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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/ml，HBeAg陽性，genotype Cであった．2009年2月HBV-DNA 2.5 log copies/mlまで下がるも，その後2009年4月HBV-DNA 6.0 log copies/ml，8月8.2 log copies/ml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viral 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[1)]．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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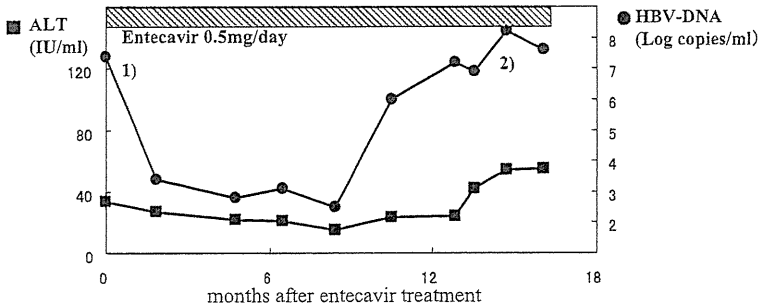

	rt181 rt184	rt202 rt204	rt250	No. of clones (Relative rate (%) of clones)
Amino acid(AB033550)	MGVGLSPFLLAQFTSAI	AFSYMDDL	NFMG	
1) At the beginning of ETV				
a) wild	----------	--------	----	32 (91.5%)
b) mutant	----------T------	--------	----	3 (8.5%)
2) 15 months after ETV				
a) wild	----------	--------	----	26 (60.5%)
b) mutant	----------T------	--------	----	17 (39.5%)

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

文献：1）Yatsuji H, Suzuki F, Sezaki H, et al. J Hepatol 2008; 48: 923—931　2）Shim JH, Suh DJ, Kim KM, et al. Hepatology 2009; 50: 1064—1071

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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Occult hepatitis B virus infection increases hepatocellular carcinogenesis by eight times in patients with non-B, non-C liver cirrhosis: a cohort study

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SUMMARY. An impact of serum hepatitis B virus (HBV) DNA on hepatocarcinogenesis has not been investigated in a cohort of patients with non-B, non-C cirrhosis. Eighty-two consecutive Japanese patients with cirrhosis, who showed negative hepatitis B surface antigen and negative anti-hepatitis C virus, were observed for a median of 5.8 years. Hepatitis B virus core (HBc) region and HBx region were assayed with nested polymerase chain reaction. Both of HBc and HBx DNA were positive in 9 patients (11.0%) and both were negative in 73. Carcinogenesis rates in the whole patients were 13.5% at the end of the 5th year and 24.6% at the 10th year. The carcinogenesis rates in the patients with positive DNA group and negative DNA group were 27.0% and 11.8% at the end of the 5th year, and 100% and 17.6% at the 10th year, respectively ($P = 0.0078$). Multivariate analysis showed that men ($P = 0.04$), presence of HBc and HBx DNA (hazard ratio: 8.25, $P = 0.003$), less total alcohol intake ($P = 0.010$), older age ($P = 0.010$), and association of diabetes ($P = 0.005$) were independently associated with hepatocellular carcinogenesis. Existence of serum HBV DNA predicted a high hepatocellular carcinogenesis rate in a cohort of patients with non-B, non-C cirrhosis.

Keywords: hepatitis B virus, hepatocellular carcinogenesis, liver cirrhosis, occult hepatitis B virus infection, proportional hazard model.

INTRODUCTION

Hepatocellular carcinoma (HCC) is a leading cause of death in many parts of sub-Saharan Africa and Asia [1,2]. It is also one of the most common neoplasms in Japan [3]. Hepatitis B virus (HBV) infection is the primary cause of cirrhosis and HCC and one of the major causes of death globally [4]. Needless to say, a cohort of patients with HBV-related chronic hepatitis and cirrhosis has a significantly high risk for HCC development [5–7]. In our retrospective cohort studies concerning HBV-related disease, cumulative hepatocellular carcinogenesis rates in chronic hepatitis ($n = 610$) and cirrhosis ($n = 180$) were 2.1% and 7.2% at the end of the 5th year, and 4.9% and 27.2% at the 10th year, respectively [5,7]. Abundant epidemiological and molecular biological evidence shows that HBV is an important factor in the development of HCC [8–10], but the precise role of HBV in the oncogenesis is still unknown.

HBV infection is usually diagnosed when the circulating hepatitis B surface antigen (HBsAg) is detected. However, the availability of highly sensitive molecular biology techniques has allowed the identification of HBV infection in HBsAg-negative individuals with or without circulating antibodies to HBsAg and/or hepatitis B core antigen (anti-HBc) [11–16]. Much evidence suggests that this so-called occult HBV infection is highly prevalent in a number of patient subgroups including those with HCV infection [16,17], cryptogenic advanced liver fibrosis [18] and HCC [17,19–27]. Although Marusawa *et al.* [28] and Uetake *et al.* [29] described the relationship between anti-HBc and HCC appearance rate in each study, impact of occult HBV infection on carcinogenesis cannot be evaluated because of lack of HBV DNA assay. As all the previous studies were performed as a pilot study or a case-controlled one, actual risk ratio of occult HBV infection for hepatocellular carcinogenesis has not been reported in a cohort study until now.

Abbreviations: AFP, alpha-fetoprotein; ALT, alanine transaminase; AST, aspartic transaminase; HBsAg, hepatitis B surface antigen; HBV, hepatitis B virus; HCC, hepatocellular carcinoma; HCV, hepatitis C virus; PCR, polymerase chain reaction.

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We, therefore, analysed a retrospective cohort of consecutive patients with cirrhosis for a long period, in order to elucidate the influence of occult HBV infection on the carcinogenesis rate from non-B, non-C cirrhosis.

PATIENTS AND METHODS

Patients

Among 103 consecutive patients diagnosed as having non-B, non-C cirrhosis by peritoneoscopic liver biopsy at Toranomon Hospital, Tokyo, Japan in the period from 1976 to 1998, initial frozen sera at the time of the diagnosis of cirrhosis were available for the assay of HBV DNA in 82 patients (79.6%). The cohort of 82 patients was retrospectively observed for a long period. All the patients showed negative HBsAg, negative anti-hepatitis C virus (HCV) and negative HCV RNA. Patients with a possible association of HCC at the time of the diagnosis of cirrhosis were strictly excluded from this study. No patient received interferon or other antiviral therapy after the diagnosis of cirrhosis.

Background and laboratory data of the patients

There were 67 men and 15 women aged 34–80 with a median age of 58 years. A total of 47 patients (57.3%) had a history of alcohol intake of more than 500 kg until the diagnosis of liver cirrhosis. Fifteen patients (18.3%) had decompensated cirrhosis with ascites, a history of encephalopathy, or both. The median value of indocyanine green retention rate at 15 min (ICG R15) was 33% (range, 7–75%), and total bilirubin concentration was 1.3 mg/dL (range 0.4–20.9 mg/dL).

Measurement of hepatitis virus markers

Hepatitis virus markers were assayed using frozen sera at −80 °C. All sera were tested for HBsAg (radioimmunoassay, Dainabot, Tokyo, Japan), anti-HCV (second-generation anti-HCV, enzyme-linked immunosorbent assay, Dainabot), and HCV RNA with reverse transcription-nested polymerase chain reaction (PCR).

HBV DNA was analysed for the region of HBc and HBx by sensitive nested PCR according to Yotsuyanagi *et al.* [30]. Fifty microlitres of STE solution [100 mmol/L Tris–HCl (pH 8.0), 100 mmol/L NaCl, 2 mmol/L ethylenediaminetetraacetic acid (pH 8.0), and 0.2% sodium dodecyl sulphate] with 20 μg of proteinase K (Boehringer, Mannheim, Germany) were added to serum samples. Mixed samples were then incubated for 2 h at 55 °C. DNA was extracted twice with phenol/chloroform, once with chloroform, and precipitated with ethanol. The DNA pellet was dissolved in 25 μL of TE buffer [10 mmol/L Tris–HCl (pH 8.0) and 1 mmol/L ethylenediaminetetraacetic acid (pH 8.0)].

