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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

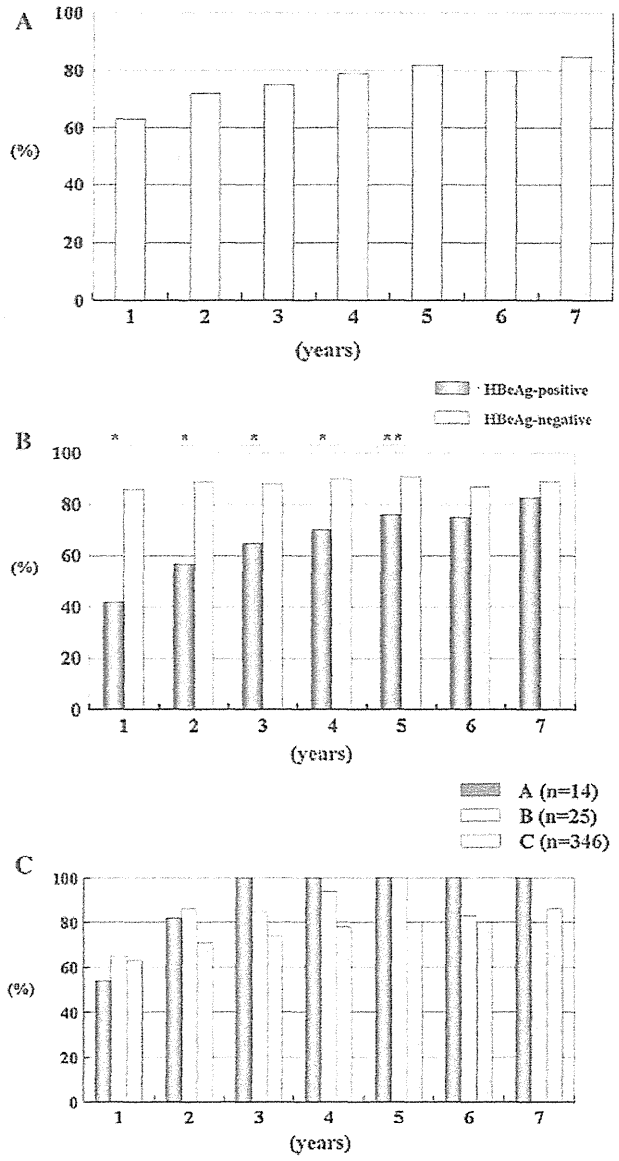

Fig. 1 Undetectable serum HBV DNA levels (<2.6 log copies/mL) in years 1 through 7, respectively. **a** All patients. **b** HBeAg status. A *single asterisk* indicates a statistical significance of $P < 0.0001$ and a *double asterisk* indicates $P = 0.0044$, as determined at the χ^2 test. **c** Genotypes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

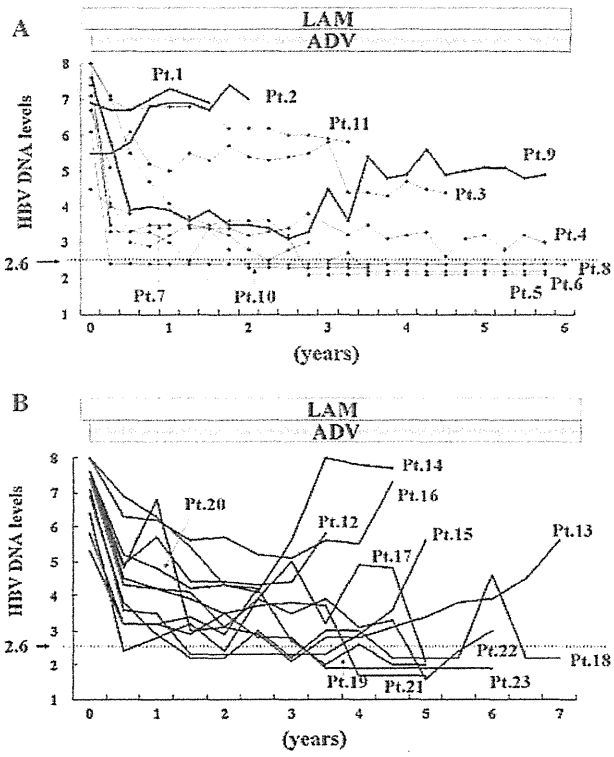

Fig. 2 Clinical course (HBV DNA load) of patients. **a** Patients with resistance associated with ADV or ETV at baseline of ADV plus LAM combination therapy. **b** Patients with resistance associated with ADV or ETV during ADV plus LAM combination therapy

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 %) M (49 %)	A (96.4 %) **T (3.5 %)**	T (99.9 %)	A (99.9 %)	S (99.9 %)	I (59.1 %) V (34.5 %)	I (99.8 %)	N (99.9 %)	M (99.8 %)	A181T, N236T
14	L (81.2 %) M (15.6 %)	A (99.4 %) **T (0.56 %)**	T (99.9 %)	A (99.7 %)	S (99.8 %)	I (99.6 %)	I (99.7 %)	N (99.8 %)	M (99.5 %) I (0.38 %)	A181T, T184I, M250L
15	L (75.3 %) M (24.4 %)	A (97.5 %) S (1.5 %) **V (0.75 %)**	T (99.7 %)	A (99.7 %)	S (99.7 %)	I (70.6 %) V (27.2 %)	I (99.7 %)	N (99.8 %)	M (99.6 %)	A181V, M250L
16	M (99.3 %) L (0.26 %)	A (99.7 %) **T (0.27 %)**	T (99.9 %)	A (99.7 %) T (0.27 %)	S (99.8 %)	V (99.5 %)	I (99.7 %)	N (99.8 %)	M (99.4 %) I (0.51 %)	A181T
17	L (99.8 %)	A (99.7 %) **T (0.25 %)**	T (99.9 %)	A (99.9 %)	S (99.9 %)	I (80.3 %) M (19.5 %)	I (99.7 %)	N (99.8 %)	M (99.7 %)	A181T
18	L (87.9 %) M (11.9 %)	A (98.7 %) T (1.3 %)	T (99.9 %)	A (99.4 %) T (0.55 %)	S (99.5 %)	I (98.2 %) V (1.7 %)	I (99.7 %)	N (99.8 %)	M (98.9 %) I (0.97 %)	A181S
19	L (99.8 %)	A (98.8 %) T (0.89 %)	T (99.9 %)	A (99.8 %)	S (99.8 %)	M (99.5 %)	I (99.6 %)	N (99.7 %)	M (99.6 %)	A181S
21	L (98.8 %) M (0.96 %)	A (98.2 %) V (0.99 %) S (0.48 %) **T (0.35 %)**	T (99.9 %)	A (99.8 %)	S (99.8 %)	I (72.3 %) M (27.0 %) V (0.49 %)	I (99.6 %)	N (99.7 %)	M (99.6 %)	A181T
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 %) M (12.3 %)	A (99.1 %) **T (0.81 %)**	T (99.9 %)	A (99.9 %)	S (99.8 %)	I (99.4 %) M (0.48 %)	I (99.8 %)	N (99.8 %)	M (99.6 %) **I (0.31 %)**	A181T, M250I

