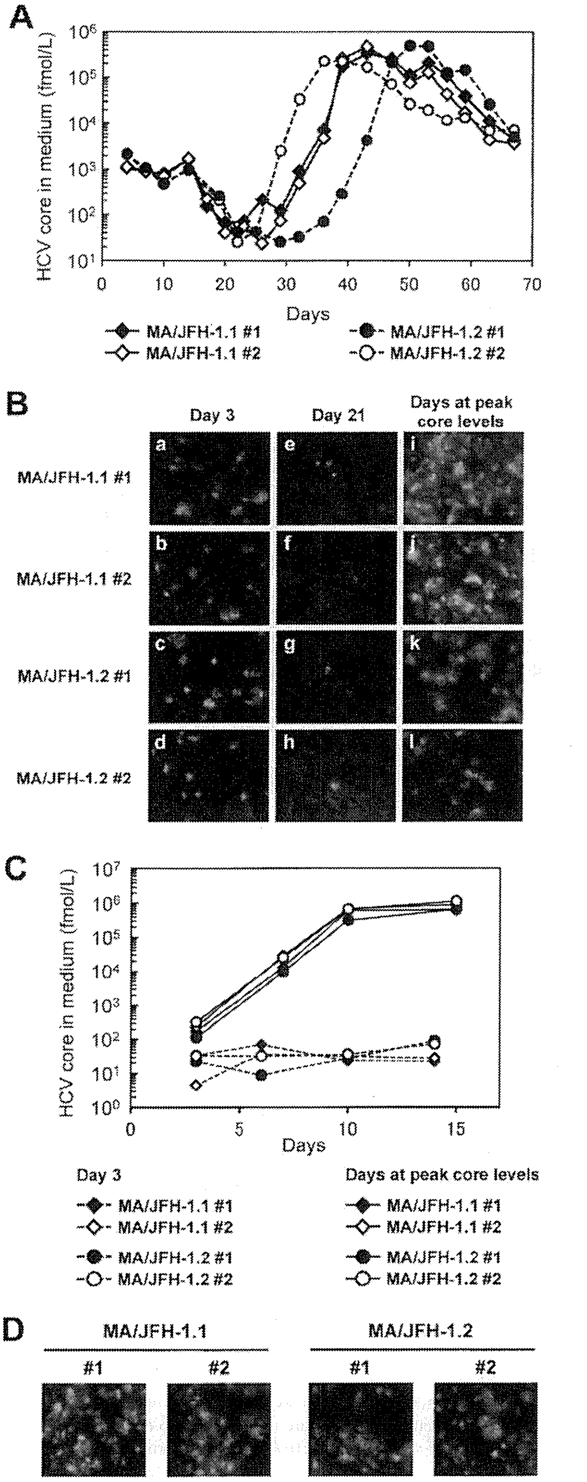


FIG 2 Long-term culture of MA/JFH-1.1 and MA/JFH-1.2 RNA-transfected cells. Ten micrograms of HCV RNA was transfected into Huh7.5.1 cells, and cells were passaged every 2 to 5 days, depending on cell status. Culture medium was collected after every passage, and HCV core protein levels were measured. Transfection was performed twice for each chimeric RNA (1 and 2 for each construct). (A) HCV core protein levels in culture medium from MA/JFH-1.1 and MA/JFH-1.2 RNA-transfected cells. (B) Immunostained cells at 3 days after transfection (a to d), at 21 days after transfection (e to h), and at the time of peak core levels (days 42 to 49). Infected cells were visualized with anti-core protein antibody (green), and nuclei were visualized with DAPI (blue). (C) Infection of naïve cells by culture medium at an MOI of 0.001. (D) Immunostained cells at 15 days after infection with medium at peak core protein levels (Fig. 2A) at an MOI of 0.001. Infected cells were visualized with anti-core antibody (green), and nuclei were visualized with DAPI (blue).

TABLE 1 HCV core protein levels and infectivity in culture medium immediately after RNA transfection (day 3) and after long-term culture (days 35 to 49)

Sample period and virus	Sample no.	Day no.[a]	HCV core (fmol/liter)	Infectivity (FFU/ml)
After transfection				
MA/JFH-1.1	1	3	1.06×10^3	5.00×10^1
	2	3	1.14×10^3	5.70×10^1
MA/JFH-1.2	1	3	2.14×10^3	7.30×10^1
	2	3	2.15×10^3	9.30×10^1
After long-term culture				
MA/JFH-1.1	1	42	3.38×10^5	1.62×10^5
	2	42	4.70×10^5	3.23×10^5
MA/JFH-1.2	1	35	2.27×10^5	1.61×10^5
	2	49	4.93×10^5	3.27×10^5

[a] For the long-term culture, the days are those of peak core protein levels.

as a 5′ UTR replacement from J6CF (genotype 2a) to JFH-1 enhanced virus production of chimeric J6CF virus harboring the region of NS2 to 3′ X of JFH-1 (J6/JFH-1) (A. Murayama et al., unpublished data). The core protein accumulation levels with MA/JFH-1.2 RNA-transfected cells were higher than those with MA/JFH-1.1 ($P < 0.05$) (Fig. 1B). Similarly, core protein and HCV RNA levels in the medium of MA/JFH-1.2 RNA-transfected cells were higher than those of MA/JFH-1.1 ($P < 0.05$) (Fig. 1C and D). Infectivity on day 3 was also higher than with MA/JFH-1.1 ($P < 0.05$) (Fig. 1E), indicating that the 5′ UTR of JFH-1 enhanced virus production. However, infectivity of medium from MA/JFH-1.2 RNA-transfected cells on day 3 remained 6.4-fold lower than that of JFH-1 although HCV RNA levels in the medium were similar to those of JFH-1 (Fig. 1D and E).

These results indicate that 2b/2a chimeric RNA is able to replicate autonomously in Huh7.5.1 cells and produce infectious virus although infectivity remains lower than that of JFH-1.

Assembly-enhancing mutation in core region introduced during long-term culture. Because MA/JFH-1.1 and MA/JFH-1.2 replicated efficiently but produced small amounts of infectious virus, we performed long-term culture of these RNA-transfected cells in order to examine whether these chimeric RNAs would continue replicating and producing infectious virus over the long term. We prepared two RNA-transfected cell lines for each construct (MA/JFH-1.1 and MA/JFH-1.2) as both of these replicated and produced infectious virus at different levels.

Immediately after transfection, core protein levels and infectivity in culture medium were low (1.06×10^3 to 2.15×10^3 fmol/liter and 5.00×10^1 to 9.30×10^1 FFU/ml, respectively) (Fig. 2A and Table 1) although a considerable number of core protein-positive cells were observed by immunostaining (Fig. 2B, frames a to d). Subsequently, core protein levels in the culture medium decreased gradually (Fig. 2A), and core protein-positive cells were rare (Fig. 2B, frames e to h). However, at 30 to 40 days after transfection, core protein levels in the supernatants of all chimeric RNA-transfected cells increased and reached 2.27×10^5 to 4.93×10^5 fmol/liter (Fig. 2A and Table 1). Infectivity in the culture medium also increased (1.61×10^5 to 3.27×10^5 FFU/ml) (Table 1), and at this point, most of the cells were core protein positive (Fig. 2B, frame i to l).

As the infectivity of culture supernatant of MA/JFH-1 RNA-transfected cells appeared to increase after long-term culture, we compared viral spread by infection with these supernatants on day 3 (immediately after transfection) and for each peak in core protein levels (after long-term culture). When naïve Huh7.5.1 cells were infected with supernatant on days corresponding to a peak in core protein levels at a multiplicity of infection (MOI) of 0.001, core protein levels in the medium increased rapidly and reached 0.64×10^6 to 1.13×10^6 fmol/liter by day 15 after infection (Fig. 2C). Immunostained images showed that most cells were HCV core protein positive on day 15 (Fig. 2D). When naïve Huh7.5.1 cells were infected with supernatant from day 3 at an MOI of 0.001, core protein levels in the medium did not increase under these conditions (Fig. 2C). These results indicate that both MA/JFH-1 chimeric viruses (MA/JFH-1.1 and MA/JFH-1.2) acquired the ability to spread rapidly after long-term culture.

As the characteristics of the MA/JFH-1 virus changed in long-term culture, we analyzed the possible mutations in the viral genome from the supernatant at each peak in core protein levels (Table 1, days at peak core levels). Nine- to 12-nucleotide mutations were found in the viral genome from each supernatant, and the detected mutations were distributed along the entire genome. Among these mutations, a common nonsynonymous mutation was found in the core region (Arg to Gly at amino acid [aa] 167, R167G).

In order to test the effects of R167G on virus production, an R167G substitution was introduced into MA/JFH-1.2 as MA/JFH-1.2 replicated and produced infectious virus more efficiently than MA/JFH-1.1. HCV core protein levels in cells and medium of MA/JFH-1.2 with R167G (MA/JFH-1.2/R167G) were higher than with MA/JFH-1.2 ($P < 0.05$) (Fig. 3A and B). HCV RNA levels in the medium of MA/JFH-1.2/R167G RNA-transfected cells were also higher than with MA/JFH-1.2 ($P < 0.05$) (Fig. 3C). Infectious virus production was also increased by the R167G mutation ($P < 0.05$) (Fig. 3D) and was 8.7-fold higher than that of JFH-1 RNA-transfected cells on day 3 ($P < 0.05$) (Fig. 3D).

We then tested whether R167G was responsible for the rapid spread observed in culture supernatant after long-term culture by monitoring virus spread after infection of naïve Huh7.5.1 with culture medium taken 3 days after RNA transfection of MA/JFH-1.2 and MA/JFH-1.2/R167G at an MOI of 0.005. Core protein levels in medium from MA/JFH-1.2/R167G-infected cells increased with the same kinetics as levels of JFH-1 (Fig. 3E), and the population of core protein-positive cells was almost the same as with JFH-1-infected cells (Fig. 3F), indicating that MA/JFH-1.2/R167G virus spread as rapidly as JFH-1 virus. In contrast, we observed no infectious foci in the MA/JFH-1.2 virus-inoculated cells (Fig. 3F). These data suggest that the R167G mutation in the core region was a cell culture-adaptive mutation and that it enhanced infectious MA/JFH-1.2 virus production.

