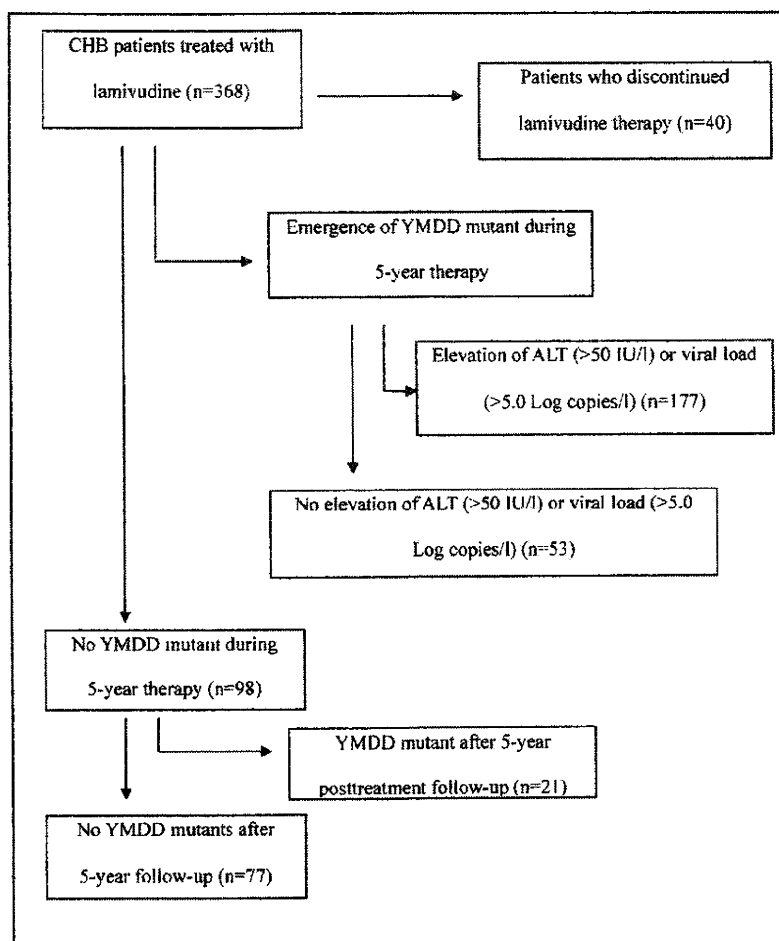[a]Data are median (range) values.

Fig. 1. Outcome of patients with lamivudine therapy. CHB, chronic hepatitis B; YMDD, tyrosine–methionine–aspartate–aspartate; ALT, alanine aminotransferase.

loss during 5-year treatment. On the other hand, in 128 patients who showed emergence of YMDD mutants, 42 (33%) achieved HBeAg loss. Analysis of various parameters showed that only the platelet count was different between the two HBeAg-positive groups; that

is, in HBeAg-positive patients, those with high platelet counts were less likely to develop YMDD mutations ($P = 0.051$).

Emergence of YMDD Mutant After 5 Years of Lamivudine Therapy

As described above, 98 patients showed no emergence of YMDD mutants during the 5-year treatment. We investigated in this group the emergence of YMDD mutants after the 5-year treatment period. Twenty-one (21%) patients showed emergence of YMDD mutants following the completion of the 5-year treatment period (Table V). Univariate analysis showed only age (>50 years) influenced the emergence of the YMDD mutants after the 5-year treatment ($P = 0.012$). At time 5 years, 94 (96%) patients were negative for HBeAg. Therefore, the status of HBeAg at 5 years did not influence the emergence of YMDD mutant. After the emergence of YMDD mutant, 4 of the 21 patients had elevated ALT and viral load; they were further treated
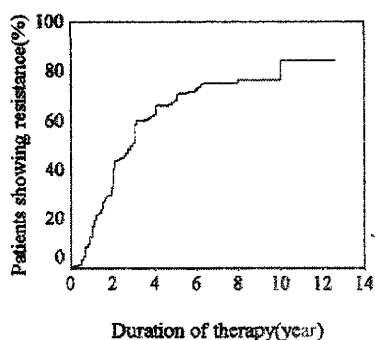

Fig. 2. Cumulative rate of patients who showed emergence of YMDD mutants during lamivudine therapy (Kaplan–Meier method). YMDD, tyrosine–methionine–aspartate–aspartate.