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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Utility of Detection of Telaprevir-Resistant Variants for Prediction of Efficacy of Treatment of Hepatitis C Virus Genotype 1 Infection

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The clinical usefulness of detecting telaprevir-resistant variants is unclear. Two hundred fifty-two Japanese patients infected with hepatitis C virus (HCV) genotype 1b received triple therapy with telaprevir–peginterferon (PEG-IFN)–ribavirin and were evaluated for telaprevir-resistant variants by direct sequencing at baseline and at the time of reelevation of the viral load. An analysis of the entire group indicated that 76% achieved a sustained virological response. Multivariate analysis identified a PEG-IFN dose of <1.3 μg/kg of body weight, an *IL28B* rs8099917 genotype (genotype non-TT), detection of telaprevir-resistant variants of amino acid (aa) 54 at baseline, nonresponse to prior treatment, and a leukocyte count of <5,000/mm^3 as significant pretreatment factors for detection of telaprevir-resistant variants at the time of reelevation of the viral load. In 63 patients who showed nonresponse to prior treatment, a higher proportion of patients with no detected telaprevir-resistant variants at baseline (54%) achieved a sustained virological response than did patients with detected telaprevir-resistant variants at baseline (0%). Furthermore, 2 patients who did not have a sustained virological response from the first course of triple therapy with telaprevir received a second course of triple therapy with telaprevir. These patients achieved a sustained virological response by the second course despite the persistence of very-high-frequency variants (98.1% for V36C) or a history of the emergence of variants (0.2% for R155Q and 0.2% for A156T) by ultradeep sequencing. In conclusion, this study indicates that the presence of telaprevir-resistant variants at the time of reelevation of viral load can be predicted by a combination of host, viral, and treatment factors. The presence of resistant variants at baseline might partly affect treatment efficacy, especially in those with nonresponse to prior treatment.

New strategies have been introduced recently for the treatment of chronic hepatitis C virus (HCV) infection based on the inhibition of protease in the nonstructural 3 (NS3)/NS4 region of the HCV polyprotein. Of the new agents currently available, telaprevir (VX-950) is used for the treatment of chronic HCV infection (1). Three studies (PROVE1, PROVE2, and a Japanese study [2–4]) showed that a 24-week regimen of triple therapy (telaprevir, peginterferon [PEG-IFN], and ribavirin) for 12 weeks followed by dual therapy (PEG-IFN and ribavirin) for 12 weeks (also called the T12PR24 regimen) achieved sustained virological response (SVR) (negative for HCV RNA for >24 weeks after the withdrawal of treatment) rates of 61%, 69%, and 73%, respectively, in patients infected with HCV genotype 1 (HCV-1). However, another study (PROVE3) found lower SVR rates to the T12PR24 regimen (39%) in nonresponders to previous PEG-IFN–ribavirin therapy infected with HCV-1 who did not achieve HCV RNA negativity during or at the end of the initial triple therapy course (5).

Telaprevir-based therapy is reported to induce resistant variants of HCV (6, 7). A recent report indicated that resistant variants are observed in most patients after failure to achieve an SVR by telaprevir-based treatment and that they tend to be replaced with wild-type viruses over time, presumably due to the lower fitness of those variants (8). However, the clinical usefulness of detecting telaprevir-resistant variants is still unclear. First of all, pretreatment factors associated with the detection of telaprevir-resistant variants at the time of reelevation of viral load have not been investigated. Furthermore, it is not clear at this stage whether the detection of telaprevir-resistant variants at baseline is useful for predicting the efficacy of telaprevir-based treatment and whether a history of the emergence of telaprevir-resistant variants affects treatment efficacy with the second course of telaprevir-based treatment.

Based on the above background, there is a need to investigate the clinical usefulness of detecting telaprevir-resistant variants. The aim of this study was to determine the pretreatment factors associated with the subsequent detection of telaprevir-resistant variants at the time of reelevation of viral load and the importance of telaprevir-resistant variants for predicting the efficacy of telaprevir-based treatment in patients infected with HCV-1b.