Prepared DNA was subjected to amplification using nested PCR technique. HBV DNA was amplified using two independent pairs of primers, with each primer complementary to sequences in the X or core region of the HBV genome [30]. Amplification was performed using a thermal cycler for a total of 40 cycles, with each cycle consisting of 94 °C for 1 min, 55 °C for 1 min and 72 °C for 1 min, in 100 μL of reaction mixture containing 200 mmol/L of each dNTP, 1X PCR buffer [50 mmol/L KCl, 10 mmol/L Tris–HCl (pH 8.3), 1.5 mmol/L $MgCl_2$ and 0.001% (w/v) gelatine], and 2 units of Ampli-Taq polymerase (Perkin Elmer Cetus Corp., Norwalk, CT, USA). The PCR products were separated in a 2% agarose gel and transferred to a nylon membrane (Schleicher and Schuell, Dassel, Germany). The membrane was then probed with digoxigenin-labelled oligonucleotides, which hybridize specifically with the core or X gene. Results were considered valid only if the same results were obtained in at least two separate experiments.

We considered the cases with positivity in at least two different viral genomic regions as HBV DNA positive. Appropriate negative controls were included in each PCR. The limit of sensitivity of our nested PCR methods ranged from 10 to 1 genome equivalents/mL.

Follow-up of patients

Follow-up of the patients was made on a monthly or bimonthly basis after diagnosis of cirrhosis by monitoring alpha-fetoprotein (AFP) and other biochemical data. Imaging diagnosis was made at least once a year for each patient with CT or US. After 1988, in order to detect HCC earlier, imagings were done three or more times per year in a majority of patients.

No patient underwent interferon therapy after the diagnosis of cirrhosis, but some of the patients received an oral or intravenous administration of medicinal herbs during the follow-up period.

All patients were finally evaluated in November 2004. The cases lost to follow-up were 13 (15.9%). The median observation period of the total patients was 5.8 years with a range of 0.1–34.8 years.

Statistical analysis

Differences of background features and laboratory data between the patients with and without HBV DNA were analysed by chi-square test, Fisher's exact test and Mann–Whitney's *U*-test. The time between diagnosis of cirrhosis and appearance of HCC was analysed using the Kaplan–Meier technique [31] and differences in curves were tested using log-rank test [32]. Those patients who had been lost to follow-up were regarded as censored data at the time of missing in the statistics. Independent risk factors associated with the appearance rate of HCC were studied using the stepwise Cox regression analysis [33]. Potential risk factors

assessed for hepatocellular carcinogenesis included the following 18 variables: age, sex, association of diabetes mellitus, total alcohol intake, history of cigarette smoking, family history of liver disease, history of blood transfusion, state of cirrhosis (presence of ascites and/or a history of encephalopathy), HBc DNA, HBx DNA, aspartic transaminase (AST), alanine transaminase (ALT), albumin, bilirubin, globulin, AFP, platelet, and ICG R15. A probability less than 0.05 was considered as significant. Data analysis was performed using computer program SPSS version 11 [34].

RESULTS

HCC appearance rate in all the patients

During the observation period, HCC appeared in 16 patients (19.5%). Median interval between the diagnosis of cirrhosis and HCC was 5.6 years (range 0.7–15.6 years) in the patients with HCC development. The cumulative HCC appearance rate in the 82 patients was 13.5% at the end of the fifth year after the diagnosis of cirrhosis, 24.6% at the end of tenth year, 33.3% at the 15th year, and 41.6% at the end of 20th year.

HCC appearance rates according to serum HBV DNA

Among the 82 patients, 9 patients (11.0%) showed positive serum HBV DNA and 73 (89.0%) negative HBV DNA. The former 9 patients had both HBc DNA and HBx DNA, and the latter 73 had neither of them. Table 1 summarizes the profiles and laboratory data of each group. There was no demographic difference between the two groups. There was also no statistically significant difference between them except for ALT value, which was lower in the patient group with positive HBV DNA ($P = 0.028$).

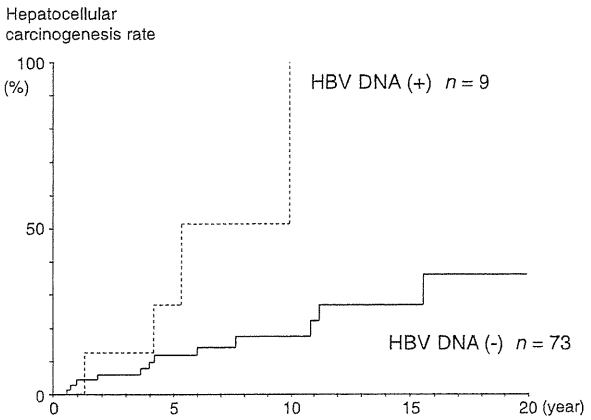

Fig. 1 Hepatocellular carcinogenesis curves of the patients with and without serum hepatitis B virus DNA. Carcinogenesis rates were 12.5% and 6.0% at the end of the third year, 27.0% and 11.8% at the fifth year, and 100% and 17.6% at the tenth year, respectively.

Figure 1 shows the curves of crude HCC appearance rate in the two patients group with and without serum HBV DNA. The third-year HCC appearance rates in the patients with and without DNA were 12.5% and 6.0%, the 5th-yr rates 27.0%, 11.8%, the tenth-yr rates 100% and 17.6%, respectively. The HCC appearance rate of the patient group

Table 1 Demography and laboratory data of patients with and without serum hepatitis B virus DNA

	HBV DNA*		
	Positive (n = 9)	Negative (n = 73)	P
Demographic and background features			
Sex – men/women	8/1	59/14	0.55
Age (median, range)	51 (45–68)	58 (34–80)	0.44
History of transfusion	1 (11.1%)	14 (19.4%)	0.55
Alcohol intake of 500 kg or more	5 (55.6%)	42 (58.3%)	0.87
Diabetes mellitus	3 (33.3%)	15 (20.8%)	0.40
Observation period (years)	5.7 (1.0–21.0)	6.1 (0.1–34.8)	0.92
Laboratory data (median, range)			
ICG R15 (%)	34 (12–51)	32.5 (7–75)	0.78
AST (IU/L)	32 (17–86)	40.5 (14–184)	0.26
ALT (IU/L)	16 (9–43)	28.5 (4–160)	0.028
Albumin (g/dL)	3.8 (2.6–4.5)	3.6 (1.7–5.2)	0.20
Bilirubin (mg/dL)	0.9 (0.5–2.8)	1.3 (0.4–20.9)	0.14
Platelet (×1000/mm^3)	142 (67–232)	104 (27–647)	0.18
AFP (ng/mL)	5 (3–9)	6 (1–98)	0.38

ICG R15, indocyanine green retention rate at 15 min; AST, aspartic transaminase; ALT, alanine transaminase; AFP, alpha-fetoprotein. *HBV DNA was assessed for HBc and HBx DNA using polymerase chain reaction

of positive HBV DNA was slightly higher than that of negative DNA (P = 0.0078, log-rank test).

Significance of serum HBV DNA in hepatocellular carcinogenesis

Cox proportional hazard model was performed for analysis of risk factors for liver carcinogenesis, using the 18 variables as mentioned above.

In the last step of stepwise regression analysis, the following five variables entered the model and could not be removed: sex (P = 0.005), serum HBV DNA (P = 0.003), past history of alcohol intake (P = 0.003), age (P = 0.035), and association of diabetes mellitus (P = 0.022) (Table 2). Accordingly, these five factors were significantly associated with hepatocellular carcinogenesis in the patients with non-B, non-C cirrhosis. Among them, gender was the strongest predictor of future HCC occurrence rate, indicating that male patients had 15.4 times as high carcinogenesis hazard as women patients. Similarly, positive HBV DNA (hazard ratio, 8.25) and little alcohol consumption of less than 500 kg (hazard ratio, 7.19) were the second and third strongest predictors for carcinogenesis, respectively. When the background factors of the cases were adjusted with the other significant factors, positive test for HBV DNA was significantly associated with the hepatocellular carcinogenesis rate.