TABLE III. Results of Multivariate Analysis of Factors Associated With Lack of Appearance
of YMDD Mutants During 5-Year Lamivudine Therapy

Factors	Risk ratio (95% confidence interval)	P-value
Pretreatment HBeAg		
0: Positive	1	
1: Negative	2.492 (1.440–4.311)	0.001
Pretreatment GGTP (IU/L)		
0: <110	1	
1: ≥110	2.226 (1.296–4.900)	0.004
Pretreatment histology		
0: LC	1	
1: Not cirrhosis	2.254 (1.037–4.900)	0.04

YMDD, tyrosine–methionine–aspartate–aspartate; HBeAg, hepatitis B envelope antigen; GGTP, gamma
glutamyltranspeptidase; LC, liver cirrhosis.

with a combination of adefovir and lamivudine. The remaining 17 patients showed no elevation of ALT or viral load, 3 of the 17 patients were treated with a combination of adefovir and lamivudine, treatment was switched in 6 of the 17 patients from lamivudine to entecavir, while 8 of the 17 patients continued lamivudine treatment. No emergence of YMDD mutant after the 5-year treatment period was noted in 77 patients, but 4 of 77 patients discontinued lamivudine therapy due to pregnancy, or loss to follow-up. Furthermore, treatment in 14 of the 77 patients was changed from lamivudine to entecavir while the remaining 59 patients continued lamivudine therapy.

Characteristics of Patients With Elevated ALT or Viral Load After Emergence of YMDD Mutant

As mentioned above, 230 (62.5%) of the 368 patients developed YMDD mutations during the 5-year treatment period, and 177 had elevated ALT or viral load level after the emergence of YMDD mutants, while 53 patients had neither ALT elevation (>50 IU/L) nor HBV DNA elevation (>5.0 log copies/ml) during the treatment period. We then explored the risk factors for the elevation of viral load and ALT level in these patients. In univariate analysis, the following seven factors correlated significantly with elevation of viral load or ALT level: HBeAg (P < 0.001), latency to emergence of YMDD mutant (P < 0.001), mixed type YMDD mutant (YIDD + YVDD) (P < 0.001), ALT level (P = 0.003), viral load (P = 0.007), and AFP level (P = 0.021). These

TABLE IV. Correlation Between GGTP and Laboratory Tests

Factors	r	n	P-value
ALT	0.562	355	<0.001
AST	0.562	355	<0.001
AFP	0.43	319	<0.001
Total bilirubin	0.264	354	<0.001
Platelet count	-0.219	330	0.019
Liver fibrosis	-0.28	276	0.641
Total cholesterol	-0.77	132	0.379
Blood glucose	0.118	115	0.355

ALT, alanine aminotransferase; AST, aspartate aminotransferase; AFP, α-fetoprotein.

variables were entered into multivariate analysis. In the last step of the analysis, the following three variables were identified as significant determinants of elevation of viral load or ALT level: latency to emergence of YMDD mutant (P < 0.001), mixed type YMDD mutant (P < 0.001), and ALT level (P = 0.016) (Table VI).

Characteristics of Patients With YMDD Mutant During and After 5-Year Treatment

Throughout the present study, YMDD mutant developed in 251 patients. As described above, 230 of these 251 patients developed YMDD mutant during the 5-year period. The remaining 21 patients developed YMDD mutant after the 5-year period. Table VII summarizes the characteristics of patients with YMDD mutant during and after the 5-year treatment. HBV genotype and HBeAg negativity were found to correlate with the development of YMDD mutants after 5-year treatment.