MATERIALS AND METHODS

Study population. From May 2008 through August 2013, 340 consecutive patients infected with HCV were selected for triple therapy with telaprevir (MP-424 or Telavic; Mitsubishi Tanabe Pharma, Osaka, Japan), PEG-IFN-α2b (PegIntron; MSD, Tokyo, Japan), and ribavirin (Rebetol; MSD, Tokyo) at the Department of Hepatology, Toranomon Hospital (located in metropolitan Tokyo, Japan). Subsequently, 252 of these patients received the triple therapy based on the following inclusion and exclusion criteria: (i) diagnosis of chronic hepatitis C, (ii) HCV-1b confirmed by sequence analysis, (iii) HCV RNA level of ≥5.0 log IU/ml as determined

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by the Cobas TaqMan HCV test (Roche Diagnostics, Tokyo, Japan), (iv) follow-up duration of ≥24 weeks after the completion of triple therapy, (v) no history of treatment with NS3/4A protease inhibitors, (vi) absence of decompensated liver cirrhosis and hepatocellular carcinoma (HCC), (vii) negative for hepatitis B surface antigen (HBsAg), (viii) no evidence of human immunodeficiency virus infection, (ix) negative history of autoimmune hepatitis, alcohol liver disease, hemochromatosis, and chronic liver disease other than chronic hepatitis C, (x) negative history of depression, schizophrenia, or suicide attempts, angina pectoris, cardiac insufficiency, myocardial infarction, severe arrhythmia, uncontrolled hypertension, uncontrolled diabetes, chronic renal dysfunction, cerebrovascular disorders, thyroidal dysfunction uncontrolled by medical treatment, chronic pulmonary disease, allergy to medication, or anaphylaxis at baseline, and (xi) pregnant or breastfeeding women or those willing to become pregnant during the study and men with a pregnant partner were excluded. The study protocol was in compliance with the guidelines for good clinical practice and the 1975 Declaration of Helsinki and was approved by the institutional review board of the Toranomon Hospital. Each patient received ample information about the goals and potential side effects of the treatment and their right to withdraw from the study at any time. Each patient provided a signed consent form before participating in this trial.

The efficacy of treatment was evaluated by the presence or absence of an HCV RNA-negative result at 24 weeks after the completion of therapy (i.e., SVR), as determined by the Cobas TaqMan HCV test (Roche Diagnostics). Furthermore, failure to achieve an SVR was classified as nonresponse (HCV RNA detected during or at the end of treatment) or relapse (at the time of reelevation of viral load after the end of treatment, even when HCV RNA result was negative at the end of treatment).

Twenty patients (8%) were assigned to a 12-week regimen of triple therapy (the T12PR12 group) and were randomly divided into two groups (10 patients each) treated with either 1,500 mg/day or 2,250 mg/day of telaprevir to evaluate the treatment efficacy during 12 weeks on treatment. Sixty patients (24%) were allocated to a 24-week regimen of the same triple therapy described above followed by dual therapy of PEG-IFN and ribavirin for another 12 weeks (the T12PR24 group) to evaluate treatment efficacy according to the response to prior treatment, and they were treated with 2,250 mg/day of telaprevir. Another group of 172 patients (68%) was treated as described above for the T12PR24 group except for the dosages of telaprevir; this group was divided into two groups treated with either 1,500 mg/day (111 patients) or 2,250 mg/day (61 patients) of telaprevir, as selected by the attending physician. Table 1 summarizes the profiles and laboratory data of the entire group of 252 patients at the commencement of treatment. They included 155 males and 97 females 21 to 73 years of age (median, 58 years). At the start of treatment, telaprevir was administered at a median dose of 30.8 mg/kg of body weight (range, 14.1 to 59.2 mg/kg) daily. One hundred thirty-one patients (52%) were treated with 2,250 mg/day of telaprevir, while the other 121 patients (48%) were treated with 1,500 mg/day of telaprevir. PEG-IFN-α2b was injected subcutaneously at a median dose of 1.5 μg/kg (range, 0.7 to 1.8 μg/kg) once a week. Ribavirin was administered at a median dose of 10.9 mg/kg (range, 4.3 to 15.8 mg/kg) daily. Each drug was discontinued or its dose reduced as required per the judgment of the attending physician, in response to a fall in hemoglobin level, leukocyte count, neutrophil count, or platelet count, or the appearance of side effects. The triple therapy was discontinued when the leukocyte count decreased to $<1{,}000/mm^3$, the neutrophil count decreased to $<500/mm^3$, the platelet count decreased to $<5.0 \times 10^4/mm^3$, or when hemoglobin decreased to <8.5 g/dl.

Follow-up. Clinical and laboratory assessments were performed at least once every month before, during, and after treatment. They were performed every week in the initial 12 weeks of treatment. Adverse effects were monitored clinically by careful interviews and a medical examination at least once every month. Compliance with treatment was evaluated by a questionnaire.

TABLE 1 Profile and laboratory data at commencement of telaprevir, peginterferon, and ribavirin triple therapy in patients infected with HCV genotype 1b

Variable	Patient data
Patient demographics	
No. of patients	252
Sex (no. of males/no. of females)	155/97
Median age (yr) (range)	58 (21–73)
Median body mass index (kg/m^2) (range)	22.8 (16.0–36.7)
Laboratory data (median [range])	
Level of viremia (log IU/ml)	6.7 (5.0–7.8)
Aspartate aminotransferase (IU/liter)	37 (15–624)
Alanine aminotransferase (IU/liter)	42 (11–525)
Albumin (g/dl)	3.9 (2.5–4.7)
Gamma-glutamyl transpeptidase (IU/liter)	34 (3–319)
Leukocyte count ($/mm^3$)	4,700 (2,000–8,400)
Hemoglobin (g/dl)	14.3 (12.1–17.6)
Platelet count ($10^4/mm^3$)	16.5 (8.5–33.8)
Treatment	
Median PEG-IFN-α2b dose (μg/kg) (range)	1.5 (0.7–1.8)
Median ribavirin dose (mg/kg) (range)	10.9 (4.3–15.8)
Median telaprevir dose (mg/kg) (range)	30.8 (14.1–59.2)
No. of patients with telaprevir dose of 1,500/2,250 mg/day	121/131
No. of patients on T12PR12/T12PR24 treatment regimen	20/232
Response to prior treatment	
No. of treatment-naive patients/no. of patients with relapse to prior treatment/no. of patients with nonresponse to prior treatment (IFN monotherapy/ribavirin combination therapy)/unknown	79/109/63 (16/47)/1
Amino acid substitutions in HCV genotype 1b	
Core aa 70 (arginine/glutamine [histidine]/ND[a])	162/88/2
Core aa 91 (leucine/methionine/ND)	139/111/2
ISDR of NS5A (wild type/non-wild type/ND)	199/24/29
IRRDR of NS5A (≤5/≥6/ND)	180/69/3
V3 of NS5A (≤2/≥3/ND)	64/185/3
IL28B genotype	
rs8099917 genotype (TT/non-TT/ND)	181/69/2
ITPA genotype	
rs112735 genotype (CC/non-CC)	186/65/1
NS3/4A protease inhibitor-resistant variants by direct sequencing[b]	
V36/T54/Q80/R155/A156/D168/V170	1/7/55/1/2/26/0

[a] ND, not determined.