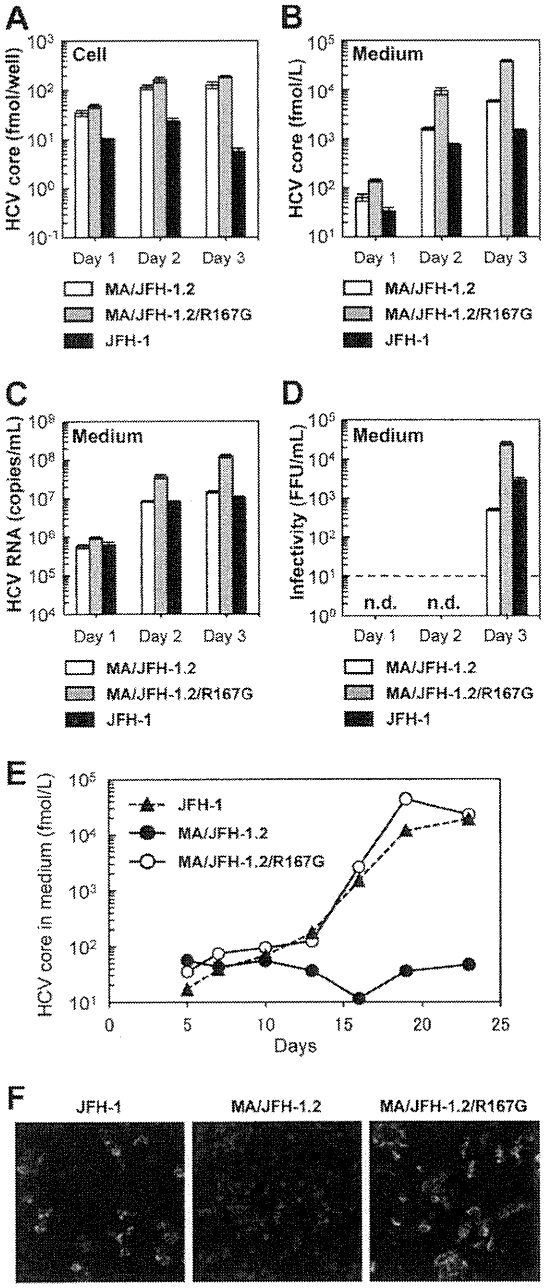


FIG 3 Effects of R167G on replication and virus production of MA/JFH-1.2 in Huh7.5.1 cells. Ten micrograms of HCV RNA was transfected into Huh7.5.1 cells, and cells and medium were harvested on days 1, 2, and 3. HCV core protein levels in the cells (A) and culture medium (B) and HCV RNA levels in the medium (C) and the infectivity of culture medium (D) from HCV RNA-transfected Huh7.5.1 cells are shown. n.d., not determined. Dashed line indicates the detection limit. Assays were performed three times independently, and data are presented as means ± standard deviation. (E) HCV core protein levels in culture medium from cells infected with medium at 3 days posttransfection at an MOI of 0.005. (F) Immunostained cells at 19 days postinfection. Infected cells were visualized with anti-core antibody (green), and nuclei were visualized with DAPI (blue).

In order to determine whether R167G enhances RNA replication or other steps in the viral life cycle, we performed a single-cycle virus production assay (11) using Huh7-25 cells, a HuH-7-derived cell line lacking CD81 expression on the cell surface (1). This cell line can support replication and infectious virus production upon transfection of HCV genomic RNA but cannot be reinfected by progeny virus, thereby allowing observation of a single cycle of infectious virus production without the confounding effects of reinfection. R167G did not affect HCV core protein levels in the chimeric RNA-transfected Huh7-25 cells (Fig. 4A), demonstrating that R167G did not enhance RNA replication. Nevertheless, R167G increased HCV core protein levels in the medium ($P < 0.05$ on days 2 and 3) and infectivity (Fig. 4B and C). These results suggest that R167G did not affect RNA replication but affected other steps such as virus assembly and/or virus secretion.

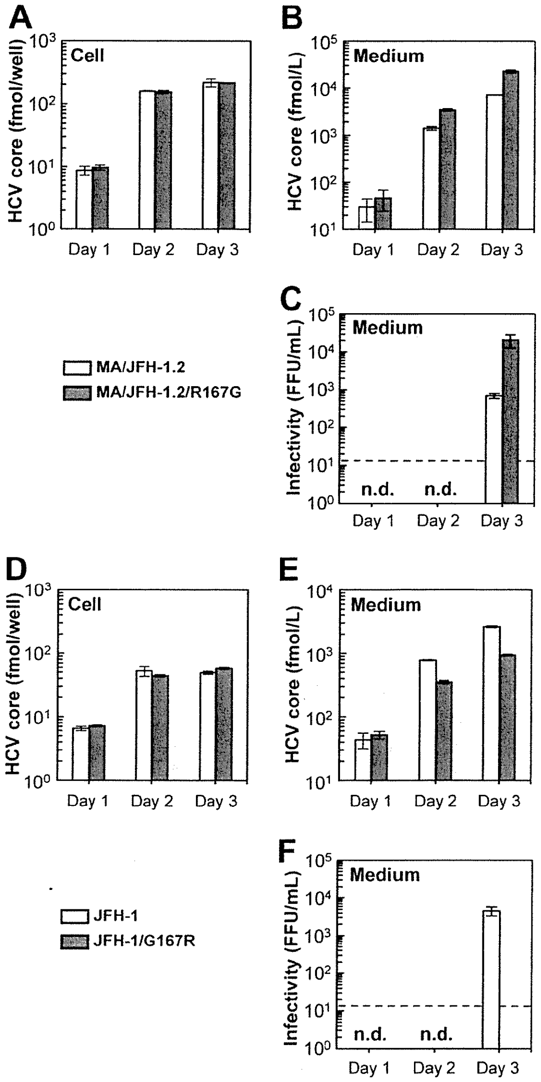
Virus particle assembly efficiency was then assessed by determining intracellular-specific infectivity from infectivity and RNA titer in the cells, as reported previously (11). As shown in Fig. 4G, R167G enhanced intracellular-specific infectivity of MA/JFH-1.2 virus 10.2-fold. Virus secretion efficiency was also calculated from the amount of intracellular and extracellular infectious virus, but R167G had no effect (Fig. 4G).

To confirm the effects of Arg167 in other HCV strains, we tested its effects on JFH-1. As aa 167 of JFH-1 is Gly, we replaced it with Arg (G167R). HCV core protein levels in the cells were not affected by G167R (Fig. 4D), and no effects on RNA replication were confirmed. HCV core protein levels in the medium and infectivity decreased after G167R mutation (Fig. 4E and F). As the G167R mutation decreased intracellular infectious virus production of JFH-1 to undetectable levels, we were unable to determine the intracellular-specific infectivity and virus secretion efficiency of JFH-1 G167R (Fig. 4G). These results indicate that Gly is favored over Arg at core position 167 for infectious virus assembly in multiple HCV strains.

MA harboring the R167G mutation, 5′ UTR, and N3H (NS3 helicase) and N5BX (NS5B to 3′ X) regions of JFH-1 replicated and produced infectious chimeric virus. In order to establish a genotype 2b cell culture system with the MA strain with minimal regions of JFH-1, we attempted to reduce JFH-1 content in MA/JFH-1.2. We previously reported that replacement of the N3H and N5BX regions of JFH-1 allowed efficient replication of the J6CF strain, which normally cannot replicate in cells (21). Thus, we tested whether the N3H and N5BX regions of JFH-1 could also support MA RNA replication.

We prepared two chimeric MA constructs harboring the 5′ UTR and N3H and N5BX regions of JFH-1, MA/N3H+N5BX-JFH1 (Fig. 5A) and MA/N3H+N5BX-JFH1/R167G. After *in vitro* transcribed RNA was transfected into Huh7.5.1 cells, intracellular core protein levels of MA/N3H+N5BX-JFH1 and MA/N3H+N5BX-JFH1/R167G RNA-transfected cells increased in a time-dependent manner and reached almost the same levels as with MA/JFH-1.2 RNA-transfected cells on day 5 (Fig. 5B). Extracellular core protein and HCV RNA levels of MA/N3H+N5BX-JFH1 and MA/N3H+N5BX-JFH1/R167G RNA-transfected cells also increased in a time-dependent manner (Fig. 5C and D). However, they were more than 10 times lower than with MA/JFH-1.2 RNA-transfected cells although intracellular core levels were comparable on day 5 (Fig. 5B to D).

We then tested whether the medium from MA/N3H+N5BX-JFH1 and MA/N3H+N5BX-JFH1/R167G RNA-transfected cells was infectious. Infectivity of the medium from MA/N3H+N5BX-JFH1 RNA-transfected cells was below the detection limit, and that of MA/N3H+N5BX-JFH1/R167G RNA-transfected cells on day 5 was very low ($3.3 \times 10^1 \pm 2.1 \times 10^1$ FFU/ml) (Fig. 5E). To confirm infectivity, the culture media were concentrated, and their infectivity was determined. Infected foci were observed after infection with concentrated medium in MA/N3H+N5BX-JFH1/R167G RNA-transfected cells (Fig. 5F), and infectivity was found



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Construct	Intracellular Specific Infectivity (FFU/ x10⁶ HCV RNA copies)	Infectious Virus Secretion (Extra/Intra)
MA/JFH-1.2	1.68 ± 0.404	20.2 ± 4.26
MA/JFH-1.2/R167G	17.1 ± 4.38	14.1 ± 1.65
JFH-1	1.78 ± 0.364	63.3 ± 6.44
JFH-1/G167R	NA	NA

FIG 4 Effects of R167G on replication and virus production of MA/JFH-1.2 and JFH-1 in Huh7-25 cells. Ten micrograms of HCV RNA was transfected into Huh7-25 cells, and cells and medium were harvested on days 1, 2, and 3. HCV core protein levels in cells (A and D) and in medium (B and E) were measured, and infectivity of medium (C and F) was determined. n.d., not determined. Dashed line indicates the detection limit. (G) Intracellular specific infectivity and virus secretion efficiency of chimeric HCV RNA-transfected cells. Intracellular and extracellular infectivity of day 3 samples was determined, and specific infectivity and virus secretion rate were calculated. Assays were performed three times independently, and data are presented as means ± standard deviation. NA, not available.

to be 7.27 × 10^2 ± 7.57 × 10^1 FFU/ml (Fig. 5G). No infected foci were observed after infection of MA/N3H+N5BX-JFH1 RNA-transfected cells, even when medium was concentrated (Fig. 5F), although intracellular and extracellular core protein levels were comparable to those with MA/N3H+N5BX-JFH1/R167G RNA-transfected cells (Fig. 5B and C). These results indicate that replacement of the 5′ UTR and N3H and N5BX regions in JFH-1 were necessary to rescue autonomous replication in the replication-incompetent MA strain and for secretion of infectious chimeric virus. However, the secretion and infection efficiencies of the virus were low.

