Table 3 Determinants of hypophosphatemia

	Univariate analysis		Multivariate analysis	
	HR (95 % CI)	*P* value	HR (95 % CI)	*P* value
Age ≥50 years	1.325 (0.836–2.100)	0.230		
Male sex	3.690 (1.600–8.475)	0.002	2.824 (1.212–6.759)	0.016
Body weight < 60 kg	1.417 (0.850–2.360)	0.181		
Current cirrhosis	1.854 (1.143–3.008)	0.012		
Current and/or history of HCC	1.824 (1.089–3.054)	0.022	1.871 (1.106–3.166)	0.020
History of diabetes mellitus	1.355 (0.546–3.362)	0.513		
History of hypertension	1.558 (0.870–2.791)	0.136		
Baseline eGFR < 80 (eGFR ≥50)	1.264 (0.788–2.029)	0.332		
Baseline IP < 3.2 mg/dl	3.155 (1.965–5.051)	<0.0001	2.833 (1.751–4.032)	<0.0001
Platelet count < 15 × 10^4/mm^3	1.472 (0.925–2.342)	0.103		

Abbreviations as in Table 2

with a fall in serum phosphate level to < 2.5 mg/dl. Patients with baseline serum phosphate of < 2.5 mg/dl ($n = 23$) were excluded from the analysis. Univariate analysis showed that male sex ($P = 0.002$), cirrhosis ($P = 0.012$), current and/or history of HCC ($P = 0.012$), and low baseline phosphate level ($P < 0.0001$) correlated with hypophosphatemia. On the other hand, multivariate analysis identified male sex ($P = 0.016$), current and/or history of HCC ($P = 0.020$), and low baseline serum phosphate level ($P < 0.0001$) as significant determinants of ADV-induced hypophosphatemia.

Further analysis showed that decreases in eGFR of more ≥30 % relative to the baseline value in 2.5 years correlated significantly with hypophosphatemia ($P = 0.007$).

Effect of modification of ADV dosing interval on hypophosphatemia and liver function

The median serum phosphate level after 1-, 2-, and 3- years of modification of ADV dose was 2.9, 3.1, and 3.0 mg/dl, respectively. Serum phosphate level fluctuated even after the dose modification. We also analyzed changes in serum ALT and HBV-DNA. After ADV dose modification, serum ALT level decreased to within the normal range (ALT < 40 IU/L) in 16 of 17 patients. Although serum ALT level of the remaining single case increased transiently after the modification, it normalized 1 year later. The HBV-DNA level was below the detection level at ADV dose modification in 14 of the 17

Table 4 Clinical features of patients with persistent ADV-induced hypophosphatemia

Case no.	Sex	Age (years)	BW (kg)	LC/CH/HCC	Baseline					Min. IP	Max. ALP	Min. UA	Max. Cr	Fall in eGFR (%)	Ostealgia
					IP	ALP	UA	Cr	eGFR						
1	F	63	64.6	LC/HCC	2.7	323	5.4	0.5	93.3	0.8	1081	1.2	0.9	47.9	+
2	F	73	57.2	CH	3.6	285	4.1	0.5	89.3	1.9	1102	2.2	0.8	41.1	+
3	M	35	61.4	CH	3.9	149	4.3	0.8	89.3	2.2	174	3.4	1.2	37.8	–
4	M	57	66.2	LC/HCC	2.9	361	2.8	0.8	77.7	2.2	742	1.7	1.2	37.1	–
5	F	40	60.4	CH	2.9	259	4.9	0.5	105.8	1.1	1012	2.5	0.7	33.1	–
6	M	47	57.4	CH	3.9	203	3.9	0.7	95.1	1.8	241	3.1	1.0	32.3	–
7	M	50	70.2	LC/HCC	3.4	300	5.4	0.6	110.2	1.1	351	5.3	0.8	29.3	–
8	M	41	80.3	LC/HCC	2.7	206	5.3	0.8	85.3	2.0	268	4.3	1.0	23.2	–
9	M	58	73.0	CH	2.6	259	2.9	0.9	67.8	2.2	378	2.2	1.1	20.5	–
10	M	31	89.0	LC	3.4	180	4.4	0.8	92.2	1.6	502	1.8	0.9	17.7	+
11	M	34	62.9	CH	2.7	111	6.4	0.6	123.7	2.2	179	4.6	0.7	16.2	–
12	M	49	83.0	CH	3.1	442	6.1	0.8	80.9	2.2	383	5.0	0.9	14.5	–
13	M	40	83.9	LC/HCC	3.7	216	6.9	0.9	75.4	1.9	383	6.0	1.0	10.9	–
14	M	39	66.0	CH	4.1	144	6.4	1.0	67.7	2.1	179	6.3	1.1	9.9	–

Fall in eGFR represents fall in eGFR relative to the baseline

BW body weight, *IP* inorganic phosphate, *ALP* alkaline phosphatase, *UA* uric acid, *Cr* creatinine, *LC* liver cirrhosis, *CH* chronic hepatitis, *HCC* hepatocellular carcinoma

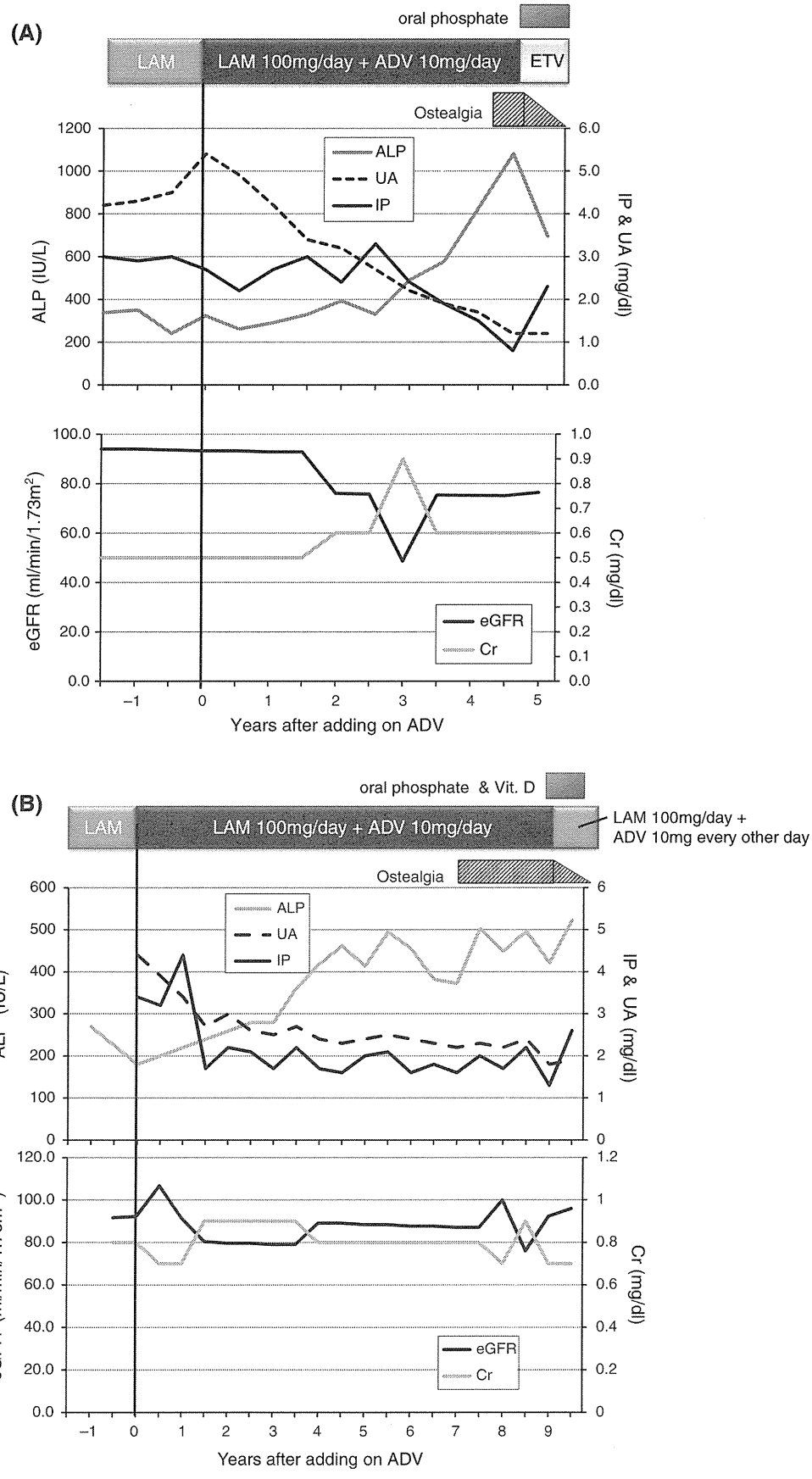

Fig. 4 Two cases who developed Fanconi's syndrome. **a** Case 1: a 63-year-old woman with HBeAg-positive liver cirrhosis. **b** Case 10: a 31 year-old man with HBeAg-positive liver cirrhosis

patients, and the level did not increase after the modification. The remaining three patients with detectable HBV-DNA at modification did not show any change in HBV-DNA.

Patients with persistent hypophosphatemia

Fourteen (5.2 %) patients developed persistent hypophosphatemia. There were no significant differences in clinical features and results of laboratory tests at baseline between patients with transient and persistent hypophosphatemia. Table 4 lists the clinical features of these patients. Three of these patients complained of bone pain during treatment. They had markedly elevated alkaline phosphatase (ALP) and low serum uric acid (UA) levels during the combination therapy. Their serum creatinine level remained normal, but their eGFR decreased relative to baseline. Figure 4 provides a summary of the clinical course of cases 1 and 10.