DISCUSSION

The aim of the present study was to identify the factors associated with the lack of emergence of YMDD mutant during long-term lamivudine therapy. Our analysis showed that negativity for HBeAg, high GGTP level (≥110 IU/L), and lack of LC protected against the appearance of YMDD mutants during the 5-year lamivudine therapy. Since positivity for HBeAg is a well-known factor associated with emergence of YMDD mutant [Yuen et al., 2001; Suzuki et al., 2003], we focused on the correlation between GGTP and other factors (Table IV). The results showed that GGTP correlated with ALT, AST, and other liver function-related parameters. Previous studies identified high pretreatment ALT level as an independent factor associated with no appearance of YMDD mutant [Tsubota et al., 2004; Chang et al., 2005]. In this regard, GGTP is regarded as a marker of fatty liver and alcoholic liver disease [Patton et al., 2008]. Fatty liver disease correlates with liver fibrosis and carcinogenesis [Yuan et al., 2004; Yu et al., 2008]. However, the influence of treatment with nucleos(t)ide analog is not clear. Based on the above results, GGTP does not seem to be related to other metabolic factors (e.g., total cholesterol and blood glucose). However, further investigation of other

TABLE V. Comparison of Clinicopathological Features of Patients With and Without Emergence of YMDD Mutants After 5-Year Posttreatment Follow-Up

Category	Without YMDD mutation (n = 77)	With YMDD mutation (n = 21)	P-value
Age (years)[a]	42 (24–76)	50 (33–69)	0.032
Sex: male/female	63/14	14/7	0.134
Genotype: A/B/C/others	1/8/65/3	0/4/16/1	0.275
Histology: no cirrhosis/cirrhosis[b]	69/8	19/2	0.636
Bilirubin (mg/dl)[a]	0.7 (0.2–12.2)	0.7 (0.4–4.4)	0.644
ALT (IU/L)[a]	135 (16–1,975)	142 (25–2,077)	0.997
GGTP (IU/L)[a]	69 (13–442)	82 (24–264)	0.878
Viral load (log copies/ml)[a]	7 (<2.7 to >7.6)	7.4 (<2.7 to >7.6)	0.394
HBeAg: positive/negative	28/49	7/14	0.797
Status of HBeAg at 5 years: positive/negative	3/74	1/20	0.860
Latency to emergence of YMDD mutation		5.6 (5–10)	

YMDD, tyrosine–methionine–aspartate–aspartate; ALT, alanine aminotransferase; GGTP, gamma glutamyltranspeptidase; HBV, hepatitis B virus; CHB, chronic hepatitis B; HBeAg, hepatitis B envelope antigen.
[a]Data are median (range) values.
[b]Chronic hepatitis and cirrhosis were confirmed by needle biopsy, peritoneoscopy, or clinically before treatment. Diagnosis of chronic hepatitis was based on elevated ALT levels over 6 months and absence of clinical evidence of portal hypertension, such as esophageal varices, ascites, hepatic encephalopathy, and imaging features suggestive of cirrhosis on ultrasonography. Viral load was measured by PCR. All viral loads below the lower limit of detection (<2.7 log copies) were set to 2 and those over upper limit of detection (>7.6) were set to 8 for calculation purposes.

metabolic factors is needed, such as body mass index, HOMA-IR, and alcohol intake. The third factor, lack of liver fibrosis and cirrhosis based on histopathological examination, was associated with lack of YMDD mutants. Previous study reported that the presence of cirrhosis correlated with emergence of YMDD mutant [Ooga et al., 2004]. Moreover, among patients with LC, those who develop YMDD mutants are more likely to have high Child-Pugh scores than those without such mutants [Liaw et al., 2004]. On the other hand, viral load has been reported to promote the emergence of YMDD mutants [Yuen et al., 2001]. In the present study, although viral load was identified as a factor in univariate analysis, it was not identified as such in multivariate analysis.

We performed additional investigation on elevation of ALT or viral load after the emergence of YMDD mutants. In this analysis, 77% of these patients (n = 177) had elevated ALT or viral load, while 23% (n = 53) had not. We found several common characteristics among patients of the high ALT/viral load group. The latency to emergence of YMDD mutants and mixed type mutants (YIDD + YVDD) were significant factors

in this group. Early emergence of YMDD mutant could reflect a rapid increase of HBV DNA. The mixed type was reported as a risk factor of HBV DNA breakthrough and breakthrough hepatitis [Akuta et al., 2003; Suzuki et al., 2006]. Previous studies reported that a low pretreatment ALT was an independent factor associated with appearance of YMDD mutants [Tsubota et al., 2004; Chang et al., 2005]. Based on the above findings, patients with low baseline ALT level and during treatment emergence of YMDD mutants seem to be at high risk of breakthrough hepatitis.