Cell culture-adaptive mutations enhanced infectious virus production of MA/N3H+N5BX-JFH1/R167G. Because MA/N3H+N5BX-JFH1/R167G replicated efficiently but produced very small amounts of infectious virus, we performed a long-term culture of the RNA-transfected cells in order to induce cell culture-adaptive mutations that could enhance infectious virus production. We prepared RNA-transfected cells using two constructs, MA/N3H+N5BX-JFH1 and MA/N3H+N5BX-JFH1/R167G; both of these replicated efficiently, and MA/N3H+N5BX-JFH1/R167G produced infectious virus at low levels while MA/N3H+N5BX-JFH1 did not. Immediately after transfection, the HCV core protein levels in the medium of each RNA-transfected cell culture peaked at 3.0 × 10^3 fmol/liter and declined thereafter. However, the core protein level in the medium with MA/N3H+N5BX-JFH1/R167G RNA-transfected cells continued to increase and reached a peak of 2.7 × 10^5 fmol/liter 54 days after transfection, at which point most cells were core protein positive (Fig. 6B). The core protein level in the medium with MA/N3H+N5BX-JFH1 RNA-transfected cells did not increase and core-positive cells were scarce on day 54 (Fig. 6B). We analyzed the viral genome in the culture supernatants from day 54 for possible mutations and identified four nonsynonymous mutations in the MA/N3H+N5BX-JFH1/R167G genome: L814S (NS2), R1012G, (NS2), T1106A (NS3), and V1951A (NS4B). In order to test whether these amino acid substitutions enhance infectious virus production, L814S, R1012G, T1106A, and V1951A were introduced into MA/N3H+N5BX-JFH1/R167G, and the product was designated MA/N3H+N5BX-JFH1/5am (where am indicates adaptive mutation). On day 1, although HCV core protein levels in the MA/N3H+N5BX-JFH1/5am RNA-transfected cells were higher than those of MA/N3H+N5BX-JFH1/R167G RNA-transfected cells, they were still lower than those of MA/JFH-1.2/R167G RNA-transfected cells; however, on days 3 and 5, they reached a level comparable to that of MA/JFH-1.2/R167G RNA-transfected cells (Fig. 6C). HCV core protein and HCV RNA levels in the medium of MA/N3H+N5BX-JFH1/5am RNA-transfected cells were higher than those of MA/JFH-1.2/R167G RNA-transfected cells ($P < 0.05$, Fig. 6D and 6E, respectively). MA/N3H+N5BX-JFH1/5am, containing the four additional adaptive mutations, produced infectious virus at the same level as MA/JFH-1.2/R167G on day 5 (Fig. 6F). These results indicate that the

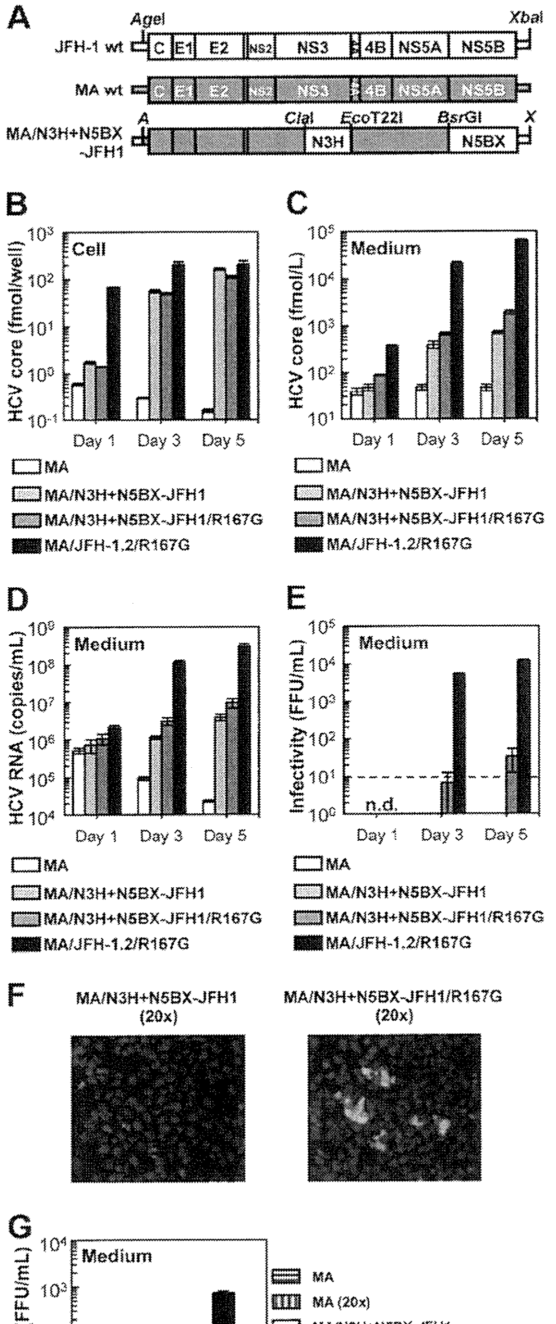

FIG 5 Replication and virus production of MA/N3H+N5BX-JFH1/R167G in Huh7.5.1 cells. (A) Schematic structures of JFH-1, MA, and MA/N3H+N5BX-JFH1. The junction of JFH-1 and MA in the 5′ UTR is an AgeI site; the junctions of MA and JFH-1 in the NS3 regions are ClaI and EcoT22I sites, and the junction in the NS5B region is a BsrGI site. A, AgeI; X, XbaI. (B to G) Chimeric HCV RNA replication in Huh7.5.1 cells. Ten micrograms of HCV RNA was transfected into Huh7.5.1 cells, and cells and medium were harvested on days 1, 3, and 5. HCV core protein levels in cells (B) and in medium (C) and HCV RNA levels in medium (D) were measured, and infectivity of medium (E) was determined. Assays were performed three times independently, and data are presented as means ± standard deviation. n.d., not determined. Dashed line indicates the detection limit. (F) Immunostained cells. Huh7.5.1 cells were infected with concentrated medium from RNA-transfected cells on day 5. Infected cells were visualized with anti-core antibody (green), and nuclei were visualized with DAPI (blue). (G) Infectivity of concentrated culture medium from HCV RNA-transfected cells. Culture medium was concentrated by 20 times. Infectivities of original and concentrated culture media were determined. Dashed line indicates detection thelimit.

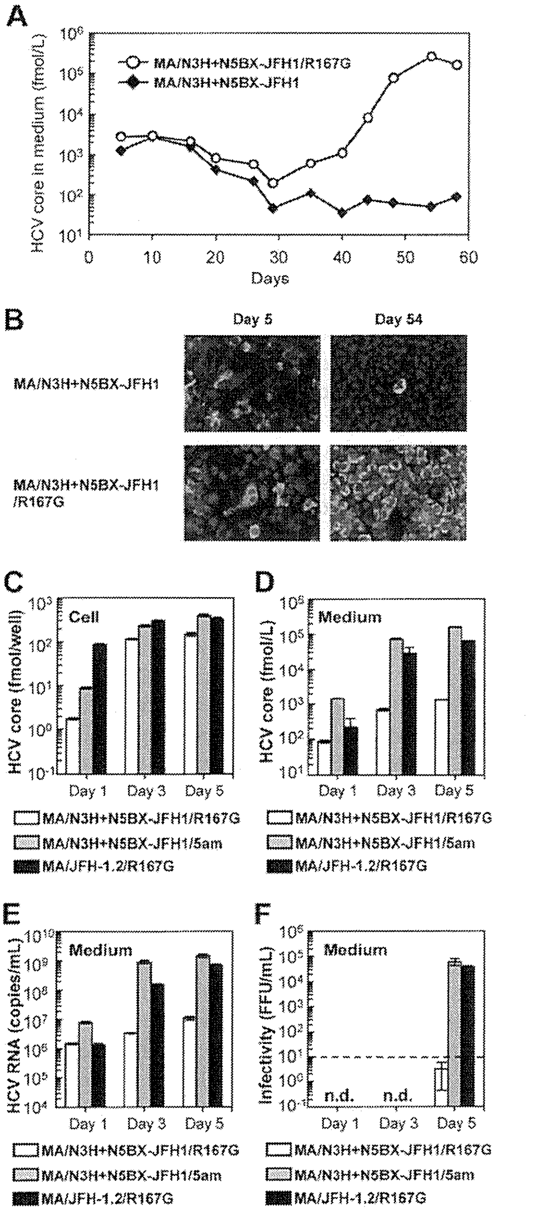

FIG 6 Cell culture-adaptive mutations enhanced infectious virus production of MA/N3H+N5BX-JFH1/R167G. (A) Long-term culture of MA/N3H+N5BX-JFH1 and MA/N3H+N5BX-JFH1/R167G RNA-transfected cells. Ten micrograms of HCV RNA was transfected into Huh7.5.1 cells, and cells were passaged every 2 to 5 days, depending on cell status. Culture medium was collected after every passage, and HCV core protein levels were measured. HCV core protein levels in culture medium from MA/N3H+N5BX-JFH1 and MA/N3H+N5BX-JFH1/R167G RNA-transfected cells are presented. (B) Immunostained cells on days 5 and 54 after transfection. Infected cells were visualized with anti-core antibody (green), and nuclei were visualized with DAPI (blue). (C to F) Effect of four additional cell culture-adaptive mutations on virus production. Ten micrograms of HCV RNA was transfected into Huh7.5.1 cells, and cells and medium were harvested on days 1, 3, and 5. HCV core levels in cells (C) and in medium (D) and HCV RNA levels in medium (E) were measured, and infectivity of medium (F) was determined. Assays were performed three times independently, and data are presented as means ± standard deviation. n.d., not determined. Dashed line indicates the detection limit.

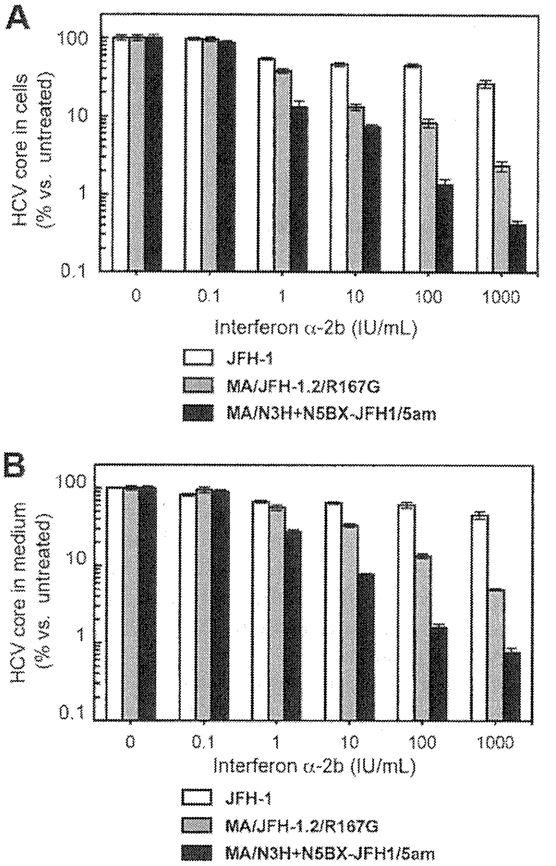

FIG 7 Comparisons of interferon sensitivity between JFH-1, MA/JFH-1.2/R167G and MA/N3H+N5BX-JFH1/5am. Two micrograms of HCV RNA was transfected into Huh7.5.1 cells, and interferon was added at the indicated concentrations at 4 h after transfection. HCV core protein levels in cells (A) and in medium (B) on day 3 were measured, and data are expressed as percent versus untreated cells (0 IU/ml). Assays were performed three times independently, and data are presented as means ± standard deviation.

four additional adaptive mutations enhance infectious virus production and that MA/N3H+N5BX-JFH1/5am RNA-transfected cells replicate and produce infectious virus as efficiently as MA/JFH-1.2/R167G RNA-transfected cells.

