Efficiency and safety of gene transfer methods are the key determinants of the clinical success of gene therapy and an unresolved problem. There are several reports of delivery of siRNA or siRNA-expression vectors to cells *in vivo*;[12,40,41] however, gene delivery methods that are safe enough to apply to clinical therapeutics are currently under development. Adenovirus vectors are one of the most commonly used carriers for human gene therapies.[42–44] Our present results demonstrate that the adenoviral delivery of shRNA is effective in blocking HCV replication *in vitro* and virus protein expression *in vivo*. Adenovirus vectors have several advantages of efficient delivery of transgene both *in vitro* and *in vivo* and natural hepatotropism when administered *in vivo*. The AxshRNA-HCV specifically blocked expression of HCV structural proteins in a conditional transgenic mouse expressing those proteins. The current adenovirus vectors may cause inflammatory reactions in the target organ,[45] however, and produce neutralizing antibodies which make repeated administration difficult. These problems may be overcome by the improved constructs of virus vectors with attenuated immunogenicity or by the development of non-viral carriers for gene delivery.[46]

In conclusion, our results demonstrate the effectiveness and feasibility of the siRNA expression system. The efficiency of adenovirus expressing shRNA that target HCV suggests that delivery and expression of siRNA in hepatocytes may eliminate the virus and that this RNA-targeting approach might provide a potentially effective future therapeutic option for HCV infection.

## Acknowledgments

This study was supported by grants from Japan Society for the Promotion of Science, 15590629 and 16590580, and partly supported by a grant from the Viral Hepatitis Research Foundation of Japan.

## References

1 Alter MJ. Epidemiology of hepatitis C. *Hepatology* 1997; **26**: 62S–65S.
2 Hadziyannis SJ, Sette H Jr, Morgan TR *et al.* Peginterferon-alpha2a and ribavirin combination therapy in chronic hepatitis C: a randomized study of treatment duration and ribavirin dose. *Ann. Intern. Med.* 2004; **140**: 346–55.
3 Fire A, Xu S, Montgomery M, Kostas S, Driver S, Mello C. Potent and specific genetic interference by double-stranded RNA in Caenorhabditis elegans. *Nature* 1998; **19**: 806–11.
4 Elbashir SM, Harborth J, Lendeckel W, Yalcin A, Weber K, Tuschl T. Duplexes of 21-nucleotide RNAs mediate RNA interference in cultured mammalian cells. *Nature* 2001; **411**: 494–8.
5 Coburn GA, Cullen BR. Potent and specific inhibition of human immunodeficiency virus type 1 replication by RNA interference. *J. Virol.* 2002; **76**: 9225–31.
6 Jacque JM, Triques K, Stevenson M. Modulation of HIV-1 replication by RNA interference. *Nature* 2002; **418**: 435–8.
7 Gitlin L, Karelsky S, Andino R. Short interfering RNA confers intracellular antiviral immunity in human cells. *Nature* 2002; **418**: 430–4.
8 Ge Q, Filip L, Bai A, Nguyen T, Eisen HN, Chen J. Inhibition of influenza virus production in virus-infected mice by RNA interference. *Proc. Natl. Acad. Sci. USA* 2004; **101**: 8676–81.
9 Wang C, Pflugheber J, Sumpter R Jr *et al.* Alpha interferon induces distinct translational control programs to suppress hepatitis C virus RNA replication. *J. Virol.* 2003; **77**: 3898–912.
10 Klein C, Bock CT, Wedemeyer H *et al.* Inhibition of hepatitis B virus replication in vivo by nucleoside analogues and siRNA. *Gastroenterology* 2003; **125**: 9–18.
11 Konishi M, Wu CH, Wu GY. Inhibition of HBV replication by siRNA in a stable HBV-producing cell line. *Hepatology* 2003; **38**: 842–50.
12 McCaffrey AP, Meuse L, Pham TT, Conklin DS, Hannon GJ, Kay MA. RNA interference in adult mice. *Nature* 2002; **418**: 38–9.
13 Shlomai A, Shaul Y. Inhibition of hepatitis B virus expression and replication by RNA interference. *Hepatology* 2003; **37**: 764–70.
14 Yokota T, Sakamoto N, Enomoto N *et al.* Inhibition of intracellular hepatitis C virus replication by synthetic and vector-derived small interfering RNAs. *EMBO Rep.* 2003; **4**: 602–8.
15 Kapadia SB, Brideau-Andersen A, Chisari FV. Interference of hepatitis C virus RNA replication by short interfering RNAs. *Proc. Natl. Acad. Sci. USA* 2003; **100**: 2014–18.
16 Kronke J, Kittler R, Buchholz F *et al.* Alternative approaches for efficient inhibition of hepatitis C virus RNA replication by small interfering RNAs. *J. Virol.* 2004; **78**: 3436–46.
17 Randall G, Grakoui A, Rice CM. Clearance of replicating hepatitis C virus replicon RNAs in cell culture by small interfering RNAs. *Proc. Natl. Acad. Sci. USA* 2003; **100**: 235–40.
18 Seo MY, Abrignani S, Houghton M, Han JH. Letter to the editor: small interfering RNA-mediated inhibition of hepatitis C virus replication in the human hepatoma cell line Huh-7. *J. Virol.* 2003; **77**: 810–12.
19 Wilson JA, Jayasena S, Khvorova A *et al.* RNA interference blocks gene expression and RNA synthesis from hepatitis C replicons propagated in human liver cells. *Proc. Natl. Acad. Sci. USA* 2003; **100**: 2783–8.
20 Guo JT, Bichko VV, Seeger C. Effect of alpha interferon on the hepatitis C virus replicon. *J. Virol.* 2001; **75**: 8516–23.
21 Tanabe Y, Sakamoto N, Enomoto N *et al.* Synergistic inhibition of intracellular hepatitis C virus replication by combination of ribavirin and interferon-alpha. *J. Infect. Dis.* 2004; **189**: 1129–39.
22 Maekawa S, Enomoto N, Sakamoto N *et al.* Introduction of NS5A mutations enables subgenomic HCV-replicon derived from chimpanzee-infectious HC-J4 isolate to replicate efficiently in Huh-7 cells. *J. Viral. Hepat.* 2004; **11**: 394–403.
23 Miyagishi M, Sumimoto H, Miyoshi H, Kawakami Y, Taira K. Optimization of an siRNA-expression system with an improved hairpin and its significant suppressive effects in mammalian cells. *J. Gene Med.* 2004; **6**: 715–23.
24 Li Y, Yokota T, Matsumura R, Taira K, Mizusawa H. Sequence-dependent and independent inhibition specific for mutant ataxin-3 by small interfering RNA. *Ann. Neurol.* 2004; **56**: 124–9.
25 Kanazawa N, Kurosaki M, Sakamoto N *et al.* Regulation of hepatitis C virus replication by interferon regulatory factor-1. *J. Virol.* 2004; **78**: 9713–20.
26 Wakita T, Pietschmann T, Kato T *et al.* Production of infectious hepatitis C virus in tissue culture from a cloned viral genome. *Nat. Med.* 2005; **11**: 791–6.
27 Zhong J, Gastaminza P, Cheng G *et al.* Robust hepatitis C virus infection in vitro. *Proc. Natl. Acad. Sci. USA* 2005; **102**: 9294–9.
28 Wakita T, Taya C, Katsume A *et al.* Efficient conditional transgene expression in hepatitis C virus cDNA transgenic mice mediated by the Cre/loxP system. *J. Biol. Chem.* 1998; **273**: 9001–6.
29 Kashiwakuma T, Hasegawa A, Kajita T *et al.* Detection of hepatitis C virus specific core protein in serum of patients by a sensitive fluorescence enzyme immunoassay (FEIA). *J. Immunol. Methods* 1996; **28**: 79–89.

 

30 Baglioni C, Nilsen TW. Mechanisms of antiviral action of interferon. *Interferon* 1983; **5**: 23–42.
31 Bridge A, Pebernard S, Ducraux A, Nicoulaz A, Iggo R. Induction of an interferon response by RNAi vectors in mammalian cells. *Nat. Genet.* 2003; **34**: 263–4.
32 Carmichael GG. Silencing viruses with RNA. *Nature* 2002; **418**: 379–80.
33 Okamoto H, Okada S, Sugiyama Y *et al.* Nucleotide sequence of the genomic RNA of hepatitis C virus isolated from a human carrier: comparison with reported isolates for conserved and divergent regions. *J. Gen. Virol.* 1991; **72**: 2697–704.
34 Kato T, Date T, Miyamoto M *et al.* Efficient replication of the genotype 2a hepatitis C virus subgenomic replicon. *Gastroenterology* 2003; **125**: 1808–17.
35 Alexopoulou L, Holt AC, Medzhitov R, Flavell RA. Recognition of double-stranded RNA and activation of NF-kB by Toll-like receptor 3. *Nature* 2001; **413**: 732–8.
36 Yoneyama M, Kikuchi M, Natsukawa T *et al.* The RNA helicase RIG-I has an essential function in double-stranded RNA-induced innate antiviral responses. *Nat. Immunol.* 2004; **5**: 730–7.
37 Sledz C, Holko M, de Veer M, Silverman R, Williams, B. Activation of the interferon system by short-interfering RNAs. *Nat. Cell. Biol.* 2003; **5**: 834–9.
38 Doench JG, Petersen CP, Sharp PA. siRNAs can function as miRNAs. *Genes Dev.* 2003; **17**: 438–42.
39 Morris KV. siRNA-mediated transcriptional gene silencing: the potential mechanism and a possible role in the histone code. *Cell. Mol. Life Sci.* 2005; **62**: 3057–66.
40 Xia H, Mao Q, Paulson HL, Davidson BL. siRNA-mediated gene silencing in vitro and in vivo. *Nat. Biotechnol.* 2002; **20**: 1006–10.
41 Zender L, Hutker S, Liedtke C *et al.* Caspase 8 small interfering RNA prevents acute liver failure in mice. *Proc. Natl. Acad. Sci. USA* 2003; **100**: 7797–802.
42 Akli S, Caillaud C, Vigne E *et al.* Transfer of a foreign gene into the brain using adenovirus vectors. *Nat. Genet.* 1993; **3**: 224–8.
43 Bajocchi G, Feldman SH, Crystal RG, Mastrangeli A. Direct in vivo gene transfer to ependymal cells in the central nervous system using recombinant adenovirus vectors. *Nat. Genet.* 1993; **3**: 229–34.
44 Davidson BL, Allen ED, Kozarsky KF, Wilson JM, Roessler BJ. A model system for in vivo gene transfer into the central nervous system using an adenoviral vector. *Nat. Genet.* 1993; **3**: 219–23.
45 Yang Y, Wilson JM. Clearance of adenovirus-infected hepatocytes by MHC class I-restricted CD4+ CTLs in vivo. *J. Immunol.* 1995; **155**: 2564–70.
46 Fleury S, Driscoll R, Simeoni E *et al.* Helper-dependent adenovirus vectors devoid of all viral genes cause less myocardial inflammation compared with first-generation adenovirus vectors. *Basic Res. Cardiol.* 2004; **99**: 247–56.

JOURNAL OF VIROLOGY, Aug. 2008, p. 8241–8242
0022-538X/08/$08.00+0 doi:10.1128/JVI.00793-08

Vol. 82, No. 16

# When Should "I" Consider a New Hepatitis B Virus Genotype?

Recently, Huy et al. described a new hepatitis B virus (HBV) strain isolated in Vietnam (3) and claimed it to be a "new genotype," "HBV genotype I," with a complex recombination involving genotypes C, A, and G. We refute both claims.

Using complete genome sequence analysis of their single isolate, VH24 (AB231908), the authors documented an over 98% similarity with three other Vietnamese strains (2). Earlier, Hannoun et al. provided comprehensive information regarding those strains, showing recombination between genotype C and an unknown genotype in the pre-S/S region (2). Mean genetic divergence from genotype C of <8% in the entire genome and evidence of recombination had prevented the authors from assigning the strains to a new genotype. The same conclusion for the strains was reached by a later study using a new methodological approach (10). By providing neither additional information nor a new analytical approach, Huy et al. (3) surprisingly conclude that their strain, with those previously reported, represent a new genotype.

First, phylogenetic analysis of the complete genome of the four Vietnamese HBV isolates shows them to cluster with subgenotypes of C (C1 to C5) and to differ from genotype C by a mean nucleotide distance of only 7.0% ± 0.4%, which falls within the range of intragenotype and not intergenotype divergence (4). Furthermore, their conclusion of a "complex A/G/C recombination" arose from the use of Simplot software that has methodological limitations, which can be overcome by using GroupScanning (10). Reanalyzing AB231908 by using GroupScanning provides no strong evidence for recombination with known human or ape HBV genotypes in the pre-S/S regions (apart from two restricted regions, with association values of >0.5), in contrast to its consistent penetration into the genotype C clade from position 1600 (Fig. 1). In the pre-S/S regions, AB231908 formed variable, inconsistent outgroup associations with a range of genotypes, including A and G (originally identified as recombination partners by Huy et al. [3], using SimPlot) and with chimpanzee variants (Fig. 1, gray line; not included in the original analysis), a recombination partner even more improbable geographically than genotype A or G.

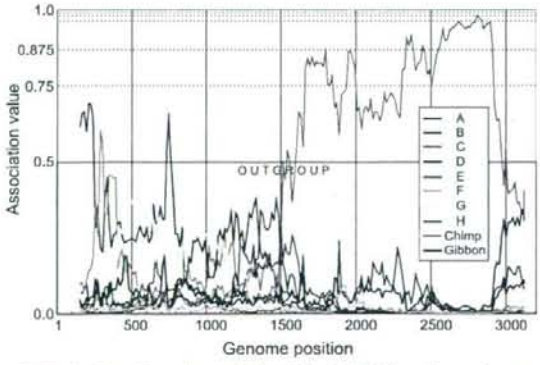


FIG. 1. GroupScanning analysis (10) of VH24 against reference groups of nonrecombinant HBV sequences of human genotypes A to H and nonhuman ape-derived variants (chimpanzee/gibbon) ($n$ = 288), incorporating all HBV sequences used for recombination detection in the Huy et al. study (3). Association values of approximately 0.5 or lower indicate an outgroup position or no phylogenetic clustering with a reference group. Analysis of previously described Vietnamese variants (AF241407 to AF241409) produced almost identical results (data not shown).