Curves of carcinogenesis rates were generated from the multivariate analysis in an imaginary positive DNA group and an imaginary negative DNA group, with average sex ratio, average alcohol intake, average age and average association rate of diabetes (Fig. 2). The difference of the carcinogenesis curves indicated 'pure' impact of positive serum HBV DNA upon the carcinogenesis, which was adjusted with significant covariates assuming a standardized study group.

Table 2 Independent factors associated with liver carcinogenesis in the patients with non-B, non-C cirrhosis

Factors	Category	Hazard ratio (95% confidence interval)	P
Sex	Women	1	
	Men	15.4 (2.24–111.1)	0.005
Serum HBV DNA*	Negative	1	
	Positive	8.25 (2.01–33.93)	0.003
Total alcohol intake	≥500 kg	1	
	<500 kg	7.19 (1.98–26.32)	0.003
Age	<60 years	1	
	≥60 years	3.98 (1.10–14.42)	0.035
Diabetes mellitus	No	1	
	Yes	3.89 (1.22–12.47)	0.022

*Positive HBV DNA: positive for both HBc DNA and HBx DNA.

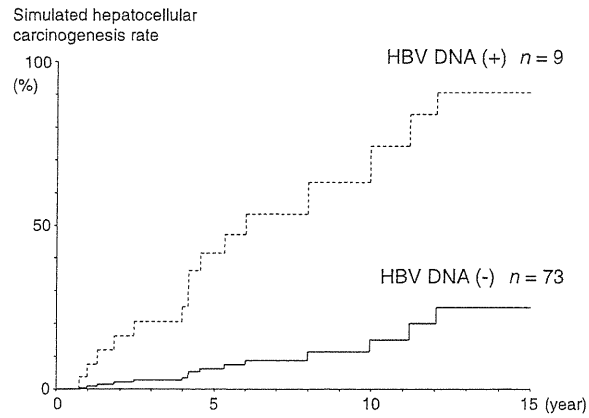

Fig. 2 'Adjusted' hepatocellular carcinogenesis rates in the positive HBV DNA group and the negative DNA group. Cox proportional hazard analysis showed that the carcinogenesis rate in the positive DNA group was significantly higher than that of the negative DNA group, when the other significant covariates were substituted with the same average parameters in the two groups.

Mortality and causes of death

During the observation period, 36 (43.9%) of 82 patients died: 5 (55.6%) of 9 patients in the positive DNA group and 31 (42.5%) of 73 patients in the negative DNA group. Cumulative survival rates in patients with and without HBV DNA were 78.8% and 74.1% at the end of the fifth year, 54.4% and 44.4% at the tenth year, 38.4% and 29.6% at the 15th year, and 33.6% and 29.6% at the 20th year, respectively. Although the survival rate in the positive HBV DNA group was lower than in the negative group, statistical significance was not shown.

Causes of death included liver failure due to liver cirrhosis in 21 (4 in positive DNA group and 17 in negative DNA group), progression of HCC in 7 patients (all in negative DNA group), and other causes in 8 (one in positive DNA group and 7 in negative DNA group).

DISCUSSION

Epidemiological and molecular virological studies in the 1970s and early 1980s established a strong aetiological association between chronic HBV infection and the hepatocellular carcinogenesis [35]. We also estimated annual carcinogenesis rates as 0.5% in chronic hepatitis and 3% in cirrhosis, from cohorts of biopsy-proven HBV disease [5,7].

Integration of HBV DNA has been reported in the majority of HBsAg positive HCCs since 1980s, and the fact suggested HBV might be oncogenic. Up to now, there is no evidence

that HBV DNA is directly oncogenic and the mechanism by which chronic HBV infection leads to carcinogenesis remains unclear. Integration of HBV DNA may stimulate cellular pro-oncogenes or suppress growth-regulating genes [36]. Integration of HBV DNA, however, has been found in varied regions of the host chromosomes and no preferential and specific site has been identified until now. The other authors suggested that integration of HBV DNA could also induce carcinogenesis via transactivation of other oncogenes [37]. Both HBx protein and the truncated pre-S/S protein are potent transactivators and are commonly found in HCC tissue but their precise role in hepatocarcinogenesis remains unknown.

Occult HBV infection is generally defined as the detection of HBV DNA in the serum or liver tissue of patients who test negative for hepatitis B surface antigen [38–41]. Occult HBV infection was first reported in the early 1980s when hybridization techniques for the detection of HBV DNA became available. These studies showed that HBV DNA could be detected in HBsAg negative patients with HCC [42]. Recent studies using more sensitive techniques confirmed the close correlation between chronic occult HBV infection and carcinogenesis. Many authors demonstrated the relationship between occult HBV infection and hepatocellular carcinogenesis, mainly by a pilot study or a case–control study [17,19–27]. Shiota *et al.* [24] reported in their case studies without control group that serum of 18 out of 26 HCC patients without HBsAg and anti-HCV were positive for either S, C, or X region on PCR and southern blotting. Pollicino *et al.* [26] described that viral DNA was detected in 68 of 107 cases of HCC tissue (63.5%) and in 63 of 192 cases of chronic hepatitis tissue (32.8%), and concluded that occult HBV is a risk factor for development of HCC. The other authors also emphasized the high incidence of HBV DNA in either serum or HCC tissue compared with that of cases without HCC development. All the literatures, except one [43] from Taipei where HBV infection was endemic and prevalent, concluded that occult HBV infection was closely associated HCC development. However, precise risk or hazard ratio for carcinogenesis has not been reported.

Current study on this topic provided strong evidence of an association between occult HBV infection and HCC. In the patient cohort of non-B, non-C cirrhosis, occult HBV infection increased the future carcinogenesis rate with a hazard ratio of 8.25 (95% confidence interval, 2.01–33.93). It has been proposed that diagnosis of occult HBV infection be made only when HBV DNA can be detected using at least two sets of primers from different areas of the HBV genome in duplicate assay [38,39]. Appropriate negative controls must be included in each assay and specificity of the amplification reaction confirmed by sequencing of the amplicons. Using this strict criterion, occult HBV infection was found in 9 (11.0%) of 82 Japanese patients with non-B, non-C cirrhosis. Background features of the nine patients with serum HBV DNA showed a slightly younger age, a lower ALT, a slightly lower bilirubin, and a slightly higher platelet count (Table 1). Although all these demographic and laboratory findings were considered to favour low carcinogenetic risk, the patients with cryptic HBV DNA infection developed HCC more frequently. After adjustment of these background covariates in the multivariate analysis, positivity of serum HBV DNA proved to be an independent risk factor for hepatocarcinogenesis (Table 2).

As this retrospective cohort consisted of only cirrhosis as an advanced liver disease, and as it included both alcoholic and non-alcoholic cirrhosis, the hazard ratio of 8.25 could not be applied for varied stages and varied aetiologies of liver disease. In order to elucidate the impact of occult HBV infection on carcinogenesis, future studies should be performed also in the other cohort of chronic liver disease, such as HCV-related disease. Although anti-HBc and anti-HBs antibody were measured in a small numbers of the patients, an exact relationship between serum HBV DNA and serum positivity of anti-HBc antibody was not analysed in this study. When we tested anti-HBc antibody in a small part of subjects, 3 of 6 patients (50.0%) with positive HBV DNA had serum anti-HBc antibody and 7 of 19 patients (36.8%) without HBV DNA had anti-HBc (Fisher's exact test, $P = 0.69$). For the convenience of clinical circumstance and practical usefulness, significance of positive anti-HBc on carcinogenesis risk should be elucidated through a large-scale cohort study with an identical assay for anti-HBc antibody.