Comparison of interferon sensitivity between JFH-1, MA/JFH-1.2/R167G, and MA/N3H+N5BX-JFH1/R167G. Using the newly established genotype 2b infectious chimeric virus, we compared interferon sensitivity between the JFH-1, MA/JFH-1.2/R167G, and MA/N3H+N5BX-JFH1/5am viruses. JFH-1 or MA chimeric viral RNA-transfected Huh7.5.1 cells were treated with 0.1, 1, 10, 100, or 1,000 IU/ml interferon α-2b, and HCV core protein levels in the cells and in culture media were compared. Interferon decreased HCV core protein levels in the JFH-1 RNA-transfected cells and in the medium in a dose-dependent manner, and production was inhibited to 26.8% ± 3.0% and 45.6% ± 4.7%, respectively, of control levels (Fig. 7A and B, respectively). In contrast, HCV core protein levels in cells and medium of MA/JFH-1.2/R167G and MA/N3H+N5BX-JFH1/5am RNA-transfected cells decreased more pronouncedly in a dose-dependent manner (Fig. 7A and B, respectively). HCV core protein levels in cells and medium from MA/N3H+N5BX-JFH1/5am RNA-transfected cells were lower than those from MA/JFH-1.2/

R167G RNA-transfected cells (Fig. 7A and B, respectively) ($P < 0.05$ at 1, 10, 100, and 1,000 IU/ml), indicating that the MA/N3H+N5BX-JFH1/5am virus was more sensitive to interferon than the MA/JFH1.2/R167G virus, which contained more regions from JFH-1.

DISCUSSION

In this study, we developed a novel infectious HCV production system using a genotype 2b chimeric virus. To improve infectious virus production, we introduced two modifications into the chimeric genome.

First, we replaced the 5′ UTR from MA with that of JFH-1. Similarly to J6/JFH-1, replacement of the 5′ UTR increased core protein accumulation in both the cells and medium when these RNAs were transfected into Huh7.5.1 cells (Fig. 1). The same trend was observed when these RNAs were transfected into Huh7-25 cells (data not shown), indicating that the 5′ UTR of JFH-1 enhanced RNA replication. There are two genetic variations in J6CF and seven in MA in the region we replaced (nt 1 to 154 for J6CF and nt 1 to 155 for MA), and some of these mutations may affect RNA replication by changing the RNA secondary structure, RNA-RNA interactions, or binding of host or viral proteins.

Second, we introduced a cell culture-adaptive mutation (R167G) in the core region. This mutation was induced by long-term culture of MA/JFH-1 RNA-transfected cells (Fig. 2). MA/JFH-1 chimeric RNA (MA/JFH-1.1 and MA/JFH-1.2) replicated when synthesized RNA was transfected into the cells. However, infectious virus production was low, and virus infection did not spread over the short term. In early stages of long-term culture, the number of core protein-positive cells gradually decreased, and core protein-positive cells were scarcely detectable. Subsequently, the population of core protein-positive cells increased, reaching almost 100%. At this time point, we identified a common mutation in the core region (R167G) of the viral genome as a cell culture-adaptive mutation and found that it enhanced infectious virus production (Fig. 3). Several nonsynonymous mutations other than R167G were identified in the viral genome from each supernatant, and these mutations may enhance infectious virus production. However, there was a discrepancy between RNA levels and the infectivity of the culture media of MA/JFH-1.2 and MA/JFH-1.2/R167G RNA-transfected cells (Fig. 3C and D). The MA/JFH-1.2/R167G mutant had a 2-log increase in viral infectivity compared to that of MA/JFH-1.2 but only a 1-log increase in secreted RNA. The replication efficiency of MA/JFH-1.2 RNA-transfected cells was comparable to that of MA/JFH-1.2/R167G RNA-transfected cells, but the efficiency of infectious virus assembly within the cells was low, indicating that mainly noninfectious virus may be produced.

Infection of MA/JFH-1.2/R167G virus spreads rapidly, similarly to that of the JFH-1 virus, when it is inoculated into naïve Huh7.5.1 cells. On a single-cycle virus production assay, we found that the R167G mutation did not affect RNA replication or virus secretion but enhanced infectious virus assembly within the cells (Fig. 4). Efficient infectious virus assembly within the cells was mainly responsible for the rapid spread and high virus production of MA/JFH-1.2/R167G.

The amino acid at 167 (aa 167) is located in domain 2 of the core region, which is important for localization of the core protein (3, 8). Lipid droplet localization of the core protein and/or NS5A is important for infectious virus production (4, 18, 26). The interaction between the core protein and NS5A is also important for infectious virus production (16). Thus, aa 167 affects infectious virus production possibly by altering subcellular localization of the core protein or interaction between the core protein and NS5A. We examined the amino acid sequence of the core protein in 2,078 strains in the Hepatitis Virus Database (http://s2as02.genes.nig.ac.jp/) and found that aa 167 is Gly in all other strains. These data strongly suggest that Gly at aa 167 is important for the HCV life cycle. As the MA strain was cloned from the serum of a patient with chronic hepatitis C, the low virus production by this Gly at aa 167 may be important for persistent infection.

We then attempted to reduce the contents of JFH-1 from MA/JFH-1.2/R167G. We previously reported that the N3H and N5BX regions of JFH-1 were sufficient for replication of the J6CF strain (21). We also reported that this effect was observed only in genotype 2a strains (J6CF, JCH-1, and JCH-4). In this study, we tested whether the N3H and N5BX regions of JFH-1 could also support replication of a genotype 2b strain, MA. We constructed an MA chimeric virus harboring the N3H and N5BX regions of JFH-1 and combined this with the 5′ UTR of JFH-1 and the R167G mutation (MA/N3H+N5BX-JFH1/R167G). This chimeric RNA was able to replicate in the cells and produce infectious chimeric virus in culture medium although infectious virus production levels were low (Fig. 5).

We showed in this paper that the N3H and N5BX regions of JFH-1 were able to support RNA replication by both genotype 2a clones and genotype 2b clones, but the nucleotide sequence similarity between JFH-1 and MA was lower than that between JFH-1 and J6CF (77% versus 89%, respectively). Compared to MA/JFH-1.2/R167G, MA/N3H+N5BX-JFH1/R167G RNA showed the same levels of RNA replication and low levels of infectious virus production. To clarify whether there were any differences in the characteristics of the secreted virus, we performed density gradient ultracentrifugation with the MA/JFH-1.2/R167G and MA/N3H+N5BX-JFH1/R167G viruses. The distributions of the HCV core protein and infectivity showed similar profiles (data not shown).

The differences between MA/JFH-1.2/R167G and MA/N3H+N5BX-JFH1/R167G are the NS2, NS3 protease domain (N3P), and NS4A to NS5A regions. Nucleotide variation(s) other than aa 167 in these regions of the MA strain may be associated with reduced virus assembly. We identified four additional cell culture-adaptive mutations, L814S (NS2), R1012G (NS2), T1106A (NS3), and V1951A (NS4B), which resulted from long-term culture of MA/N3H+N5BX-JFH1/R167G RNA-transfected cells. Consequently, cells transfected with MA/N3H+N5BX-JFH1/5am constructed by insertion of these four adaptive mutations into MA/N3H+N5BX-JFH1/R167G replicated and produced infectious virus as efficiently as MA/JFH-1.2/R167G RNA-transfected cells (Fig. 6).

This system is able to contribute to studies into the development of antiviral strategies. It has been reported that HCV genotype 2a was more sensitive to interferon therapy than HCV genotype 2b in a clinical study (20). To assess the interferon resistance of genotype 2b, a cell culture system with multiple genotype 2b strains is necessary. The previously reported replicable genotype 2b chimeric virus harbored only structural regions of 2b strains (6, 27). The 2b/JFH-1 chimeric virus containing the region of the core protein to NS2 from the J8 strain (genotype 2b) and the region of NS3 to 3′ X of JFH-1 was able to replicate and showed that there were no differences in interferon sensitivity among the JFH-1 chimeric viruses of other genotypes (6, 27). Another 2b/JFH-1 chimeric virus containing the regions of the core protein to NS2 (nt 342 to 2867) of a genotype 2b strain and of NS2 to 3′ UTR (nt 2868) of JFH-1 has been reported (6, 27). The authors reported that their 2b/JFH-1 chimeric virus was more sensitive to interferon than JFH-1 (6, 27). We developed the genotype 2b HCV cell culture system with another HCV genotype 2b strain (MA). We identified a virus assembly-enhancing mutation in the core region, the minimal JFH-1 regions necessary for replication, and four additional adaptive mutations that enhance infectious virus production and demonstrated that MA harboring the five adaptive mutations and the 5′ UTR and N3H and N5BX regions of JFH-1 (MA/N3H+N5BX-JFH1/5am) could replicate and produce infectious virus efficiently.

Using these novel genotype 2b chimeric viruses, we assessed interferon sensitivity. We found that MA/JFH-1.2/R167G chimeric virus and MA/N3H+N5BX-JFH1/5am virus were more sensitive to interferon than the JFH-1 virus (Fig. 7). Furthermore, we found that MA/N3H+N5BX-JFH1/5am was more sensitive to interferon than MA/JFH-1.2/R167G, indicating that the genetic variation(s) in the NS2, N3P, and NS4A to NS5A regions affect interferon sensitivity. Although genotype 2a viruses are more sensitive to interferon than genotype 2b viruses in clinical studies, JFH-1 displayed interferon resistance in our study.

These results suggest that the JFH-1 regions in the 2b/JFH-1 virus affect the interferon sensitivity of the chimeric virus. Moreover, it was reported that amino acid variations in E2, p7, NS2, and NS5A were associated with the response to peginterferon and ribavirin therapy in genotype 2b HCV infection (10). Therefore, our MA/JFH-1 chimeric virus harboring minimal regions from JFH-1 (MA/N3H+N5BX-JFH1/5am) is more suitable for assessing the characteristics of the MA strain than the MA/JFH-1 chimeric virus, which includes a nonstructural region from JFH-1 (MA/JFH-1.2/R167G). We showed here that replacement of the 5′ UTR and N3H and N5BX regions in MA with those from JFH-1 is able to convert MA into a replicable virus. Using the same strategy, numerous HCV cell culture systems with various genotype 2b strains, as well as genotype 2a strains, may be available.

In conclusion, we established a novel HCV genotype 2b cell culture system using a chimeric genome in MA harboring minimal regions from JFH-1. This cell culture system using the chimeric genotype 2b virus will be useful for characterization of genotype 2b viruses and the development of antiviral strategies.