Younger patients had less opportunity to develop YMDD mutations after the 5-year treatment. We reported previously that age was not associated with emergence of YMDD mutant [Kawaoka et al., 2007]. However, the duration of treatment in our previous study was <5 years. Patients free of YMDD mutants during the 5-year treatment might have adequate immune response to suppress the development of YMDD mutants. The immune response is lower in elderly patients [Adler and Nagel, 1994; Marcus and Tur-Kaspa, 1997]. Considered together, younger patients seem to be more immune against the emergence

TABLE VI. Factors Associated With Elevation of ALT or Viral Load After Emergence of YMDD Mutant

Factors	Hazard ratio (95% confidence interval)	P-value
Latency to emergence of YMDD mutant		
0: ≥1 year	1	
1: <1 year	7.429 (4.769–11.572)	<0.001
YMDD mutant type		
0: YIDD or YVDD	1	
1: Mixed (YIDD + YVDD) type	2.939 (1.834–4.677)	<0.001
Pretreatment ALT level (IU/L)		
0: >160	1	
1: ≤159	1.583 (1.089–2.301)	0.016

YMDD, tyrosine–methionine–aspartate–aspartate; ALT, alanine aminotransferase; HBV, hepatitis B virus; YIDD, tyrosine–isoleucine–aspartate–aspartate; YVDD, tyrosine–valine–aspartate–aspartate.

TABLE VII. Comparison of Clinicopathological Features of Patients With YMDD Mutants During and After 5-Year Treatment Period

Category	With YMDD mutation during 5-year (n = 230)	With YMDD mutation after 5-year (n = 21)	P-value
Age (years)[a]	44 (23–71)	50 (33–69)	0.109
Sex: male/female	194/36	14/7	0.063
Genotype: A/B/C/others	11/9/203/7	0/4/16/1	0.0184
Histology: no cirrhosis/cirrhosis[b]	185/43	19/2	0.384
Bilirubin (mg/dl)[a]	0.7 (0.2–16.5)	0.7 (0.4–4.4)	0.570
ALT (IU/L)[a]	118.5 (14–2,274)	142 (25–2,077)	0.527
GGTP (IU/L)[a]	58 (16–402)	82 (24–264)	0.382
Viral load (log copies/ml)[a]	7.2 (<2.7 to >7.6)	7.4 (<2.7 to >7.6)	0.936
HBeAg: positive/negative	128/102	7/14	0.0496

YMDD, tyrosine–methionine–aspartate–aspartate; ALT, alanine aminotransferase; GGTP, gamma glutamyltranspeptidase; HBV, hepatitis B virus; CHB, chronic hepatitis B; HBeAg, hepatitis B envelope antigen.
[a]Data are median (range) values.
[b]Chronic hepatitis and cirrhosis were confirmed by needle biopsy, peritoneoscopy, or clinically before treatment. Diagnosis of chronic hepatitis was based on elevated ALT levels over 6 months and absence of clinical evidence of portal hypertension, such as esophageal varices, ascites, hepatic encephalopathy, and imaging features suggestive of cirrhosis on ultrasonography. Viral load was measured by PCR. All viral loads below the lower limit of detection (<2.7 log copies) were set to 2 and those over upper limit of detection (>7.6) were set to 8 for calculation purposes.

of YMDD mutant in long-term lamivudine treatment than elderly patients.