Case 1 was a 63-year-old woman with HBeAg-positive liver cirrhosis. She was first treated with LAM for chronic hepatitis, but ADV was added 17 months later due to the development of LAM resistance. The laboratory data (serum phosphate, ALP, UA and creatinine) were within normal ranges at baseline, and she had no other health problems. Continuous treatment with ADV for about 3 years resulted in increase in ALP level and decrease in UA and serum phosphate. After 4.5 years, she developed lumbago and right ankle pain. Blood tests showed ALP of 1102 IU/ml, UA of 1.2 mg/dl, and serum phosphate of 0.8 mg/dl. Other laboratory tests demonstrated metabolic acidosis, aminoaciduria, low tubular reabsorption of phosphate (34.8 %; normal value 85–98 %), and high fractional excretion of uric acid (47.6 %; normal value 4–14 %). These results indicated generalized dysfunction of the proximal renal tubules. A technetium bone scan showed increased uptake in bilateral ribs, carpal bones, lumbar spine, and bilateral calcaneus. She was diagnosed with acquired Fanconi's syndrome with hypophosphatemic osteomalacia associated with ADV therapy. ADV was discontinued and replaced with entecavir (ETV) while hypophosphatemia was treated with oral phosphate. Three months after cessation of ADV and oral phosphate supplementation, the patient reported symptomatic improvement and blood tests showed normalization of phosphate level and low ALP level.

Case 10 was a 31-year-old man with HBeAg-positive liver cirrhosis. He was also first treated with LAM, and ADV was added on 16 months later. The laboratory data were within the normal ranges at baseline. Treatment for 1.5 year with ADV resulted in decrease in serum phosphate and UA, and 4-year treatment increased ALP level. After 7 years, the right metatarsal bone broke in an accident. After 9 years of treatment, blood tests showed serum phosphate of 1.3 mg/dl. Detailed clinical examination was conducted at that stage. Other laboratory tests showed aminoaciduria, low tubular reabsorption of phosphate (65.5 %), and high fractional excretion of uric acid (19.1 %). A technetium bone scan showed increased uptake in bilateral ribs, bilateral ankles, tarsal bones, and right metatarsal. He was also diagnosed with acquired Fanconi's syndrome and hypophosphatemic osteomalacia associated with ADV therapy. ADV dosing interval was changed from 10 mg every day to 10 mg every other day, and oral phosphate supplementation and calcitriol were added to the treatment. Treatment for 2 months resulted in improvement of symptoms and normalization of phosphate level.

Discussion

Renal impairment is one of the most serious adverse effects of ADV. The following mechanism is considered to explain ADV-induced nephrotoxicity: the human organic anion transporter-1 (hOAT1) is a renal membrane protein expressed at the basolateral membrane of the proximal tubule cells. hOAT1 can efficiently transport cyclic nucleoside phosphonate, and thus contribute to ADV nephrotoxicity by accumulation of the drug in renal proximal tubules [18, 19].

Previous studies indicated that the ADV-related nephrotoxicity is dose-dependent [12]. In a large-scale clinical trial, 8 % of patients treated with 30 mg/day ADV for 48 weeks had high serum creatinine (≥0.5 mg/dl), relative to baseline. On the other hand, none of the patients treated with 10 mg/day ADV showed increase in creatinine (≥0.5 mg/dl), relative to baseline [20]. Thus, ADV at a dose of 10 mg/day has been used previously for the treatment of patients with CHBI. However, renal dysfunction has been reported even after the use of ADV at this dose, especially after long-term administration [13–15]. For example, in a study of the 10 mg ADV combined with LAM, serum creatinine increased in 38 % of patients following median treatment duration of 38 months [14]. In another retrospective study of 687 patients, during a median treatment period of 27 months, 10.5 % of patients developed renal impairment, which was defined as a decrease in eGFR of more than 20 % relative to the baseline [15]. In our study, 9.6 % of patients developed renal impairment during a median treatment duration of 64.3 months. Our results also showed that 20.2 % of the patients exhibited more than 30 % decrease in eGFR, and a much larger proportion (43.2 %) of the patients showed more than 20 % decrease in eGFR. These rates are higher than those reported previously. Furthermore, as shown in

Fig. 2a, patients with rapid falls in eGFR within the first 2 years of treatment should be carefully monitored for any renal dysfunction. Based on the results of our study, it seems that longer dosing period is associated with higher incidence of renal dysfunction.

We also analyzed the risk factors of renal impairment defined by a decrease in eGFR to less than 50 ml/min/1.73 m^2. Ha et al. [13] reported that age >50 years, mild renal impairment at baseline, hypertension and/or diabetes mellitus, and male sex were significant predictors of renal impairment characterized by decrease in eGFR of ≥20 % relative to baseline. Furthermore, Yu et al. [15] also reported that age ≥50 years was a significant predictor of renal dysfunction in those patients treated with ADV. In our study, age was also identified as a significant and independent determinant of the primary endpoint, together with liver cirrhosis and history of arterial hypertension. Considered together, these data indicate that care should be taken when ADV-based therapy is used for elderly patients with CHBI.

Cross-sectional studies have demonstrated a decline in GFR with age [21, 22]. Moreover, hypertension and diabetes mellitus are also reported to worsen the rate of decline of renal function [23–25]. Renal failure is common and often severe in patients with cirrhosis due to the activation of various vasoconstrictor systems, including the renin–angiotensin system and the sympathetic nervous system [26]. Taken together, eGFR is more likely to decrease during ADV therapy in patients with older age, hypertension, diabetes mellitus, cirrhosis, mild renal dysfunction at baseline.

ADV-induced proximal tubule failure can lead to hypophosphatemia. In a randomized clinical control trial using 120 mg/day ADV for treatment of patients with HIV, hypophosphatemia occurred in 50 % of patients after 48 weeks and in 61 % of patients after 72 weeks of ADV treatment [27]. On the other hand, in another study using 10 mg/day ADV for patients with CHBI, there was no overall change in serum phosphorus level during the 96-week study period [28]. However, in recent years, several reports have described the development of hypophosphatemia in patients treated with ADV at a daily dose of 10 mg [14, 29]. In our study, 27.1 % of patients developed hypophosphatemia during the combination therapy. Although 21.9 % of patients developed transient hypophosphatemia, 5.2 % of patients who had normal phosphate level at baseline developed persistent hypophosphatemia. In this regard, one previous study reported that approximately 2 % of hospitalized patients had hypophosphatemia [30]. Collectively, the above results and our findings indicate that ADV-based treatment is associated with a high incidence of hypophosphatemia. Tamori et al. [14] reported that serum phosphate level decreased to less than 2.5 mg/ml in 16.2 % of their patients during the 38-month combination therapy. Gara et al. [29] reported that 14 % of their patients treated with nucleotide analog therapy (10 mg/day ADV combined with 100 mg/day LAM, or 300 mg/day tenofovir monotherapy) developed persistent hypophosphatemia. Analysis of our data identified male sex, presence and/or history of HCC, and low serum phosphate level at baseline as significant determinants of hypophosphatemia. Furthermore, a decrease in eGFR by ≥30 % relative to baseline within 2.5 years was also associated with the development of hypophosphatemia.

Hepatic insufficiency is associated with impairment in 25-hydroxylation of vitamin D in the liver, which can lead to reduced synthesis of 1, 25 (OH) 2D3, with subsequent worsening of hypophosphatemia based on reduced intestinal absorption of phosphorus [31, 32]. In our study, 73 % of patients with HCC had liver cirrhosis, and the presence and/or history of HCC was a predictor of hypophosphatemia. Another mechanism of hypophosphatemia is protein and calorie malnutrition, which is a common feature of chronic liver disease. Furthermore, invasive treatment of HCC may itself cause hypophosphatemia. The present study also analyzed the relation between gender and hypophosphatemia. In a study that enrolled more than 4500 community-dwelling Italians of broadly diverse age, serum phosphorus levels were similar in males and females until the age of 45 years [33]. Interestingly, serum phosphate level increased in females aged between 45 and 54 years but fell after 55 years of age. The increase in serum phosphate level in females is probably related to menstrual status [33]. In the present study, serum phosphate level was higher in females than in males at baseline (3.51 vs. 3.18, $P < 0.0001$). Thus, male sex was a significant determinant of hypophosphatemia. These findings call for careful monitoring of serum phosphate level in patients treated with ADV, especially male patients, patients with HCC, and patients with renal dysfunction.

Several studies described the development of Fanconi's syndrome and subsequent hypophosphatemic osteomalacia in patients treated with 10 mg/day ADV [14, 16, 17]. Fanconi's syndrome is characterized by generalized transport defect in the proximal tubules, leading to renal losses of glucose, phosphate, uric acid, amino acids, bicarbonate, and other organic compounds [34]. Severe hypophosphatemia seems to cause inadequate mineralization of bone matrix, with subsequent osteomalacia [35, 36]. The electrolyte imbalance and osteomalacia cause symptoms of muscle weakness, fatigue, ostealgia, and bone fractures [37]. Acquired renal tubular defect resulting in Fanconi's syndrome have been described in association with many exogenous agents, including valproate, aminoglycosides, tetracycline, and acyclic nucleoside phosphonates [34].

Various approaches have been used for the treatment of osteomalacia associated with Fanconi's syndrome. Clarke et al. [38] reported successful treatment of osteomalacia associated with acquired Fanconi's syndrome with calcium, phosphate and vitamin D, regardless of the underlying cause of the disease. Eight cases of Fanconi's syndrome with ADV-related hypophosphatemic osteomalacia were reported in the past 5 years [14, 16, 17, 39–41]. Three of the 8 patients were treated with oral phosphate only; while 3 other patients received oral phosphate and vitamin D, and one patient was treated with the combination of oral phosphate, vitamin D and calcium. In all cases, treatment increased serum phosphate level and improved musculoskeletal symptoms. Similar to the eight cases reported in the literature, our 2 patients showed normalization of phosphate level and symptomatic improvement after treatment. Treatment with oral phosphate for ADV-related hypophosphatemic osteomalacia is considered effective.