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Original Article

Recommendation of lamivudine-to-entecavir switching treatment in chronic hepatitis B responders: Randomized controlled trial

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Aim: In the 2007–2008 guidelines of the study group (Ministry of Health, Labor and Welfare of Japan), lamivudine (LAM)-continuous treatment was recommended in patients treated with LAM for more than 3 years who maintained hepatitis B virus (HBV) DNA less than 2.6 log copies/mL, because in these patients LAM resistance might exist and switching treatment to entecavir (ETV) might cause ETV resistance. However, there was no evidence on whether switching treatment to ETV- or LAM-continuous treatment was better in those patients. In the present study, we performed a randomized controlled trial of LAM-to-ETV switching treatment.

Methods: Twenty-seven patients treated with LAM for more than 3 years whose HBV DNA levels were less than 2.6 log copies/mL were enrolled and randomly divided into two groups, LAM-continued group or switching to ETV group. Then, we examined incidence of virological breakthrough (VBT) and breakthrough hepatitis (BTH) in each group.

Results: There was no BTH in any of the patients. VBT was observed in six patients of the LAM group (6/15, 40%), and no patient of the ETV group (0/11, 0%) ($P = 0.02$). The differences of the proportion of cumulated VBT using a log–rank test with Kaplan–Meier analysis were significant between the LAM and ETV groups ($P = 0.025$).

Conclusion: In patients treated with LAM for more than 3 years maintaining HBV DNA less than 2.6 log copies/mL, switching treatment to ETV is recommended at least during the 2 years' follow-up period.

Key words: chronic hepatitis B, entecavir, lamivudine, lamivudine resistance, randomized controlled trial, switching treatment

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INTRODUCTION

OVER THE PAST two decades, treatment of chronic hepatitis B (CHB) has greatly improved with the availability of nucleos(t)ide analogs (NA), including lamivudine (LAM), adefovir dipivoxil (ADV), entecavir (ETV), telbivudine, clevudine and tenofovir. NA target

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the reverse transcriptase of hepatitis B virus (HBV), and are highly effective in suppressing HBV replication and clinical progression to liver cirrhosis and hepatocellular carcinoma in CHB patients.[1–4]

Lamivudine, ADV and ETV are commonly available in Japan. LAM, the first approved NA, has been shown to provide benefit for CHB patients with respect to the reduction of HBV DNA, normalization of alanine aminotransferase (ALT) and improvement of liver histology.[5,6] However, a serious problem of LAM is the high incidence of drug resistance during long-term treatment. The detection rate of LAM resistance has been reported to be 24% at 1 year and 70% after 5 years of treatment.[7–10] Even when the HBV DNA level was maintained at less than 2.6 log copies/mL, the accumulated incidence of LAM resistance reached 65% in patients treated with LAM for a long period (3 to ~10 years).[11] LAM resistance is caused by amino acid substitution(s) at rtM204V/I within the reverse transcriptase domain of the HBV polymerase gene.[12–14] The emergence of a LAM-resistant strain leads to virological breakthrough (VBT) and breakthrough hepatitis (BTH).

Recently, ETV has been demonstrated to exert antiviral efficacy in both NA-naïve and LAM-resistant CHB patients.[15–17] The frequency of ETV resistance has been reported to be 1.2% after 5 years of treatment in NA-naïve CHB patients.[18,19] On the other hand, in switching treatment to ETV for LAM-resistant CHB patients, the cumulative probability of ETV resistance increases.[17,20] After 5 years of treatment, 51% of LAM-refractory patients treated with ETV showed genotypic ETV resistance.[21]

The 2007–2008 guidelines of the study group (Ministry of Health, Labor and Welfare of Japan) for patients on LAM therapy are summarized in Table 1.[22] Regardless of duration of LAM administration, in cases where HBV DNA is more than 2.6 log copies/mL with BTH, ADV add-on treatment was recommended. In patients treated with LAM for less than 3 years who maintained HBV DNA of less than 2.6 log copies/mL or HBV DNA of 2.6 log copies/mL or more without BTH, switching to ETV was recommended. On the other hand, in patients treated with LAM for more than 3 years who maintained HBV DNA of less than 2.6 log copies/mL or HBV DNA of 2.6 log copies/mL or more without BTH, LAM-continuous treatment was recommended because in these patients LAM resistance might exist, and switching treatment to ETV might cause ETV resistance. However, there is insufficient evidence on whether switching treatment to ETV- or LAM-continuous treatment is better for CHB patients treated with LAM for more than 3 years with HBV DNA of less than 2.6 log copies/mL.

In the present study, we performed a randomized controlled trial of LAM-to-ETV switching treatment in CHB patients treated with LAM for more than 3 years who maintained HBV DNA of less than 2.6 log copies/mL.

METHODS

Patients

A TOTAL OF 27 CHB patients (mean age 55 ± 9 years, 17 men) from 11 institutions all over Japan (Hokkaido University Hospital, Tohoku University Hospital, Akita City Hospital, Kuramitsu Clinic, Juntendo University Hospital, Chukyo Hospital, Nagoya City University Hospital, Okayama University Hospital, Kawasaki Medical University Hospital, Ehime University Hospital, Shin-Kokura Hospital) were enrolled from April 2008. All the patients were followed at least 6 months after they were diagnosed with CHB. Their characteristics are shown in Table 2. They were treated with LAM (100 mg/day) for more than 3 years (median 50 months, range 36–106 months). Before starting LAM administration, all patients were positive for hepatitis B surface antigen (HBsAg) in serum, abnormal for ALT, detectable for HBV DNA, and were not

Table 1 2007–2008 guidelines of the study group (Ministry of Health, Labor and Welfare of Japan) for patients on lamivudine treatment

Duration of lamivudine treatment HBV DNA		<3 years	≥3 years
<2.6 log copies/mL, persistently		May be switched to ETV 0.5 mg/day	LAM 100 mg/day
≥2.6 log copies/mL	No BTH†	May be switched to ETV 0.5 mg/day	LAM 100 mg/day
	With BTH	Add on ADV 10 mg/day	Add on ADV 10 mg/day

†After checking for absence of LAM resistance.
ADV, adefovir; BTH, breakthrough hepatitis; ETV, entecavir; HBV, hepatitis B virus; LAM, lamivudine.

Table 2 Characteristics of LAM continuous group and ETV switch group at baseline

	LAM (n = 15)	ETV (n = 11)	*P*-value
Male	10	6	NS
Age	53 ± 7	57 ± 7	NS
Duration of LAM administration (month)	59 ± 23	55 ± 18	NS
ALT (IU/L)	33 ± 29	28 ± 22	NS
HbeAg positive	1	1	NS

ALT, alanine aminotransferase; ETV, entecavir; HBeAg, hepatitis B e-antigen; LAM, lamivudine; NS, not significant.

infected with hepatitis C virus and HIV. Patients diagnosed with alcoholism, primary biliary cirrhosis or autoimmune hepatitis were excluded.

Study design

The overview of this study design is shown in Figure 1. Twenty-seven patients treated with LAM for more than 3 years were enrolled, who showed HBV DNA of less than 2.6 log copies/mL at entry. They were randomly divided into two groups by each institution, the LAM-continued group (LAM group) or switching to the ETV group (ETV group). The primary end-points were the incidences of VBT and BTH in each group. VBT was defined as having more than 1 log copies/mL increase of HBV DNA level from the nadir on at least two occasions after initial virological response. BTH was defined as showing abnormal ALT level due to LAM or ETV resistance. All subjects were monitored at least every 3-month intervals. At every visit, routine examination with biochemical (ALT, bilirubin, albumin) and virological (HBV DNA level, hepatitis B e-antigen [HBeAg], anti-HBe) assessments took place. The mean follow-up period was 24 ± 3 months.

This study was registered in the University Hospital Medical Information Network Clinical Trials Registry (UMIN-CTR) on 4 April 2008 as "A randomized trial of lamivudine continuous therapy and entecavir switching therapy for chronic hepatitis B patients treated with lamivudine monotherapy" (no. UMIN000001120).

The study protocol conformed to the Declaration of Helsinki, and was approved by the Committee for Ethics of Medical Experiments on Human Subjects of all the institutions, and written informed consent was obtained from every participant.

Serological and virological markers of HBV

Hepatitis B surface antigen, antibody against HBsAg (anti-HBs), HBeAg and antibody against HBeAg (anti-HBe) were determined using commercially available enzyme immunoassays. HBV DNA was determined by an Amplicor HBV Monitor (Roche Molecular Systems, Branchburg, NJ, USA; detection limit 2.6 log copies/mL)

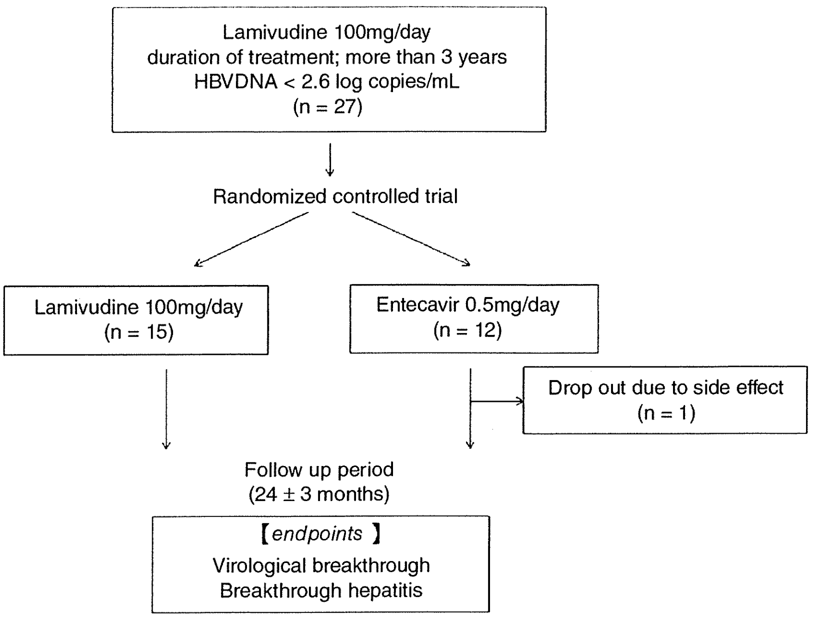

Figure 1 Overview of this study design. Twenty-seven patients treated with lamivudine for more than 3 years whose hepatitis B virus (HBV) DNA was maintained at <2.6 log copies/mL were enrolled. They were randomly divided into two groups by each institution, lamivudine-continued group or switching to entecavir group. We examined the incidence of virological breakthrough and breakthrough hepatitis in each group.

or COBAS AmpliPrep-COBAS TaqMan HBV test (Roche Molecular Systems; detection limit 2.1 log copies/mL). Positive results (signals) below the quantitative HBV DNA concentrations are referred to as "detected" and negative signals are "not detected" when registered by COBAS AmpliPrep-COBAS TaqMan HBV test. The presence of LAM-resistant rtM204V/I and rtL180M substitutions was analyzed by direct sequencing of the HBV DNA polymerase reverse transcriptase site.