[b] The NS3/4A protease inhibitor-resistant variants detected by direct sequencing included V36A/C/M/L/G, T54A/S, Q80K/R/H/G/L, R155K/T/I/M/G/L/S/Q, A156V/T/S/I/G, D168A/V/E/G/N/T/Y/H/I, and V170A (19, 20).

Measurement of HCV RNA. The antiviral effects of the triple therapy on HCV were assessed by measuring blood plasma HCV RNA levels. In this study, HCV RNA levels during treatment were evaluated at least once every month before, during, and after therapy. HCV RNA concentrations were determined using the Cobas TaqMan HCV test (Roche Diagnostics). The linear dynamic range of the assay was 1.2 to 7.8 log IU/ml, and undetectable samples were defined as negative.

Determination of *IL28B* and *ITPA* genotypes. The *IL28B* rs8099917 and *ITPA* rs112735 genotypes have been reported as predictors of treatment efficacy and side effects to PEG-IFN–ribavirin dual therapy, and they were genotyped by using the Invader assay, TaqMan assay, or direct sequencing, as described previously (9–13).

Detection of amino acid substitutions in core and NS5A regions of HCV-1b. With the use of HCV-J (GenBank accession no. D90208) as a reference type (14), the sequence of amino acids (aa) 1 to 191 in the core protein of HCV-1b was determined and then compared with the consensus sequence constructed in a previous study to detect substitutions at aa 70 of arginine (Arg70) or glutamine/histidine (Gln70/His70) and at aa 91 of leucine (Leu91) or methionine (Met91) (15). The sequence of aa 2209 to 2248 in the NS5A of HCV-1b (the interferon sensitivity-determining region [ISDR]) reported by Enomoto and coworkers (16) was determined, and the number of amino acid substitutions in the ISDR was defined as wild type (≤1) or non-wild type (≥2) compared to that of HCV-J. Furthermore, the sequence of aa 2334 to 2379 in the NS5A region of HCV-1b (the IFN/ribavirin resistance-determining region [IRRDR]) reported by El-Shamy and coworkers (17), including the sequence of aa 2356 to 2379 referred to as the variable region 3 (V3), was determined and then compared with the consensus sequence constructed in a previous study. The numbers of amino acid substitutions in the IRRDR and V3 regions were divided into two groups for analysis (those with ≤5 and ≥6 aa substitutions in the IRRDR, and those with ≤2 and ≥3 aa substitutions in the V3). In the present study, the amino acid substitutions of the core region and the NS5A-ISDR/IRRDR/V3 of HCV-1b were analyzed by direct sequencing.

Assessment of NS3/4A protease inhibitor-resistant variants. The genome sequence of 609 nucleotides (203 amino acids) in the N terminal of the NS3 region of HCV isolates from the patients was examined. HCV RNA was extracted from 100 μl of blood serum sample, and the nucleotide sequences were determined by direct sequencing and deep sequencing. The primers used to amplify the NS3 region were NS3-F1 (5′-ACA CCG CGG CGT GTG GGG ACA T-3′, nucleotides 3295 to 3316) and NS3-AS2 (5′-GCT CTT GCC GCT GCC AGT GGG A-3′, nucleotides 4040 to 4019) as the first (outer) primer pair and NS3-F3 (5′-CAG GGG TGG CGG CTC CTT-3′, nucleotides 3390 to 3407) and NS3-AS2 as the second (inner) primer pair (18). Thirty-five cycles of first and second amplifications were performed as follows: denaturation for 30 s at 95°C, annealing of primers for 1 min at 63°C, extension for 1 min at 72°C, and final extension at 72°C for 7 min. The PCR-amplified DNA was purified after agarose gel electrophoresis and then used for direct sequencing and ultradeep sequencing.

Patients were examined for NS3/4A protease inhibitor-resistant variants by direct sequencing at baseline and at the time of reelevation of viral loads. Furthermore, patients who did not have an SVR with the first course of triple therapy with telaprevir and received the second course of the triple therapy with telaprevir were analyzed for telaprevir-resistant variants by ultradeep sequencing at baseline and at the time of reelevation of viral loads. NS3/4A protease inhibitor-resistant variants included V36A/C/M/L/G, T54A/S, Q80K/R/H/G/L, R155K/T/I/M/G/L/S/Q, A156V/T/S/I/G, D168A/V/E/G/N/T/Y/H/I, and V170A. Telaprevir-resistant variants (at aa 36, aa 54, aa 155, aa 156, and aa 170) and TMC435-resistant variants (at aa 80, aa 155, and aa 168) were evaluated (19, 20).

Direct sequencing was analyzed by the Dye Terminator method. Dideoxynucleotide termination sequencing was performed with the BigDye deoxy terminator version 1.1 cycle sequencing kit (Life Technologies, Carlsbad, CA) (18). The sequence data were deposited in GenBank. Also, ultradeep sequencing was performed using the Ion Personal Genome Machine (PGM) sequencer (Life Technologies). 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 8 cycles. Subsequently, the library was purified using AMPure beads (Beckman Coulter, Brea, CA) and the concentration determined using the StepOnePlus real-time PCR (Life Technologies) and Ion Library quantitation kit, according to the instructions provided by the manufacturers. Emulsion PCR was performed using the Ion OneTouch (Life Technologies) in conjunction with the Ion OneTouch 200 template kit version 2 (Life Technologies). Enrichment for templated Ion Sphere particles (ISPs) was performed using the Ion OneTouch enrichment system (Life Technologies) according to the instructions provided by the manufacturer. Templated ISPs were loaded onto an Ion 314 chip and subsequently sequenced using 130 sequencing cycles according to the Ion PGM 200 sequencing kit user guide. The total output read length per run was >10 Mb (0.5 million tags, 200-base read) (21). The results were analyzed with the CLC Genomics Workbench software (CLC bio, Aarhus, Denmark) (22).