We also examined the clinical characteristics of the 14 patients who developed persistent hypophosphatemia. Three of the 14 patients developed ostealgia during the treatment. Patients 1 and 10 were diagnosed with acquired Fanconi's syndrome with subsequent hypophosphatemic osteomalacia. Although we could not confirm the diagnosis of Fanconi's syndrome in patient 2 because she was transferred to another hospital, she was considered to have developed Fanconi's syndrome based on the clinical course. Despite persistent hypophosphatemia, serum creatinine remained within the normal range. In addition, 6 of the 14 patients also had low eGFR ($\geq$30 % decrease relative to baseline), and two patients with Fanconi's syndrome showed $\geq$40 % decrease in eGFR, relative to baseline. Based on the above features, patients can develop marked hypophosphatemia and serious complications, such as Fanconi's syndrome, following significant fall in eGFR, irrespective of the level of serum creatinine. In the three patients who developed Fanconi's syndrome, a gradual increase in serum ALP level and simultaneous fall in serum uric acid were noted more than one year before the appearance of ostealgia. Based on the above findings, we recommend reducing the dose or changing medications to other nucleotide analogues in patients who develop hypouricemia, hyper-ALPemia, hypophosphatemia, and low eGFR, to avoid the development of ADV-induced Fanconi's syndrome.

In our study, the dosing interval of ADV was modified by the attending physician following increase in serum creatinine level. Seventeen (5.8 %) patients required such modification, their eGFR and serum phosphate showed significant improvement at 6 and 12 months after the modification, in agreement with previous reports [13, 42]. However, the modification in ADV dosing interval from 10 mg every day to every other day neither affected HBV-DNA level nor the antiviral effect. Therefore, the ADV dose should be modified in patients who show decrease in eGFR and/or serum phosphate.

In conclusion, our results showed that even at low dose of 10 mg/day, long-term combination therapy of ADV and LAM can cause renal impairment and hypophosphatemia, and lead to Fanconi's syndrome in a subgroup of patients. ADV-based treatment tends to reduce eGFR and serum phosphate especially in elderly male patients and those with HCC. We recommend regular monitoring of serum phosphate and evaluation of eGFR, in addition to serum creatinine, in patients treated with ADV. Suspicion of Fanconi's syndrome requires early reduction of ADV dose or switching to other antiviral agents.

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Conflict of interest None.

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ORIGINAL ARTICLE—LIVER, PANCREAS, and BILIARY TRACT

Long-term efficacy and emergence of multidrug resistance in patients with lamivudine-refractory chronic hepatitis B treated by combination therapy with adefovir plus lamivudine

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Abstract
Background Few studies have investigated the emergence of multidrug resistance to adefovir dipivoxil (ADV) plus lamivudine (LAM) combination therapy for patients with LAM-refractory chronic hepatitis B (CHB). In this retrospective study, we investigated the long-term clinical course of these patients with or without multidrug resistance mutations.
Methods We analyzed 406 Japanese patients with LAM-refractory CHB treated with combination therapy with follow-up for a median of 5.4 (0.5–9.5) years. Multidrug resistance of hepatitis B virus (HBV) DNA was analyzed using direct sequencing or cloning methods at baseline and viral breakthrough or insufficient decline during combination therapy.
Results Ratio of patients with undetectable serum HBV DNA levels (<2.6 log copies/mL) during combination therapy was 63, 72, 75, 79, 82, 80 and 85 % at years 1 through 7, respectively. Substitutions associated with multidrug resistance were identified in 11 patients (2.7 %) at baseline, and in 12 patients (3 %) during therapy. HBV DNA levels of patients with rtA181S mutation at baseline and emergence of rtA181T + rtN236T double mutation or a wide variety of mutations during combination therapy could not be suppressed. Moreover, using ultra-deep sequencing, rtA181T/V mutations were detected at baseline in 7 of 10 patients with emergent multidrug resistance during combination therapy, although 6 of these 7 patients had very low frequency (<1 %) variants.
Conclusion Long-term ADV plus LAM combination therapy is effective in LAM-refractory patients. However, HBV DNA levels of the patients with multidrug resistance at baseline or during combination therapy sometimes could not achieve complete suppression or were re-elevated after a decrease.

Keywords Adefovir dipivoxil · Lamivudine · Hepatitis B virus · Ultra-deep sequence · Multidrug resistance

Abbreviations

HBV	Hepatitis B virus
IFN	Interferon
NA	Nucleoside/nucleotide analogues
LAM	Lamivudine
ADV	Adefovir dipivoxil
ETV	Entecavir
TDF	Tenofovir disoproxil fumarate
CHB	Chronic hepatitis B
HBeAg	Hepatitis B e antigen
ALT	Alanine aminotransferase
HBsAg	Hepatitis B surface antigen
PCR	Polymerase chain reaction
CLEIA	Chemiluminescent enzyme immunoassay
rt	Reverse transcriptase

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VBT Viral breakthrough
AST Aspartate aminotransferase
CI Confidence interval
Pt Patient

Introduction

Hepatitis B virus (HBV) infection is a common disease that can induce a chronic carrier state, and is associated with the risk of developing progressive disease and hepatocellular carcinoma [1]. Interferon (IFN) and several nucleoside/nucleotide analogues (NA) such as lamivudine (LAM), adefovir dipivoxil (ADV), entecavir (ETV), and tenofovir disoproxil fumarate (TDF) are currently approved for treatment of chronic hepatitis B (CHB) in most countries [2–8]. Successful treatment of CHB with clearance of hepatitis B e antigen (HBeAg), reduction in serum HBV DNA levels, and normalization of alanine aminotransferase (ALT) levels are associated with favorable long-term outcomes, independent of the antiviral drug used [9–11].

LAM is effective in suppressing HBV replication, improving transaminase levels and liver histology, and enhancing the rate of loss of HBeAg. A major problem with the long-term use of lamivudine, however, is its potential to induce viral resistance, with associated increases in HBV DNA and serum transaminases [3, 12, 13]. ADV is reportedly effective in suppressing HBV replication and is approved as a standard therapy in LAM-resistant patients in Japan [14, 15]. However, data concerning the long-term efficacy of ADV treatment in LAM-resistant CHB patients remain limited.

Although both experimental and clinical studies have shown that ADV suppresses not only wild-type but also LAM-resistant strains, the potential for ADV-resistance mutation has emerged. Selection of the rtA181V/T or rtN236T mutant was associated with ADV [13, 16]. Moreover, we previously reported that the emergence of ADV-resistant mutations before and during combination therapy for a period of 2 years was rare [17]. However, ADV-resistant mutations emerging before and during combination therapy might be caused by a poor response to therapy. Moreover, long-term clinical and virological data concerning ADV- or ETV-resistant mutations in LAM-resistant CHB patients receiving long-term ADV plus LAM combination therapy are limited.

The aims of this study were to evaluate the long-term efficiency of ADV plus LAM combination therapy based on virological response (VR), HBeAg clearance, and Hepatitis B surface antigen (HBsAg) clearance, and to investigate the emergence of ADV-, ETV-, or TDF-resistant (or multidrug resistant) mutations before and during combination therapy, and the clinical course of these patients.

Patients and methods

Patients

A total of 406 consecutive adult Japanese patients with chronic HBV infection were treated with ADV in addition to ongoing LAM treatment from 2002 at Toranomon Hospital (Table 1). Several of these patients were included in previous reports [14, 15, 17, 18]. Enrollment in this study and the start of ADV treatment were determined by the following criteria. First, an increase in serum HBV DNA levels of $\geq$1 log copies/mL during LAM treatment compared with the nadir of initial antiviral efficacy on at least two consecutive occasions, or a serum HBV DNA level of $\geq$5 log copies/mL after 1 year of LAM monotherapy; and second, no history of treatment with other NAs such as ETV or TDF. Exclusion criteria were a serum creatinine level $\geq$1.2 mg/dL; coinfection with hepatitis C virus or HIV; and history of other liver diseases, such as autoimmune hepatitis, alcoholic liver disease, or metabolic liver disease. The study was conducted in accordance with the ethical principles of the Declaration of Helsinki and was approved by the Toranomon Hospital Ethical

Table 1 Characteristics of patients at the commencement of adefovir dipivoxil plus lamivudine combination therapy

Demographic data	
Total number	406
Sex (female/male)	86/320
Age, years (range)	48 (25–78)
Duration of treatment, years (range)	5.4 (0.5–9.5)
History of IFN therapy (+/−)	157/249
Laboratory data	
Aspartate aminotransferase, IU/L (range)	54 (12–1413)
Alanine aminotransferase, IU/L (range)	76 (9–1563)
Bilirubin, mg/dL (range)	0.7 (0.2–15.5)
Albumin, g/dL (range)	3.9 (1.9–4.7)
Platelets, $\times 10^3/\mu$L (range)	160 (28–452)
Staging of liver histology (CH/LC)	325/81
Serum HBV DNA, log copies/mL (range)	6.7 (<2.6 to >7.6)
HBeAg, positive/negative/unknown	208/193/5
HBV genotype (A/B/C/D/F)	14/25/364/2/1
rtM204 mutant (%)	365 (90 %)

Values are expressed as the median and range in parentheses, or number and percentage in parentheses

IFN interferon, *HBV* hepatitis B virus, *CH* chronic hepatitis, *LC* liver cirrhosis, *HBeAg* hepatitis B e antigen

Committee (approval no. 714). Informed consent was obtained from all patients.