Finally, Huy et al. (3) "justified" assigning the four Vietnamese strains into a new genotype on the basis of seven "unique" conserved amino acids: $His^{56}$, $Ala^{60}$, $Asn^{87}$, $Val^{90}$, $Val^{91}$, $Ile^{136}$, and $Lys^{198}$. From the databases, it is evident that $His^{56}$ is present in subgenotype B1 and genotype C; $Ala^{60}$ is the consensus for genotype D and present in subgenotypes C2 to C4; $Val^{90}$, found in only three of the four Vietnamese sequences, is present in subgenotype C2; $Val^{91}$ is common in genotype A; and $Lys^{198}$ is found in subgenotypes B1 to B4, C3, F1, and F2 and genotypes E and H. $Ile^{136}$ and $Asn^{87}$ are therefore the only amino acids unique to the four Vietnamese strains, a far-from-recognized criterion of HBV genotyping.

Since 1988, when nucleotide diversity of >8% in the entire genome was first proposed for genotyping (9), eight genotypes have been described and named A to H (1, 7, 8, 11), and their geographical distribution and clinical relevance have been extensively reported (5, 6). In addition to the eight currently recognized genotypes, intergenotype recombination generates novel HBV variants, with over 24 phylogenetically independent recombinant variants described (10, 13). These recombinants can spread in humans and develop specific distributions and epidemiology as shown for the B/C recombinant, which accounts for the majority of genotype B strains in mainland Asia (12). Since sequencing and phylogenetic analyses are widely available, numerous further reports on HBV variation can be expected. If every new recombinant is assigned to a new genotype, we would soon be running out of alphabet letters. Principles of HBV classification must be established and accepted by the international community of experts in the field in order to ensure that genotyping is consistent, relevant, and significant.

## REFERENCES

1. **Arauz-Ruiz, P., H. Norder, B. H. Robertson, and L. O. Magnius.** 2002. Genotype H: a new Amerindian genotype of hepatitis B virus revealed in Central America. J. Gen. Virol. **83**:2059–2073.
2. **Hannoun, C., H. Norder, and M. Lindh.** 2000. An aberrant genotype revealed in recombinant hepatitis B virus strains from Vietnam. J. Gen. Virol. **81**:2267–2272.
3. **Huy, T. T. T., T. T. Ngoc, and K. Abe.** 2008. New complex recombinant genotype of hepatitis B virus identified in Vietnam. J. Virol. **82**:5657–5663.
4. **Kramvis, A., K. Arakawa, M. C. Yu, R. Nogueira, D. O. Stram, and M. C. Kew.** 2008. Relationship of serological subtype, basic core promoter and precore mutations to genotypes/subgenotypes of hepatitis B virus. J. Med. Virol. **80**:27–46.
5. **Kramvis, A., M. Kew, and G. Francois.** 2005. Hepatitis B virus genotypes. Vaccine **23**:2409–2423.
6. **Miyakawa, Y., and M. Mizokami.** 2003. Classifying hepatitis B virus genotypes. Intervirology **46**:329–338.
7. **Norder, H., A. M. Courouce, and L. O. Magnius.** 1994. Complete genomes, phylogenetic relatedness, and structural proteins of six strains of the hepatitis B virus, four of which represent two new genotypes. Virology **198**:489–503.
8. **Norder, H., A. M. Courouce, and L. O. Magnius.** 1992. Molecular basis of hepatitis B virus serotype variations within the four major subtypes. J. Gen. Virol. **73**:3141–3145.
9. **Okamoto, H., F. Tsuda, H. Sakugawa, R. I. Sastrosoewignjo, M. Imai, Y. Miyakawa, and M. Mayumi.** 1988. Typing hepatitis B virus by homology in nucleotide sequence: comparison of surface antigen subtypes. J. Gen. Virol. **69**:2575–2583.

10. **Simmonds, P., and S. Midgley.** 2005. Recombination in the genesis and evolution of hepatitis B virus genotypes. J. Virol. **79**:15467–15476.
11. **Stuyver, L., S. De Gendt, C. Van Geyt, F. Zoulim, M. Fried, R. F. Schinazi, and R. Rossau.** 2000. A new genotype of hepatitis B virus: complete genome and phylogenetic relatedness. J. Gen. Virol. **81**:67–74.
12. **Sugauchi, F., E. Orito, T. Ichida, H. Kato, H. Sakugawa, S. Kakumu, T. Ishida, A. Chutaputti, C. L. Lai, R. Ueda, Y. Miyakawa, and M. Mizokami.** 2002. Hepatitis B virus of genotype B with or without recombination with genotype C over the precore region plus the core gene. J. Virol. **76**:5985–5992.
13. **Suwannakarn, K., P. Tangkijvanich, A. Theamboonlers, K. Abe, and Y. Poovorawan.** 2005. A novel recombinant of hepatitis B virus genotypes G and C isolated from a Thai patient with hepatocellular carcinoma. J. Gen. Virol. **86**:3027–3030.

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Virology 376 (2008) 408–415

Contents lists available at ScienceDirect

Virology

journal homepage: www.elsevier.com/locate/yviro

# Characteristics of hepatitis B virus genotype G coinfected with genotype H in chimeric mice carrying human hepatocytes☆

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ARTICLE INFO

*Article history:*
Received 14 February 2008
Returned to author for revision
18 March 2008
Accepted 1 April 2008
Available onlin 13 May 2008

*Keywords:*
HBV genotype G
HBV genotype H
Chimeric mice
MSM
Replication
Fibrosis

ABSTRACT

Accumulated evidence indicated that hepatitis B virus genotype G (HBV/G) is present exclusively in coinfection with other HBV genotypes. In Mexico, HBV/G from 6 men who had sex with men were coinfected with HBV/H. Phylogenetically complete genomes of the 6 Mexican HBV/G strains were closely related to previous ones from the US/Europe. Using uPA/SCID mice with human hepatocytes, monoinfection with HBV/G did not result in detectable HBV DNA in serum, whereas superinfection with HBV/G at week 10 inoculated HBV/H when HBV/H DNA was elevated to $>10^7$ copies/mL has enhanced the replication of HBV/G. The HBV/G was enhanced in another 3 inoculated with a serum passage containing HBV/G with a trace of HBV/H. Coinfection of mice with HBV/G and H induced fibrosis in the liver. In conclusion, the replication of HBV/G can be enhanced remarkably when it is coinfected with HBV/H. Coinfection with HBV/G may be directly cytopathic in immunosuppressive conditions.



## Introduction

On the basis of the nucleotide sequence divergence exceeding 8% throughout the complete genome sequence, hepatitis B virus (HBV) has been classified into eight genotypes designated by capital letters A (HBV/A) through H (HBV/H) (Arauz-Ruiz et al., 2002; Norder et al., 1994; Okamoto et al., 1988; Stuyver et al., 2000). The genotypes have different geographical distributions, virological characteristics and clinical manifestations (Magnius and Norder, 1995; Miyakawa and Mizokami, 2003).

One of the less studied genotypes is the HBV/G. It was first described in 2000, among inhabitants of France and Georgia, USA (Stuyver et al., 2000). The isolated strains had 36 base-pairs' insertion in the core gene and two stop codons in the precore region depriving ability of the virus to translate HBeAg. Nevertheless, some of the carriers were HBeAg positive (Stuyver et al., 2000) that was shortly after explained by the coexistence of the "HBeAg-potent" HBV/A strains in coinfection (Kato et al., 2002a,b). Further studies reported circulation of the genotype in Thailand (Suwannakarn et al., 2005), Japan (Ozasa et al., 2006) and Mexico (Sanchez et al., 2007) indicating global distribution and association of the infection with specific risk groups, such as injection drug users (IDU) and men who had sex with men (MSM). The studies also demonstrated that throughout the world HBV/G strains possess unprecedented genetic homology and are mainly presented in coinfection with another endemic genotype. However, little is known about peculiarities of interaction of the HBV/G with various genotypes as well as about virological and clinical concerns of the coinfection.

Produced by genetic engineering, a mouse with severe combined immunodeficiency, carrying urokinase-type plasminogen activator transgenes controlled by albumin promoter (uPA/SCID) with transplanted human hepatocytes (Heckel et al., 1990; Rhim et al., 1994) was recently shown as an appropriate animal model for studying HBV (Dandri et al., 2001; Tsuge et al., 2005). Using this model it was demonstrated that during monoinfection, HBV/G might be able to replicate in hepatocytes at low level; but its replication was

*Abbreviations:* HBV, hepatitis B virus; HBeAg, hepatitis B e antigen; HBsAg, hepatitis B surface antigen; HBcrAG, antigens related to HBV core; uPA/SCID, severe combined immunodeficiency transgenic with urokinase-type plasminogen activator.

☆ Supported by a grant-in-aid from the Ministry of Education, Culture, Sports, Science, and Technology, and a grant-in-aid from the Ministry of Health, Labour, and Welfare of Japan.

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doi:10.1016/j.virol.2008.04.001

significantly enhanced by coinfection with HBV/A or C (Sugiyama et al., 2007).

Our purpose is to determine the complete sequences of HBV/G coinfected with HBV/H in sera obtained from MSM in Mexico and to elucidate the characteristics of HBV/G in coinfection with HBV/H using recently developed *in vivo* model.

## Results

### *Phylogenetic relatedness of HBV complete genome sequences in Mexico*

Six HBV/G strains in coinfection with HBV/H among MSM in Mexico were described in our previous study (Sanchez et al., 2007). In the present study, the complete genome sequences of not only 6 HBV/G strains but also 6 HBV/H strains from the same patients were determined by each specific PCR. The phylogenetic analyses indicated that the 6 HBV/G strains were close to those previously reported from the United States (US), France and Germany, and the 6 HBV/H strains were related to the previously reported ones in the US (Fig. 1). All 6 coinfected patients were positive for HBeAg, and asymptomatic carriers of chronic HBV infection at the time of sample collection (the details unknown).

### *Characteristics of HBV/G strains in Mexico*

Sequence analyses revealed unique insertion of 36 nt in the core gene, two stop codons in the precore region and double mutation in the core promoter (CP) in all Mexican HBV/G strains, whereas no related mutations were found in the corresponding HBV/H strains (Fig. 2a and b). These data suggest that the HBeAg detected in serum of those patients had been produced by HBV/H. Additionally, several mutations, which might have affected the replication of the virus genome and amino acid substitutions of HBx, were found in the first half of the CP region, including the above double mutation (nt 1701–1765) (Fig. 2a).

### *Examining the genetic diversity and recombination of HBV/G*

Comparing the complete sequences, both overall genetic distance among the HBV/G strains (0.0037±0.0005 per site) and percent nucleotide homology (0.30±0.24%) were much lower than those among the other intra-genotype groups. In consideration of previously reported recombination between HBV/A and HBV/G strains (i.e. AB056516) (Kato et al., 2002a), we have examined the Mexican HBV/G strains for possible event of intergenotypic recombination. Complete sequences of 3 to 5 clones isolated from each of the 6 HBV/G carriers revealed; no evidence of recombination by similarity and bootstrap scan (data not shown).

### *Intracellular expression of HBV DNA and antigens*

Huh7 cells were transfected with a pUC19 vector carrying 1.24-fold the HBV genome. Three days post-transfection, they were harvested, lysed with NP-40 and tested for HBV DNA and antigens. The density of single-stranded (ss) HBV DNA was compared between HBV/G and H by Southern blotting. The expression of HBV DNA was higher for HBV/H than G, indicating that HBV/G had very low replication *in vitro* (Fig. 3a). As well, HBsAg, HBeAg and HBcrAg levels were much higher in HBV/H (Fig. 3b).

### *Superinfection with HBV/G on mice infected with HBV/H*

Chimeric mice were infected with HBV/G and H particles propagated in Huh7 cells in order to confirm the infective efficiency. Monoinfection with HBV/G from the Huh7 cells culture medium did not result in detectable HBV DNA in mice serum (data not shown).

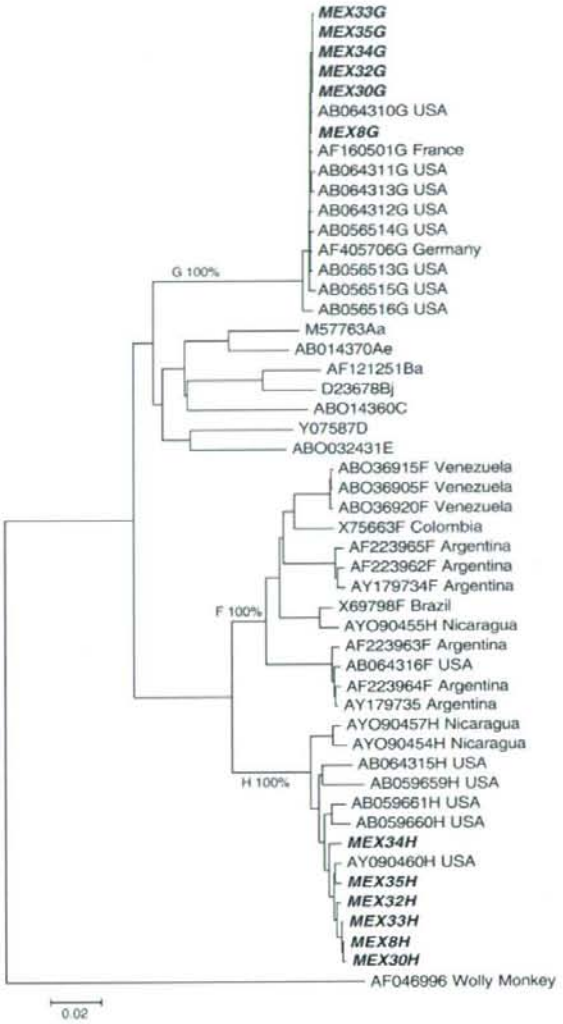


**Fig. 1.** A phylogenetic tree constructed using the complete nucleotide sequences of 50 HBV strains. The 6 HBV/G strains coinfected with HBV/H in Mexico (MEX), shown in bold italic, were compared with reference sequences recruited from GenBank/DDBJ/EMBL databases; 10 HBV/G, 7 HBV/H, 13 HBV/F, 7 representing genotypes A–E and 1 outgroup (Wolly Monkey). Aa and Ae are subgenotypes of HBV/A (Sugauchi et al., 2004). Ba and Bj are subgenotypes of HBV/B (Sugauchi et al., 2002). The country of origin is indicated after the accession number for each HBV/F, HBV/H and HBV/G strain. Bootstrap values are shown at the nodes of the main branches.