We also included a control experiment to validate the error rates in ultradeep sequencing of the viral genome. In this study, the amplification products of the second-round PCR were ligated with a plasmid and transformed in *Escherichia coli* by using a cloning kit (TA Cloning; Invitrogen, Carlsbad, CA). A plasmid-derived NS3 sequence was determined as the template, in a control experiment. The fold coverages evaluated per position for aa 36, aa 54, aa 155, aa 156, and aa 170 in the NS3 region were 359,379×, 473,716×, 106,435×, 105,979×, and 49,058×, respectively. Thus, using the control experiment based on a plasmid carrying the HCV NS3 sequence, amino acid mutations were defined as amino acid substitutions at a frequency of >0.2% among the total coverage. This frequency ruled out putative errors caused by the ultradeep sequence platform used in this study (23).

Statistical analysis. Nonparametric variables were compared between the groups by the chi-square and Fisher's exact probability tests. Univariate and multivariate analyses for factors affecting the presence of telaprevir-resistant variants by direct sequencing at the reelevation of viral load were performed by the chi-square test and logistic regression, respectively. Patients who achieved an SVR were said to have no detection of resistant variants at the reelevation of viral load. The sensitivity, specificity, positive predictive value (PPV), and negative predictive value (NPV) were calculated to determine the reliability of the predictors of the response to therapy.

Nucleotide sequence accession numbers. The N-terminal sequences of the NS3 regions of the telaprevir-resistant variant isolates were deposited in GenBank under accession numbers AB709241, AB709263, AB709264, AB709276, AB709279, AB709283, AB709286, AB709289, AB709295, AB709296, AB709300, AB709303, AB709307, AB709310, AB709311, AB709312, AB709317, AB709319, AB709321, AB709322, AB709345, AB709348, AB709352, AB709353, AB709354, AB709356, AB709357, AB709358, AB709360, AB709370, AB709377, AB709382, AB709383, AB709384, AB709388, AB709390, AB709392, AB709396, AB709398, AB709399, AB709401, AB709405, AB709409, AB709410, AB709414, AB709418, AB709422, AB709426, AB709437, AB709444, AB709445, AB709451, AB709456, AB709461, AB709474, AB709476, AB709481, AB709484, AB709485, AB709486, AB709488, AB709489, AB709490, AB709491, AB709492, AB709493, AB709502, AB709507, AB709508, AB709514, AB709515, AB709525, AB709526, AB709527, and AB826566 to AB826684.

RESULTS

Virological response to therapy. An analysis of the entire group showed that 76% (192 of 252 patients) achieved an SVR. According to the treatment regimen, an SVR was achieved by 45% (9 of 20 patients) and 79% (183 of 232 patients) of the T12PR12 and T12PR24 groups, respectively. Taking into consideration the response to prior treatment, an SVR was achieved by 86% (68 of 79 patients), 84% (91 of 109 patients), and 35% (32 of 63 patients) of the treatment-naive patients, patients who showed relapse following prior treatment, and nonresponders to prior treatment, respectively. In the 231 patients of the T12PR24 group, an SVR was achieved by 88% (61 of 69 patients), 85% (89 of 105 patients), and

TABLE 2 Frequencies of the subjects in whom NS3/4A protease inhibitor-resistant variants were detected by direct sequencing at baseline and at the time of reelevation of viral loads[a]

Time of variant detection	% (*n*) by aa position[b]:						
	36	54	80	155	156	168	170
Baseline	0.4 (1)	3 (7)	22 (55)	0.4 (1)	0.8 (2)	10 (26)	0 (0)
Reelevation of viral load	7 (18)	12 (30)	5 (11)	0.4 (1)	4 (10)	1.2 (3)	0.4 (1)

[a] NS3/4A protease inhibitor-resistant variants included V36A/C/M/L/G, T54A/S, Q80K/R/H/G/L, R155K/T/I/M/G/L/S/Q, A156V/T/S/I/G, D168A/V/E/G/N/T/Y/H/I, and V170A (19, 20).

[b] The data represent the percentages (*n*) of patients in whom NS3/4A protease inhibitor-resistant variants were detected by direct sequencing. Patients who achieved a sustained virological response were said to have no detection of resistant variants by direct sequencing at the time of reelevation of the viral load.

56% (32 of 57 patients) of the treatment-naive patients, patients who showed relapse following prior treatment, and nonresponders to prior treatment, respectively. Furthermore, an SVR was achieved by 86% (12 of 14 patients) and 47% (20 of 43 patients) of the nonresponders to prior IFN monotherapy and ribavirin combination therapy, respectively.

NS3/4A protease inhibitor-resistant variants detected by direct sequencing at baseline and at the time of reelevation of viral loads. All of the 252 patients were evaluated for resistant variants by direct sequencing at baseline. Sixty patients who did not achieve an SVR were also analyzed for resistant variants by direct sequencing at the time of reelevation of viral load. One hundred ninety-two patients who achieved SVR were said to have no detection of resistant variants as determined by direct sequencing at the reelevation of viral load.

As a whole, the frequency of the subjects in whom telaprevir-resistant variants were detected increased from 5% (12 of 252 patients) at baseline to 18% (45 of 252 patients) at the time of reelevation of viral load. On the other hand, the frequency of the subjects in whom TMC435-resistant variants were detected decreased from 31% (78 of 252 patients) at baseline to 6% (14 of 252 patients) at the time of reelevation of viral load. Table 2 shows the frequencies of subjects in whom resistant variants were detected at baseline and at the time of reelevation of viral load per position for aa 36, aa 54, aa 80, aa 155, aa 156, aa 168, and aa 170 in the NS3 region.