Patients received a single daily oral administration of ADV 10 mg, in addition to ongoing LAM treatment (100 mg/day). The dosing interval of ADV was modified by the attending physician when serum creatinine level increased to >1.2 mg/dl. Liver cirrhosis was defined by the presence of stage 4 fibrosis on histopathological examination and/or clinical evidence of portal hypertension.

Blood tests and serum viral markers

Routine biochemical tests were performed using standard procedures before and during therapy at least once every 3 months. Levels of HBsAg, HBeAg, and anti-HBe were determined using radioimmunoassay kits (Abbot Diagnostics, Chicago, IL, USA) or Chemiluminescent enzyme immunoassay (CLEIA; Lumipulse System, Fujirebio, Inc. Tokyo, Japan). Serum HBV DNA was quantified using the polymerase chain reaction (PCR)-based Amplicor HBV Monitor assay (Roche Diagnostics, Indianapolis, IN; lower limit of detection, 2.6 log copies/mL).

Determination of nucleotide sequences of HBV DNA

DNA was extracted from 100 μL of serum. PCR reactions for detection of the reverse transcriptase (rt) region (nt 130–1161) of HBV DNA were performed in two parts. The first and second PCR reactions for detection of the first part of the rt region were performed using primers BGF1 (sense; 5′-CTGTGGAAGGCTGGCATTCT-3′) and BGR2 (antisense; 5′-GGCAGGATAGCCGCATTGTG-3′), and PreSBamH1 (sense; 5′-CTTGGGATCCAGAGCTAC AGCATGG-3′) and BR112 (antisense; 5′-TTCCGTCG ACATATCCCATGAAGTTAAGGGA-3′), respectively, under conditions of initial denaturation for 4 min, 35 cycles of amplification with 94 °C for 1 min, 55 °C for 2 min, 72 °C for 3 min, and a final extension at 72 °C for 7 min. The first and second PCR reactions for detection of the second part of the same region were performed using primer pairs B11F (sense; 5′-GGCCAAGTCTGTACAA CATC-3′) and B12R (antisense; 5′-TGCAGAGGTG AAGCGAAGTG-3′), and B11F and B14R (antisense; 5′-GATCCAGTTGGCAGCACACC-3′), respectively, under the same conditions. The amplified PCR products were used for direct sequencing or cloning methods as previously described [19, 20]. When mutations as a mixed viral population with the wild type sequence for direct sequencing were present, PCR was performed using a cloning method. Sequences of 9–26 independent clones from the sample were determined and analyzed. Measurement of sequences in the rt region was performed at the start of ADV treatment, and on viral breakthrough (VBT) during ADV plus LAM combination therapy. VBT was defined as any increase in serum HBV-DNA by >1 log copies/mL from the nadir or redetection of serum HBV-DNA at levels tenfold the lower limit of detection of the HBV-DNA assay after having an undetectable result. Moreover, sequences for serum HBV DNA level of ≥4 log copies/mL after 1 or 2 years of ADV plus LAM combination therapy were also measured.

Measurement of LAM-, ADV-, ETV- and TDF-resistant variants using ultra-deep sequencing

Ultra-deep sequencing was performed using the Ion Personal Genome Machine (PGM) Sequencer (Life Technologies), as described previously [21]. An Ion Torrent adapter-ligated library was prepared using an Ion Xpress Plus Fragment Library Kit (Life Technologies). Briefly, 100 ng of fragmented genomic DNA was ligated to the Ion Torrent adapters P1 and A. The adapter-ligated products were nick-translated and PCR-amplified for a total of eight cycles. Subsequently, the library was purified using AM-Pure beads (Beckman Coulter, Brea, CA) and the concentration was determined using the StepOne Plus Real Time PCR (Life Technologies) and Ion Library Quantitation Kit in accordance with the manufacturer's instructions. Emulsion PCR was performed using Ion OneTouch (Life Technologies) in conjunction with an Ion OneTouch 200 Template Kit v2 (Life Technologies). Enrichment for templated ion spheres particles (ISPs) was performed using the Ion OneTouch Enrichment System (Life Technologies) in accordance with the manufacturer's instructions. Templated ISPs were loaded onto an Ion 314 chip and subsequently sequenced using 130 sequencing cycles in accordance with the Ion PGM 200 Sequencing Kit user guide. Total output read length per run is over 10 M base (0.5 M-tag, 200 base read). The results were analyzed with the CLC Genomics Workbench software (CLCbio, Aarhus, Denmark). A control experiment was included to validate the error rates in ultra-deep sequencing of the viral genome. In this study, amplification products of the second-round PCR were ligated with plasmid and transformed in Escherichia coli in a cloning kit (TA Cloning; Invitrogen, Carlsbad, CA). A plasmid-derived rt sequence was determined as the template by the control experiment. Coverage per position for aa180, aa181, aa184, aa194, aa202, aa204, aa233, aa236 and aa250 in the rt region was 63320, 63890, 67737, 49273, 57410, 57211, 40155, 34801 and 42914, respectively. Thus, using the control experiment based on the plasmid encoding rt sequence, amino acid mutations were defined as amino acid substitutions at a ratio of more than 0.25 % of total coverage. This frequency ruled out putative errors caused by the deep sequence platform used in this study.

HBV genotype

The major genotypes of HBV were determined using the enzyme-linked immunosorbent assay (ELISA, Institute of Immunology, Tokyo, Japan) or the PCR-invader assay (BML, Inc, Tokyo, Japan) according to the method described by Usuda et al. [22] or Tadokoro et al. [23].

Statistical analysis

Differences between groups were examined for statistical significance using the χ^2 or Fisher's exact test where appropriate. Independent risk factors predicting the achievement of HBeAg seroclearance were studied using stepwise Cox regression analysis. The following 14 potential predictors of HBeAg seroclearance were assessed in this study: age, sex, pretreatment with IFN, severity of liver disease (CH or liver cirrhosis), duration from LAM to ADV, substitution of rtM204, HBV genotype, and levels of aspartate aminotransferase (AST), ALT, bilirubin, albumin, γ-glutamyl transpeptidase, platelets, and HBV DNA. Each was transformed into categorical data consisting of two simple ordinal numbers for univariate and multivariate analyses. All factors found to be at least marginally associated with HBeAg seroclearance ($P < 0.10$) were tested in the multivariate Cox proportional hazards model, and hazard ratios and 95 % confidence intervals (CIs) were calculated to assess the relative risk confidence. The above calculations were performed using the Windows IBM SPSS version 19.0.0 software (IBM Corp., Armonk, NY, USA). A Kaplan–Meier estimate was also performed using the SPSS software.

Results

Study population

Clinical and virological profiles of the 406 patients at the start of ADV plus LAM combination therapy are shown in Table 1. At the start of combination therapy, 81 patients (20 %) had cirrhosis and 208 (51 %) were positive for HBeAg. Fourteen (3 %), 25 (6 %), 364 (90 %), 2 (0.5 %), and 1 (0.2 %) patients were infected with HBV genotypes A, B, C, D, and F, respectively. During the clinical course, 48 of 406 patients (12 %) showed an elevation in serum creatinine >1.2 mg/dL, and their ADV dose was accordingly reduced to 10 mg every second day.

Response to ADV plus LAM combination therapy

The ratio of patients with undetectable serum HBV DNA levels (<2.6 log copies/mL) was 63 % (231/367), 72 % (254/352), 75 % (249/331), 79 % (235/297), 82 % (210/256), 80 % (137/171), and 85 % (94/110) at years 1 through 7, respectively (Fig. 1a). Among HBeAg-positive patients at baseline, undetectable rates of serum HBV DNA levels gradually increased from 1 to 7 years (42, 57, 65, 70, 76, 75, 83 % at years 1 through 7, respectively; $n = 208$). In contrast, ratios in HBeAg-negative patients at baseline were >80 % at all points (86, 89, 88, 90, 91, 87, 89 % at years 1 through 7, respectively; $n = 193$). The undetectable rates of serum HBV DNA in HBeAg-negative patients

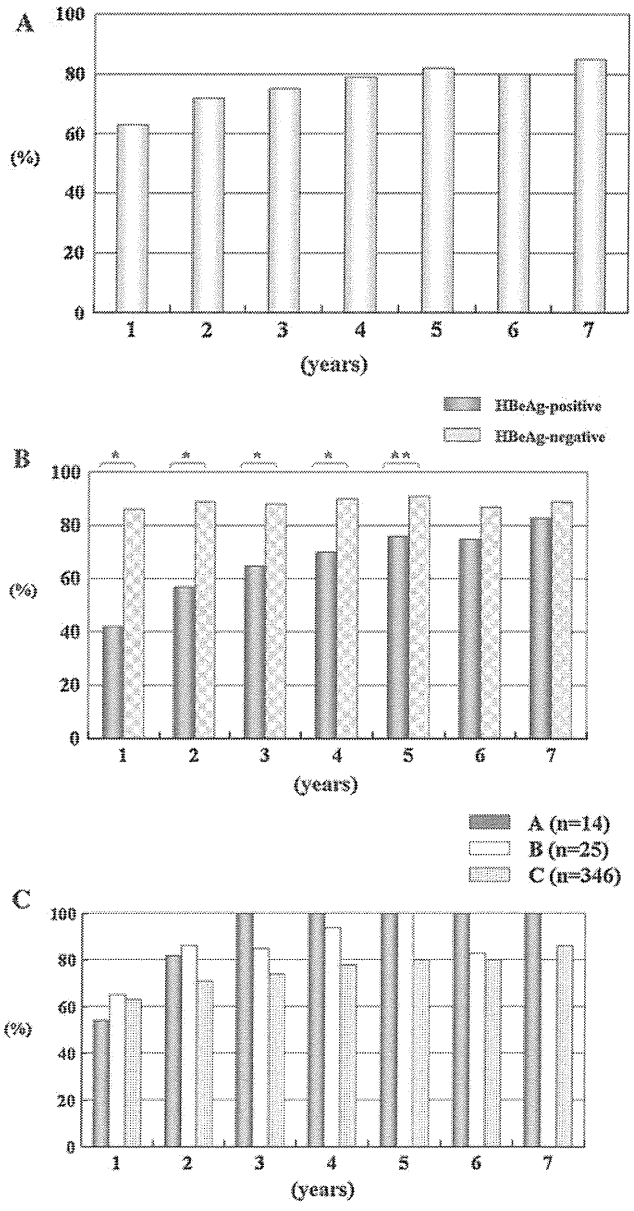

Fig. 1 Undetectable serum HBV DNA levels (<2.6 log copies/mL) in years 1 through 7, respectively. **a** All patients. **b** HBeAg status. A *single asterisk* indicates a statistical significance of $P < 0.0001$ and a *double asterisk* indicates $P = 0.0044$, as determined at the χ^2 test. **c** Genotypes A, B and C

were significantly higher than those in HBeAg-positive patients at years 1 through 5 ($P < 0.0001$ at years 1 through 4, and $P = 0.0044$ at year 5) (Fig. 1b).