Retrospective analysis

Using a conserved serum sample, we examined the existence of LAM-resistant rtM204V/I or rtL180M at baseline in patients with VBT. We also measured HBV DNA by COBAS AmpliPrep-COBAS TaqMan HBV test, and we evaluated the subsequent occurrence of VBT according to the DNA level (not detected/detected/2.1 to <2.6 log copies/mL).

Statistical analysis

Categorial variables were compared between groups by the χ^2-test or Fisher's exact test, and non-categorical variables by Mann–Whitney's *U*-test. The cumulated VBT rate was compared between each group using a log-rank test with Kaplan–Meier analysis. All data were analyzed using SPSS ver. 15.0J software. $P < 0.05$ was considered statistically significant.

RESULTS

Baseline characteristics of the patients

BASED ON THIS randomized controlled trial, 12 patients were placed in an ETV group and 15 in a LAM group. One patient in the ETV group dropped out because of skin rash by ETV. The baseline characteristics of the patients are described in Table 2. At the entry, one patient was positive for HBeAg in each group. There was no difference in sex, age, duration of LAM administration and ALT level between the two groups.

Incidence of VBT and BTH

There was no BTH in any of the patients. The incidence of VBT was six patients out of 15 (40%) in the LAM group, and no patient in the ETV group ($P = 0.02$). The Kaplan–Meier curve for the proportion of cumulated VBT is shown in Figure 2. The differences in the rates of VBT were significant between the LAM and ETV groups (log-rank test $P = 0.025$).

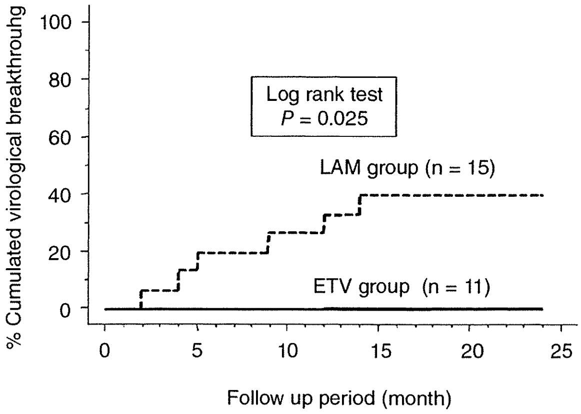

Figure 2 Proportion of cumulated virological breakthrough in lamivudine (LAM) and entecavir (ETV) group. The cumulated rate of virological breakthrough was higher in patients treated with LAM than those with ETV (40% vs 0%, $P = 0.025$ by log-rank test).

Characteristics of patients with VBT in LAM group

Details of the six VBT cases in the LAM group are described in Table 3. Assessment of LAM-resistant mutations at the time of VBT showed that both rtM204V and rtL180M were observed in all cases. For five of the six cases, HBV DNA was detected by COBAS AmpliPrep-COBAS TaqMan HBV test at baseline, although the HBV DNA level was very low. With respect to LAM-resistant mutation at baseline, rtM204V and rtL180M were observed in one of six cases. In contrast, no LAM-resistant mutations were observed in 20 non-VBT cases at baseline.

Incidence of VBT based on the HBV DNA level by COBAS AmpliPrep-COBAS TaqMan HBV test

Incidence of VBT based on the HBV DNA level according to COBAS AmpliPrep-COBAS TaqMan HBV test at baseline is shown in Figure 3. HBV DNA levels were less than 2.6 log copies/mL by Amplicor HBV Monitor in all cases. However, HBV DNA levels in the LAM group were "not detected" in five cases, "detected" in eight cases and 2.1 log copies/mL or more in two cases by COBAS AmpliPrep-COBAS TaqMan HBV test. VBT was observed in five of the 10 cases whose results were either "detected" or 2.1 log copies/mL or more and in one of the five "not detected" cases. On the other hand, although HBV DNA levels in the ETV group were

Table 3 Characteristics of patients with virological breakthrough in LAM group

		At baseline				At virological breakthrough		
Age	Sex	Duration of LAM administration (month)	HBeAg	HBV DNA by TaqMan HBV (log copies/mL)	Mutant of LAM resistance	Period of VBT (months)	HBV DNA (log copies/mL)	Mutant of LAM resistance
49	M	37	Negative	Detected	None	14	4.9	L180M/M204V
54	F	106	Negative	Detected	None	5	2.8	L180M/M204V
63	F	81	Negative	Not detected	None	9	4.5	L180M/M204V
57	F	43	Negative	Detected	None	10	3	L180M/M204V
55	M	84	Negative	Detected	None	12	2.8	L180M/M204V
57	M	36	Negative	2.3	L180M/M204V	2	4	L180M/M204V

ALT, alanine aminotransferase; ETV, entecavir; HBeAg, hepatitis B e-antigen; HBV, hepatitis B virus; LAM, lamivudine; VBT, virological breakthrough.

"detected" in six cases by COBAS AmpliPrep-COBAS TaqMan HBV test, there was no incidence of VBT: HBV DNA levels of five patients were undetectable and that of one patient was "detected" at the last follow-up point after switching to ETV.

DISCUSSION

AT PRESENT, LAM, ADV and ETV are only approved for treatment of CHB patients in Japan. ETV has become the first-line treatment for NA-naïve patients, because the ETV resistance is much less frequent than LAM-resistance.[8,23,24] On the other hand, in switching treatment to ETV for LAM-resistant CHB patients, the frequency of ETV resistance was increased.[17,20,25–27] It has also been reported that ADV add-on treatment suppressed HBV replication more effectively than ETV or ADV monotherapy in patients with LAM-resistant CHB.[25,28] Therefore, it is desirable to examine LAM-resistant mutants before switching to ETV in patients treated with LAM. However, as the assay for the LAM-resistant mutants is not covered by the Japanese health insurance system at present, the Japanese guidelines for CHB management after LAM therapy were based on HBV DNA, duration of LAM administration and incidence of BTH (Table 1).[22] In patients treated with LAM for more than 3 years, maintaining HBV DNA of less than 2.6 log copies/mL or HBV DNA of 2.6 log copies/mL or more without BTH, LAM-continuous treatment was recommended because in these patients, LAM-resistance might exist, and switching treatment to ETV might cause ETV-resistance. It was reported that although LAM-resistant strains were detected in 34% cases treated with LAM for more than 3 years and whose HBV DNA level was suppressed to less than 2.6 log copies/mL, switching to ETV maintained undetectable HBV DNA level over 2 years.[29] In addition, Kurashige *et al.* reported that LAM-to-ETV switching treatment maintained an undetectable HBV DNA level in patients with baseline HBV DNA of less than 2.6 and 2.6 to less than 4.0 log copies/mL for a period of ETV treatment ranging 10–23 (median 20) months.[30] In the present study, randomized controlled trial evidenced that switching treatment to ETV or LAM-continuous treatment would be recommended in CHB patients treated with LAM for more than 3 years and maintained HBV DNA of less than 2.6 log copies/mL. Interestingly, even though HBV DNA had been suppressed to less than 2.6 log copies/mL, a high rate of VBT was observed in the LAM group, whereas no VBT over 24 months was observed in the ETV group. Of the six patients with VBT,

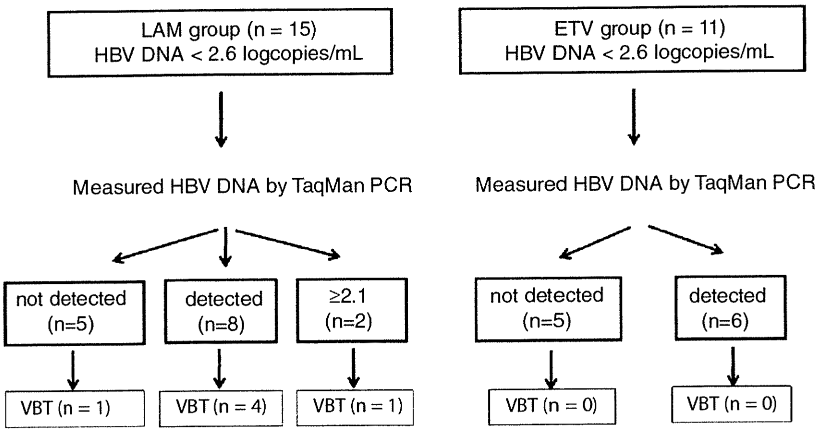

Figure 3 Incidence of virological breakthrough (VBT) based on the hepatitis B virus (HBV) DNA level at baseline by COBAS AmpliPrep-COBAS TaqMan HBV test (TaqMan PCR). The subsequent occurrence of VBT according to the DNA level by TaqMan PCR (not detected/detected/2.1 to <2.6 log copies/mL) was evaluated. In the lamivudine (LAM) group, VBT was observed in five of the 10 cases in which the results were either "detected" or ≥2.1 log copies/mL and in one of the five "not detected" cases. On the other hand, HBV DNA levels in the entecavir (ETV) group were "detected" in six, but there was no incidence of VBT.

five had no LAM resistance at baseline. However, the LAM resistance of rtM204V and rtL180M were found in all the patients with VBT in the LAM group. Moreover, a retrospective assessment by COBAS AmpliPrep-COBAS TaqMan HBV test showed that HBV DNA was detectable in 10 patients in the LAM group and six patients in the ETV group. Only five of the 10 patients in the LAM group had VBT, but none in the ETV group. In addition, one patient had VBT in the LAM group even though DNA was not detected by the TaqMan test, suggesting that switching to ETV was preferable. Hence, our data supported the 2010 Japanese guidelines which recommend switching to ETV in patients whose HBV DNA levels are less than 2.1 log copies/mL by TaqMan PCR.

A potential limitation of the present study is that the number of the cases was small. Nevertheless, our randomized controlled trial indicated significant difference in the incidence of VBT between the LAM and ETV groups. Therefore, this study is valuable for the purpose of verifying the 2007–2008 guidelines in Japan. In the present study, although no LAM-resistant mutant was observed in the ETV group at baseline, a very low level of LAM-resistant mutants may derive ETV resistance for long-term therapy. The results of switching to ETV in the present study were favorable during the 24-month observation period, but we have to be careful of possible emergence of ETV-resistant mutants in long-term follow up.

In conclusion, in patients treated with LAM for more than 3 years maintaining HBV DNA of less than 2.6 log copies/mL, switching treatment to ETV is recommended in at least a 2-year follow-up period.

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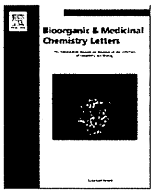

Antiviral activity of novel 2′-fluoro-6′-methylene-carbocyclic adenosine against wild-type and drug-resistant hepatitis B virus mutants

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ABSTRACT

Novel 2′-fluoro-6′-methylene-carbocyclic adenosine (**9**) was synthesized and evaluated its anti-HBV activity. The titled compound demonstrated significant antiviral activity against wild-type as well as lamivudine, adefovir and double lamivudine/entecavir resistant mutants. Molecular modeling study indicate that the 2′-fluoro moiety by a hydrogen bond, as well as the van der Waals interaction of the carbocyclic ring with the phenylalanine moiety of the polymerase promote the positive binding, even in the drug resistant mutants.