Pretreatment factors associated with detection of telaprevir-resistant variants by direct sequencing at the time of reelevation of viral load. Univariate analysis of the data of the entire group identified eight pretreatment factors that were significantly associated with the detection of telaprevir-resistant variants by direct sequencing at the time of reelevation of viral load: *IL28B* rs8099917 genotype (genotype non-TT) ($P < 0.001$), nonresponse to prior treatment ($P < 0.001$), PEG-IFN dose of <1.3 μg/kg ($P = 0.001$), detection of variants at aa 54 at baseline ($P = 0.002$), Gln70/His70 substitution of aa 70 ($P = 0.003$), gamma-glutamyl transpeptidase (GGT) level of ≥50 IU/liter ($P = 0.006$), leukocyte count of <5,000/mm^3 ($P = 0.026$), and ribavirin dose of <8.0 mg/kg ($P = 0.026$). Multivariate analysis that included the above variables identified five pretreatment factors that were independently associated with the detection of telaprevir-resistant variants at the time of reelevation of viral load: PEG-IFN dose of <1.3 μg/kg (odds ratio [OR], 9.71; $P < 0.001$), *IL28B* rs8099917 genotype (genotype non-TT) (OR, 8.61; $P < 0.001$), detection of variants at aa 54 at baseline (OR, 33.4; $P = 0.002$), nonresponse to prior treatment (OR, 2.66, $P = 0.018$), and leukocyte count of <5,000/mm^3 (OR, 2.46; $P = 0.042$) (Table 3).

Prediction of treatment efficacy by the combination of response to prior treatment and presence of telaprevir-resistant variants by direct sequencing at baseline. The SVR rates based on the combination of response to prior treatment and the presence of telaprevir-resistant variants by direct sequencing at baseline are shown in Fig. 1. In 79 treatment-naive patients, the SVR rates were not different between those patients in whom there were no detected telaprevir-resistant variants (86% [65 of 76 patients]) and those in whom variants were detected (67% [2 of 3 patients]). In 109 patients who showed relapse following prior treatment, the SVR rates were not different between those patients in whom there were no detected variants (83% [86 of 104 patients]) and those in whom variants were detected (100% [5 of 5 patients]). In contrast, in 63 patients who showed nonresponse to prior treatment, a higher proportion of patients with undetected telaprevir-resistant variants (54% [32 of 59 patients]) achieved an SVR than did patients in whom telaprevir-resistant variants were detected (0% [0 of 4 patients]) ($P = 0.053$). Thus, with the combination of nonresponse to prior treatment and detection of telaprevir-resistant variants, the sensitivity, specificity, PPV, and NPV for those with non-SVR were 7% (4 of 60 patients), 100% (191 of 191 patients), 100% (4 of 4 patients), and 77% (191 of 247 patients), respectively. These results indicated that the use of the combination of the above two factors has high specificity and PPV for the prediction of a non-SVR.

TABLE 3 Multivariate analysis of factors associated with detection of telaprevir-resistant variants by direct sequencing at the reelevation of viral load, to telaprevir, peginterferon, and ribavirin triple therapy in patients infected with HCV genotype 1b

Detection factors	Category	Odds ratio (95% CI[a])	*P*[b]
PEG-IFN-α2b dose (μg/kg)	≥1.3	1	
	<1.3	9.71 (3.23–29.4)	<0.001
IL28B rs8099917 genotype	TT genotype	1	
	Non-TT genotype	8.61 (3.48–21.3)	<0.001
Variants of aa 54 at baseline	No detection	1	
	Detection	33.4 (3.77–295)	0.002
Response to treatment	Naive or relapse	1	
	Nonresponse	2.66 (1.18–5.96)	0.018
Leukocyte count (/mm^3)	≥5,000	1	
	<5,000	2.46 (1.03–5.85)	0.042

[a] CI, confidence interval.

[b] Only variables that achieved statistical significance ($P < 0.05$) on multivariate logistic regression analysis are shown.

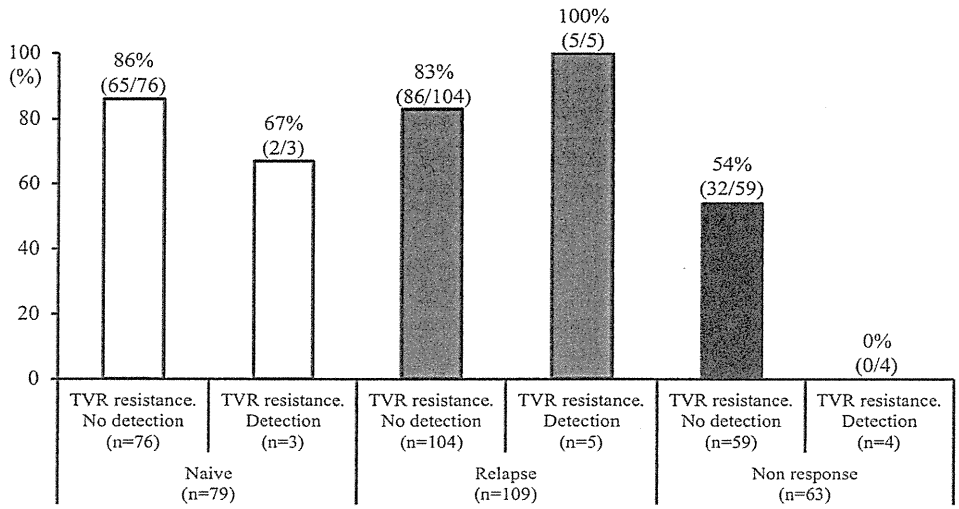

FIG 1 The rates of sustained virological response by the combination of response to prior treatment and presence of telaprevir (TVR)-resistant variants by direct sequencing at baseline are shown. Of those who showed nonresponse to prior treatment, a higher proportion of patients with undetected TVR-resistant variants (54%) achieved a sustained virological response than patients with detected TVR-resistant variants (0%) ($P = 0.053$).