By genotype, serum HBV DNA levels were undetectable after 3 years in 100 % of those with genotype A (54, 82, 100, 100, 100, 100, 100 % at years 1 through 7, respectively; $n = 14$), and in >80 % after 2 years in those with genotype B (65, 86, 85, 94, 100, 83, 80 %, at years 1 through 7, respectively; $n = 25$). In contrast, ratios in patients with genotype C gradually increased from 1 to 7 years (63, 71, 74, 78, 80, 80, 86 %, at years 1 through 7, respectively; $n = 364$) (Fig. 1c).

Moreover, the ratio of patients with ALT normalization (≤30 IU/L) was 66 % (250/380), 73 % (262/358), 78 % (255/327), 77 % (226/292), 77 % (194/251), 76 % (125/165), and 77 % (81/105) at years 1 through 7, respectively.

HBeAg clearance

Eighty-four of 208 HBeAg-positive patients (40 %) achieved seroclearance of HBeAg. Cumulative HBeAg seroclearance rates from the commencement date of ADV plus LAM combination therapy were 13 % at 1 year, 24 % at 3 years, 35 % at 5 years, and 52 % at 7 years (Kaplan–Meier method; Supplementary Figure). No patients experienced the reappearance of HBeAg after seroclearance. Six factors found to be associated with the achievement of HBeAg seroclearance in univariate analysis were: AST upper limit of normal (ULN: 30 IU/L)×2<($P = 0.017$), bilirubin 1.1 < mg/dL ($P = 0.020$), ALT ULN×3 <($P = 0.040$), history of IFN therapy ($P = 0.068$), platelets 150<×10^3 μL ($P = 0.074$), and non C genotype ($P = 0.081$). In multivariate analysis, independent factors predicting the achievement of HBeAg seroclearance were history of IFN therapy ($P = 0.009$), AST ($P = 0.016$), bilirubin ($P = 0.030$), and genotype ($P = 0.042$) (Table 2).

HBsAg clearance

Eight of 406 patients (1.9 %) achieved seroclearance of HBsAg (Supplementary Table). All patients were older than 40 years, and all but one was male. Three, two, and three patients were infected with HBV genotypes A, B, C, respectively; two patients were HBeAg-positive at baseline of combination therapy; and five patients had a history of IFN therapy. The duration of HBsAg seroclearance was 2.1–6.8 years.

Genotypic analysis of ADV- and ETV-resistant mutants at baseline of combination therapy and clinical course

Genotypic resistance to LAM, ADV, ETV or TDF was analyzed in baseline samples before the start of ADV plus LAM combination therapy. Substitutions were assessed by direct sequencing or cloning, namely those at rtL180 or rtM204 associated with LAM resistance; rtA181, rtI233, or rtN236 associated with ADV resistance; rtT184, rtS202, or rtM250 associated with ETV resistance; and rtA194 associated TDF resistance. At baseline, substitutions associated with resistance to ADV or ETV were identified in 11 patients (2.7 %) (Table 3). RtA181S/T mutations without substitution at rtM204 were identified in four patients, whereas rtA181T mutation with substitution at rtM204 on the same clones was identified in three patients. RtA181T mutation and rtM204V/I mutation, which existed together on other clones, was identified in two patients. Substitutions related with ETV resistance were identified in the remaining two patients. All but one (Pt. 11) patient was HBeAg-positive and most were younger (<40 years old) and had a high viral load at baseline of LAM therapy. In the remaining 395 patients, rtM204 mutations without substitutions associated with resistance to ADV, ETV or TDF were identified in 358 patients, whereas 37 patients had no substitutions associated with resistance to LAM, ADV, ETV or TDF.

Table 2 Factors associated with HBeAg seroclearance due to ADV plus LAM combination therapy on univariate and multivariate analyses

Parameter	Univariate analysis		Multivariate analysis	
	Hazard ratio (95 % CI)	*P*	Hazard ratio (95 % CI)	*P*
AST (≤UNL×2/UNL×2<)	1.717 (1.102–2.676)	0.017	1.750 (1.112–2.754)	0.016
Bilirubin (≤1.1/1.1<)	1.783 (1.095–2.903)	0.020	1.743 (1.056–2.876)	0.030
ALT (≤UNL×3/UNL×3<)	1.577 (1.008–2.468)	0.040		
History of IFN therapy (−/+)		0.068	1.824 (1.164–2.857)	0.009
Platelets (≤150 × 10^3/150 × 10^3<)		0.074		
Genotype (C/non C)		0.081	2.096 (1.025–4.274)	0.042

HBeAg hepatitis B e antigen, *ADV* adefovir dipivoxil, *LAM* lamivudine, *CI* confidence interval, *AST* aspartate aminotransferase, *UNL* upper limit of normal: 30 IU/L, *ALT* alanine aminotransferase, *IFN* interferon

Table 3 Characteristics of patients with resistance to ADV, ETV or TDF at baseline of ADV plus LAM combination therapy

No.	Baseline of LAM therapy					Baseline of ADV plus LAM combination therapy	
	Age	Sex	Genotype	HBeAg	HBV DNA level	Mutation type (rt region)	Duration from start of LAM to emergence of mutation (years)
1	29	M	C	+	7.6<	A181S	3.3
2	32	M	C	+	7.6<	A181T	1.3
3	23	M	C	+	7.6	A181T	2
4	34	M	C	+	nd	A181T	5
5	35	M	C	+	7.6<	A181T (17/19), L180M + M204V (2/19)	1
6	37	M	C	+	6.5	A181T (7/24), M204I (15/24), L180M + M204V (2/24)	1.3
7	51	M	C	+	7.4	A181T + M204I	1.3
8	38	F	C	+	nd	A181T + M204I (7/13), M204I (6/13)	4
9	33	M	C	+	nd	A181T + M204I (10/21), A181T + M204V(1/21), M204I (10/21)	1.3
10	25	F	D	+	nd	L180M + S202G + M204V	5
11	31	F	C	−	7.6<	L180M + M204V + M250L	6

No. of clones with combined mutations in rt region/total clones are shown in parentheses

ADV adefovir dipivoxil, *ETV* entecavir, *TDF* tenofovir disoproxil fumarate, *LAM* lamivudine, *HBV* hepatitis B virus, *HBeAg* hepatitis B e antigen, *nd* not done, *rt* reverse transcriptase, *M* male, *F* female

Following ADV plus LAM combination therapy, HBV DNA levels of four patients (Pt. 5, 6, 8, 10) were undetectable (<2.6 log copies/mL) (Fig. 2a), while those of the remaining seven were ≥2.6 log copies/mL. One patient (Pt. 7) achieved HBeAg clearance at 2 weeks, while HBeAg reappeared in a second patient (Pt. 11) at 40 weeks. Ratios of patients with undetectable levels of HBV DNA were 9 % (1/11) at 1 year, 22 % (2/9) at 2 years and 50 % (4/8) at 3 years. Three patients (Pt. 1, 2, 9) received TDF plus LAM or TDF plus ETV therapy after ADV plus LAM combination therapy due to insufficient virological response. Mutations of rtA181T + rtM204I, rtA181T + rtM204V and rtM204I in Pt. 9 changed to rtA181T + rtN236T and rtL180V + rtM204V after 3 years of combination therapy, and HBV DNA level was again thereafter elevated.