Then, according to our previous method (Sugiyama et al., 2007), the dynamics of HBV DNA, HBsAg and HBeAg assessed in 3 chimeric mice (ChiM_H1–H3) with HBV/G on H superinfection, are shown in Fig. 4 (a–c). Initially each of the mice received inoculation of around $10^5$ copies of HBV/H recovered from the Huh7 cells culture supernatants, and the dynamics of HBV/H DNA indicated approximately 2 logs elevation within the following 5 weeks. At week 10 when HBV/H DNA level exceeded concentration of $>10^7$ copies/mL, the chimeric mice were superinfected by inoculation of HBV/G. The HBV/G DNA level increased within 5 weeks after the superinfection and plateaued around $10^7$ copies/mL. Two HBV antigens (HBsAg and HBeAg) waxed and waned in profiles similar to that of HBV DNA.

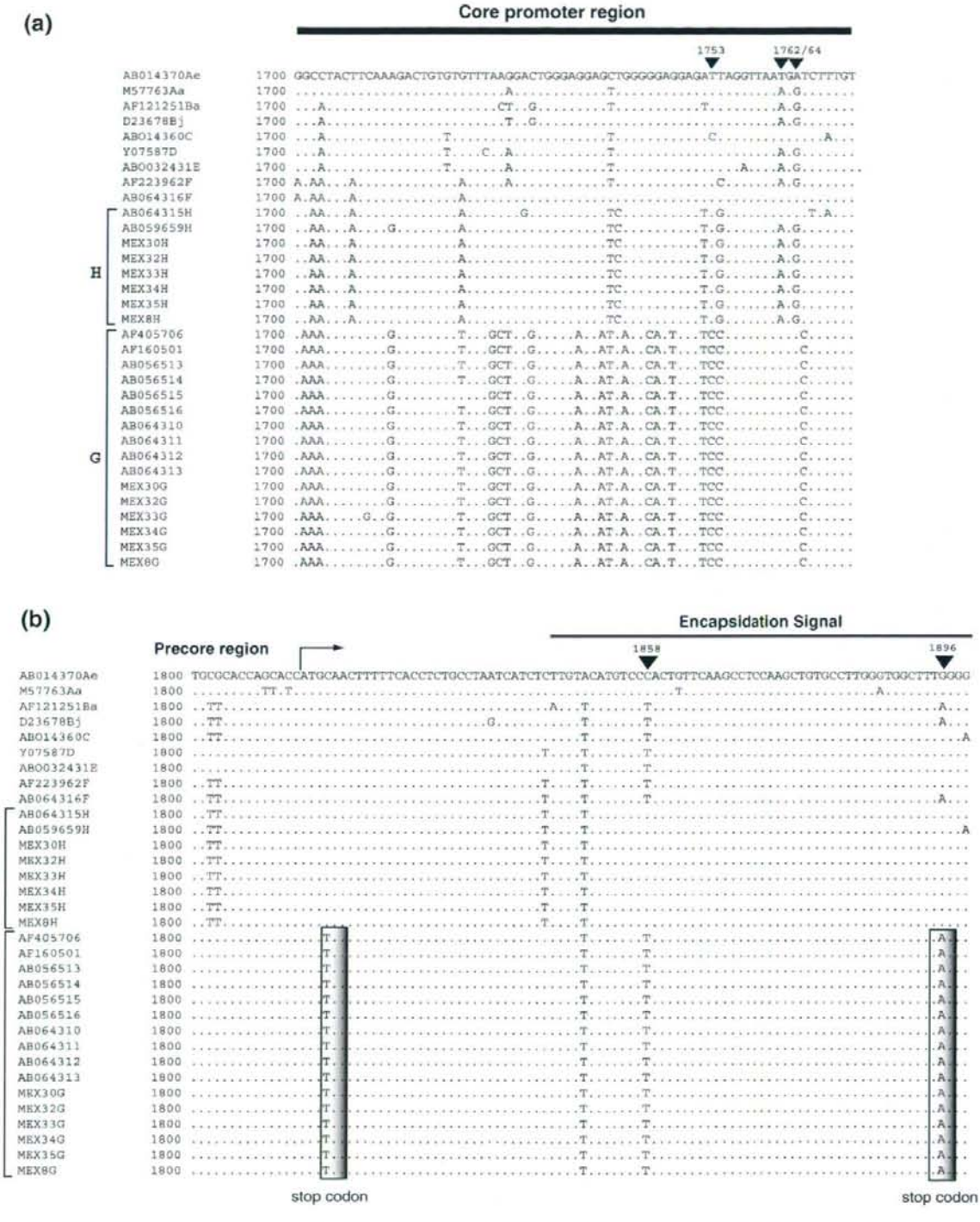


**Fig. 2.** Nucleotide sequences spanning (a) core promoter and (b) precore gene in HBV genotypes A–H. The reference sequence is shown for the AB014370Ae. The precore region includes pregenome encapsidation signal. Positions of the double mutation (A1762T and G1764A), T1753C, and C1858T making a pair with G1896A are indicated by inverted triangles. Two stop codons in the precore region are shaded.

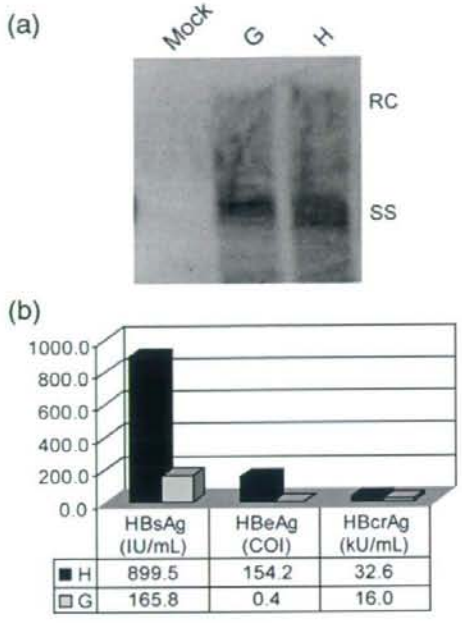


**Fig. 3.** Intracellular expression of HBV DNA and antigens. (a) The density of single-stranded (ss) HBV DNA was compared between HBV/G and H by Southern blotting. RC: relaxed circular double stranded DNA forms. (b) HBsAg, HBeAg and HBcrAg levels were also compared.

*Coinfection of mice with HBV/H and G by inoculation with a mouse passage of G-on-H superinfection*

Another 3 chimeric mice (ChiM202-17, ChiM212-22 and ChiM314-12) received serum from sacrificed ChiM_H2 with G-on-H superinfection taken at week 34 when the HBV/G and H DNA was around $5\times10^6$, $10^8$ copies/mL, respectively (Fig. 4b). Profiles of HBV/H and G, after inoculation with $10^6$ copies of HBV DNA, were similar among the 3 chimeric mice. Despite receiving the inoculation with a mouse passage supposedly containing HBV/G strain, the HBV/G DNA was not detectable until week 4 after the passage. At the week 4 when HBV/H DNA level exceeded concentration of $>10^7$ copies/mL, HBV/G started to increase and plateaued around $10^8$ copies/mL at week 16 (Fig. 4d).

*Cloning and sequencing HBV DNA in chimeric mice coinfected with HBV/H and G*

HBV DNA clones from sera of the ChiM_H1 and ChiM_H2 sampled at 26 and 34 weeks, respectively (Fig. 4a and b) included those of HBV/H and G invariably. At least 5 clones were propagated and completely sequenced in each serum; but no mutation was observed when the clones were compared to the original inoculum of either genotype. No evidence of recombinations was detected between HBV/H and G on the basis of complete genome analyses.

*Pathology in the liver of chimeric mouse infected with HBV/G and H*

Fig. 5a shows histology of liver of a chimeric mouse 26 weeks after superinfection with HBV/G on H (ChiM_H1). The mouse coinfected with HBV/G and H revealed fibrosis of stage 1 (F1) and inflammation of grade 2 (A2) with Hematoxlin–Eosin and Masson's trichrome stain (Fig. 5a), whereas the mouse monoinfected with HBV/H had no fibrosis (Fig. 5b). ChiM_H2 also had F1A1 at week 34, but ChiM_H3 was not available for histological examination due to sudden death. Interestingly, a chimeric mouse (ChiM202-17) received serum from ChiM_H2 with G-on-H superinfection revealed F2A2 at week 24 (Fig. 5c). It might be difficult to evaluate its statistical significance due to small number.

## Discussion

The HBV/G was initially reported in the US, Canada and Europe in coinfection with HBV/A (Kato et al., 2002a,b; Osiowy and Giles, 2003; Stuyver et al., 2000), which is the one of the prevalent genotypes in both of the regions. Recently, coinfection of HBV/G with H as well as G/C recombinant were reported in Mexico and Thailand, respectively (Sanchez et al., 2002, 2007; Suwannakarn et al., 2005), and accumulated data indicated trend to preferential occurrence of the HBV/G coinfection in population of MSM and IDU, possibly via particular infectious routes of transmission. A phylogenetic analysis of the complete genome of HBV/G strains isolated in the present study indicated their close relationship with those previously reported, despite the fact that they were all isolated from HBV carriers infected with different genotypes that were prevalent in the respective area. These suggest that the HBV/G is genetically homologous and has no specific preference for HBV genotype to be coinfected. Thus, the HBV/G may be found among HBV carriers in any part of the world regardless of the prevalent genotype.

Invariably coinfected with other genotypes, HBV/G was once deemed a defective virus that cannot replicate by itself. Recently, however, Chudy and his associates reported plasmapheresis and platelet donor who was infected with HBV/G alone and had transmitted it to two recipients in look-back studies (Chudy et al., 2006). Since the donor and two recipients were not coinfected with HBV of the other genotypes by the reversed hybridization assay (Hussain et al., 2003), capable of detecting HBV infection of any genotype in low titers, the authors concluded that HBV/G can monoinfect human beings without help from coinfecting HBV of other genotypes (Chudy et al., 2006).

The uPA/SCID mouse with the liver replaced for human hepatocytes (Heckel et al., 1990) is a very useful model for studies on hepatitis virus infection and replication *in vivo* (Dandri et al., 2001; Tsuge et al., 2005). Using this model we have previously demonstrated that despite of apparent dependence on other genotype strain (HBV/A or HBV/C) in replication, the viral load of the HBV/G eventually outgrows and takes over the coinfecting strain in the chimeric mice (Sugiyama et al., 2007).

In the present study, the chimeric mice had undetectable HBV DNA in the serum when monoinfected with HBV/G, whereas superinfection on HBV/H enhanced replication of the HBV/G. This observation is concordant with previous experimental study which indicated a rapid takeover in mice initially infected with HBV/A or C and superinfected with HBV/G (Sugiyama et al., 2007). The takeover was significantly enhanced in mice infected with HBV/G on HBV/A when compared to HBV/G on HBV/C; with the mean time required for a 10-fold increase (log time) in the HBV/DNA level 1.6 vs. 3.3 weeks, respectively (Sugiyama et al., 2007). Interestingly, the present study demonstrates that pattern of the genotypic interaction between HBV/G and H was similar to that described for HBV/G on C; with the HBV DNA log time 3.0 weeks, suggesting that HBV/G is better sustained in human population by its association with HBV/A than with other HBV genotypes. These experimental results were also supported by clinical observations of the takeover which was demonstrated in a patient coinfected with HBV/G and A by cloning and sequencing (Kato et al., 2002a). However, such a heavy dependence of HBV/G on other genotype strain does not seem to require intergenotypic recombination between them, as no recombination event was observed in chimeric mice coinfected with HBV/G and any other genotype strain. The mechanism how HBV/G depends on other genotypes for replication had been pursued in cotransfection experiments in Huh7 cells; our previous *in vitro* study showed that trans-complementation with core protein of HBV/A would be required for HBV/G to replicate