Several new nucleos(t)ide analogs, for example, adefovir and entecavir, are available at present [Gish et al., 2007; Marcellin et al., 2008]. These new drugs have greater inhibitory effects on HBV replication and their use is associated with a lower incidence of drug resistance. However, resistant to the new drugs has already been reported [Suzuki et al., 2007; Baldick et al., 2008]. Lamivudine was the first nucleoside analog and has been used over a long time worldwide. Based on the result of our study, younger patients (<50 years) who continued lamivudine monotherapy without emergence of YMDD mutant during 5-year period showed less opportunity to develop mutants after a 5-year follow-up and were able to continue lamivudine monotherapy. After the cessation of lamivudine therapy, flare up of ALT accompanied with elevation of HBV DNA was observed at a high frequency [Song et al., 2000; Dienstag et al., 2003a; Akuta et al., 2005]. Moreover, we reported previously HBsAg clearance from the serum in some patients who received long-term lamivudine therapy [Kobayashi et al., 2007]. Taken together, it seems that before any treatment, one can predict a less likelihood of development of YMDD mutants during long-term lamivudine therapy in young patients with genotype C who are HBeAg negative, have no cirrhosis, and no elevated GGTP level. Tables II and VII suggest that patients with genotype B are also less likely to develop YMDD mutant, but their numbers are too small to make a firm conclusion. Further studies of larger number of patients with genotype B, A, and others are needed to clarify this issue.

In conclusion, factors associated with lack of appearance of YMDD mutants during 5-year lamivudine therapy in patients with HBV infection are HBeAg negativity, lack of cirrhosis, and high GGTP level. Patients who do not show the emergence of YMDD mutants during 5-year lamivudine therapy, younger age protected against the emergence of such mutants during the following 5 years of follow-up. On the other hand, in those who show emergence of YMDD mutant, elevation of ALT or viral load correlate with a short latency to emergence of YMDD mutants, presence of mixed (YIDD + YVDD) type, and low baseline ALT level.

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＜短　　報＞

核酸アナログ未使用のB型慢性肝炎症例へのエンテカビル治療中に
rtA181T変異ウイルスが増殖した1症例

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緒言：核酸アナログ未使用のB型慢性肝炎患者への
エンテカビル治療中に，既報のエンテカビル耐性ウイ
ルスが出現していないにもかかわらず，viral rebound
を生じた症例を経験したため，報告する．

症例：51歳女性．1978年にB型慢性肝炎と診断され，
2008年6月よりエンテカビル（0.5 mg／日）治療を開始
した．治療開始時 HBV-DNA 7.2 log copies／m*l*，HBeAg
陽性，genotype C であった．2009年2月 HBV-DNA
2.5 log copies／m*l* まで下がるも，その後2009年4月 HBV-
DNA 6.0 log copies／m*l*，8月 8.2 log copies／m*l* と viral
rebound が出現し，トランスアミナーゼの上昇も認めた
（Fig. 1）．

**治療開始時および治療中の HBV-DNA polymerase
RT 領域のアミノ酸配列の比較検討**：患者血清から抽出
された HBV-DNA は PCR 法にて増幅したのち，direct
sequence 法にて塩基配列を決定した．クローニング解
析もあわせて行った．ダイレクトシークエンスでは核
酸アナログ未使用であるにもかかわらず，エンテカビ
ル開始時に rtA181T 変異のわずかな混在を認め，クロー
ニング解析では 8.5%（3／35クローン）に rtA181T
変異を確認した．また治療開始後15カ月ではダイレク
トシークエンスにて rtA181T 変異の混在の割合が増加
しており，クローニング解析にて rtA181T 変異は 39.5%
（17／43クローン）に増加していた．尚，エンテカビル
開始時および治療中に rtA181 以外の既報のエンテカビ

ル耐性に関与するアミノ酸（rtL180，T184，S202，
M204，M250）に変異は認められなかった（Fig. 1）．

考察：今回我々は，エンテカビル投与にて rtA181T
変異が増殖した症例を経験した．本症例はエンテカビ
ル投与中に viral rebound を生じ，その際既報のエンテ
カビル耐性ウイルスは出現せず，治療開始時よりわず
かに認められていた rtA181T 変異ウイルスが増殖して
いた．クローニング解析にて rtA181T 変異ウイルスは
治療開始時 8.5% から治療開始15カ月後に 39.5% に増
加し，他に有意なアミノ酸変異を認めないことから，
rtA181T 変異がエンテカビル耐性に関与している可能
性が考えられた．しかし本症例で出現した rtA181T
変異ウイルスのエンテカビル耐性への関与を証明する
ためには，今後本症例の血清を使用した in vitro の実験
にて評価する必要があると考える．また本症例では vi-
ral rebound と同時にトランスアミナーゼ上昇も認めた
が，軽度上昇にとどまっているため，現在もエンテカ
ビル治療を継続し厳重にフォローしている．