Genotypic analysis of ADV- and ETV-resistant mutants during combination therapy and clinical course

Genotypic resistance to ADV, ETV or TDF was analyzed during ADV plus LAM combination therapy in 395 patients without ADV- or ETV-resistant mutants at baseline. During combination therapy, substitutions associated with resistance to ADV or ETV were identified in 12 patients (3 %) (Table 4). All patients were genotype C and had a high viral load (>5.0 log copies/ml) at baseline of combination therapy. Substitutions of rtM204 were identified in all but one patient (Pt. 19) at baseline. RtA181V/S/

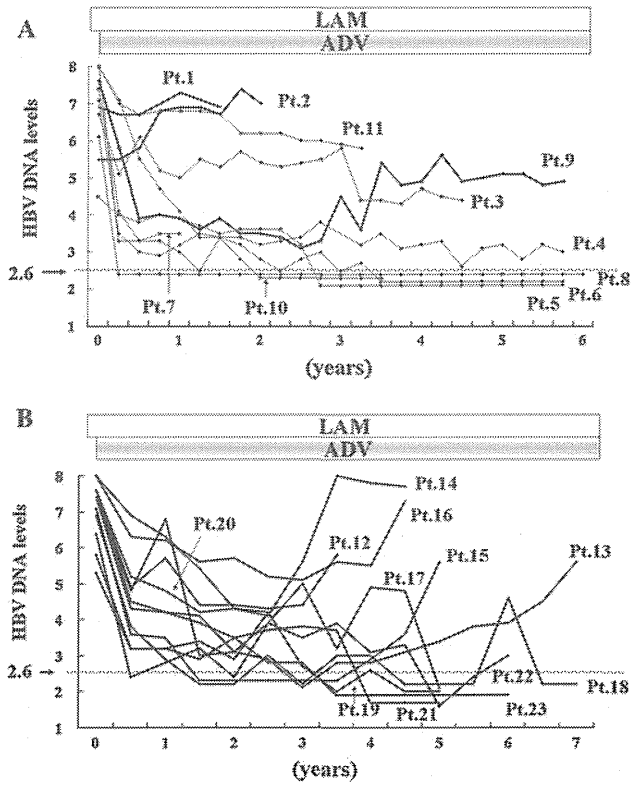

Fig. 2 Clinical course (HBV DNA load) of patients. **a** Patients with resistance associated with ADV or ETV at baseline of ADV plus LAM combination therapy. **b** Patients with resistance associated with ADV or ETV during ADV plus LAM combination therapy

Table 4 Characteristics of patients with emergence of resistance to ADV, ETV or TDF during ADV plus LAM combination therapy

No.	Baseline of ADV plus LAM combination therapy						During ADV plus LAM combination therapy	
	Age	Sex	Genotype	HBeAg	HBV DNA level	rtM204 mutant type	Mutation type(rt)	Duration from start of ADV + LAM to emergence of mutations (years)
12	32	M	C	+	7.6	M204I/V	A181T + N236T (12/16), L180M + N236T (1/16), A181T (1/16), L180M + A181T + M204V (1/16), L180M + M204V + N236T (1/16)	1
13	29	M	C	+	7.6	M204I/V	A181T + M204I + M250L (13/18), L180M + M204V + M250L (2/18), L180M + T184I + M204I + M250L(1/18), L180M + M204I + M250L(1/18), A181T + M204I (1/18)	5
14	58	M	C	+	7.6 <	M204I	L180M + T184I + M204I + M250L(16/26), L180M + T184I + M204I(6/26), A181T(4/26),	3.5
15	49	M	C	+	5.1	M204I/V	A181V + M250L	5
16	46	M	C	+	7.6	M204V	A181T + N236T	3
17	30	F	C	+	7.4	M204I	A181T	0.2
18	40	M	C	+	6.9	M204I	A181S	4
19	40	M	C	+	5.3	M204	A181S	2.3
20	49	M	C	+	7.6	M204V	A181V	0.1
21	63	M	C	−	5.8	M204I	A181T(10/11), A181T + M204I(1/11)	2
22	56	M	C	−	6.4	M204V	A181S	0.6
23	36	M	C	+	7.4	M204I	M180M + A181T(5/9), L180M + A181T + M204I + M250I (3/9), L180M + M204I + M250I(1/9)	1

No. of clones with combined mutations in the rt region/total clones are shown in parentheses

ADV adefovir dipivoxil, *ETV* entecavir, *TDF* tenofovir disoproxil fumarate, *LAM* lamivudine, *HBV* hepatitis B virus, *HBeAg* hepatitis B e antigen, *rt* reverse transcriptase, *M* male, *F* female

T mutation with or without substitution at rtM204 was identified in all patients, whereas rtT184I or rtM250I/L mutation with or without substitution at rtM204 was identified in 4 patients. Moreover, rtA181T + N236T double mutation related with ADV resistance was identified in two patients (Pt. 12 and 16). Interestingly, substitutions of rtM204 were not detected in five patients (Pt 15, 17, 18, 19, 22) when these ADV- or ETV-related mutations emerged.

Following ADV plus LAM combination therapy, the ratio of patients with undetectable levels of HBV DNA was 0 % (0/12) at 1 year, 25 % (3/12) at 2 years, 27 % (3/11) at 3 years, and 20 % (2/10) at 4 years (Fig. 2b). The HBV DNA levels of five patients (Pt. 12–16) were re-elevated after a decrease, and these patients were then switched to a different treatment (TDF plus LAM or TDF plus ETV in four patients and ETV plus ADV in one). Two of these five patients (Pt. 12 and 16) had rtA181T + rtN236T double mutation-related ADV resistance, while three (Pt. 12–14) had a wide variety of mutations. In contrast, HBV DNA levels of patients who had HBeAg clearance (Pt. 17–19, 23) during ADV plus LAM combination therapy were sustained at ≤5 Log copies/mL after 1 year, and only three patients (Pt. 19, 21, 22) showed sustained levels of ≤2.6 Log copies/mL after 4 years.

Evolution of LAM-, ADV-, ETV- and TDF-resistant variants using ultra-deep sequencing

In 10 of 12 patients with emergent substitutions associated with resistance to ADV or ETV during combination therapy, LAM-, ADV-, ETV- and TDF-resistant variants were analyzed by ultra-deep sequencing at baseline (Table 5). Patients 13 and 20 could not be analyzed due to insufficient stored serum. RtA181T/V mutations were detected in all 7 patients by ultra-deep sequencing at baseline, although 6 of these 7 patients had very low frequency (<1 %) variants. Interestingly, rtA181S mutation in 3 patients could not be

Table 5 Detection of resistance to ADV, ETV or TDF by ultra-deep sequencing at baseline in patients with emergence of resistance during ADV plus LAM combination therapy

No.	Baseline of ADV plus LAM combination therapy (ultra-deep sequencing)									During therapy
	rtL180	rtA181	rtT184	rtA194	rtS202	rtM204	rtI233	rtN236	rtM250	Mutation type(rt)
12	L (50.7 %)	A (96.4 %)	T (99.9 %)	A (99.9 %)	S (99.9 %)	I (59.1 %)	I (99.8 %)	N (99.9 %)	M (99.8 %)	A181T,
	M (49 %)	**T (3.5 %)**				V (34.5 %)				N236T
14	L (81.2 %)	A (99.4 %)	T (99.9 %)	A (99.7 %)	S (99.8 %)	I (99.6 %)	I (99.7 %)	N (99.8 %)	M (99.5 %)	A181T, T184I,
	M (15.6 %)	**T (0.56 %)**							I (0.38 %)	M250L
15	L (75.3 %)	A (97.5 %)	T (99.7 %)	A (99.7 %)	S (99.7 %)	I (70.6 %)	I (99.7 %)	N (99.8 %)	M (99.6 %)	A181V,
	M (24.4 %)	S (1.5 %)				V (27.2 %)				M250L
		V (0.75 %)								
16	M (99.3 %)	A (99.7 %)	T (99.9 %)	A (99.7 %)	S (99.8 %)	V (99.5 %)	I (99.7 %)	N (99.8 %)	M (99.4 %) I (0.51 %)	A181T
	L (0.26 %)	**T (0.27 %)**		T (0.27 %)						
17	L (99.8 %)	A (99.7 %)	T (99.9 %)	A (99.9 %)	S (99.9 %)	I (80.3 %)	I (99.7 %)	N (99.8 %)	M (99.7 %)	A181T
		T (0.25 %)				M (19.5 %)				
18	L (87.9 %)	A (98.7 %)	T (99.9 %)	A (99.4 %)	S (99.5 %)	I (98.2 %)	I (99.7 %)	N (99.8 %)	M (98.9 %)	A181S
	M (11.9 %)	T (1.3 %)		T (0.55 %)		V (1.7 %)			I (0.97 %)	
19	L (99.8 %)	A (98.8 %)	T (99.9 %)	A (99.8 %)	S (99.8 %)	M (99.5 %)	I (99.6 %)	N (99.7 %)	M (99.6 %)	A181S
		T (0.89 %)								
21	L (98.8 %)	A (98.2 %)	T (99.9 %)	A (99.8 %)	S (99.8 %)	I (72.3 %)	I (99.6 %)	N (99.7 %)	M (99.6 %)	A181T
	M (0.96 %)	V (0.99 %)				M (27.0 %)				
		S (0.48 %)				V (0.49 %)				
		T (0.35 %)								
22	M (99.4 %)	A (99.8 %)	T (99.8 %)	A (99.8 %)	S (99.8 %)	V (99.8 %)	I (99.6 %)	N (99.8 %)	M (99.6 %)	A181S
23	L (87.5 %)	A (99.1 %)	T (99.9 %)	A (99.9 %)	S (99.8 %)	I (99.4 %)	I (99.8 %)	N (99.8 %)	M (99.6 %)	A181T, M250I
	M (12.3 %)	**T (0.81 %)**				M (0.48 %)			**I (0.31 %)**	

Bold values indicate emergent substitutions during combination therapy

ADV adefovir dipivoxil, *ETV* entecavir, *TDF* tenofovir disoproxil fumarate, *LAM* lamivudine, *rt* reverse transcriptase

detected at baseline. In contrast, rtT184I, rtN236T or M250I/L mutations were detected in 1 of 4 patients with emergent mutations during combination therapy.

Discussion

Although ADV plus LAM combination therapy is a standard rescue treatment for patients with LAM-refractory HBV, the virological benefits of long-term therapy have not yet been fully assessed. Here, we evaluated the long-term efficacy of ADV plus LAM combination therapy in 406 LAM-refractory patients over a median follow-up period of 5.4 years. We also investigated baseline factors associated with HBeAg clearance and HBsAg clearance. We found long-term combination therapy produced a gradual virological improvement. In particular, virological response was higher in patients who were HBeAg-negative at baseline, and genotype A and B. Toyama et al. [24] recently evaluated the long-term (median 41 months, 158 patients) efficacy of add-on ADV treatment for patients with LAM-resistant HBV and reported a rate of virological response of 90.8 % at 4 years. Inoue et al. [25] reported that HBV-DNA levels were undetectable (<2.6 log copies/mL) on long-term ADV plus LAM combination therapy (median 47 months; 28 patients, including 7 genotype B) in 56, 80, 86, and 92 % of patients at 12, 24, 36, and 48 months, respectively, whereas Aizawa et al. [26] reported undetectable levels on the same long-term regimen (median 46 months, 72 patients) in 61, 74, 81, 84, and 85 % at 12, 24, 36, 48, and 60 months, respectively, a pattern of response that was similar to our present findings. These differences in virologic response among these Japanese studies might have been due to treatment duration, genotype, or number of patients. Nevertheless, all these long-term studies in Japanese showed a gradual increase in virological response rate for 7 years, and that combination therapy with ADV plus LAM was effective for LAM-refractory patients without multidrug-resistant HBV.