Table 4 summarizes the profiles of 4 patients with nonresponse to prior treatment and in whom telaprevir-resistant variants were detected by direct sequencing at baseline. All of these 4 patients did not achieve an SVR with triple therapy. Interestingly, both T54S as a telaprevir-resistant variant and Q80L as a TMC435-resistant variant (19) were detected by direct sequencing at baseline.

Evolution of telaprevir-resistant variants over time as investigated by ultradeep sequencing in patients who received the second course of triple therapy. Two of 60 patients who did not achieve an SVR with the first course of triple therapy with telaprevir received the second course of triple therapy with telaprevir. They were analyzed for telaprevir-resistant variants by ultradeep sequencing at baseline and at the time of reelevation of viral loads.

Figure 2A shows the clinical course of case 1. In the first course of triple therapy with telaprevir (T12PR24) in a 57-year-old, V36C (0% of 32,413× coverage) was not detected by ultradeep sequencing at baseline of the first course, but very-high-frequency variants of V36C (97.2% of 36,757× coverage) were detected at the time of reelevation of viral loads. In the second course of triple therapy with telaprevir (T12PR54) when the patient was 59 years old, very-high-frequency variants of V36C (98.1% of 94,547× coverage) persisted at baseline of the second course, despite the passing of 2 years after cessation of the first therapy course. Case 1 achieved HCV RNA-negative status at 20 weeks after the start of the second course (late virological response), so PEG-IFN and ribavirin therapy was extended to 54 weeks. In conclusion, case 1 achieved an SVR after the second course of triple therapy with telaprevir, despite the persistence of very-high-frequency variants.

Figure 2B shows the clinical course of case 2. In the first course of triple therapy with telaprevir (T12PR24) in a 61-year-old patient, R155Q (0% of 23,751× coverage) and A156T (0% of 16,040× coverage) were not detected by ultradeep sequencing at baseline of the first course, but very-low-frequency variants of R155Q (0.2% of 11,572× coverage) and A156T (0.2% of 16,040× coverage) were detected at the time of reelevation of viral loads. In the second course of triple therapy with telaprevir (T12PR20) when the patient was 64 years old, R155Q (0% of 80,572× coverage) and A156T (0% of 87,686× coverage) were not detected by ultradeep sequencing at baseline of the second course, which was 2 years after cessation of the first course. In conclusion, case 2 achieved an SVR by the second course of triple therapy with telaprevir, despite the history of the emergence of variants.

TABLE 4 Profiles of 4 patients with nonresponse to prior treatment and detection of telaprevir-resistant variants by direct sequencing at baseline

Case no.	Sex	Age (yr)	Response to prior treatment[a]	Amino acid detected at aa position: 36	54	80	155	156	168	170	Time of HCV RNA-negative result during treatment (wks)	Efficacy of triple therapy
1	Male	70	Nonresponse to IFN monotherapy	V	S	L	R	A	D	I	2	Non-SVR
2	Male	47	Nonresponse to IFN monotherapy	V	S	L	R	A	D	I	4	Non-SVR
3	Male	61	Nonresponse to RBV combination therapy	V	S	L	R	A	D	I	3	Non-SVR
4	Female	60	Nonresponse to RBV combination therapy	V	S	L	R	A	D	I	4	Non-SVR

[a] RBV, ribavirin.