Although a lot of epidemiological and clinicopathological evidence of the relationship has been published, precise role of occult HBV in this setting has been still unclear. Patients with occult hepatitis B overlap with those who previously have been classified as having recovered [44]. In fact, the distinction between recovery and occult hepatitis B is likely to be somewhat arbitrary, as recovery does not necessarily imply eradication of infection in all cases [30], but includes the possibility of complete suppression in some cases by a broad and vigorous immune response [44]. One of the most important clinical questions is whether occult hepatitis B merely represents a marker of past infection, or whether HBV genome persistence contributes to liver disease. It is very likely that occult HBV is a cofactor in the development of HCC. Several studies found that patients co-infected with HBV and HCV have increased risks of HCC compared with those with mono-infection. Our cohort studies [45] also showed that a risk factor of a history of heavy drinking interacted with HBV or HCV subtypes in a characteristic manner from the viewpoint of carcinogenesis in cirrhosis. The other important problem is whether occult HBV infection alone causes HCC. To address this question, studies on occult HBV infection in patients with HCC might provide details on other causes of chronic liver disease including nonalcoholic fatty liver disease, which may masquerade as cryptogenic cirrhosis, hemochromatosis, alfa-1-antitrypsin deficiency, and autoimmune liver disease [46]. Recently,

Castillo *et al.* [47] reported a clinical state of occult HCV infection, which shows negative serum anti-HCV, negative serum HCV RNA, and positive HCV RNA in liver biopsy specimen. Although we did not tested the possibility of occult HCV infection in this study, future studies should be also aimed at the influence of latent HCV infection on hepatocarcinogenesis.

In conclusion, occult HBV infection significantly increased the incidence of hepatocellular carcinogenesis in patients with non-B, non-C cirrhosis. Although non-B, non-C cirrhosis seemed to include varied aetiology of liver disease, cryptic HBV infection should be taken account in the prediction of future HCC development.

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GASTROENTEROLOGY

Efficacy of entecavir treatment for lamivudine-resistant hepatitis B over 3 years: Histological improvement or entecavir resistance?

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Key words
entecavir, chronic hepatitis, hepatitis B virus, lamivudine, YMDD mutants.

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Abstract

Background and Aims: Long-term lamivudine therapy is required for patients with chronic hepatitis B, because hepatitis reappears frequently after it has withdrawn. However, hepatitis B virus (HBV) mutants resistant to lamivudine emerge frequently accompanied by breakthrough hepatitis.

Methods: Effects of entecavir were evaluated in 19 patients who had developed breakthrough hepatitis during lamivudine therapy for longer than 5 years. This study is a subgroup analysis of a previously reported study. Entecavir, in either 0.5 or 1.0 mg/day doses, was given to 10 and nine patients for 52 weeks, respectively, and then all received 1.0 mg/day entecavir for an additional 68–92 weeks.

Results: There were no differences in biochemical and virological responses in the two groups of patients with respect to the two different initial doses of entecavir. Serum levels of alanine aminotransferase were normalized in 17 (90%) patients, and hepatitis B e antigen (HBeAg) disappeared from the serum in two (14%) of the 14 patients who were HBeAg-positive before. Furthermore, a decrease in histological activity index score greater than 2 points was achieved in nine of the 11 (82%) patients in whom annual liver biopsies were performed during 3 years while they received entecavir. HBV mutants resistant to entecavir emerged in five of the 19 (26%) patients, and hepatitis flare occurred in two of them (40%).

Conclusion: Entecavir in the long term would be useful for histological improvement of breakthrough hepatitis induced by lamivudine-resistant HBV mutants in patients with chronic hepatitis B. However, the relatively high rate of entecavir resistance is a concern, and other strategies need to be considered when available.

Introduction

Worldwide, an estimated 400 million people are infected with hepatitis B virus (HBV) persistently, and some of them develop fatal liver disease, such as decompensated cirrhosis and hepatocellular carcinoma.[1] In 1995, lamivudine was introduced to the treatment of chronic hepatitis B for which interferon (IFN) had previously been the only option.[2,3] Although lamivudine is efficient for treatment of chronic hepatitis B, drug-resistant HBV variants with mutations in the tyrosine–methionine–aspartate–aspartate (YMDD) motif occur increasingly more frequently with treatment duration, to higher than 60% within 5 years.[4–7] Furthermore, these YMDD mutants are often accompanied by breakthrough hepatitis, and it is difficult to obtain disease control with lamivudine.

Subsequently, adefovir dipivoxil has been approved for treatment of chronic hepatitis B,[8,9] and more recently entecavir.[10–12] Entecavir is superior to lamivudine as the first-line treatment, and both adefovir add-on lamivudine and entecavir as switch therapy have also been employed for treatment of breakthrough.[13,14]

The present study represent a subgroup analysis of our previously reported multicenter randomized controlled trial.[12] From a single center, biological and virological responses to entecavir were examined among 19 patients who had developed hepatitis breakthrough during long-term lamivudine therapy, with particular focus on histological responses to entecavir over 3 years and the rate of development of entecavir resistance. Because patients had been randomized to both the low (0.5 mg) and higher (1.0 mg) doses of entecavir, we were also able to compare results between these two different doses.

Methods

Patients

During 10 years from November 1995 to December 2004, 704 patients with chronic hepatitis B received 100 mg lamivudine/day and were followed for more than 5 years in the Department of Hepatology of Toranomon Hospital in metropolitan Tokyo. Lamivudine-resistant YMDD mutants developed in 274 (39%) of the patients, accompanied by breakthrough hepatitis in 176 (64% of those with mutants). Medication was changed so they received the other antivirals. The present study is a subgroup analysis of our previously reported multicenter randomized controlled trial.[12] After entecavir became available, 19 of them were switched to it and the treatment was continued for up to 3 years. None of them were infected with hepatitis C virus (HCV) or HIV type 1, or had autoimmune hepatitis. They were followed for liver function tests and serum markers of HBV infection monthly. At the start of entecavir therapy, chronic hepatitis was diagnosed in them all by liver biopsies performed under laparoscopy and/or ultrasonic imaging; cirrhosis was detected in no patients. Liver biopsies were performed annually for 3 years on 12 of the 19 (63%) patients, for evaluating the efficacy of long-term entecavir in improving histology of the liver. The study design conformed to the 1975 Declaration of Helsinki, and was approved by the ethics committee of the institution. All patients gave their informed consent to participate in this study.

Markers of HBV infection

Hepatitis B surface antigen (HBsAg) and the corresponding antibody (anti-HBs) were determined by hemagglutination (MyCell; Institute of Immunology, Tokyo, Japan), and hepatitis e antigen (HBeAg) by enzyme-linked immunosorbent assay (ELISA) (F-HBe; Sysmex, Kobe, Japan). HBV-DNA was determined by reverse transcription polymerase chain reaction (RT-PCR) with commercial kits (Amplicor, Tokyo, Japan; Roche, Tokyo, Japan), and the result was expressed in log genome equivalents (LGE)/mm with the cut-off value of 2.6 LGE/mL over a dynamic range of 2.6–7.6 LGE/mL. The six major genotypes (A–F) were determined serologically by ELISA (HBV Fenotype EIA; Institute of Immunology). The method employs the combination of epitopes on preS2-region products that is specific for each genotype.[15,16]

Analyses for viral resistance

YMDD mutants were determined by PCR followed by restriction fragment length polymorphism after the method of Chayama *et al.*[4] HBV mutants resistant to entecavir were examined at the baseline and sequentially while patients received entecavir. HBV-DNA was extracted from the serum and amplified by PCR, and nucleotides corresponding to amino acids 1–344 of the reverse transcriptase were sequenced directly by the dideoxy-chain method of Sanger *et al.*[17]

Treatment with entecavir

The 19 patients were randomized to receive two different regimens of entecavir in a double-blind study. Thus, 0.5 and 1.0 mg entecavir was given daily to 10 and nine patients, respectively, for the first 52 weeks. Thereafter, patients in both groups received 1.0 mg/day entecavir, and the treatment was continued for an additional 68–92 weeks (120–144 weeks in total).