The rate of HBeAg clearance at the end of follow-up in our study of 40 % was compatible with previous reports [13, 24]. The strongest predictor of HBeAg clearance on multivariate analysis was IFN history, as in a previous report [24]. Moreover, we recently reported that HBsAg clearance during NA therapy in patients with HBeAg was influenced by previous IFN therapy and HBV genotype [27]. These results suggest that previous IFN therapy might have an immunomodulatory effect on NA therapy. In addition, baseline levels of AST and bilirubin were also significantly associated with HBeAg clearance in this study. Our results agree with those of many clinical studies that have shown baseline transaminase levels to be the strongest predictor of HBeAg seroconversion in response to both IFN [11] and NA therapy [6, 28]. On the other hand, the rate of HBsAg clearance at the end of follow-up in the present study was only 1.9 %. As mentioned above, we reported that HBsAg clearance during NA therapy was influenced by previous IFN therapy and HBV genotype as well as HBsAg level at baseline or by a decrease in HBsAg level within 6 months [27]. That study [27] included patients originally treated with LAM monotherapy or ETV therapy who switched to LAM monotherapy along with ADV plus LAM combination therapy. In this regard, further study to evaluate factors affecting HBsAg clearance in ADV plus LAM combination therapy is necessary.

We previously reported the emergence of ADV-resistant mutations (rtA181T, rtA181S and rtA181T + rtN236T) in 3 of 132 patients at baseline and in 2 during subsequent combination therapy for a period of 2 years [17]. Moriconi et al. [29] reported that rtA181S and rtT184S mutations, either alone or with rtM204 mutation, at baseline in combination therapy in patients with viral breakthrough during LAM monotherapy correlated negatively with virologic response. Moreover, Heo et al. [30] reported that the presence of the rtA181V/T mutation at baseline was associated with a decreased rate of virologic response at 12 months of combination therapy. In the present study, we analyzed more patients with multidrug resistance during combination therapy over a longer clinical course. Substitutions associated with resistance to ADV or ETV were identified at baseline in 11 of 406 patients (2.7 %), most of whom were HBeAg-positive, of younger age, and had a high viral load. Moreover, a virological response during combination therapy was obtained in only four patients. On this basis, substitution of rtA181 without rtM204 mutation might correlate with a poor virological response in combination therapy. In contrast, virological response rate in patients with mutations associated with ETV (Pt. 10 and 11) was 50 %. Inoue et al. [25] detected ETV-resistant mutations of rtT184S and rtS202C during ADV plus LAM combination therapy, and noted that these patients also showed an ADV resistance profile on in vitro analysis. Moreover, a previous report showed that A181S, A181S + M204I, and L180M + T184S + M204V/I mutations were associated with a poor response to ADV plus LAM combination therapy [29]. In light of these results, A181S mutation and A181T without rtM204I/V mutation at baseline might be associated with multidrug resistance.

On the other hand, substitutions associated with resistance to ADV or ETV were identified in 12 of 395 patients (3 %) during combination therapy. Two patients (Pt. 12 and 16) in this group and a patient (Pt. 9) with rtA181T + M204V/I mutations at baseline developed rtA181T + rtN236T double mutation-related ADV resistance. Considering our clinical study, rtA181T + rtN236T

double mutation correlated with a poor virological response. Moreover, a wide variety of mutations (Pt. 12–14) might be correlated with a poor virological response. Inoue et al. reported that 1 of 28 patients developed virologic breakthrough after combination therapy and sequence analysis identified a wide variety of mutations, including L180M + A200V + M204V + N236T, L180M + A200V + M204V, L180M + M204V, L180M + T184S + M204V and L180M + S202C + M204V [25]. The replication capacity of each clone differed [25], and accordingly a wide variety of mutations might be associated with the development of multidrug resistance. Although rtA181S mutation emerged in three patients (Pt. 18, 19, 22), their HBV DNA level was sustained below 5 log copies/mL. This might be explained by the fact that two of these patients (Pt. 18, 19) had HBeAg clearance during combination therapy while the third (Pt. 22) was HBeAg-negative at baseline. In contrast, Lampertico et al. [31] reported that 9 of 145 (6 %) LAM-resistant patients developed rtA181T/V mutation before and during combination therapy for 4 years, but that HBV DNA levels progressively declined to become undetectable in 7 (78 %). In that report, however, rtA181T and rtA181V mutations were detected as a mixed population together with the wild-type sequence rtA181 in all serum samples. In our study, in contrast, rtA181S/T/V mutations were the major population and may accordingly have influenced the poor virologic response. In any case, response to combination therapy may be influenced by amino acid substitutions other than the well-known mutations associated with LAM, ADV, or ETV resistance, and further in vivo and in vitro studies are required.

Moreover, rtA181T/V mutations were detected by ultra-deep sequencing at baseline in 7 of 10 patients with emergent substitutions associated with resistance to ADV or ETV during combination therapy. It was possible that these mutant viruses increased during combination therapy. However, rtA181S, rtT184I or rtN236T or M250L were not detected at baseline. These data indicate that resistant variants of a minor population increased in some cases, whereas de novo resistant variants emerged during combination therapy in others. However, the number of patients analyzed by ultra-deep sequencing in this study was small; and we did not obtain data from patients without emergent substitutions associated with resistance during combination therapy. Further studies should be performed to interpret the significance of the presence of low frequency variants detected by ultra-deep sequencing.

In conclusion, this study shows that long-term ADV plus LAM combination therapy is effective for LAM-refractory patients. A history of IFN therapy, AST, bilirubin, and genotype were important factors in predicting HBeAg seroclearance. However, some patients did not achieve complete viral suppression of HBV DNA level (<2.6 Log copies/mL). We speculate that incomplete suppression might favor further selection of drug-resistant mutants, albeit that the frequency of multidrug resistance in the present study (5.7 %, 23/406) was low. Moreover, the presence of rtA181S mutation at baseline and emergence of rtA181T + rtN236T double mutation or a wide variety of mutations during combination therapy might be associated with a poor virological response. Several recent reports have indicated the effectiveness of TDF for ADV- or ETV-refractory patients [32–34]. Where indicated, HBV DNA and virological analysis should be carefully monitored.

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Conflict of interest The authors declare that they have no conflict of interest.

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ORIGINAL ARTICLE—LIVER, PANCREAS, AND BILIARY TRACT

Clearance of hepatitis B surface antigen during long-term nucleot(s)ide analog treatment in chronic hepatitis B: results from a nine-year longitudinal study

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Abstract
Background Clearance of hepatitis B surface antigen (HBsAg) is considered the ultimate goal in chronic hepatitis B treatment. One treatment option is long-term nucleot(s)ide analog (NA) therapy. We followed a group of long-term NA therapy patients to evaluate the efficacy of this treatment in promoting clearance and longitudinal declines of HBsAg.
Method The study included 791 NA therapy patients who received lamivudine as their first drug. At the baseline, 442 patients were hepatitis B e antigen (HBeAg)+ and 349 were HBeAg−. All analyses were performed after separating the HBeAg+ and HBeAg− cohorts. Cox proportional hazards models were used to determine which factors were associated with HBsAg clearance.
Results HBsAg clearance was observed in 18 (4.1 %) of the HBeAg+ patients and 20 (5.7 %) of the HBeAg− patients at baseline, giving seroclearance rates of 6.4 and 6.9 %, respectively, over the nine-year study period. HBsAg clearance was influenced by several independent factors that varied according to HBeAg cohort. For HBeAg+ patients, these included previous interferon therapy, infection with hepatitis B virus (HBV) genotype A, a ≥0.5 log IU/mL decline in HBsAg level within six months, and clearance of HBeAg at six months. For HBeAg− patients, these included infection with HBV genotype A, decline in HBsAg at six months, and a baseline HBsAg level of <730 IU/mL.
Conclusion This study suggests that both direct antiviral potential and host immune response are needed to achieve HBsAg clearance by NA therapy. Viral genotype strongly influenced HBsAg clearance during NA therapy.

Keywords Hepatitis B surface antigen · Nucleot(s)ide analog · Lamivudine · Interferon

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Introduction

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 analogs (NAs) have been used as a mainstay therapeutic strategy against chronic hepatitis B. Five such antiviral agents—lamivudine (LAM), entecavir (ETV), telbivudine, adefovir dipivoxil (ADV), and tenofovir disoproxil fumarate—which inhibit viral replication [e.g., hepatitis B virus DNA (HBV DNA) priming, reverse transcription of negative-stranded HBV DNA, and synthesis of positive-stranded HBV DNA] have been approved; these NAs vary in both the strength and the rapidity with which they suppress HBV DNA [3–10]. Sustained viral suppression by NA therapy can improve liver fibrosis and clinical outcomes of patients [11, 12]. LAM was the first NA to be approved to treat chronic hepatitis B in Japan, followed by ADV and ETV.