　本症例は，核酸アナログ未使用のB型慢性肝炎症例
であったにもかかわらず，エンテカビル治療開始前よ
り rtA181T 変異が存在していた．核酸アナログ未使用
症例にラミブジン耐性に関与する rtL180M，rtM204V
変異が存在するという報告はあるが，本症例のように
rtA181T 変異が核酸アナログ使用前に存在したという
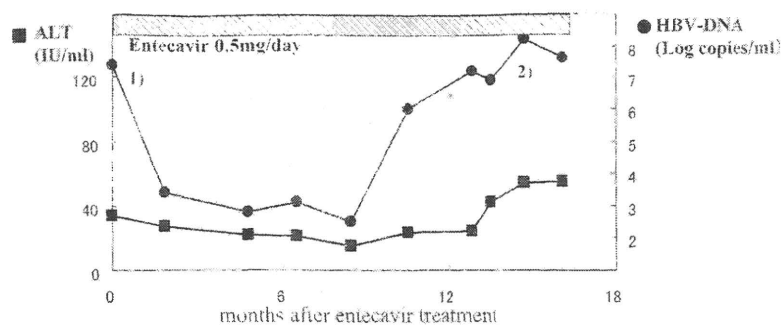報告は過去になく，初めての報告である．

　rtA181T 変異は以前よりアデホビル耐性に関与する
アミノ酸変異として知られていたが，最近ではラミブ
ジンとアデホビルの交差耐性のある変異であることが
わかっている．このため rtA181T 変異に対してエンテ
カビルの効果が期待されている．しかし海外からは
ラミブジン耐性ウイルスに対するアデホビル単独治療

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Fig. 1　Clinical course and clonal analysis of samples from patient with viral rebound during entecavir therapy

中に耐性ウイルス (rtA181T/V または N236T 変異ウイルス) が出現した症例は，ラミブジン耐性ウイルスのみの症例に比べ，エンテカビル治療におけるウイルス抑制効果が低いという報告があり[2]，また本症例のようにエンテカビル治療にて rtA181T 変異ウイルスが増加する症例も存在することから，今後 rtA181T 変異ウイルスに対する治療として，エンテカビル以外の核酸アナログ (テノフォビル，その他新規薬剤等) の有効性も検討していく必要があると考えられる．

索引用語：エンテカビル，耐性ウイルス，
　　　　　rtA181T

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英文要旨

Increase of rtA181T mutant strains during entecavir therapy for a patient with chronic hepatitis B virus infection

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A 51-year-old Japanese woman with chronic hepatitis B who had never treated with nucleotide analogues was admitted to our hospital and treated with entecavir. In this patient, entecavir successfully reduced the HBV level, but viral and biochemical breakthrough was observed at 10 months after the beginning of therapy. The HBV viral load reached up to 8.2 log copies/ml, but direct sequence analysis showed no LAM and ETV resistant-related mutation (rtT184, S202, M204, M250). Comparison by clonal analysis of samples obtained before and after the viral breakthrough showed the increase of the rtA181T mutant strains (8.5% versus 39.5%). It was considered that the rtA181T mutant

strain in this case might be related to entecavir resistance.

Key words: entecavir, drug-resistant mutant, rtA181T

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HEPATOLOGY

Long-term follow-up of patients with hepatitis B e antigen negative chronic hepatitis B

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Abstract

Background and Aim: After hepatitis B virus (HBV) e antigen (HBeAg) seroconversion, HBV-DNA continues to replicate, and HBeAg-negative patients still face the risk of liver disease progression. We investigated the predictive factors for alanine aminotransferase (ALT) elevation, antiviral drug use, and hepatocellular carcinoma (HCC) occurrence in HBeAg-negative patients.

Methods: Age, sex, ALT, platelet counts, HBV-DNA levels, genotype, antidiabetic drug use, body mass index, smoking, and alcohol consumption were analyzed for a total of 244 HBV carriers who were HBeAg-negative.