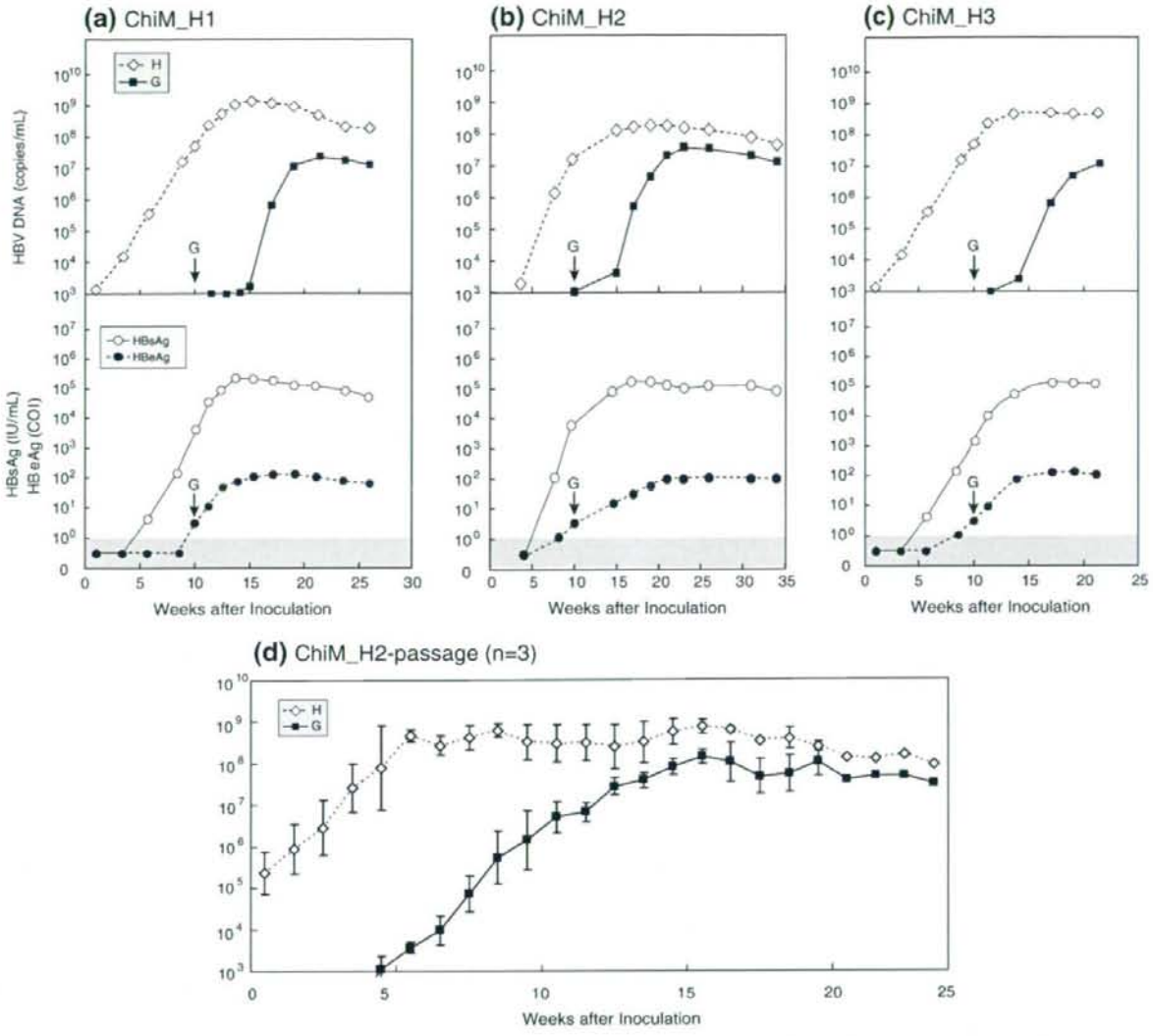


**Fig. 4.** Superinfection with HBV/G on chimeric mice infected with HBV/H [(a) ChiM_H1, (b) ChiM_H2, (c) ChiM_H3]. Inoculation with genotype G is indicated by large arrows. The dynamics of HBV DNA, HBsAg and HBeAg assessed superinfection of 3 chimeric mice (ChiM_H1–H3) are shown in panels a–c. Another 3 chimeric mice received serum from ChiM_H2 with G-on-H superinfection taken at week 34 when HBV/G DNA plateaued around $10^7$ copies/mL (Fig. 4b). Profiles of HBV/H and G, after inoculation with $10^6$ copies of HBV DNA, were similar among the 3 chimeric mice. Mean HBV DNA and standard deviation (bar) were shown in panel d.

actively (Sugiyama et al., 2007), suggesting that the replication of HBV/G might be also enhanced by core protein of HBV/H. Two other functional analyses of HBV/G had been already reported. Kremsdorf et al. have proposed the involvement of polymerase encoded by HBV/G in active replication (Kremsdorf et al., 1996) and Li et al. showed that lack of HBeAg expression rather than a replication defect could be the primary determinant for the rare occurrence of HBV/G monoinfection (Li et al., 2007). Hence, possibility remains for other viral elements beyond core protein from coinfecting genotypes to enhance the replication of HBV/G. Further studies are needed to elucidate the mechanism of HBV/G replication by cotransfection of other proteins beyond core protein of HBV/H or construction of domain-switch experiments between the genome of HBV/G and H.

Considering that coinfection with HBV/G may be associated with pathological manifestations, liver histology was investigated in tissue obtained from the mice used in this study. The chimeric mouse co-infected with HBV/G and H had developed fibrosis and inflammation (F1–2, A1–2) in the liver that was not observed in mice with HBV/G or H monoinfection. This might be supported by clinical data in Mexico; Mexican patients infected with the most prevalent HBV/H have milder liver damage when it is in monoinfection rather than in coinfection with other genotypes (personal communication). Our recent study also showed fibrosis of F1–F2 stage in the majority of the mice superinfected with HBV/G on A or C (Sugiyama et al., 2007). Clinically, Lacombe and her colleagues reported more severe fibrosis in human immunodeficiency type-1 (HIV)-positive French patients who were infected with HBV/G than the others (Lacombe et al., 2006). Taken together, clinical and experimental observations indicate that in immunodefficient conditions HBV/G possesses stronger disease-inducing capacity when it is coinfected with other genotype. Unfortunately, studied patients did not have exact diagnosis due to neither histopathological examination nor abdominal ultrasonography, although they were asymptomatic.

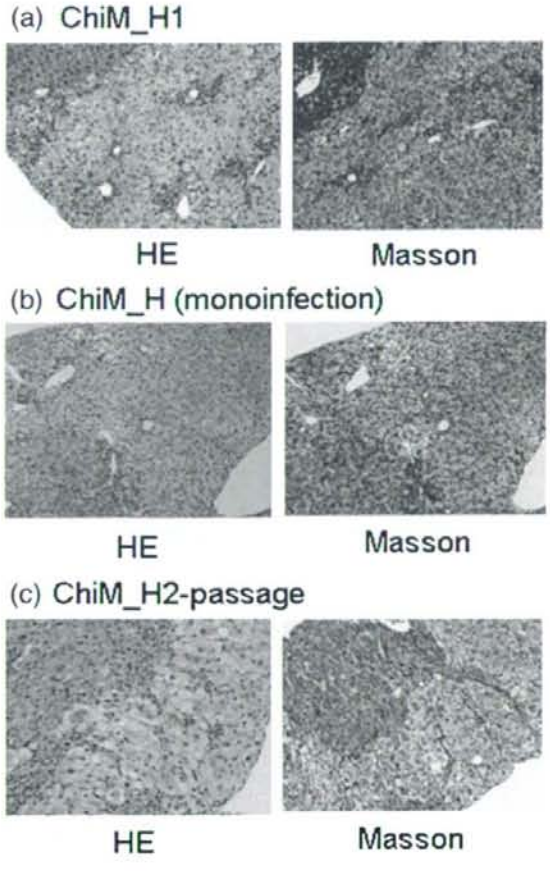


**Fig. 5.** Liver histology in chimeric mice superinfected with HBV/G on H. (a) A chimeric mouse 26 weeks after superinfection with HBV/G on H (ChiM_H1) revealed F1A2 with Hematoxlin–Eosin (HE) and Masson's trichrome stain. (b) A chimeric mouse 24 weeks after monoinfection with HBV/H had no fibrosis. The peak of HBV DNA was around $10^8$ copies/mL. (c) Another chimeric mouse (ChiM202-17) received serum from ChiM_H2 with G-on-H superinfection revealed F2A2 at week 24.

Further prospected studies are required to investigate whether HBV DNA levels (viral replication) and/or other factors would affect liver fibrosis in immunosuppressive conditions.

Two remarkable viral genomic characteristics of the HBV/G have been established by previous reports; one of them is the unique insertion of 36 bp in the core gene, which is shared by all HBV/G strains studied herein and previously (Fig. 2). Although screening of the entire DNA Genome Bank (BLAST search) did not reveal any homologous to the insertion parts within other sequences including those of human, we took the advantage of these peculiar insertion sequences for designing the type-specific primers to be used for screening (Kato et al., 2001) and quantification of the genotype (Sugiyama et al., 2007). In respect to the function of this insertion, it may induce modifications of both the encapsidation signal sequence and the core protein structure, as previously proposed (Junker-Niepmann et al., 1990). Furthermore, HBV/G strains include two stop codons in the precore region at positions 2 and 28, both of which prohibit the translation of the HBeAg precursor (Carman et al., 1989; Okamoto et al., 1990), assumably resulting in HBeAg-negative phenotype of all HBV/G strains. In this study all patients infected with HBV/G, however, were positive for HBeAg. The coinfection with HBV/H would explain the presence of HBeAg in individuals infected with HBV/G, which would be consistent with a previous report (Kato et al., 2002a).

In conclusion, the replication of HBV/G can be enhanced remarkably when it is coinfected with HBV/H prevalent in Mexico. Coinfection with HBV/G may be directly cytopathic in immunosuppressive conditions. Further epidemiological, clinical and *in vitro* studies are required to confirm the clinical manifestation of the HBV/G coinfection with various genotypes and evaluate its genotypic peculiarities.

## Methods

### *Serum samples*

Nineteen HBsAg-positive sera were obtained from previously described MSM cohort (age range 22–30 years) in Mexico (Sanchez et al., 2007). HBeAg was detected with chemiluminescent enzyme immunoassay (Ortho Clinical Diagnostics, Tokyo, Japan).

### *Determination of HBV genotypes and the complete sequences of HBV*

Initially, HBV genotypes were determined by EIA with monoclonal antibodies directed to the preS2 epitopes (Usuda et al., 1999, 2000), with use of commercial kits (HBV GENOTYPE EIA, Institute of Immunology Co., Ltd., Tokyo, Japan), allowing the determination of HBV/A–F and HBV/H. HBV/G was confirmed by the G-specific PCR with one of the primers deduced from the sequence of 36 nt. insertion in the core gene (Kato et al., 2001). The complete genomes were further determined. In brief, two partially overlapping fragments were amplified by nested PCR using two sets of primers with LA Taq (TaKaRa Bio Inc., Tokyo, Japan) (Table 1). Similarly, the complete genomes of HBV/H strains were also amplified as two overlapping fragments using different set of primers shown in the Table 2. Thereafter, the PCR products were cloned in a plasmid pGEM-T easy vector (Promega Corp., Madison, WI, US) and sequenced using sequencing primers (Tables 1 and 2) with Prism Big Dye (Applied Biosystems, Foster City, CA, US) on the ABI 3100 DNA automated sequencer. Reference sequences for comparative analyses were retrieved from the DDBJ/EMBL/GenBank database.

### *Plasmid constructs of HBV DNA*

HBV DNA from a Mexican patient (MEX33) was extracted from 100 μL of serum using the QIAamp DNA blood kit (QIAGEN, GmbH, Hilden, Germany). Two overlapping fragments, fragment A and fragment B approximately 1700 bp long, covering the entire genome

**Table 1**
HBV DNA oligonucleotide primers for complete genomes of genotype G

| Primer | Nucleotide sequence (5′–3′) | Position* | Polarity |
|---|---|---|---|
| *1) Fragment A* | | | |
| HBVG3157F | CCTCCTGCCTCCACCAATCG | 3157–3176 | Sense |
| HBVG1917R | AGCCAAAAAGGCCATATGGCA | 1937–1917 | Antisense |
| HBVG3187F | AGGCAGCCTACTCCCATCTC | 3187–3206 | Sense |
| HBVG1797R | CATGGTGCTGGTGCGCAGAC | 1816–1797 | Antisense |
| *2) Fragment B* | | | |
| HBVG1601F | ACGTTACATGGAAACCGCCA | 1601–1620 | Sense |
| HBVG103R | GATTGACGAGATGTGAGAGGCA | 124–103 | Antisense |
| HBVG1630F | CTCATCATCTGCCAAGGCAGT | 1630–1650 | Sense |
| HBVG56R | GAACTGGAGCCACCAGCAGG | 75–56 | Antisense |
| *3) Sequencing primers* | | | |
| HBSF2 | CTTCATCCTGCTGCTATGCCT | 407–426 | Sense |
| HBVG894F | AAGTTGGGGTACTTTGCCAC | 894–913 | Sense |
| HBVG1013R | TGGGTAAAAGGAGCAGCGAAAC | 1034–1013 | Antisense |
| HBVG2052F | GGGAATCCTTAGAGTCCTCTG | 2052–2072 | Sense |
| HBVG2491F | TTCCTTGGACTCACAAGGTG2 | 2491–2510 | Sense |

* Nucleotide position of reference sequence (AB056513).

**Table 2**
HBV DNA oligonucleotide primers for complete genomes of genotype H

| Primer | Nucleotide sequence (5′–3′) | Position | Polarity |
|---|---|---|---|
| *1) Fragment A* | | | |
| HBVH55F | TCCTGCTGGTGGCTCC | 55–70 | Sense |
| HBVH1801R | GTTGCATGGTGCTGGTGAAC | 1820–1801 | Antisense |
| HB6R | AACAGACCAATTTATGCCTA | 1803–1784 | Antisense |
| *2) Fragment B* | | | |
| HBVH1611F | GAGACCACCGTGAACGCCC | 1611–1629 | Sense |
| HBVH285R | GCCAGGACACCCGGGTGGTA | 304–285 | Antisense |
| HBVH229R | CGAGTCTAGACTCTGTGGTATTGTGAGG | 256–229 | Antisense |
| *3) Sequencing primers* | | | |
| HB2F | TGCTGCTATGCCTCATCTTC | 414–433 | Sense |
| HBVH760F | GCCAAATCTGTGCAGCATCTTGAG | 760–783 | Sense |
| HB5F | CTCTGCCGATCCATACTGCGGAA | 1256–1278 | Sense |
| HBVH1859F | ACTGTTCAAGCCTCCAAGCTGT | 1859–1880 | Sense |
| HBVH2415F | GTCGCAGAAGATCTCAATCTC | 2415–2435 | Sense |
| HBVH2814F | GGGTCACCATATTCCTGGGAA | 2814–2834 | Sense |

*Nucleotide position of reference sequence (AB059659).

of HBV, were amplified by nested PCR (primers sequences shown in Table 2). Primers used for fragment A were HBVH55F and HBVH1801R for 1st PCR and HBVH55F and HB6R for 2nd PCR. Primers used for fragment B were HBVH1611F and HBVH285R for 1st PCR and HBVH1611F and HBVH229R for 2nd PCR. Then these fragments were ligated into pGEM-T vector (Promega, Madison, WI) and cloned in DH5α cells. Ten clones each (pGEM-fragA-1 to 10, pGEM-fragB-1 to 10) were obtained and the nucleotide sequences were determined. As reported previously (Fujiwara et al., 2005; Sugiyama et al., 2006), these fragments were constructed into the pUC19 vector deprived of promoters (Invitrogen Corp., Carlsbad, CA) by digestion with HindIII and EcoRI, resulting in 1.24-fold the HBV genome, just enough to transcribe over-sized pregenome and precore mRNA. Cloned HBV DNA sequences were determined with Prism Big Dye (Applied Biosystems, Foster City, CA) in the ABI 3100 automated sequencer. Based on our previous report (Sugiyama et al., 2007), a plasmid of HBV/G with 1.24-fold the HBV genome was also constructed in this study.