Responses to antiviral treatments can be evaluated by monitoring serum HBV DNA levels, hepatitis B e antigen (HBeAg) and antibody levels, and hepatitis B surface

antigen (HBsAg) and antibody levels. Serum HBsAg levels appear to reflect the amount of intrahepatic covalently closed circular DNA (cccDNA), which acts as a template for the transcription of viral genes [13–15]. Previous studies have shown that both interferon (IFN) and NA therapy result in a reduction of intrahepatic cccDNA [16, 17], suggesting that these treatments may be helpful in achieving the ultimate therapeutic goal of antiviral therapy for chronic hepatitis B (i.e., total clearance of HBsAg).

Very low rates of HBsAg clearance have been reported in the past [18–22]. Recent work has shown that over a one-year period, pegylated (PEG)-IFN therapy is more successful than ETV at reducing serum HBsAg [23]; furthermore, PEG-IFN therapy has also been reported to promote the complete clearance of HBsAg [24–27]. Several studies have detailed similar successes achieved by NA therapy but over relatively short (<5 years) treatment durations [18–20, 22, 28, 29]. The kinetics of HBsAg during long-term (>5 years) treatment remain unknown. NA therapy leads to time-dependent decreases in intrahepatic cccDNA and serum HBsAg levels if sustained viral suppression is longer term, and may therefore increase the rates of HBsAg clearance.

In order to evaluate this possibility empirically, we conducted a ten-year-long study in which we followed patients who received NA therapy initiated by the administration of LAM. We evaluated the resulting clearance and longitudinal declines of HBsAg using highly sensitive assays. Our aim was to determine whether long-term NA therapy can lead to HBsAg clearance, as suggested; if so, we also wished to elucidate the factors associated with its success.

Methods

Study population

Over a period of 12 years (September 1995 to September 2007), 949 consecutive patients who were chronically monoinfected with HBV (confirmed HBsAg positivity for at least six months), were treated with LAM monotherapy at the Department of Hepatology, Toranomon Hospital, Metropolitan Tokyo. The indication for antiviral therapy was abnormal ALT levels accompanying the increase in HBV DNA (over 4 log copies/mL) as a rule. However, in cases where ALT levels were normal, patients with advanced fibrosis were administered LAM. We did not treat patients without fibrosis who had low HBV DNA and normal ALT levels as a rule. We selected 791 patients for the final study after we had excluded all those who had been treated with LAM for <6 months, were co-infected with hepatitis C virus, had not provided sufficient serum samples, and/or had insufficient clinical records (Fig. 1). No patient was co-infected with human immunodeficiency virus in this cohort. Seven hundred ninety-one patients were enrolled in this cohort study. Of these 791 patients, 442 were HBeAg+ and 349 were HBeAg− at baseline. All analyses were performed after separating the HBeAg+ and HBeAg− cohorts. Written informed consent was obtained from each patient. The study protocol conformed to the ethical guidelines of the 1975 Declaration of Helsinki and was approved a priori by the institution's human research committee. This study has been registered in the University Hospital Medical Information Network Clinical Trials Registry (UMIN CTR) as the number UMIN000007993.

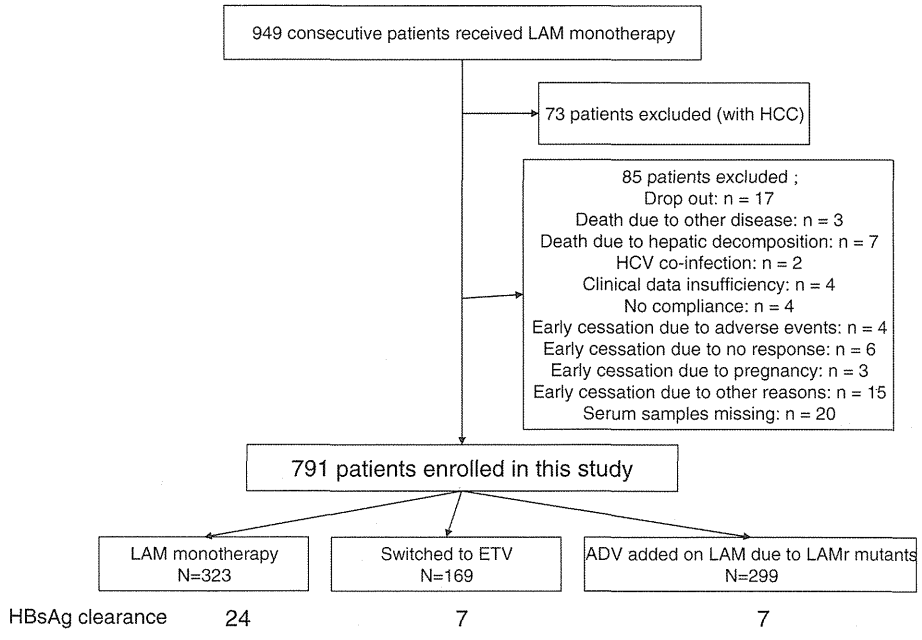

Fig. 1 Schematic of study protocol. *LAM* lamivudine, *HCC* hepatocellular carcinoma, *HCV* hepatitis C virus, *ETV* entecavir, *ADV* adefovir dipivoxil, *HBsAg* hepatitis B surface antigen

Antiviral therapy and drug resistance

All 791 patients received 100 mg LAM daily as an initial therapy, but a LAM-resistant rtM204I/V mutation developed in 439 (55 %) of these patients. Over time, 334 (42 %) individuals experienced an increase in HBV DNA (≥1 log copies/mL) [e.g., virological breakthrough (VBT)] and, as a result, 299 (98.5 %) individuals were also provided with ADV treatment (10 mg) added onto LAM as a rescue therapy. The remaining patients continued to receive LAM monotherapy and were lost to follow-up before the administration of ADV because of the lack of approval for ADV administration in Japan at the time. The resistant mutation for rtM204I/V was detected in 312 of 334 patients who experienced VBT using a commercial kit (as described below). Patients who had achieved an optimal or suboptimal virological response or who wished to participate in the clinical trial of ETV for LAM-refractory patients (ClinicalTrials.gov: NCT 1037166)—152 and 17 patients, respectively—switched from LAM to ETV (0.5 mg/day). Additionally, patients in whom subsequent ADV- or ETV-resistant mutants emerged received an optimal rescue therapy with other NAs (ETV + ADV combination for ADV resistance, and LAM + ADV combination for ETV resistance).

NA treatment was continued as a rule; median NA treatment duration was 75 months (25th–75th percentile, 55–102) in the HBeAg+ cohort and 92 months (67–119) in the HBeAg− cohort. Ultimately, 55 (7 %) of the 791 patients discontinued treatment; 16 of these individuals terminated treatment after achieving HBsAg seroclearance. Follow-ups were conducted for all patients, regardless of length of treatment, for as long as possible.

Clinical data collection and follow-ups

Data on patient characteristics, biochemistry, hematology, virology, histology, and previous treatments were collected and registered in our institute's database at the time of patient enrollment. Prior to beginning LAM, all patients were surveyed about the presence of a family history of HBV infection. Data on treatment dose and duration of previous IFN therapy were collected from our hospital's IFN therapy database or requested from other hospitals as necessary. Complete details on the previous treatment were lacking for 29 (9.7 %) of 297 patients who received IFN therapy before starting LAM.

At least every 1–3 months, liver function and virological markers of HBV infection were measured in all patients. All serum HBsAg titers were measured from frozen serum samples collected at six months, one year, three years, five years, and once annually for 6–10 years, and then stored at −80 °C. The day of HBsAg clearance was defined by the measurement in consecutive available serum samples before it was undetected in subsequent samples. A genotypic analysis of drug resistance was performed in cases of insufficient virological response or VBT, defined as an increase in serum HBV DNA levels ≥1 log above the nadir measured after the initial virological response. Cirrhosis was diagnosed by laparoscopy, liver biopsy, or clinical data such as imaging modalities and portal hypertension. The primary outcome for this study was HBsAg clearance. The endpoint of the follow-up was HBsAg clearance or last visit before January 2011.

Markers of HBV infection

Serum HBsAg titers were measured using ARCHITECT HBsAg QT assay kits (Abbott Laboratories, Tokyo, Japan), which have a lower limit of detection of 0.05 IU/mL and an upper limit of detection of 250 IU/mL. To expand the upper range from 250 to 125,000 IU/mL, serum samples, going off the scale, were diluted stepwise to 1:20 and 1:500 with ARCHITECT diluents as the product document described. HBeAg was determined by enzyme-linked immunosorbent assay with a commercial kit (HBeAg EIA; Institute of Immunology, Tokyo, Japan). HBV DNA was quantified using the Amplicor monitor assay (Roche Diagnostics, Tokyo, Japan), which has a dynamic range of 2.6–7.6 log copies/mL, or COBAS TaqMan HBV v.2.0 (Roche Diagnostics, Tokyo, Japan), which has a dynamic range of 2.1–9.0 log copies/mL. A commercial kit (HBV Genotype EIA; Institute of Immunology) was used to serologically determine HBV genotypes using the combination of epitopes expressed on the pre-S2 region product, which is specific to each of the seven major genotypes (A–G). YMDD mutants (rt M204I/V) were determined by polymerase chain reaction-based enzyme-linked mini-sequence assay with a commercial kit (Genome Science Laboratories, Tokyo, Japan).

Statistical analyses

Categorical data were compared between groups using chi-square or Fisher's exact tests. Continuous variables with a nonparametric distribution were analyzed with Mann–Whitney *U* tests, while those with a parametric distribution were analyzed with Student's *t* tests. When appropriate, Kruskal–Wallis tests were used to conduct pairwise comparisons of specific variables. Cox regression analyses were used to assess which variables were significantly associated with HBsAg clearance. Cut-off values were provided using the area under the receiver operating characteristic curve (ROC) only after rejecting the null hypothesis for the ROC curve. All baseline factors that were found to be significantly associated with HBsAg clearance by univariate analysis