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Chronic hepatitis B virus (HBV) infection is one of the leading causes of morbidity and mortality worldwide. Chronic infection with HBV occurs in approximately 350 million of the world population, including 1.7 million in the USA.[1] HBV infection can persist for the life of the host, often leading to severe consequences such as liver failure, cirrhosis and eventually hepatocellular carcinoma, resulting in annually 0.5–1.2 million deaths worldwide.[2] HBV is an incomplete double-stranded DNA virus. Its DNA replication is unique because it includes a reverse transcription step. The HBV DNA polymerase/reverse transcriptase is an essential and multifunctional enzyme, which operates as a DNA polymerase/reverse transcriptase, an RNAse H, through coordinating the assembly of viral nucleocapsids, as well as catalyzing the generation of DNA primers.[3] Nucleoside analogues can suppress HBV replication by inhibiting the viral polymerase/reverse transcriptase. The pivotal role of nucleoside/nucleotide analogues such as lamivudine, adefovir, telbivudine, entecavir, clevudine, and tenofovir has been demonstrated by their therapeutic efficacy in clinical practice. However, long-term therapy with these drugs is often associated with viral resistance, which significantly compromises the clinical application of these agents. For example, the extensive use of lamivudine resulted in the emergence of mutants that are resistant to the anti-HBV activity; 24% after a 1-year therapy, increasing to over 70% after 4 years of therapy. Adefovir has been used for the patients, who develop lamivudine-resistant mutants, however, a significant number of patients (29% after 5 years of use) also develop the adefovir resistant mutant (N236T).

Entecavir is a carbocyclic 2′-deoxyguanosine analog that demonstrates potent anti-HBV activity[4] and is recommended for patients with the wild-type strain as well as for those patients harboring lamivudine-resistant strains.[5] However, a recent study by Tanaka and his co-workers suggest that the viral breakthrough was observed in the lamivudine-refractory group in 4.9% of patients at baseline and increase to 14.6%, 24% and 44.8% at weeks 48, 96 and 144, respectively.[6]

In view of the fact that currently adefovir and entecavir are the most prescribed drugs for the treatment of chronic HBV infection, it is critical to discover the agents that do not confer cross-resistance with the adefovir and lamivudine/entecavir-mutants for the future treatment of drug resistant patients. In this report we try to demonstrate that our newly discovered compound **9** may potentially play a significant role for that purpose.

Carbocyclic nucleosides are an interesting class of compounds in which the methylene group replaces the oxygen atom of a furanose ring. As a consequence, the glycosidic bond is resistant to nucleoside phosphorylase as well as nucleoside hydrolase, which makes the carbocyclic nucleosides more stable towards metabolic

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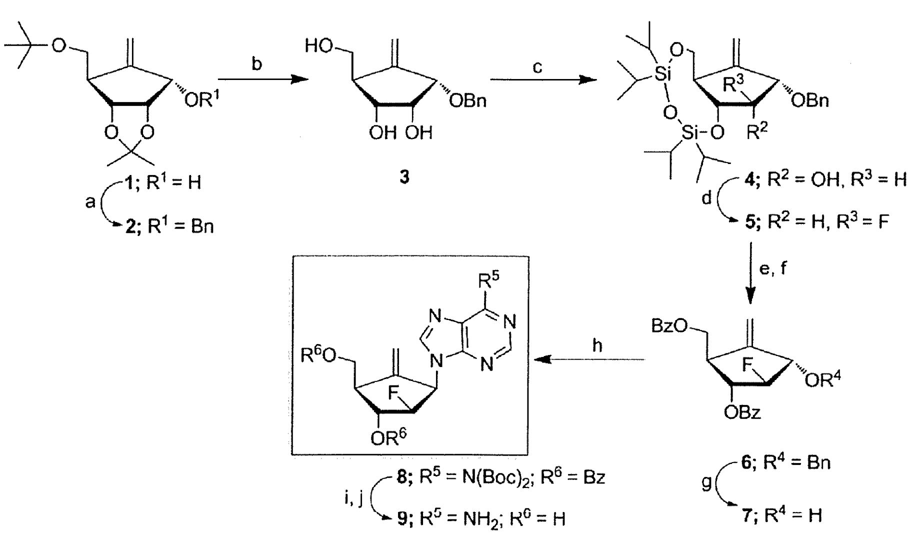

Scheme 1. Synthesis of target compound **9**. Reagents and conditions: (a) NaH, BnBr, DMF, 0 °C; (b) TFA/H_2O (2:1), 50 °C; (c) $TIDPSCl_2$/imidazole, DMF, 0 °C; (d) DAST, CH_2Cl_2, rt; (e) TBAF/AcOH, THF, rt; (f) BzCl, pyridine, rt; (g) BCl_3, CH_2Cl_2, −78 °C; (h) *N,N*-dibocprotected adenine, DIAD, Ph_3P, THF, 0 °C; (i) TFA, CH_2Cl_2, rt; (j) DIBAL-H, CH_2Cl_2, −78 °C.

degradation.[7] Due to these features, carbocyclic nucleosides have received much attention as potential chemotherapeutic agents.[8] Carbovir and entecavir are examples of results of these efforts.

It is also well known that incorporation of a fluorine atom at the 2′-position of nucleosides can increase the stability of the glycosyl bond towards chemical and metabolic degradation.[9,10] A fluorine substitution on the carbocyclic sugar moiety has been proven to be useful in producing effective antiviral agents as demonstrated by our group in 2′-fluoro-5-methyl-β-L-arabinofuranosyluracil (L-FMAU or clevudine)[11] as well as in clofarabine.[12]

In view of the 2′-F substitution[9,10] as well the introduction of an exocyclic double bond to carbocyclic nucleosides,[4] which have been beneficial for anti-HBV activity such as in entecavir, 2′-fluoro-6′-methylene-carbocyclic adenosine or (+)-9-[(1*R*,2*R*,3*R*,4*R*)-2-fluoro-3-hydroxy-4-(hydroxymethyl)-5-methylenecyclopentan-1-yl] adenine **9** was synthesized and evaluated for its antiviral activity against wild-type HBV as well as adefovir, lamivudine and lamivudine/entecavir (double)-resistant mutants in vitro.

The synthesis of the target nucleoside **9** commenced with compound **7** as the key intermediate (Scheme 1). Compound **1** was synthesized according to the reported procedure from our group.[13] The allylic hydroxyl group of **1** was protected with a benzyl group and subsequent deprotection of the acetonide and the *t*-butyl group of compound **2** gave **3** in 86% yield. The 3, 5-hydroxy groups of **3** were selectively protected with 1,3-dichloro-1,1,2,2-tetraisopropyl disilazine to give **4** in 95% yield. Transformation of the 2-β-hydroxyl group to 2-α-fluoro was accomplished by treating the alcohol **4** with DAST to give 47% yield of compound **5**. However, debenzylation of **5** was unsuccessful under the Birch reduction or the Lewis acid (BCl_3) conditions. Therefore, the silyl group of **5** was removed by using tetrabutyl ammonium fluoride (TBAF/HOAc) to yield 82% of a diol, which was re-protected by benzoyl chloride in pyridine to give the fully protected intermediate **6** in 86% yield. The compound **6** was then treated with BCl_3 at −78 °C to obtain the key intermediate **7** in 76% yield. *N,N*-diboc protected adenine was synthesized according to the reported protocol in literature[14] and condensed with **7** to obtain **8** in 51% yield. The deprotection of the Boc group was carried out by TFA to afford 82% yield. Eventually, the treatment of DIBAL-H gave the target compound **9**[15] in 76% yield.

The synthesized nucleoside **9** was evaluated for its antiviral activity against wild-type HBV as well as adefovir, lamivudine and lamivudine/entecavir-drug resistant mutants in vitro,[16] and the results are summarized in Table 1. As the compound **9** is a derivative of an adenine analog, we directly compared its antiviral activity to that of adefovir instead of entecavir (a guanine analog) although the carbocyclic moiety is similar to that of entecavir. Furthermore, compound **9**, an adenine analogue, can interact with the thymidine moiety in the DNA template-primer site while entecavir interacts with the cytosine moiety at the same site in the active site. Thus, the base moiety is the major deciding factor, not the sugar moiety in determining the mode of action.

The target compound **9** demonstrated a significant antiviral in vitro activity against wild-type (WT) HBV with an EC_{50} value of 1.5 μM. The antiviral potency was similar to that of adefovir, while being 7-fold less potent than lamivudine. However, the concentration of the compound **9** required to inhibit 90% (EC_{90}) of wild-type HBV is 4.5 μM, which is 1.5-fold more potent than adefovir (EC_{50} 7.1 μM; Table 1).

The compound **9** also showed excellent activity against both lamivudine and adefovir resistant HBV mutants.[17] Particularly, the compound **9** showed a 4.5-fold enhanced potency of EC_{50} (1.7 μM) and a 7.8-fold more favorable EC_{90} (4.6 μM) against adefovir mutant rtN236T. For lamivudine mutants, rtM204V and rtM204I, the compound **9** showed an EC_{50} value of 1.8 versus 1.6 μM for adefovir, and 1.0 versus 1.9 μM for compound **9** and adefovir, respectively, while in the EC_{90} value, compound **9** demonstrated more favorable anti-HBV activity for both mutants, rtM204 V (4.7 vs 7.0 μM) and rtM204I (5.0 vs 8.0 μM). For mutant rtL180M, the antiviral activity of compound **9** was similar to that of lamivudine in the EC_{50} 2.1 versus 1.5 μM, while the compound **9** exhibited a 4.3-fold increased antiviral activity in the EC_{90} value (5.1 vs 22.0 μM).