*Cell culture and transfection*

Huh7 cells were transfected with plasmids equivalent to 5 μg of HBV DNA constructs with use of the Fugene 6 transfection reagent (Roche Diagnostics, Indianapolis, IN), and harvested after 3 days in culture. Transfection efficiency was monitored by enzymatic activity of secreted alkaline phosphatase (SEAP) in the supernatant of culture with addition of 0.5 μg of reporter plasmids expressing the SEAP.

*Determination of HBV markers*

HBsAg and HBeAg were determined by chemiluminescent enzyme immunoassay (CLEIA) with commercial kits in a fully automated Lumipulse CLEIA analyzer (Fujirebio Inc., Tokyo, Japan). HB core-related antigen (HBcrAg) was measured in serum using the CLEIA described previously (Kimura et al., 2002). Briefly, 150 μL of serum was incubated with 150 μL pretreatment solution containing 15% sodium dodecylsulfate at 60 °C for 30 min. The pretreated serum was added to a well coated with three monoclonal antibodies against denatured HBcAg and HBeAg. After washing, two other alkaline phosphatase-labelled monoclonal antibodies against denatured HBcAg and HBeAg were added as secondary antibodies. 200 μL substrate (AMPPD:(3-(2′-spiroadamantan)-4-methoxy-4- (3′-phosph oryloxy) phenyl-1, 2-dioxetane disodium salt) (Applied Biosystems, Bedford, MA, USA) solution was added and the assay tube was incubated for 5 min at 37 °C. HBcrAg assay with the relative chemiluminescence intensity was measured with chemiluminescent enzyme immunoassay (CLEIA) system for fully automated Lumipulse f CLEIA analyzer (Fujirebio Inc., Tokyo, Japan), and the HBcrAg concentration was estimated by comparison to a standard curve generated using recombinant HBeAg. In the present study, the cutoff value was tentatively set at 3.0 log U/mlmL. Sera containing over 7.0 log U/ml mL of HBcrAg were diluted 10- or 100-fold in normal human serum and re-tested to obtain the end titer.

*Detection and quantification of serum HBV DNA*

For HBV/G-specific real-time detection PCR (RTD-PCR), previously reported set of primers was used, where one of the primers contained sequence of the HBV/G unique 36-bp insertion (Sugiyama et al., 2007). For HBV/H DNA quantification, following primers were applied; HBVH29F: 5′-GTT CCA CCA AGC ACT GTT GG-′3, HBV229R: 5′-CGA GTC TAG ACT CTG TGG TAT TGT GAG G-′3. Amplification and detection were performed using SYBR Green PCR Master Mix (Applied Biosystems) on the ABI Prism 7700 Sequence Detection System (Applied Biosystems). The quantification standard was prepared by serial dilution of a known amount of the cloned plasmid of HBV/G or H. The specificity of these primers was confirmed in every PCR run by dissociation curve analysis (ABI Prism 7700 dissociation curve software; Applied Biosystems). In assays for HBV DNA in mouse sera, in which only 10 μL of sample is used, the sensitivity of the assay allowed detection of 1000 copies/mL of HBV/G or HBV/H DNA.

*Molecular evolutionary analysis*

Nucleotide sequences of HBV were aligned by the program CLUSTAL X, and the genetic distance was estimated with the 6-parameter method (Gojobori et al., 1982) in the Hepatitis Virus Database (Robertson et al., 1998). Based on these values, a phylogenetic tree was constructed by the neighbor-joining method (Saitou and Nei, 1987). To confirm the reliability of the phylogenetic tree, bootstrap resampling test was performed 1,000 times (Felsenstein, 1985).

*Examination for recombination*

Intergenotypic recombination was searched for using the method of Robertson et al. (Robertson et al., 1995) with use of the SimPlot program and bootscanning analysis (Lole et al., 1999). The mean genetic distances were calculated with a window size of 200 bp and a step size of 50 bp in this study.

*Southern blot hybridizations*

Southern blot hybridizations were performed with a full-length probe of HBV/G or H by previous methods (Fujiwara et al., 2005). No significant differences were observed in the detection between internal control HBV DNA and each probe.

*Inoculation of chimeric mice with the liver repopulated for human hepatocytes*

uPA$^{+/+}$/SCID$^{+/+}$ mice with the liver repopulated for human hepatocytes (chimeric mice) were purchased from Phoenix Bio Co., Ltd. (Hiroshima, Japan). The human hepatocytes were obtained from a single donor (female, 6 years, African American). Human serum albumin was measured by ELISA with commercial assay kits (Eiken Chemical Co.Ltd, Tokyo, Japan). They were inoculated with HBV recovered from culture supernatants of Huh7 cells transfected with plasmids containing 1.24-fold HBV genome constructs of the HBV/G or H (Sugiyama et al., 2006, 2007).

*Histopathological examination*

Liver tissues were fixed in formaldehyde, embedded in paraffin and stained with hematoxylin–eosin (H–E) or Masson's trichrome. The fibrosis stage and inflammation grade were evaluated by independent expert pathologists.

## Acknowledgments

We thank Mr. T. Nakamura and T Shimada (PhoenixBio Co., Ltd., Higashi-Hiroshima, Japan) for providing chimeric mice with a high replacement for hepatocytes, and Ms. Y. Yotani in our laboratory for constructing HBV clones.

## References

Arauz-Ruiz, P., Norder, H., Robertson, B.H., Magnius, L.O., 2002. Genotype H: a new Amerindian genotype of hepatitis B virus revealed in Central America. J. Gen. Virol. 83 (Pt 8), 2059–2073.

Carman, W.F., Jacyna, M.R., Hadziyannis, S., Karayiannis, P., McGarvey, M.J., Makris, A., Thomas, H.C., 1989. Mutation preventing formation of hepatitis B e antigen in patients with chronic hepatitis B infection. Lancet 2 (8663), 588–591.

Chudy, M., Schmidt, M., Czudai, V., Scheiblauer, H., Nick, S., Mosebach, M., Hourfar, M.K., Seifried, E., Roth, W.K., Grunelt, E., Nubling, C.M., 2006. Hepatitis B virus genotype G monoinfection and its transmission by blood components. Hepatology 44 (1), 99–107.

Dandri, M., Burda, M.R., Torok, E., Pollok, J.M., Iwanska, A., Sommer, G., Rogiers, X., Rogler, C.E., Gupta, S., Will, H., Greten, H., Petersen, J., 2001. Repopulation of mouse liver with human hepatocytes and in vivo infection with hepatitis B virus. Hepatology 33 (4), 981–988.

Felsenstein, J., 1985. Confidence limits on phylogenesis: an approach using the boostrap. Evolution 39, 783–791.

Fujiwara, K., Tanaka, Y., Paulon, E., Orito, E., Sugiyama, M., Ito, K., Ueda, R., Mizokami, M., Naoumov, N.V., 2005. Novel type of hepatitis B virus mutation: replacement mutation involving a hepatocyte nuclear factor 1 binding site tandem repeat in chronic hepatitis B virus genotype E. J. Virol. 79 (22), 14404–14410.

Gojobori, T., Ishii, K., Nei, M., 1982. Estimation of average number of nucleotide substitutions when the rate of substitution varies with nucleotide. J. Mol. Evol. 18 (6), 414–423.

Heckel, J.L., Sandgren, E.P., Degen, J.L., Palmiter, R.D., Brinster, R.L., 1990. Neonatal bleeding in transgenic mice expressing urokinase-type plasminogen activator. Cell 62 (3), 447–456.

Hussain, M., Chu, C.J., Sablon, E., Lok, A.S., 2003. Rapid and sensitive assays for determination of hepatitis B virus (HBV) genotypes and detection of HBV precore and core promoter variants. J. Clin. Microbiol. 41 (8), 3699–3705.

Junker-Niepmann, M., Bartenschlager, R., Schaller, H., 1990. A short cis-acting sequence is required for hepatitis B virus pregenome encapsidation and sufficient for packaging of foreign RNA. EMBO J. 9 (10), 3389–3396.

Kato, H., Orito, E., Sugauchi, F., Ueda, R., Gish, R.G., Usuda, S., Miyakawa, Y., Mizokami, M., 2001. Determination of hepatitis B virus genotype G by polymerase chain reaction with hemi-nested primers. J. Virol. Methods 98 (2), 153–159.

Kato, H., Orito, E., Gish, R.G., Bzowej, N., Newsom, M., Sugauchi, F., Suzuki, S., Ueda, R., Miyakawa, Y., Mizokami, M., 2002a. Hepatitis B e antigen in sera from individuals infected with hepatitis B virus of genotype G. Hepatology 35 (4), 922–929.

Kato, H., Orito, E., Gish, R.G., Sugauchi, F., Suzuki, S., Ueda, R., Miyakawa, Y., Mizokami, M., 2002b. Characteristics of hepatitis B virus isolates of genotype G and their phylogenetic differences from the other six genotypes (A through F). J. Virol. 76 (12), 6131–6137.

Kimura, T., Rokuhara, A., Sakamoto, Y., Yagi, S., Tanaka, E., Kiyosawa, K., Maki, N., 2002. Sensitive enzyme immunoassay for hepatitis B virus core-related antigens and their correlation to virus load. J. Clin. Microbiol. 40 (2), 439–445.

Kremsdorf, D., Garreau, F., Capel, F., Petit, M.A., Brechot, C., 1996. In vivo selection of a hepatitis B virus mutant with abnormal viral protein expression. J. Gen. Virol. 77 (Pt 5), 929–939.

Lacombe, K., Massari, V., Girard, P.M., Serfaty, L., Gozlan, J., Pialoux, G., Mialhes, P., Molina, J.M., Lascoux-Combe, C., Wendum, D., Carrat, F., Zoulim, F., 2006. Major role of hepatitis B genotypes in liver fibrosis during coinfection with HIV. Aids 20 (3), 419–427.

Li, K., Zoulim, F., Pichoud, C., Kwei, K., Villet, S., Wands, J., Li, J., Tong, S., 2007. Critical role of the 36-nucleotide insertion in hepatitis B virus genotype G in core protein expression, genome replication, and virion secretion. J. Virol. 81 (17), 9202–9215.

Lole, K.S., Bollinger, R.C., Paranjape, R.S., Gadkari, D., Kulkarni, S.S., Novak, N.G., Ingersoll, R., Sheppard, H.W., Ray, S.C., 1999. Full-length human immunodeficiency virus type 1 genomes from subtype C-infected seroconverters in India, with evidence of intersubtype recombination. J. Virol. 73 (1), 152–160.

Magnius, L.O., Norder, H., 1995. Subtypes, genotypes and molecular epidemiology of the hepatitis B virus as reflected by sequence variability of the S-gene. Intervirology 38 (1–2), 24–34.

Miyakawa, Y., Mizokami, M., 2003. Classifying hepatitis B virus genotypes. Intervirology 46 (6), 329–338.

Norder, H., Courouce, A.M., Magnius, L.O., 1994. Complete genomes, phylogenetic relatedness, and structural proteins of six strains of the hepatitis B virus, four of which represent two new genotypes. Virology 198 (2), 489–503.

Okamoto, H., Yotsumoto, S., Akahane, Y., Yamanaka, T., Miyazaki, Y., Sugai, Y., Tsuda, F., Tanaka, T., Miyakawa, Y., Mayumi, M., 1990. Hepatitis B viruses with precore region defects prevail in persistently infected hosts along with seroconversion to the antibody against e antigen. J. Virol. 64 (3), 1298–1303.

Okamoto, H., Tsuda, F., Sakugawa, H., Sastrosoewignjo, R.I., Imai, M., Miyakawa, Y., Mayumi, M., 1988. Typing hepatitis B virus by homology in nucleotide sequence: comparison of surface antigen subtypes. J. Gen. Virol. 69 (Pt 10), 2575–2583.

Osiowy, C., Giles, E., 2003. Evaluation of the INNO-LiPA HBV genotyping assay for determination of hepatitis B virus genotype. J. Clin. Microbiol. 41 (12), 5473–5477.

Ozasa, A., Tanaka, Y., Orito, E., Mizokami, M., 2006. Influence of genotypes and precore mutations on fulminant or chronic outcome of acute hepatitis B virus infection. Hepatology. 44, 326–334.

Rhim, J.A., Sandgren, E.P., Degen, J.L., Palmiter, R.D., Brinster, R.L., 1994. Replacement of diseased mouse liver by hepatic cell transplantation. Science 263 (5150), 1149–1152.

Robertson, D.L., Hahn, B.H., Sharp, P.M., 1995. Recombination in AIDS viruses. J. Mol. Evol. 40 (3), 249–259.

Robertson, B., Myers, G., Howard, C., Brettin, T., Bukh, J., Gaschen, B., Gojobori, T., Maertens, G., Mizokami, M., Nainan, O., Netesov, S., Nishioka, K., Shin i, T., Simmonds, P., Smith, D., Stuyver, L., Weiner, A., 1998. Classification, nomenclature, and database development for hepatitis C virus (HCV) and related viruses: proposals for standardization. International Committee on Virus Taxonomy. Arch. Virol. 143 (12), 2493–2503.