Response to entecavir

Biochemical response was defined by the normalization of serum alanine aminotransferase (ALT; < 50 IU/L in our laboratory), virological response by the disappearance of HBV-DNA from serum detectable by Amplicor (sensitivity, < 2.6 LGE/mL), and histological response by a decrease in histology activity index (HAI) score of 2 points or more. Necroinflammatory activity and fibrosis were evaluated by the METAVIR score as well.

Statistical analysis

Frequencies were compared between groups by the Mann–Whitney *U*-test and Fisher's exact test, and medians by the Wilcoxon signed rank test. Normalization in ALT levels and loss of HBV-DNA from the serum, as well as the development of entecavir-resistant HBV mutants, were compared by the method of Kaplan–Meier, and differences were evaluated by the log–rank test with use of the production limit method. $P < 0.05$ was considered significant. Analysis of data was performed with SPSS software (SPSS, Chicago, IL, USA).

Results

Comparison of baseline characteristics between patients given 0.5 and 1.0 mg entecavir daily for 52 weeks and then 1.0 mg for an additional 68–92 weeks

Table 1 compares demographic, biochemical, hematological and virological characteristics between 10 and nine patients with chronic hepatitis B who were randomized to receive 0.5 and 1.0 mg entecavir, respectively, daily for the initial 52 weeks. Thereafter, they all received 1.0 mg entecavir daily for an additional 68–92 weeks (120–144 weeks in total). There were no differences in age, sex, pretreatment ALT levels, platelet counts, frequency of HBeAg, distribution of HBV genotypes, HBV-DNA levels and types of YMDD mutants between the two groups of patients.

Normalization of ALT and loss of HBV-DNA from the serum in patients who received long-term entecavir treatment

Figure 1 a depicts ALT levels in 10 and nine patients who received 0.5 and 1.0 mg entecavir daily, respectively, during the initial 52 weeks; thereafter, they all received 1.0 mg entecavir daily for an additional 68–92 weeks (120–144 weeks in total). In both groups, ALT levels increased slightly during 2–4 weeks after the start of entecavir therapy, and then decreased sharply. ALT levels were lowered within the upper limit of normal (≤ 50 IU/L) 12 and 8 weeks after the start of 0.5 and 1.0 mg entecavir daily, respectively. After then, ALT levels decreased and stayed within the

Table 1 Patients with breakthrough hepatitis induced by lamivudine-resistant hepatitis B virus (HBV) mutants who were treated with two doses of entecavir during the initial 52 weeks

		Initial daily dose of entecavir	
	Total ($n = 19$)	0.5 mg ($n = 10$)	1.0 mg ($n = 9$)
Duration of entecavir (weeks)	120–144	120–144	124–140
Age (years)	38 (29–65)	37 (29–65)	39 (30–49)
Men	17 (89%)	9 (90%)	8 (89%)
ALT (IU/L)	119 (46–1708)	111 (46–1708)	275 (49–442)
Platelets (x 10^3/mm^3)	190 (93–265)	180 (93–235)	190 (108–265)
HBeAg	14 (74%)	7 (70%)	7 (78%)
Genotypes (A : B : C)	1:0:18	1:0:9	0:0:9
HBV-DNA (LGE/mL)	7.2 (5.2–8.6)	7.2 (5.2–8.6)	6.6 (5.7–8.2)
YMDD mutants (I : V : I/V)	11:3:5	6:2:2	5:1:3

Median values are shown with the range in parentheses, and the ratio of HBV genotypes, as well as YIDD, YVDD and both YMDD mutants, is indicated. ALT, alanine aminotransferase; HBeAg, hepatitis e antigen; LGE, log geometric equivalents.

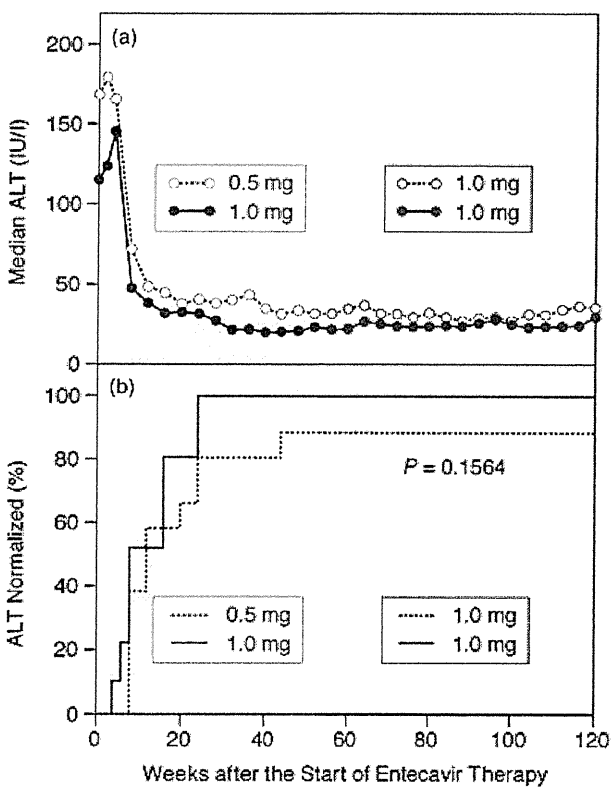

Figure 1 Alanine aminotransferase (ALT) levels in the 19 patients with breakthrough hepatitis induced by lamivudine-resistant hepatitis B virus mutants who received entecavir for 120 weeks. Of them, 10 patients received 0.5 mg and the remaining nine 1.0 mg entecavir daily during the initial 52 weeks (shaded), and thereafter both groups received 1.0 mg entecavir daily. The mean ALT levels (a) and the normalization of serum ALT (≤ 50 IU/L) (b) are illustrated.

normal limit among patients in both groups. Collectively in the 19 patients, the ALT level was normalized in 47% at week 12 and in 83% at week 24. Figure 1(b) compares the normalization of ALT levels between patients who received 0.5 and 1.0 mg entecavir daily during the initial 52 weeks. There were no statistical differences in the normalization of ALT levels between patients given 0.5 and 1.0 mg entecavir. Of the 14 patients positive for HBeAg at the start of entecavir, two (14%) lost HBeAg and seroconverted to anti-HBe, while HBsAg was not cleared from the serum in any of the 19 patients.

The loss of HBV-DNA from serum was compared between patients given 0.5 and 1.0 mg entecavir daily during the initial 52 weeks. A sharp decrease in HBV-DNA by more than 2 logs was achieved at 4 weeks in patients given the initial 0.5 mg entecavir daily, and at 8 weeks in those receiving the initial 1.0 mg entecavir daily. Twenty-four weeks after the start, HBV-DNA levels stabilized and stayed approximately 1 log lower in the patients with the initial 0.5 than 1.0 mg entecavir daily. The loss of HBV-DNA detectable by the quantitative method varied in patients with two different initial entecavir doses. At 24 weeks after the start of entecavir therapy, HBV-DNA became undetectable in 20% and 11%, respectively, of the patients with the initial 0.5 and 1.0 mg entecavir daily; the loss increased to 50% and 33% at 120 weeks, respectively. However, there were no significant differences in the loss of HBV-DNA between the patients receiving 0.5 and 1.0 mg entecavir daily during the initial 25 weeks.