Compound **9** was also evaluated against the lamivudine double mutant, rtL180M/rtM204V, and it exhibited the EC_{50} 2.2 μM that was equal to the adefovir, while the EC_{90} value of 5.5 μM of compound **9** was more effective than that of adefovir (8.5 μM). In addition, deamination studies with adenosine deaminase from calf thymus indicated that the compound **9** was completely stable.[18]

In preliminary studies, compound **9** was also evaluated against lamivudine/entecavir double resistant clone (L180M + S202I + M202V), in which compound **9** demonstrated significant anti-HBV activity (EC_{50} 0.67 μM) against the mutant. In the case of lamivudine and entecavir, there are significant decrease in their

Table 1
In vitro anti-HBV activity against adefovir, lamivudine and entecavir drug-resistant mutants in the intracellular HBV DNA replication assay[16,17]

Strains	Compound **9** (μM)				Adefovir (μM)			Lamivudine (μM)			Entecavir (μM)		
	EC$_{50}$[b]	EC$_{90}$[c]	CC$_{50}$[d,e]	Fold resistance[f] (EC$_{90}$)	EC$_{50}$	EC$_{90}$	Fold resistance (EC$_{90}$)	EC$_{50}$	EC$_{90}$	Fold resitance (EC$_{90}$)	EC$_{50}$	EC$_{90}$	CC$_{50}$
Wild Type	1.5	4.5	>100	—	1.3	7.1	—	0.2	0.6	—	0.008	0.033	28
rtM204V	1.8	4.7	>100	1.0	1.6	7.0	1.0	>100	>100	>166	NT[h]	NT	NT
rtM204I	1.0	5.0	>100	1.1	1.9	8.0	1.1	>100	>100	>166	NT	NT	NT
rtL180M	2.1	5.1	>100	1.1	5.5	7.7	1.1	1.5	22.0	36.7	NT	NT	NT
rtLM/rtMV[a]	2.2	5.5	>100	1.2	2.1	8.5	1.2	>100	>100	>166	NT	NT	NT
rtN236T	1.7	4.6	>100	1.0	7.8	36.0	5.1	0.2	0.9	1.5	NT	NT	NT
rtLM/rtMV/rtSG[g]	0.67	NT	NT	—	NT	NT	—	>500[i]	NT	—	1.20[j]	NT	NT

[a] rtLM/rtMV = rtL180M/rtM204V double mutant.
[b] Effective concentration required to inhibit 50% of HBV-DNA.
[c] Concentration required to reduce infectious virus titer by 90%.
[d] The > sign indicates that the 50% inhibition was not reached at the highest concentration tested.
[e] The drug concentration required to reduce the cellular viability by 50% as assayed by an MTT assay.
[f] Fold resistance = (mutant EC$_{90}$)/(wt EC$_{90}$).
[g] rtLM/rtMV/rtSG = rtL180M/rtM204V/rtS202G.
[h] NT = not tested.
[i] Ref. 19.
[j] Ref. 20.

antiviral potency (EC$_{50}$ > 500 and 1.2 μM, respectively) as shown in Table 1.[19,20]

It was of interest to know how the compound **9** demonstrated the favorable anti-HBV activity in comparison to that of adefovir. Therefore, molecular modeling studies were conducted to obtain the insight of the molecular mechanism of compound **9** by using the Schrodinger suite.[21] The homology model of HBV RT was constructed based on the published X-ray crystal structure of HIV reverse transcriptase (PDB code: 1RTD),[22] which was previously used for molecular mechanism studies of several anti-HBV nucleosides.[23] In the homology model of HBV polymerase, the relative position of α-, β- and γ-phosphates of compound **9** with respect to the catalytic triad were assumed to occupy the similar position to the dNTP in the crystal structure of the HIV-1 RT-DNA-dNTP complex. The molecular docking[24] of compound **9** shows that the triphosphate forms all the network of hydrogen bonds with the active site residues, S85, A86, A87, R41, K32 (Fig. 1a). The γ-phosphate of compound **9** retains a critical H-bonding with the OH of S85 with connection of hydrogen bonds between S85 and N236. Generally, the N236T mutant loses the hydrogen bond to S85, which results in destabilization of the S85 to γ-phosphate interaction, thus causes resistance. However, compound **9** (as its triphosphate) maintains a critical H-bonding with S85 (Fig. 1b) similar to that as observed in wild type HBV (Fig. 1a).

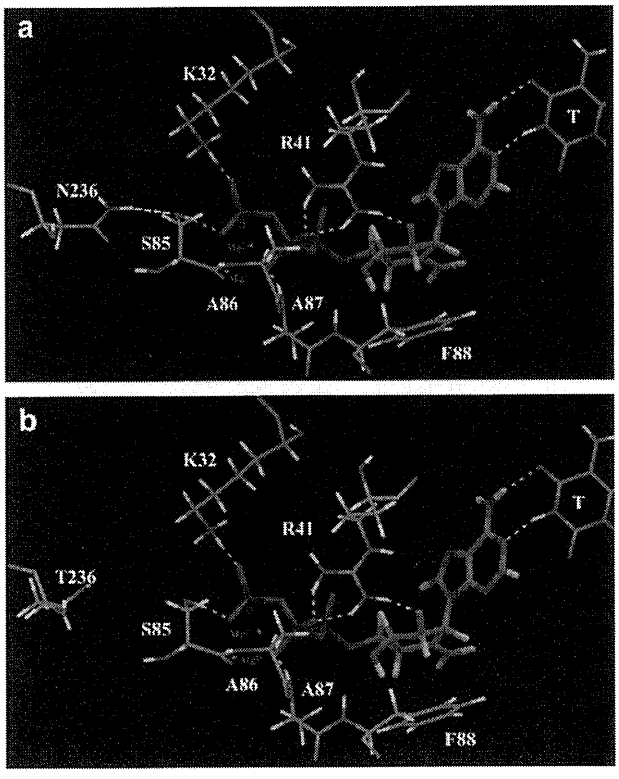

Figure 1. Binding mode and van der Waals interaction of compound **9** (a) in wild-type HBV and (b) in N236T adefovir mutant HBV. Yellow dotted lines are hydrogen bonding interactions (<2.5 Å).

The carbocyclic ring with an exocyclic alkene of compound **9** occupies the hydrophobic pocket (residues F88, L180 and M204) and makes the favorable van der Waals interaction with F88 (Fig. 1a and b). The 2′-fluorine substituent in the carbocyclic ring of compound **9** appears to promote an additional binding with R41 as shown in Figure 1a and b, which corroborates with the antiviral activity of compound **9** shown in Table 1. Overall, the modeling studies can qualitatively explain the favorable anti-HBV activity of the newly discovered compound **9** in WT (Fig. 1a) as well as against adefovir resistant mutant, N236T (Fig. 1b). These modeling studies are qualitative, and therefore, more quantitative calculation is warranted in the future.

In summary, a novel carbocyclic adenosine derivative **9** was synthesized, and evaluated for its anti-HBV activity. From these studies, the target nucleoside demonstrated significant anti-HBV activity against both the wild-type as well as the major nucleoside-resistant HBV mutants (adefovir and lamivudine), including the lamivudine/entecavir double mutant. In view of these promising anti-HBV activities, further biological and biochemical studies of the nucleoside **9** is warranted to assess the full potential as an anti-HBV agent.

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Supplementary data

Supplementary data associated with this article can be found, in the online version, at doi:10.1016/j.bmcl.2011.08.113.

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15. *Compound* **9**: $[\alpha]_D^{25}$ + 151.80° (c 0.23, CH_3OH); mp 215–217 °C; UV (H_2O) λ_{max} 259.0 nm (e 14,000, pH 2), 260.0 nm (e 15,600, pH 7), 260.0 nm (e 15,600, pH 11); ^1H NMR (500 MHz, CD_3OD) d 8.26 (s, 1H), 8.10 (d, *J* = 2.5 Hz, 1H), 5.90 (d, *J* = 2.5 Hz, 1H), 5.46 (s, 1H), 5.01–4.89 (m, 2H), 4.46–4.42 (m, 1H), 391–3.81 (m, 2H), 2.81 (br, 1H); ^{19}F NMR (500 MHz, CD_3OD) δ −192.93 (m); ^{13}C NMR (125 MHz, CD_3OD) d 155.9, 152.5, 149.9, 146.0, 141.1, (d, J = 5.3 Hz), 117.8, 111.7, 109.8, 95.9 (d, *J* = 184 Hz) 72.9 (d, *J* = 23.6 Hz), 61.7, 57.5 (d, *J* = 17.4 Hz), 51.0; Anal. Calcd For $C_{12}H_{14}FN_5O_2$: C, 51.61; H, 5.05; N, 25.08; Found C, 51.74; H, 5.09; N, 24.92.
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Cross-species transmission of gibbon and orangutan hepatitis B virus to uPA/SCID mice with human hepatocytes

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ABSTRACT

To investigate the potential of cross-species transmission of non-human primate HBV to humans, severe combined immunodeficiency mice transgenic for urokinase-type plasminogen activator, in which the mouse liver has been engrafted with human hepatocytes, were inoculated with non-human primate HBV. HBV-DNA positive serum samples from a gibbon or orangutan were inoculated into 6 chimeric mice. HBV-DNA, hepatitis B surface antigen (HBsAg), and HB core-related antigen in sera and HBV cccDNA in liver were detectable in 2 of 3 mice each from the gibbon and orangutan. Likewise, applying immunofluorescence HBV core protein was only found in human hepatocytes expressing human albumin. The HBV sequences from mouse sera were identical to those from orangutan and gibbon sera determined prior to inoculation. In conclusion, human hepatocytes have been infected with gibbon/orangutan HBV.

1. Introduction

Hepatitis B is caused by hepatitis B virus (HBV), a hepatotropic virus of the family *Hepadnaviridae*. This family comprises two genera, Avihepadnavirus and Orthohepadnavirus which can infect birds and mammals, respectively (Mason et al., 2005). As for humans, approximately 350 million chronic carriers have been infected by HBV worldwide (Lavanchy, 2004) and 15–40 percent have developed liver cirrhosis and hepatocellular carcinoma (Lee, 1997; McQuillan et al., 1989; Sharma et al., 2005). In addition to humans, HBV also infects higher non-human primates (apes) such as orangutans (*Pongo pygmaeus*), gibbons (*Hylobates* sp. and *Nomascus* sp.), gorillas (*Gorilla gorilla*), and chimpanzees (*Pan troglodytes*) (Grethe et al., 2000; MacDonald et al., 2000; Makuwa et al., 2003; Noppornpanth et al., 2003; Sall et al., 2005; Sa-nguanmoo et al., 2008; Starkman et al., 2003; Warren et al., 1998). In comparison with human HBV, non-human primate HBVs contain a 33 nucleotide deletion in the *PreS1* gene and all non-human primate HBVs cluster within their respective group separate from each human HBV genotype (Grethe et al., 2000; Kramvis et al., 2005; Robertson, 2001; Takahashi et al., 2000).

Several experiments have been conducted to study cross-species transmission of human HBV to non-human primates. Human HBsAg positive sera were intravenously inoculated into chimpanzees. In all experiments, inoculated chimpanzees displayed HBsAg in their sera (Kim et al., 2008; Tabor et al., 1980). In 1977, Bancroft et al. inoculated pooled saliva collected from 5 human carriers into gibbons. Gibbons which received subcutaneous injections of the pooled saliva developed serological markers of HBV infection. In contrast, gibbons infected via either the nasal or oral route did not show evidence of HBV infection (Bancroft et al., 1977). However, the negative results in this study are probably attributable to the lack of a sufficiently sensitive test available at that time. Alter et al. transmitted semen and saliva of carrier patients to chimpanzees. Chimpanzees developed HBsAg and elevated ALT after inoculation (Alter et al., 1977). In 1980, Scott et al. inoculated semen donated by HBsAg and HBeAg positive patients

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