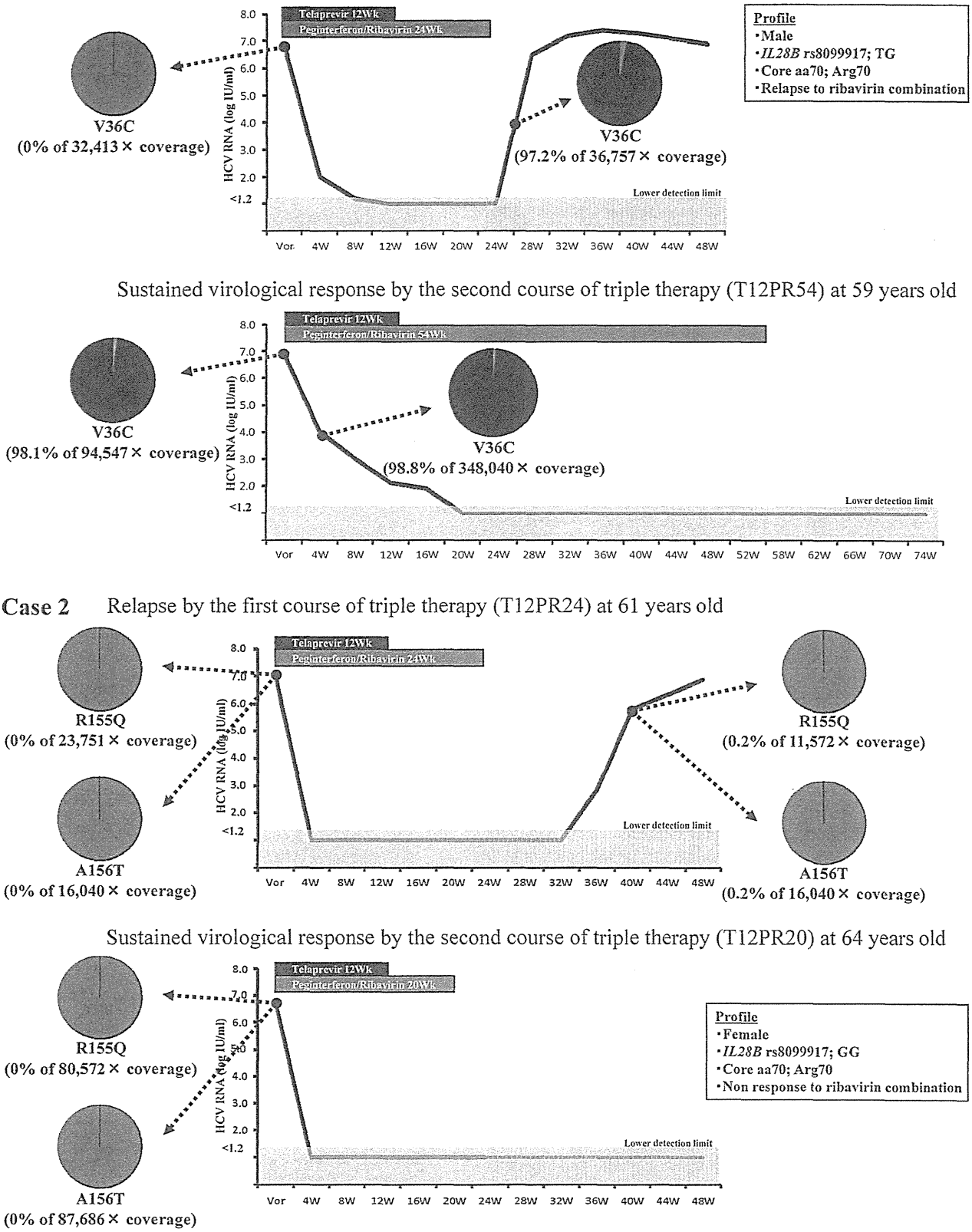

FIG 2 Two patients who did not achieve a sustained virological response with the first course of triple therapy with telaprevir received the second course of the triple therapy with telaprevir. They were analyzed for telaprevir-resistant variants by ultradeep sequencing at baseline and at the time of reelevation of viral loads. (A) Case 1 achieved a sustained virological response with the second course of therapy despite the persistence of very-high-frequency variants. (B) Case 2 achieved a sustained virological response with the second course of therapy despite the history of the emergence of variants.

DISCUSSION

Patients who fail to achieve an SVR to triple therapy need to be identified to avoid unnecessary side effects, high costs, and the emergence of telaprevir-resistant variants. Host genetic factors (e.g., *IL28B* genotype), and viral factors (e.g., amino acid substitutions in the core/NS5A region) have often been used as pretreatment predictors of poor virological response to PEG-IFN–ribavirin dual therapy (9–11, 15, 17) and telaprevir–PEG-IFN–ribavirin triple therapy (24–26). However, the pretreatment factors associated with the detection of telaprevir-resistant variants at the time of reelevation of viral load are still unknown. The present study identified that the detection of telaprevir-resistant variants at the time of reelevation of viral load can be predicted by a combination of host (*IL28B* rs8099917 genotype and leukocyte count), viral (variants of aa 54 at baseline), and treatment factors (PEG-IFN dose). All of the 4 patients with nonresponse to prior treatment and in whom telaprevir-resistant variants were detected at baseline did not achieve an SVR with triple therapy, and the use of the combination of nonresponse to prior treatment and the detection of telaprevir-resistant variants at baseline had high specificity and PPV for the prediction of a non-SVR. This finding suggests that there is a complex relationship between host susceptibility to IFN and viral sensitivity to NS3/4A protease inhibitors in determining treatment efficacy. Interestingly, in all of the 4 patients, both T54S as a telaprevir-resistant variant and Q80L as a TMC435-resistant variant (19) were detected by direct sequencing at baseline. This result suggests that patients with the above two factors should be carefully introduced to NS3/4A protease inhibitors besides telaprevir because of the high risk of the emergence of resistant variants. However, the present study was performed with a small number of patients, so further studies based on a larger number of patients should be performed.

In the present study employing ultradeep sequencing technology, 2 patients who did not achieve an SVR with the first course of triple therapy with telaprevir received the second course of the triple therapy with telaprevir. They achieved an SVR with the second course, despite the persistence of very-high-frequency variants (case 1, 98.1% for V36C) or a history of the emergence of variants (case 2, 0.2% for R155Q and 0.2% for A156T) as determined by ultradeep sequencing. This finding may be due to one or more reasons. One reason is probably related to the high susceptibility of telaprevir-resistant variants to IFN. One previous study indicated that mice infected with the resistant strain (A156F [99.9%]) developed only low-level viremia, and the virus was successfully eliminated with IFN therapy (27). In the other clinical report, telaprevir-resistant variants that emerged during 24-week telaprevir monotherapy were eliminated by the combination therapy of PEG-IFN plus ribavirin (28). Furthermore, this finding probably suggests that a small number of mutant-type viral RNAs may be incomplete or defective, since a large proportion of viral genomes are thought to be defective due to their high replication and mutation rates (29). Further studies employing ultradeep sequencing should be performed to evaluate whether a history of the emergence of NS3/4A protease inhibitor-resistant variants, besides telaprevir-resistant variants, affects the efficacy of a second course of NS3/4A protease inhibitor-based treatment.

The results of the present study should be interpreted with caution, since the study was performed with a small number of Japanese patients infected with HCV-1b. Any generalization of the results should await confirmation by a multicenter randomized trial based on a larger number of patients, including patients of other races and those infected with HCV-1a. Furthermore, the other limitation of the present study is that the loss of telaprevir-resistant variants was not investigated long after the cessation of therapy. Further large-scale studies should be performed to investigate the impacts of telaprevir-resistant variants on the response to treatment using new drugs, including direct-acting antiviral agents.

In conclusion, this study based on Japanese patients infected with HCV-1b indicates that telaprevir-resistant variants at the time of reelevation of viral load can be predicted by a combination of host, viral, and treatment factors. In those patients with no response to prior treatment, the present results suggest that telaprevir-resistant variants at baseline might partly affect the efficacy of triple therapy treatment. This finding indicates the clinical utility of detecting telaprevir-resistant variants to predict treatment efficacy, and it suggests a complex relationship between host susceptibility to IFN and viral sensitivity to NS3/4A protease inhibitors in determining treatment efficacy. Further large-scale prospective studies are needed to investigate the clinical usefulness of telaprevir-resistant variants and to develop more effective therapeutic regimens in patients infected with HCV-1.

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Antiviral Therapy

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