Saitou, N., Nei, M., 1987. The neighbor-joining method: a new method for reconstructing phylogenetic trees. Mol. Biol. Evol. 4 (4), 406–425.

Sanchez, L.V., Maldonado, M., Bastidas-Ramirez, B.E., Norder, H., Panduro, A., 2002. Genotypes and S-gene variability of Mexican hepatitis B virus strains. J. Med. Virol. 68 (1), 24–32.

Sanchez, L.V., Tanaka, Y., Maldonado, M., Mizokami, M., Panduro, A., 2007. Difference of hepatitis B virus genotype distribution in two groups of mexican patients with different risk factors High prevalence of genotype h and g. Intervirology 50 (1), 9–15.

Stuyver, L., De Gendt, S., Van Geyt, C., Zoulim, F., Fried, M., Schinazi, R.F., Rossau, R., 2000. A new genotype of hepatitis B virus: complete genome and phylogenetic relatedness. J. Gen. Virol. 81 (Pt 1), 67–74.

Sugauchi, F., Orito, E., Ichida, T., Kato, H., Sakugawa, H., Kakumu, S., Ishida, T., Chutaputti, A., Lai, C.L., Ueda, R., Miyakawa, Y., Mizokami, M., 2002. Hepatitis B virus of genotype B with or without recombination with genotype C over the precore region plus the core gene. J. Virol. 76 (12), 5985–5992.

Sugauchi, F., Kumada, H., Acharya, S.A., Shrestha, S.M., Gamutan, M.T., Khan, M., Gish, R.G., Tanaka, Y., Kato, T., Orito, E., Ueda, R., Miyakawa, Y., Mizokami, M., 2004. Epidemiological and sequence differences between two subtypes (Ae and Aa) of hepatitis B virus genotype A. J. Gen. Virol. 85 (Pt 4), 811–820.

Sugiyama, M., Tanaka, Y., Kato, T., Orito, E., Ito, K., Acharya, S.A., Gish, R.G., Kramvis, A., 2006. Influence of hepatitis B virus genotypes on the intra-and extracellular expression of viral DNA and antigens. Hepatology 44, 915–924.

Sugiyama, M., Tanaka, Y., Sakamoto, T., Maruyama, I., Shimada, T., Takahashi, S., Shirai, T., Kato, H., Nagao, M., Miyakawa, Y., Mizokami, M., 2007. Early dynamics of hepatitis B virus in chimeric mice carrying human hepatocytes monoinfected or coinfected with genotype G. Hepatology 45 (4), 929–937.

Suwannakarn, K., Tangkijvanich, P., Theamboonlers, A., Abe, K., Poovorawan, Y., 2005. A novel recombinant of Hepatitis B virus genotypes G and C isolated from a Thai patient with hepatocellular carcinoma. J. Gen. Virol. 86 (Pt 11), 3027–3030.

Tsuge, M., Hiraga, N., Takaishi, H., Noguchi, C., Oga, H., Imamura, M., Takahashi, S., Iwao, E., Fujimoto, Y., Ochi, H., Chayama, K., Tateno, C., Yoshizato, K., 2005. Infection of human hepatocyte chimeric mouse with genetically engineered hepatitis B virus. Hepatology 42 (5), 1046–1054.

Usuda, S., Okamoto, H., Iwanari, H., Baba, K., Tsuda, F., Miyakawa, Y., Mayumi, M., 1999. Serological detection of hepatitis B virus genotypes by ELISA with monoclonal antibodies to type-specific epitopes in the preS2-region product. J. Virol. Methods 80 (1), 97–112.

Usuda, S., Okamoto, H., Tanaka, T., Kidd-Ljunggren, K., Holland, P.V., Miyakawa, Y., Mayumi, M., 2000. Differentiation of hepatitis B virus genotypes D and E by ELISA using monoclonal antibodies to epitopes on the preS2-region product. J. Virol. Methods 87 (1–2), 81–89.

# BASIC—LIVER, PANCREAS, AND BILIARY TRACT

## Direct Cytopathic Effects of Particular Hepatitis B Virus Genotypes in Severe Combined Immunodeficiency Transgenic With Urokinase-Type Plasminogen Activator Mouse With Human Hepatocytes

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***Background & Aims:*** **Little is known about the direct cytopathic effect of hepatitis B virus (HBV) and its association with particular viral genotypes or genetic mutations. We investigate HBV genotype–related differences in viral replication, antigen expression, and histopathology in severe combined immunodeficiency transgenic with urokinase-type plasminogen activator mice harboring human hepatocytes.** ***Methods:*** **Mice were inoculated with wild-type of different genotype strains (3 for each HBV/A2, B1, and C2) recovered from preinfected-mice sera or patient sera.** ***Results:*** **Histologic analysis of mice infected with HBV/C2 for 22–25 weeks showed abundant ground-glass appearance of the hepatocytes and fibrosis in the humanized part of the murine liver owing to the activation of hepatic stellate cells mediated by oxidative stress through transforming growth factor-$\beta$1 signaling, whereas neither was observed with HBV/A2 and B1. The HBV-DNA level in sera was the highest in mice infected with HBV/C2 compared with those with HBV/A2 and HBV/B1 ($10^9$, $10^7$, and $10^4$ log copies/mL, respectively, $P < .05$) during 6–8 weeks postinoculation. HB core-related antigen excretion had a similar trend among the genotypes, whereas secretion of HB surface antigen was more pronounced for HBV/A2 followed by HBV/C2 and much less for HBV/B1. Introduction of precore stop-codon mutation in the HBV/B1 caused a significant increase in viral replication, antigen expression, and a histopathologic picture similar to HBV/C2.** ***Conclusions:*** **By using a humanized in vivo model, we show that different HBV genotypes and even particular mutations resulted in different virologic and histopathologic outcomes of infection, indicating that particular genetic variants of HBV may be directly cytopathic in immunosuppressive conditions.**

With an estimated 420 million chronic carriers, hepatitis B virus (HBV) infection is one of the most prevalent chronic viral infections of human beings. The chronic infection often leads to cirrhosis and/or hepatocellular carcinoma, which is responsible for at least 1 million deaths annually worldwide.[1] The precise mechanism by which chronic viral hepatitis results in hepatocellular carcinoma (HCC) is not known. However, evidence now is available concerning the direct effects of HBV in this process.[2,3] The important issue of a distinct impact of the various HBV genotypes on the virulence has not been addressed directly so far.[4,5]

Genotypes are subdivided further into subgenotypes on the basis of phylogenetic relationships.[6] Evidence for the influence of HBV genotypes/subgenotypes on liver diseases in acute, fulminant, and chronic infection have been reported increasingly.[7–13] Involvement of genetic mutations of HBV in its pathogenesis is another open question. Previous reports have indicated that mutations in basal core promoter, precore/core, envelope, and X coding regions may be associated with HCC.[14] The term *precore mutants* refers to HBV strains with nonsense frameshift or initiation codon mutation in the precore region that prevent translation of hepatitis B e antigen (HBeAg) precursor and are associated with an increase of viral replication via stabilization of the pregenomic encapsidation signal.[15] However, little is known about the histopathologic implication of the mutants. Complexity

*Abbreviations used in this paper:* α-SMA, α-smooth muscle actin; PCm, precore stop-codon mutation; HBcrAg, antigens related to hepatitis B virus core; HSC, hepatic stellate cell; 8-OHdG, 8-hydroxydeoxyguanosine; PCR, polymerase chain reaction; ROS, reactive oxygen species; TGF-$\beta$1, transforming growth factor-$\beta$1.


0016-5085/09/$36.00
doi:10.1053/j.gastro.2008.10.048

**Table 1.** Inoculum Profiles on HBV Isolates of Distinct Genotypes/Subgenotypes

| Genotype (Subgenotype) | Isolates | Mice (n) | Accession No. | Precore (1896) | HBeAg |
|---|---|---|---|---|---|
| A (A2/Ae) | A2_US | 4 | AB246337 | Wild | + |
| | A2_JPN1 | 3 | AB246338 | Wild | + |
| | A2_JPN2 | 3 | AB362931 | Wild | + |
| C (C2/Ce) | C2_JPN22 | 4 | AB246344 | Wild | + |
| | C2_JPNAT | 4 | AB246345 | Wild | + |
| | C2_JPN31 | 3 | AB362932 | Wild | + |
| B (B1/Bj_wild) | B1_JPN35w | 4 | AB246341 | Wild | + |
| | B1_JPN56w | 3 | AB246342 | Wild | + |
| | B1_JPN58w | 4 | AB362933 | Wild | + |
| B (B1/Bj_PCm)* | B1_JPN35m | 3 | [a] | Mutant | − |
| | B1_JPN56m | 3 | [a] | Mutant | − |
| | B1_JPN58m | 3 | [a] | Mutant | − |

[a]Accession numbers are not shown because these 3 clones identical to the above described HBV/B clones were constructed with G1896A point mutation.

of the host and environmental factors complicates evaluation of the veritable virologic differences between genetic variants of HBV in a clinical study. Therefore, a model that eliminates these factors and allows a direct comparison of early dynamics of HBV genotypes is essential for such investigation.

Recently engineered severe combined immunodeficient mice transgenic for urokinase-type plasminogen activator received human hepatocyte transplants (hereafter referred to as *chimeric mice*)[16-18] and are suitable for the experiments with hepatitis viruses in vivo,[19,20] and offer a rare opportunity in modeling the early kinetics of the HBV replication.[21]

In the present study, infecting human hepatocytes in chimeric mice, we show that different HBV genotypes and even particular mutations within the same genotype have distinct virologic characteristics that may have contributed to the distinct histologic outcomes.

## Materials and Methods

### *Inoculation of Chimeric Mice With the Liver Repopulated for Human Hepatocytes*

The chimeric mice were purchased from Phoenix Bio Co, Ltd (Hiroshima, Japan). Human hepatocytes were imported from BD Biosciences (San Jose, CA). The human serum albumin was measured by enzyme-linked immunosorbent assay using commercial kits (Eiken Chemical Co Ltd, Tokyo, Japan). The serum levels of the human albumins and the body weight were required to be identical among all of the mice to provide reliable comparison. All mice were infected successfully with HBV recovered from preinfected-mice sera or sera of patients as described in our previous report.[21] Briefly, a mixture of immature virions can be present in supernatants of cell culture transfected with plasmids expressing HBV[22,23]; therefore, to avoid direct use of the supernatants in experimental mice, the preinfected mice were infected instead, using the culture media, and then were used as a source of HBV inoculums for the experimental mice. Three clones for each HBV/A2, C2, B1_wild, or B1_PC mutant (precore stop-codon mutation [PCm]) were used in this study (Table 1), and each clone was inoculated to 3 or 4 mice.

### *Patients*

Sera were obtained from 6 patients, 3 of whom had acute hepatitis B and the remaining 3 had fulminant hepatitis B. All sera were subjected to HBV extraction and direct sequencing, which determined genotype B (subgenotype Bj/B1) in all of them. HBV genome sequence analysis of the HBV clones isolated from 3 patients with fulminant hepatitis revealed both the presence of the PC mutation (G1896A) and the absence of any other featured mutations such as core promoter or tyrosine methionine aspartate aspartate mutations (Table 2). HBV strains isolated from the 3 acute hepatitis patients were wild type without core

**Table 2.** Characteristics of Patients From Whom HBV Isolates of Distinct Genotypes/Subgenotypes Were Recovered

| Genotype/subgenotype | Isolates | Precore (1896) | Diseases | HBeAg | HBV (LGE[a]/mL) |
|---|---|---|---|---|---|
| B1/Bj_wild | B1_JPN1 | Wild | AHB | + | 6.8 |
| | B1_JPN2 | Wild | AHB | + | 7.0 |
| | B1_JPN3 | Wild | AHB | + | 6.7 |
| B1/Bj_PCm | B1_JPN4 | Mutant | FHB | − | 8.7 |
| | B1_JPN5 | Mutant | FHB | − | 8.0 |
| | B1_JPN6 | Mutant | FHB | − | 8.6 |

AHB, acute hepatitis B; FHB, fulminant hepatitis B.
[a]Log genome equivalents.

promoter, precore, and tyrosine methionine aspartate aspartate mutations. The study design conformed to the 1975 Declaration of Helsinki, and was approved by the Ethic Committees of the participating institutions. Written informed consent was obtained from each patient.

### *Histopathologic Examination*

Liver tissues were fixed in buffered formalin, embedded in paraffin, and stained with H&E, Masson's trichrome (MT), or orcein staining. To detect α-smooth muscle actin (α-SMA) and human nuclei, polyclonal antibodies against anti-α-SMA (Lab Vision Corp, Fremont, CA) and monoclonal antibody against anti-human nuclei (Chemicon International, Inc, Temecula, CA) were used as primary antibodies, respectively. The fibrosis stage was evaluated by an expert pathologist who was blinded to the nature of inocula (S.T.).

### *Dihydroethidium Labeling of Reactive Oxygen Species in Liver Tissue*

In situ reactive oxygen species (ROS) production was evaluated by staining with dihydroethidium (Invitrogen, Carlsbad, CA) as previously reported with minor modification.[24] Briefly, in the presence of ROS, dihydroethidium is oxidized to ethidium bromide and stains nuclei bright red by intercalating with the DNA. The fluorescence was detected with laser scanning confocal microscopy. The relative stained area was quantified using National Institutes of Health image analysis for 5 randomly selected areas of digital images in each specimen.

### *Detection of 8-Hydroxydeoxyguanosine in Liver Tissue*

Immunohistochemical detection of 8-hydroxydeoxyguanosine (8-OHdG) was performed as previously reported with minor modification.[25] The detailed protocol is shown in the Supplementary Materials and Methods section (see Supplementary material online at www.gastrojournal.org).