Improvement of liver histology in the patients who were switched to entecavir after the development of breakthrough hepatitis during long-term lamivudine treatment

Of the 19 patients switched to receive entecavir, 12 (63%) underwent serial liver biopsies at the baseline and annually for 3 years while they were treated with entecavir. METAVIR scores for fibrosis stages at the start of entecavir were: F1 in six (50%) patients; F2 in three (25%); and F3 in three (25%). Activity grades were: A1 in six (50%) patients and A2 in six (50%). After they had received entecavir for 1 year, the fibrosis stage improved in two (17%), was

Table 2 Improvement in histology activity scores after entecavir during 3 years in the 12 patients who had developed breakthrough hepatitis induced by lamivudine-resistant HBV mutants

Features		Before	After	Decrement	Differences (*P*-value)
Periportal and/or bridging necrosis	Median (range)	1 (0–3)	0 (0–1)	1 (0–3)	0.003
	Mean ± SD	1.2 ± 0.9	0.1 ± 0.3	1.1 ± 0.8	
Lobular degeneration and focal necrosis	Median (range)	2 (0–3)	1 (0–1)	1 (0–2)	0.014
	Mean ± SD	2.0 ± 1.0	0.9 ± 0.3	1.0 ± 1.0	
Portal inflammation	Median (range)	1 (0–3)	1 (0–1)	1 (0–2)	0.015
	Mean ± SD	1.8 ± 1.0	0.8 ± 0.4	0.9 ± 0.9	
Fibrosis	Median (range)	2 (1–3)	1 (1–3)	0 (0–2)	0.059
	Mean ± SD	2.0 ± 1.0	1.4 ± 0.8	0.5 ± 1.1	
Total HAI score	Median (range)	6 (3–12)	3 (2–5)	3 (1–8)	0.002
	Mean ± SD	7.0 ± 2.7	3.2 ± 0.9	3.5 ± 2.4	

HAI, histology activity index; SD, standard deviation.

unchanged in nine (75%), and worsened in the remaining one (8%). The activity grade improved in nine (75%) patients and was unchanged in the remaining three (25%); it did not worsen in any patient.

One of the 12 patients could not receive liver biopsy 3 years after the start of therapy, because entecavir-resistant HBV mutants developed. Table 2 summarizes changes in HAI scores in the 11 patients who had received long-term entecavir treatment. After 3 years on entecavir therapy, improvement in HAI scores by 2 points or greater was achieved in nine (82%) of the 11 patients. Significant improvement was gained in the total HAI score, as well as scores for periportal and/or bridging necrosis, lobular degeneration/focal necrosis, and portal inflammation. Fibrosis score did not improve significantly ($P = 0.059$); it increased in two patients.

Clinical and virological courses of the representative patient are illustrated in Figure 2 and histological findings in yearly biopsies in Figure 3. The patient developed resistance to lamivudine and was switched to IFN. Hepatitis was exacerbated in him, however, and he was started on lamivudine again. IFN was given intermittently to him when ALT levels were elevated. Because he did not respond to IFN, entecavir was given to him. At that time, he had a HBV-DNA level of more than 7.6 LGE/mL and an HAI score of 8 in the liver biopsy. Soon after entecavir was started, HBV-DNA levels decreased sharply along with the normalization of ALT levels. He seroconverted from HBeAg to anti-HBe 1 year after the start of entecavir treatment. Histological improvement, increasing in parallel with the duration of entecavir treatment, was demonstrated by yearly liver biopsies in comparison with the baseline findings (Fig. 3). Necroinflammatory signs decreased remarkably along with narrowed portal areas, although the stage of fibrosis did not improve appreciably.

HBV mutants resistant to entecavir

Figure 4 illustrates the development of entecavir-resistant HBV mutants that increased in parallel with the duration of treatment. Entecavir-resistant HBV mutants developed in three of the 10 (30%) patients by 18, 84 and 120 weeks; and two of the nine (22%) patients by 132 and 148 weeks, respectively, who received 0.5 and 1.0 mg entecavir daily during the first year; thereafter, they all were given 1.0 mg entecavir daily for the next 68–92 weeks. During the initial 130 weeks (~2.5 years), therefore, entecavir-resistant HBV mutants developed in three of the 10 (30%) patients with the initial entecavir dose of 0.5 mg daily, in remarkable contrast to no emergence of such mutants in any of the nine patients that received 1.0 mg daily.

Alanine aminotransferase levels were elevated in only two of the five (40%) patients infected with entecavir-resistant HBV mutants, however. These two patients were switched to receive adefovir in combination with lamivudine, and breakthrough hepatitis resolved in them both. All the five patients who developed entecavir-resistant HBV mutants had been infected with lamivudine-resistant YMDD mutants with M204V in the presence or absence of M204I. In outstanding contrast, entecavir-resistant HBV mutants did not develop in any of the 11 patients who had been infected with YMDD mutants with M204I alone.

No adverse effects developed in any of the 19 patients. Breakthrough hepatitis occurred in only one of the five (20%) patients in whom entecavir-resistant mutants emerged.

Discussion

We have previously reported in the Journal that entecavir suppresses serum HBV-DNA to undetectable levels and normalizes ALT levels in more than 30% , respectively, in lamivudine-resistance patients with chronic hepatitis B at 52 weeks.[12] In the present report, we have followed 19 patients from one of the participating centers for 3 years so as to establish longer-term histological efficacy and rates of viral resistance with entecavir treatment of lamivudine-resistant chronic hepatitis B.

As in the earlier report,[12] among the 19 patients described here, ALT levels were normalized in more than 90% of them 8–12 weeks after the start of entecavir until the end of treatment. Although the median HBV-DNA level dropped by 3 logs and remained low during the entecavir therapy, they became undetectable in only 20–40% of the 19 patients. In a previous report, also, the loss of detectable HBV-DNA from the serum was achieved in only 27 of the 141 (19%) patients with lamivudine-resistant HBV mutants after they had received 1.0 mg entecavir daily for 52 weeks.[14] In a remarkable contrast, entecavir is much more efficient in treatment-naive patients who had received it for 1–2 years; HBV-DNA disappeared from the serum in 67–90% of them.[10,11,18] These differences could be attributed to some lamivudine-resistant