Results: Of 244 HBeAg-negative patients, 158 (64.8%) showed normal ALT levels at baseline. Multivariate Cox hazard regression analysis identified high HBV-DNA levels and high ALT at baseline as independent risk factors for ALT elevation in the patients with normal ALT at baseline. The threshold ALT and HBV-DNA levels were determined to be 31 IU/L and 5.3 logcopies/mL, respectively. Seventeen (7.0%) patients used antiviral drugs. Multivariate Cox hazard regression analysis identified high HBV-DNA levels (threshold, 5.7 log copies/mL), the use of antidiabetic drugs, and daily alcohol consumption at baseline as an independent risk factor for the use of antiviral drugs in HBeAg-negative patients. In 10 patients (4.1%), HCC was detected, and a low platelet count (threshold, $10.0 \times 10^4/mm^3$) was associated with the occurrence of HCC.

Conclusion: This study identified predictors of future active liver disease in HBeAg-negative patients, i.e. ALT elevation, unavoidable use of antiviral drugs, and occurrence of HCC.

Introduction

Chronic hepatitis caused by hepatitis B virus (HBV) often follows a fluctuating course characterized by periods of active hepatitis interspersed with quiescence. Therefore, close follow-up is necessary to understand the natural history of HBV patients. On the other hand, patients in which HBV is truly inactive have persistently quiescent disease with an excellent prognosis. Determining an accurate prognosis for HBV carriers based on clinical presentation is important for clinical management of the disease. Various studies have been performed to distinguish the positive and negative prognostic factors among HBV carriers.[1-3]

Hepatitis e antigen (HBeAg) seroconversion is an important event in the natural history of HBV infection. HBV-infected patients usually have a very good prognosis after HBeAg seroconversion.[4] Therefore, HBeAg seroconversion has become an important treatment goal during follow-up of HBV carriers.[5] However, it has also been shown that HBV-DNA replication and hepatic inflammation in seroconverted patients continue despite the

persistent loss of HBeAg; thus, HBeAg-negative patients are likely to develop liver cirrhosis or hepatocelluar carcinoma.[6] In this study, we focused on the natural history of patients with HBeAg-negative chronic hepatitis B, particularly with respect to alanine aminotransferase (ALT) elevation, antiviral drugs, and hepatocellular carcinoma (HCC).

Recently, prognostic factors for HBeAg-negative patients have been investigated in Taiwan and Canada.[7,8] We expect to identify a unique constellation of prognostic factors for HBeAg-negative chronic hepatitis B in the Japanese population, due to differences in race and HBV genotype.

Methods

Patients

Between January 1985 and April 2007, all patients visiting the Chiba University Hospital with HBV infection were approached for participation in the study. This study was carried out only at

one institute, Chiba University Hospital and was approved by ethical the committee of Chiba University. Written informed consent was obtained from all of the patients in accordance with the Declaration of Helsinki. New patients since 1985 and those who were already being followed-up in 1985 were eligible for inclusion in the study. A total of 881 patients were enrolled; of which, 862 were HBsAg positive at enrollment, and 319 were hepatitis B e antibody (HBeAb) positive. Patients who were positive for hepatitis C virus antibody or hepatitis D virus antibody or who had other potential cause of chronic liver diseases (autoimmune hepatitis, primary biliary cirrhosis) were excluded. Patients followed for less than 12 months were also excluded from the analysis. In total, 244 patients were included in the analysis. Serum samples from patients were stored at −20°C and the oldest sample for each patient was used for defining the level of HBV-DNA. The date of evaluation of HBV DNA level by PCR was defined as the baseline. Patient consent was obtained for storage and analysis of serum samples.

Laboratory methods

Serum ALT level was measured using a routine automated method. HBeAg and HBeAb were measured by standard enzyme-linked immunosorbent assays. Patients were screened for hepatitis C virus, hepatitis delta virus, and human immunodeficiency virus antibodies by a third-generation enzyme-linked immunosorbent assay.

HBV-DNA quantitative assay and genotyping

To investigate the level of HBV-DNA in serum, we chose polymerase chain reaction (PCR) assay with an accurate range of 500–200 000 copies/mL (Amplicor HBV monitor test, Roche Diagnostic Systems, Basel, Switzerland). The six major genotypes of HBV (A–F) were determined by enzyme-linked immunosorbent assay (ELISA) (HBV Genotype EIA, Institute of Immunology, Co., Ltd, Tokyo, Japan).