## Results

### *Differences of Replication Efficiency Among HBV Genotypes*

The inoculums, each containing approximately $10^5$ copies of any 1 of the 4 clones: HBV/A2, C2, B1_wild, and B1_PC mutant (PCm), were inoculated to 3 or 4 mice. HBV DNA was quantified in murine sera weekly. One week after inoculation, HBV DNA was detected in both the HBV/A2 and C2 groups. The titer increased approximately by 2 logs within the next 2 weeks, and continued to increase until 7–12 weeks before reaching a plateau. HBV-DNA levels were 2 logs higher in the mice inoculated with HBV/C2 than HBV/A2 at 6–8 weeks postinoculation ($P < .05$) (Figure 1*A*).

To assess the role of the PC mutation, 2 variants of HBV/B1 were included in the comparison between the genotypes: the HBV/B1_wild and HBV/B1_PCm. Differently from HBV/A2 and HBV/C2, both of the HBV/B1 variants had shown a so-called *window* period; characterized by the HBV-DNA levels remaining undetectable until weeks 4–5 after the inoculation. However, after the window period, the HBV-DNA level of the B1_PCm detected at week 5 had rapidly increased in titer, reaching the levels of HBV/C2 and A2 by week 11 (Figure 1*A*). Interestingly, HBV-DNA levels of B1_wild did not show this rapid increment during the whole follow-up period (until week 25). HBV-DNA titer was 3 logs lower in mice inoculated with HBV/B1_wild compared with those with the other genotypes ($P < .01$). To evaluate the replication dynamics of the different genotypes, the time required for a 10-fold increment of the viral load (*log time*) was estimated. When the window periods of HBV/B1_PCm were excluded from the comparison, the log time was similar between the HBV/C2 and B1_PCm, ranging from 7.3 to 8.4 days, whereas HBV/A2 had a longer index (12.9 days), suggesting slower replication. However, the lowest replication efficiency was observed for HBV/B1_wild, with a log time of 27.7 days.

### *Distinct Characteristics on Antigen Production Among HBV Genotypes*

The expression of hepatitis B surface antigen (HBsAg) and hepatitis B core-related antigen (HBcrAg) (depicted in Figure 1*B*) did not correspond with that of HBV DNA (Figure 1*A*) for HBV/B1_PCm, which had rapidly increased antigen expression in the early phase, and then decreased sharply. HBeAg of HBV/B1_PCm was undetectable as expected to confirm the function of the stop codon mutation. In contrast, dynamics of HBcrAg and HBeAg expression by HBV/C2 and HBV/A2 resembled those of HBV DNA. The HBcrAg levels of HBV/B1_PCm without HBeAg expression revealed lower levels than those of HBV/A2 or C2. To detect core protein alone without detecting HBeAg, only hepatitis B core antigen (HBcAg) was assessed in each mice group at the peak point of HBcrAg by enzyme-linked immunosorbent assay. The value of HBV/B1_PCm shown was equal to that of HBV/C2, and higher than that of HBV/A2 (data not shown). HBV antigens of HBV/B1_wild group were detectable, although they had extremely low levels, suggesting a very low replication level for this group. Core protein levels in liver tissue, with adjustment for human albumin levels, showed a similar trend to that of sera (data not shown).

### *Confirmation of HBV/B1_Wild Infectivity by Using Human Sera*

Virus titer of the HBV/B1_wild group was very low and the log time was long in the present study. To further confirm these findings, we used 6 sera: 3 from

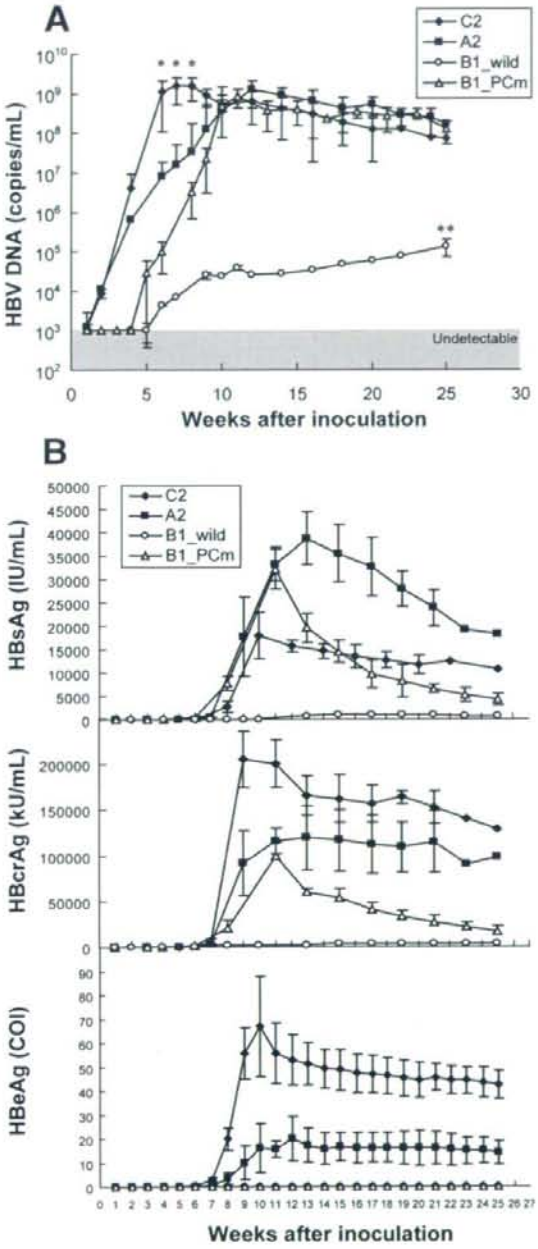


**Figure 1.** Comparative dynamic profile of HBV-DNA and antigen levels in sera of mice inoculated with preinfected-mice sera recovered from culture media transfecting HBV construct. (*A*) Levels of HBV DNA in sera of the chimeric mice inoculated with HBV/A2, C2, B1_wild, or B1_PCm. Shaded in *gray* is an area below the detection limit (<$10^3$ copies/mL) of the real-time detection PCR assay. *Statistical differences with a *P* value of less than .05. **Statistical differences with a *P* value of less than .01. (*B*) Dynamic profiles of HBV antigen expression, as revealed by quantification of HBsAg, HBeAg, and HBcrAg in sera of the chimeric mice (see Supplementary Materials and Methods section). For each group, mean values observed in 9–11 chimeric mice are depicted with the standard deviation bars.

acute hepatitis B patients harboring precore wild-type HBV/B1 and the other 3 from fulminant hepatitis B patients harboring precore nonsense-mutation B1 (B1_PCm) (Table 2). Three mice were inoculated with each one of the 6 serum specimens adjusted to contain approximately $10^6$ copies of HBV DNA (Figure 2*A* and *B*). Serum HBV-DNA levels increased immediately after inoculation of HBV/B1_PCm and continued to increase until they reached a plateau at week 6 (Figure 2*A*), showing extremely high replication efficiency. The window period was shortened to 2 weeks in the acute hepatitis B serum group with HBV/B1_wild; however, the peak of mean HBV-DNA levels still was low ($5 \times 10^5$ copies/mL), which was similar to the results by inoculation of preinfected-mice sera (Figure 1*A*). Neither serum levels of the human albumin nor the body weight differed among the mice groups. Based on direct sequencing, no mutations were detected in the HBV complete genomes from any mice 25 weeks after inoculation in comparison with those of inoculated strains.

HBV antigen expression levels of the groups inoculated with human serum samples were compared with those of the groups inoculated with the preinfected-mice sera (Figure 2*B*). HBV antigens of HBV/B1_PCm waxed and waned in profiles similar to that of the groups inoculated with the mice sera in the early phase.

### *Liver Pathology of Chimeric Mice Infected With Each Genotype*

Figure 3 shows the histology of liver in representative chimeric mice infected with HBV/A2, C2, B1_wild, or B1_PCm during weeks 22–25. The immunofluorescence staining was performed using anti-HBcAg and anti-human albumin polyclonal antibody to confirm the location of HBV infection (Supplementary Figure 1; see Supplementary material online at www.gastrojournal.org). Colocalization of HBcAg and human hepatocytes was shown by double staining for HBcAg and human albumin. Almost all of the mice did not reveal apparent steatosis of hepatocytes with H&E stain. The majority of HBV/C2- or B1_PCm-infected human hepatocytes had a ground-glass appearance on H&E stain, fibrosis of stage 2 with MT stain, as well as neutrophil or monocyte invitation. In contrast, the mice infected with HBV/A2 or B1_wild had neither a ground-glass appearance nor fibrosis. To confirm the ground-glass appearance, these specimens were stained by orcein staining. The orcein staining clearly showed cytoplasmic positivity of human hepatocytes infected with HBV/B1_PCm or C2, but not the other group, including control mice.

### *Immunostaining Analysis on Expression of α-SMA*

Active hepatic stellate cells (HSCs) express α-SMA in the early phase of fibrogenesis. To estimate the activation of stellate cells, we performed immunostaining

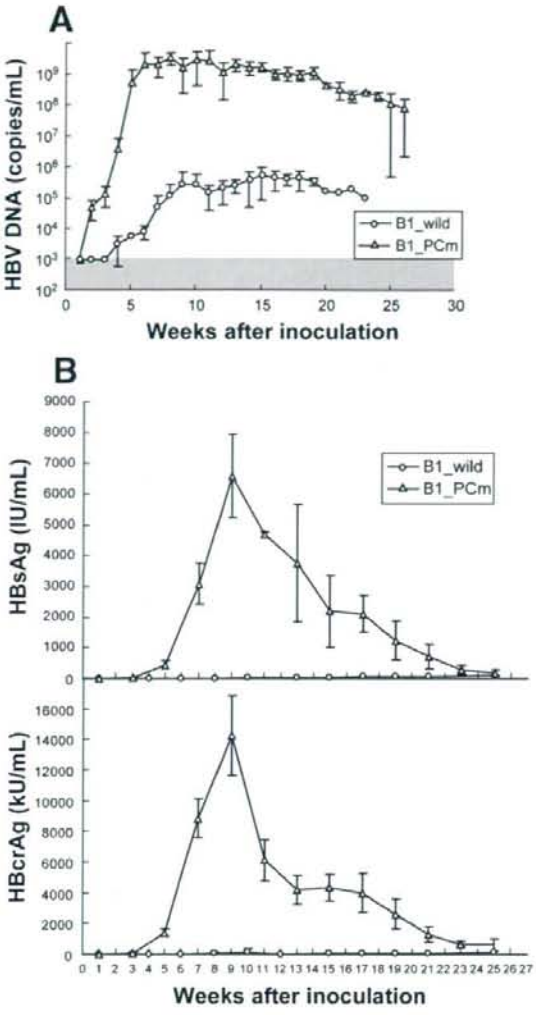


**Figure 2.** Comparative dynamic profile of HBV-DNA antigen levels in sera of mice inoculated with patient sera from HBV/B1_wild (PC wild-type) and HBV/B1_PCm (PC mutant). (*A*) Mice inoculated with sera from HBV/B1_wild–infected carriers developed acute hepatitis B or from HBV/B1_PCm-infected carriers developed fulminant hepatitis B and were assessed for levels of HBV DNA in mice sera with real-time detection PCR weekly. The area below the detection limit (<$10^3$ copies/mL) is shaded in *gray*. (*B*) Dynamic profiles of HBV antigens including HBsAg and HBcrAg in mice corresponding to panel *A*. For each genotype, mean values observed in 9–11 chimeric mice are depicted with the standard deviation bars.

using anti-α-SMA antibody. Immunostaining analysis showed strong staining of α-SMA around fibrosis, which was found by MT staining (Figure 4*A*). These results indicated that liver fibrosis of HBV/C2 and B1_PCm occurred via profibrotic cytokines from the activated HSCs but not artifacts. The specimen was double-stained for human nuclei and α-SMA to distinguish between human and mouse cells. As shown in Figure 4*B*, α-SMA and human nuclei did not stain in the same cells, suggesting that the active HSCs were of mouse origin.

### *Increased Oxidized State in Liver by HBV Infection*

In the fibrosis process, current knowledge establishes that the production of ROS plays a critical role in HSC activation involving transforming growth factor-β1 (TGF-β1) signaling.[26] Because α-SMA expressed by HSCs was detected in chimeric mice liver, we next investigated ROS production in mice liver. The ROS production was confirmed by dihydroethidium staining (Figure 5*A*). The level of ROS production was increased statistically when mice were infected with HBV/B1_PC or C2 compared with HBV/A2 or B1_wild ($P < .01$) (Figure 5*B*). Figure 5*C* shows representative immunohistochemical staining for 8-OHdG, which is a marker of oxidative DNA damage, in liver; 8-OHdG-positive cells were recognized in both HBV/C2 and B1_PCm groups, whereas few 8-OHdG-positive cells were detected in the other groups. These data were consistent with those of ROS production.