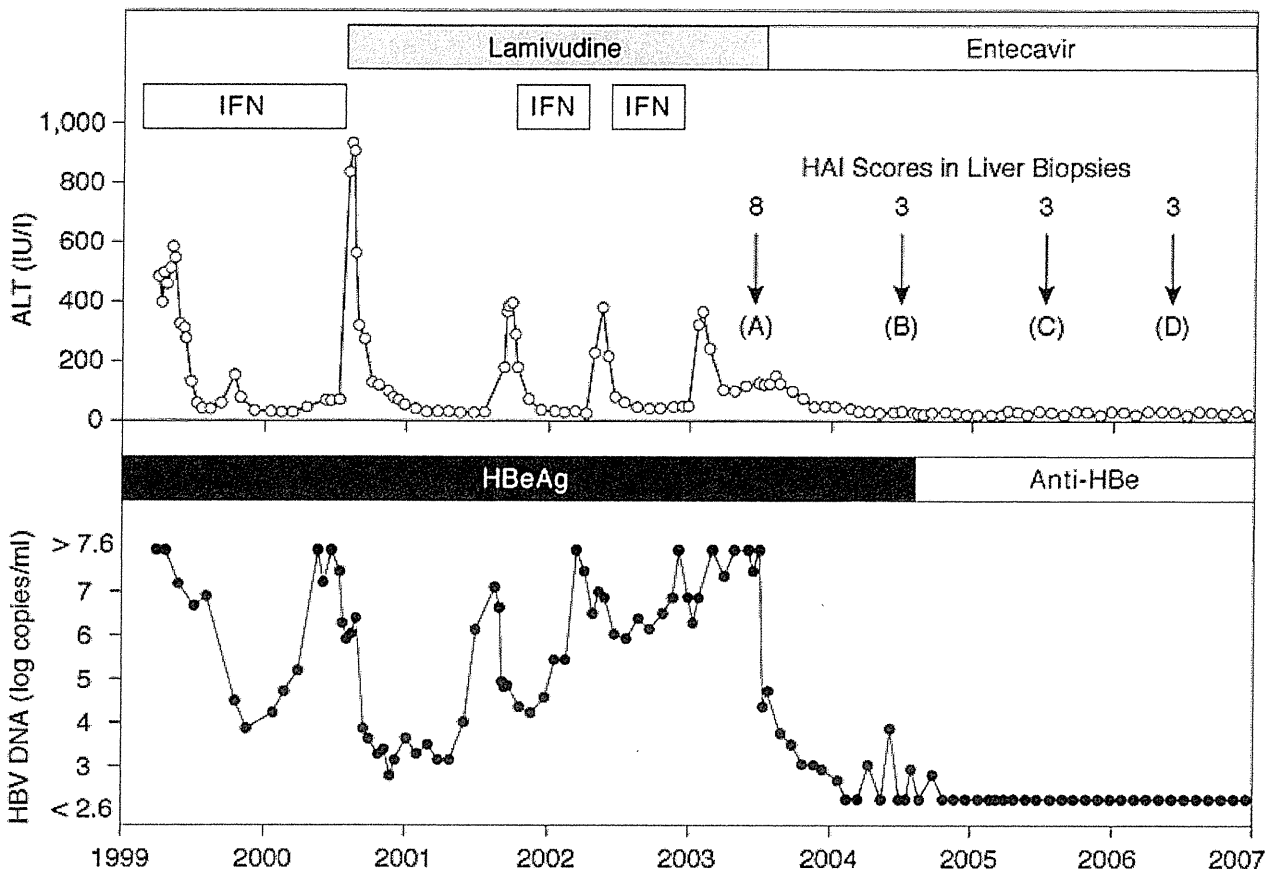

Figure 2 Clinical course of the representative patient. Fluctuating levels of alanine aminotransferase (ALT) and hepatitis B virus (HBV)-DNA are illustrated. Antiviral treatments as well as duration of hepatitis B e antigen (HBeAg) and anti-HBe are indicated by horizontal bars. Also given are time points when four liver biopsies were undertaken, along with histological activity index scores on the top. IFN, interferon.

HBV mutants contributing to the development of entecavir-resistance.[13,18]

Entecavir is a cyclopentyl guanosine analog and can inhibit the polymerase of hepadnaviridae selectively by interfering with priming and reverse transcription, as well as synthesis of minus- and plus-stranded HBV-DNA species.[19] In an *in vitro* expression system with HepG2 cells, entecavir exhibited an antiviral activity with EC_{50} of 0.00375 μM, which is 1500-fold higher than 10 μM of lamivudine.[20] Dose-dependent pharmacological activity of entecavir was evident in a randomized double-blind trial.[21] Although 0.01 mg entecavir daily decreased HBV-DNA by 2.41 logs at 22 weeks, the antiviral activity was significantly lower than 4.31 and 4.72 logs, respectively, of 0.1 and 0.5 mg daily; they were both higher than 3.36 logs by 100 mg lamivudine daily, however. Accordingly, normalization of ALT was more frequent by treatments with 0.1 and 0.5 mg entecavir daily (69% and 83%, respectively) than with 100 mg lamivudine daily (59%).

Significant decrease in HAI scores has been reported in patients with chronic hepatitis B who had received lamivudine for 1–3 years.[22,23] Furthermore, decreases in hepatic inflammation may improve the fibrosis stage. Entecavir therapy for 52 weeks has achieved histological improvement in 55–72% of patients in phase III clinical trials.[10,11,14] In corroboration of these results, fibrosis stage and inflammation grade improved in the present series of patients who had received entecavir for 3 years, with a significant decrease in the HAI score (Table 2). Histological improvement would have been gained by long-term entecavir therapy, and it may further increase, should entecavir be continued further.

Long-term entecavir treatment, however, may be hampered by the development of drug-resistant mutants. Although entecavir-resistant HBV mutants rarely occur in treatment-naive patients,[18] they can emerge rather frequently in the patients infected with lamivudine-resistant HBV mutants.[14,24] In the present study, entecavir-resistant HBV mutants developed in five of the 19 (26%) lamivudine-resistant patients during 144 weeks of treatment. The incidence was comparable with 32% in the lamivudine-resistant patients who had received entecavir for 3 years.[24] Only two (40%) of them developed hepatitis flares and they were switched to receive adefovir in combination with lamivudine. Entecavir-resistant HBV mutants emerging in patients with lamivudine-resistant mutants are reported to be replication-impaired and rarely induce breakthrough hepatitis.[25] It should be found out how entecavir-resistant HBV mutants can be managed with antiviral nucleos(t)ide analogs other than lamivudine and entecavir, or

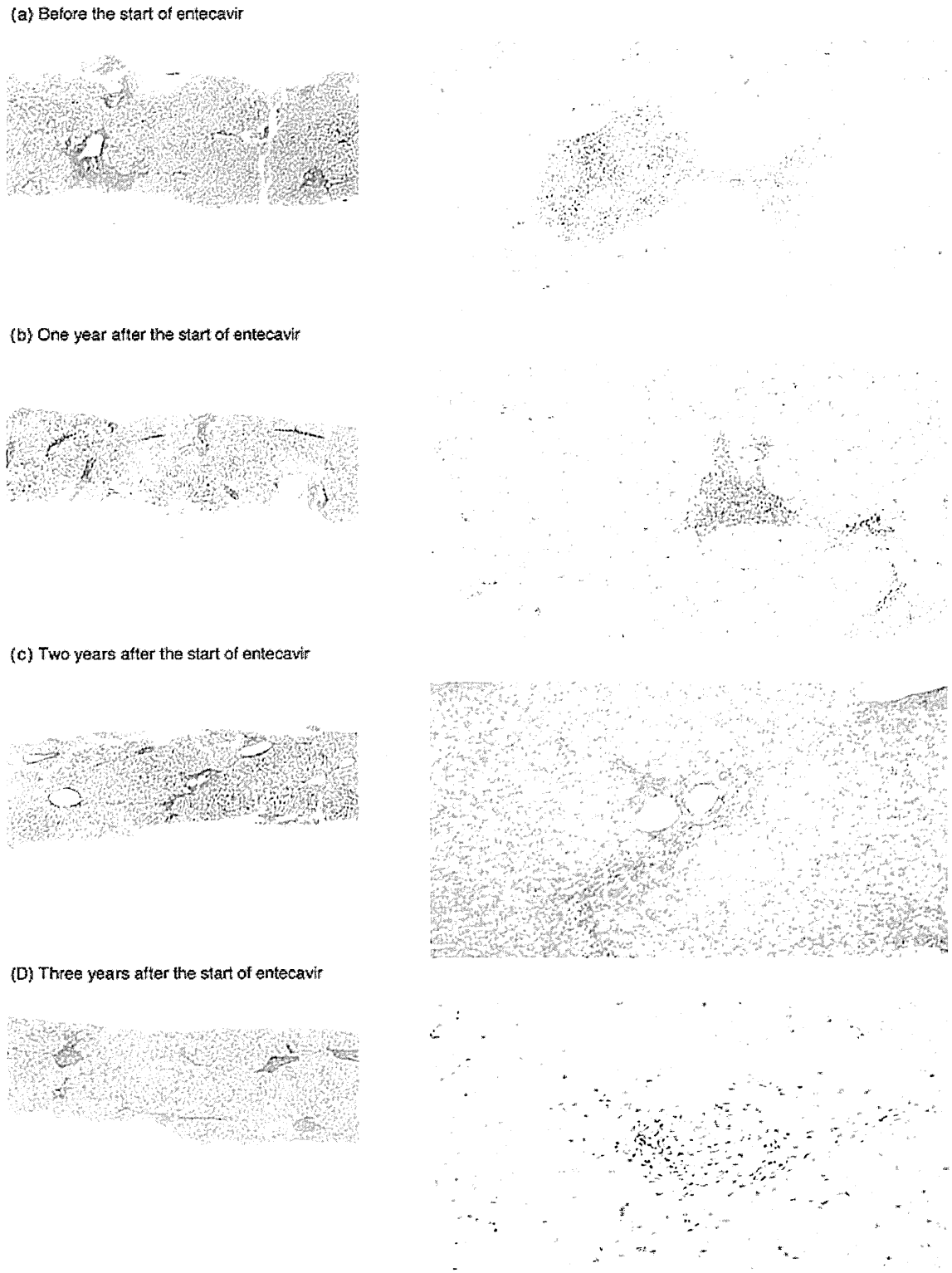

Figure 3 Histological changes in the representative patient during 3-year entecavir treatment (Fig. 2). With hematoxylin–eosin stain on the left, marked enlargement of portal areas is evident along with infiltration of mononuclear cells before the switch from lamivudine to entecavir (a). They decreased increasingly during the 3-year treatment with entecavir (b–d). Stage of fibrosis did not change appreciably by the staining for silver on the right.