Statistical analysis

ALT elevation was defined as a change from normal ALT (< 42 IU/L) to elevated ALT (≥ 42 IU/L), and normalization was defined as a change from elevated ALT to normal from one visit to the next. Baseline data are presented as mean ± standard deviation (SD). Differences in clinical parameters between groups were analyzed by unpaired *t*-test, Welch *t*-test, and χ^2 tests. The Cox proportional hazards model was used to identify predictive factors for future ALT elevation/normalization, use of antviral drugs, and HCC occurrence using SPSS version 16.1 software (SPSS Inc., Chicago, IL, USA).

Results

Patient characteristics

To investigate the natural course of HBV carriers with HBeAb, 244 carriers (HBeAg-negative and HBeAb-positive) were enrolled in the study. Follow-up was terminated when the use of

antiviral drugs was started or the occurrence of HCC. The baseline clinical and virological characteristics of the 244 HBeAg-negative carriers are shown in Table 1. Because liver biopsy was performed only in 44 (18.0%) out of 244 patients, liver biopsy results could not be analyzed further. Age, sex, ALT, platelet count (PLT), HBV-DNA level, genotype, antidiabetic drug use, body mass index, smoking, and alcohol consumption were analyzed. The average (± SD) period of follow-up was 103.6 ± 74.8 months. Seventeen (7.0%) patients used antiviral drugs (lamivudine in eight and entecavir in nine) and HCC was detected in 10 (4.1%) patients. Two (0.82%) patients died of HCC. In addition, one died of intrahepatic cholangiocarcinoma, one of liver failure due to gastrointestinal bleeding, and one of tongue cancer during the follow-up period. In Japan, the majority of HBV cases are genotype C and B and these genotypes do not cause HBV carrier by way of horizontal infection in adults; therefore, the HBV infection in our HBV carriers mainly occurred by vertical infection or infection during childhood.[9] Thus, the period of HBV infection roughly coincided with the age of HBV carriers in Japan.

ALT and HBV-DNA levels

One hundred and fifty-eight of 244 (64.8%) HBeAg-negative patients had normal ALT levels at baseline. Of these 158 subjects, 85 (53.8%) continued to have normal ALT levels during follow-up, whereas 73 (46.2%) showed fluctuation of ALT levels with intermittently elevated ALT (Fig. 1). A total of 34 (21.5%) patients had ALT ≥ 84 IU/L (more than double the normal limit). Of the 86 patients who had elevated ALT levels at baseline, ALT elevation persisted in 10 (11.6%) and 76 (88.4%) showed ALT fluctuations with intermittently elevated ALT. Although HBV-DNA levels were associated with higher ALT levels in general, correlation was weak ($r^2 = 0.13$).

Platelet count

Patients were sub classified based on PLT as follows: (I) < 100 000 (II) 100 000–149 000 (III) 150 000–199 000 (IV) 200 000–249 000 (V) > 250 000 and more (/mm³). The numbers of patients in groups I, II, III, IV, and V were 17, 28, 73, 68, and 58, respectively. A total of 84 (34.4%) patients reached a lower platelet count at the end of follow-up.

Risk factors for future ALT elevation in patients with normal ALT levels

Although 158 (64.8%) out of 244 HBeAb-positive patients had normal ALT levels at baseline, 73 patients showed fluctuation of ALT levels with intermittently elevated ALT. We investigated the risk factors for future ALT elevation in these patients. The predictive factors of ALT elevation (ALT > 42 IU/L) in patients with normal ALT levels were HBV-DNA and ALT levels at baseline (Table 2). We carried out an additional univariate analysis changing the threshold of HBV DNA from 3.5 to 7.0 log copies/mL in 0.1 log increments and that of ALT from 15 to 41 IU/L in 1.0 increments. We determined the threshold when the value of probability was smallest; the thresholds for ALT and HBV-DNA levels were 31 IU/L and 5.3 logcopies/mL, respectively. The time