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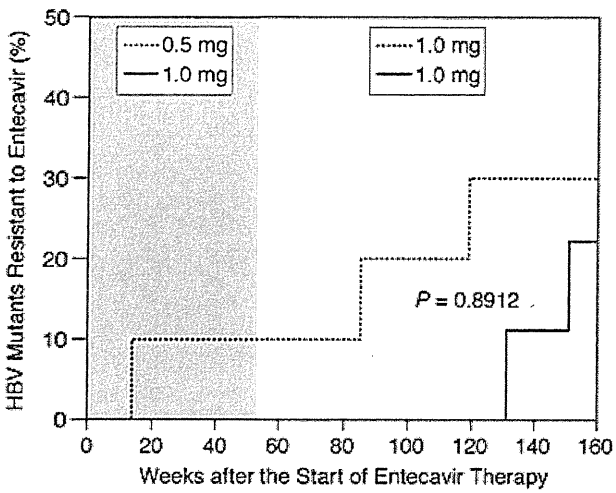

Figure 4 Development of entecavir-resistant hepatitis B virus (HBV) mutants during the 3-year treatment. The 10 patients with the initial entecavir dose of 0.5 mg daily and the nine with that of 1.0 mg daily are compared.

combination thereof. It has been proposed that adefovir add-on lamivudine is efficacious with negligible drug resistance over 3 years.[26,27]

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＜速　報＞

核酸アナログ療法中のB型関連肝癌に対する肝癌再発予測マーカーとしてのHBコア関連抗原の有用性

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緒言：B型肝疾患に対する核酸アナログ療法の有効性は広く知られており，ラミブジンにおいては投与により発癌率を抑制することが既に報告されている[1)2)]．しかしながら経過観察期間が長くなるにつれ肝発癌例も増加しつつある．また血中HBV-DNA量が抑制されているにもかかわらず，肝癌根治後の再発例も散見される．そこで今回我々は核酸アナログ投与中の肝癌について，肝癌根治療法後の再発予測マーカーとしてのHBコア関連抗原（HBcrAg）の有用性を検討した．

対象と方法：2001年～2008年までに当院で初発の肝細胞癌と診断されたB型肝癌症例で核酸アナログ投与中に肝発癌した54例を対象とした．肝癌発症時の核酸アナログ投与内容の内訳はラミブジン29例，ラミブジン＋アデフォビル併用17例，エンテカビル8例であった．肝癌治療法の内訳は外科切除36例，経皮的局所治療18例であった．HBcrAg測定は既報のごとくCLEIA法を[3)]，HBV-DNA量はアンプリコア法を用いた．肝癌根治後の再発に寄与する因子についてCox比例ハザードモデルを用いて，単変量及び多変量解析を行い検討した．

結果：発癌時のAST/ALT値は31/29 IU/l（中央値），genotype Cが92.6%（50/54）で，HBe抗原陽性例は42.6%（23/54），血清HBV-DNA量は＜2.6 log copies/ml（中央値）であった．血清HBcrAg量は5.0 logU/ml（中央値）であった．血清HBV-DNA量＜2.6 log copies/mlであった症例35例中，HBcrAg量≧3.0 logU/mlであった症例が29例（82.9%），≧4.8 logU/mlであった症例は13例（37.1%）であった．核酸アナログ投与開始から発癌までの投与期間は2.2年（中央値）であった．

肝癌再発は38.9%（21/54）で認め，根治後から再発までの期間は14カ月（中央値）であった．再発に寄与する因子について単変量解析を行ったところ，HBV-DNA量≧3.0 log copies/ml，HBcrAg≧4.8 logU/ml，腫瘍数多発，門脈浸潤ありの4因子が抽出され，さらに多変量解析を行ったところ，独立因子としてHBcrAg≧4.8 logU/ml，門脈浸潤の2因子が抽出された（Table）．

考察：今回の検討では核酸アナログ投与中の発癌例は血清HBV-DNA量が低値に抑制されているにもかかわらず，HBcrAg量は十分抑制されていない例が認められた[4)]．核酸アナログが投与されていないB型肝癌において，血清HBV-DNA量が肝癌再発に関係するという報告はされている[5)]．しかしながら今回の対象症例のように核酸アナログ投与中の場合はHBV-DNA量よりHBcrAg量の方が肝癌根治後の再発予測マーカーとして有用であると考えられる．

索引用語：HBコア関連抗原，肝癌再発予測，核酸アナログ

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Table Factors associated with recurrence of HCC by univariate and multivariate analysis.

	Univariate		Multivariate	
factors	Hazard Ratio (95%CI)	P	Hazard Ratio (95%CI)	P
HBeAg (Positive)	1.53 (0.63-3.70)	0.343		
HBV DNA ($\geq$ 3.0 logcopies/mL)	2.49 (1.03-6.00)	0.042		
HBcrAg ($\geq$ 4.8 logU/mL)	10.4 (2.39-45.0)	0.002	8.50 (1.95-37.1)	0.004
AST ($\geq$ 50 IU/L)	2.47 (0.98-6.20)	0.055		
ALT ($\geq$ 40 IU/L)	2.37 (0.99-5.71)	0.054		
Platelets count ($<$ 10^5 /mm^3)	2.20 (0.81-6.02)	0.123		
Serum Albumin ($<$ 3.5 g/dl)	1.39 (0.53-3.63)	0.505		
Serum bilirubin ($\geq$ 1.5 mg/dl)	1.11 (0.62-2.00)	0.713		
Prothorombin time ($<$ 80%)	2.23 (0.51-9.82)	0.286		
ICG-R 15 ($\geq$ 30%)	0.54 (0.16-1.87)	0.332		
AFP levels ($\geq$ 100 ng/mL)	1.81 (0.74-4.44)	0.194		
DCP levels ($\geq$ 100 mAU/mL)	2.09 (0.81-5.39)	0.129		
Tumor size ($\geq$ 21 mm)	2.02 (0.81-5.07)	0.133		
Tumor number (multiple)	4.03 (1.31-12.4)	0.015		
Presence of portal vein invasion	5.39 (1.69-17.2)	0.004	3.63 (1.15-11.5)	0.028

Abbreviation: AST, aspartate aminotransferase; ALT, alaine aminotransferase; ICG-R15: indocyanine green retention test at 15 min; AFP, alpha-fetoprotein; DCP, des-γ-carboxylprothorombin,

英文要旨

Low hepatitis B virus core-related antigen is a predictor of absence in post-treatment recurrence of hepatocellular carcinoma during antiviral therapy

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The tumor recurrence rate of hepatocellular carcinoma (HCC) is still high even in patients who receive a curative therapy. We analyzed predictive value of HBV-related viral markers, including HBcrAg, HBV DNA, and HBeAg, for HCC recurrence in the patients who developed HCC during antiviral nucleot(s)ide analogues therapy. By univariate analysis, HBV DNA, HBcrAg, tumor number and presence of portal vein invasion were significant predictive factors. By multivariate analysis, HBcrAg and presence of portal vein invasion were independent and significant predictive factors of recurrence after curative therapy for HCC. We conclude that HBcrAg is useful as a predictor of post-treatment recurrence of HCC after curative therapy in patients who received antiviral therapy.

Key words: HB core-related antigen, prediction of recurrence of HCC, nucleot(s)ide analogues

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