### *Gene Expression of Fibrosis Markers in the Mice Liver*

As for the change of factors associated with TGF-β1 signaling in the mice, serum alanine aminotransferase (ALT) and TGF-β1 levels were increased in the fibrosis group (B1_PC and C2) as compared with the nonfibrosis group (A2 and B1_wild) (Figure 6*A* and *B*). The TGF-β1 levels in the fibrosis group showed significant difference ($P < .01$). To determine whether the representative fibrosis-related genes were of human or mouse origin, we established species-specific primer sets. Polymerase chain reaction using the species-specific primers gave bands of specific size showing reliable specificity (Figure 6*C*) and dissociation curves (data not shown) (the detailed protocol is provided in the Supplementary Materials and Methods section). Gene expression levels of tissue inhibitor of metalloproteinase 1, matrix metalloproteinase 2, and collagen type 1α2 were quantified by real-time detection reverse-transcription PCR analyses. Specifically, gene expression of human tissue inhibitor of metalloproteinase 1 and mouse collagen type 1α2 represented significantly higher expression in the fibrosis group than that of the nonfibrosis or control groups ($P < .001$). Matrix metalloproteinase 2 and collagen type 1α2 messenger RNA (mRNA) of human origin were undetectable because these genes are produced predominantly in mesenchymal cells.[27]

## Discussion

In the present study, the severe combined immunodeficient mice transgenic for urokinase-type plasminogen activator mouse with human hepatocytes was applied to evaluate genotype-dependent differences in the

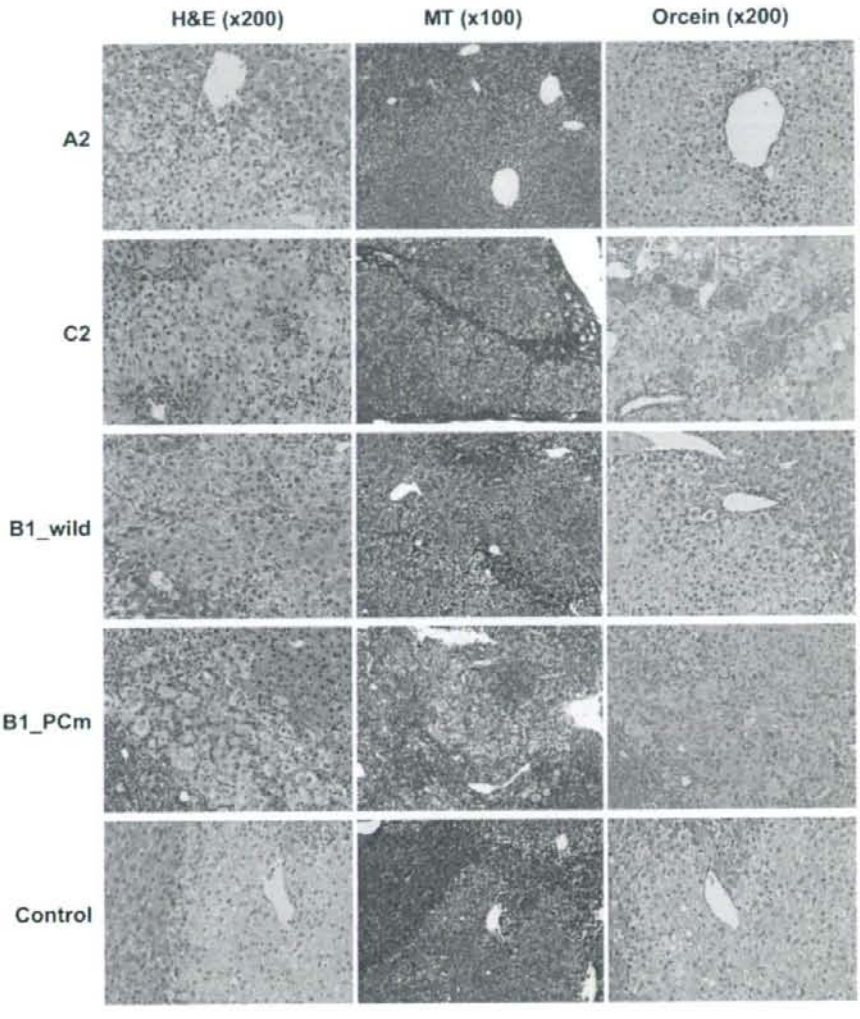


**Figure 3.** Immunohistochemical analysis of liver tissue. Comparison of liver histology in mice long-term (25 weeks) infected with HBV/A2, C2, B1_wild, B1_PCm, and noninfected control. Liver sections stained with H&E, MT, or orcein are shown. After deparaffinization, tissue slides were stained according to each method. Representative staining of C2 and B1_PCm showed a ground-glass appearance, fibrosis, and cytoplasmic positivity of human hepatocytes by orcein staining (brown), whereas these were absent in A2, B1_wild, and control mice. Original magnifications: H&E and orcein, 200×; MT, 100×.

expression of HBV DNA and antigens. This has allowed for an assessment of the direct cytopathic potential of different HBV genotypes (ie, particular subgenotypes) to be investigated without the host-related bias, under conditions of the absence of immune pressure. In addition, this may represent a novel mouse model for human liver fibrosis associated with ROS production leading to the activity of TGF-$\beta$ by viral infection but not chemical trigger. The study thereby has shown that infection with HBV/C2 in contrast to HBV/A2 or B1_wild has induced an abundant ground-glass appearance of the human hepatocytes along with an increased fibrosis in the humanized liver of the chimeric mice in an immunosuppressive condition. A strong staining of $\alpha$-SMA observed around areas of fibrosis indicated activation of HSCs in cases of HBV/C2 and B1_PCm, but not in A2 and B1_wild. In the chimeric mice, therefore, ROS production could play a critical role in HSC activation. In connection with this study, we have evaluated the liver damages in chimeric mice killed at 3 months postinfection (early phase dynamics). The viral dynamics and ROS production of HBV/C2 or B1_PCm evaluated in the early phase indicated levels of alterations similar to those observed after long-term infection (Supplementary Figure 2; see Supplementary material online at www.gastrojournal.org). Fibrosis stage and orcein staining levels (ground-glass appearance), however, were expressed in lesser levels than in the long-term infected mice, suggesting that the liver damage can be detected even in the early stage of the infection, but its level correlates with the duration of exposure to oxidative stress.

Our previous report showed that the intracellular virion retention and endoplasmic reticulum stress were the highest for HBV/C2.[21] Our data obtained in vitro and

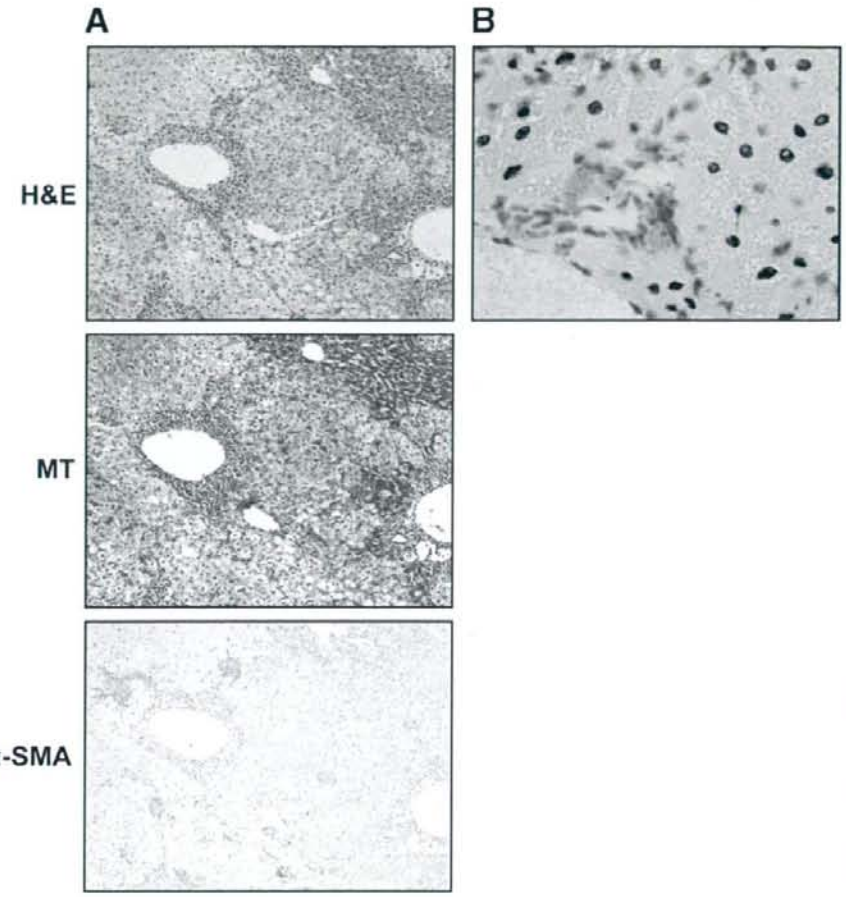


**Figure 4.** Confirmation of liver fibrosis by immunostaining using anti–α-SMA antibody. (*A*) Liver sections stained with H&E, MT, or immunostaining using anti–α-SMA antibody (as described in the Materials and Methods section). (*B*) Nuclei stained *brown* with the antibodies indicate human origin, and α-SMA is stained in *red*, located in the cytoplasm without a stained nucleus. Shown are representative staining of images expressing fibrosis. Original magnification, 200×.



in vivo may explain in part previous results accumulated from clinical studies indicating that HCC more often was associated with HBV/C and the mean age of patients with HCC is younger in the HBV/C-infected group compared with the HBV/B1-infected group.[28,29] On the other hand, the low replicative capacity and hepatic injury of HBV/A2 may contribute to the ability of the subgenotype to evade the immune response and chronically persist in up to 10% of acutely infected adults (which is exceptionally rarely observed with HBV/C or HBV/B).[11,30–32] High levels of HBsAg secretion for HBV/A2 are in contrast with its low replicative activity, and this may be an important mechanism for the immune escape. However, some cautions must be exercised when extrapolating the results of in vivo models to patients because immune responses are not taken into account.

The hepatic injury during acute and chronic HBV infection genuinely is considered to be caused by the host's immune response against the infected hepatocytes.[33] However, in some immunosuppressed chronic HBV patients, high viremia and liver fibrosis may occur.[34,35] Previous reports have shown that HBV genotypes E or G cause intracellular changes and hepatocellular damage in human hepatocytes in severe combined immunodeficient mice transgenic for urokinase-type plasminogen activator.[2,3] We showed here that activation of oxidative stress led to TGF-β1 production in chimeric mice as reported in previous studies.[26] Accumulation of oxidative damage, 8-OHdG, might enhance the possibility of carcinogenesis as observed in HCC patients. These findings suggest that hepatic injuries could arise in the absence of a mature immune system and the difference of genotype would affect the cytopathic potential of the virus.

Chimeric mice were infected with HBV recovered from serum or culture medium containing virion from Huh7 cells transfected with HBV construct.[2,20,21,36,37] In our previous study, by using a single clone corresponding to HBV/A or C, we showed 2 logs difference during weeks 4–7 in the serum levels of HBV DNA between the cohort of mice inoculated with HBV/C and HBV/A.[21] In the present study, we extended the examination of the geno-

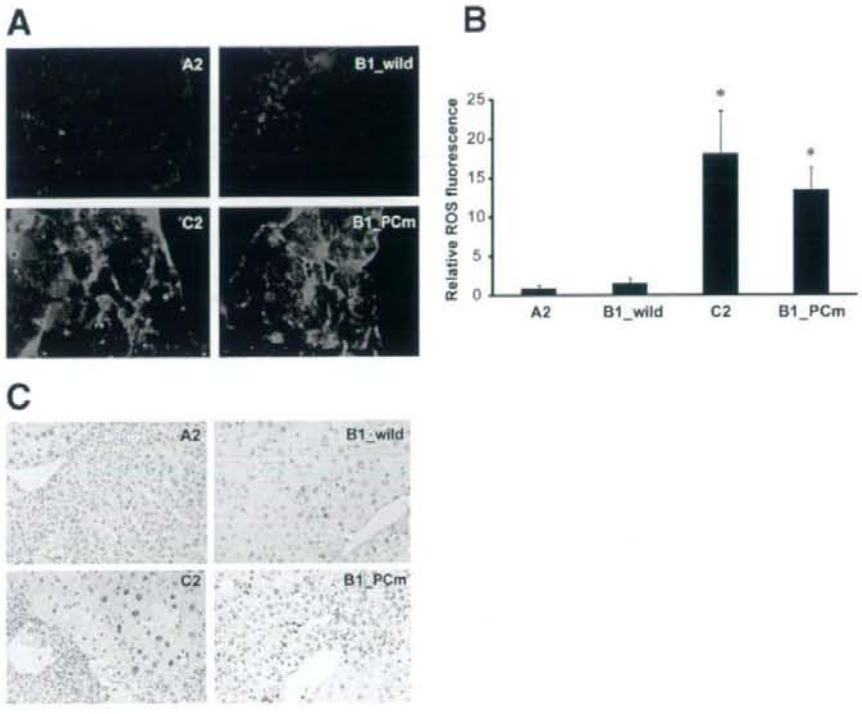


**Figure 5.** Differences in production of oxidative damage among HBV genotypes. (*A*) Frozen liver sections of mice inoculated with different HBV genotypes were stained by dihydroethidium. Fluorescence was detected with a laser scanning microscope. (*B*) Fluorescence intensities in randomly selected areas of digital images were quantified by National Institutes of Health image analysis software. *$P < .01$: A2 or B1_wild vs C2 or B1_PCm. (*C*) Oxidative damages in liver tissue were evaluated by staining of 8-OHdG–positive nuclei. Original magnifications, 200×.

type differences by using 3 clones, representative of each genotype. The results of the present study in concordance with our previous study showed that the replication efficiency of HBV/C is significantly higher than that of HBV/A, as was indicated by 2 logs difference during weeks 6–8 in the levels of HBV DNA detected in murine sera ($P < .05$). The ability of HBV/A to express more HBsAg, and that of HBV/C to produce more HBcrAg revealed in our previous in vitro study,[21] were both thereby confirmed by the present in vivo replication model using the chimeric mice.

Previous clinical observations on HBV/B1[11,28] prompted a deeper investigation on the impact of the PC mutation on the virologic characteristics of the genotype. The unique characteristic of HBV/B1_wild stood out among genotypes harboring no major mutations. The HBV/B1_wild group revealed low replication efficiency with window periods and low antigen expression. The lower replicative activity and hepatic injuries of HBV/A2 and B1_wild may partially explain why carriers with either HBV/A2 or HBV/B1 often are asymptomatic in contrast to those with HBV/C infection.[28,38,39] In our study, the PC mutation was the only difference between HBV/B1_PCm and HBV/B1_wild clone, and the former showed higher replication efficiency and severe damage in liver tissue. The antigen levels of the HBV/B1_PCm increased rapidly and decreased earlier than those of the HBV/A2 or C2 clone, whereas HBV/B1_wild showed that the concentrations of HBV antigens remained low for several months postinfection. These particular characters were observed for the HBV/B1_PCm group inoculated with sera from both preinfected mice and patients with fulminant hepatitis. The majority of patients with fulminant hepatitis and fatal acute exacerbation have been found to have the G1896A mutation.[11,40,41] A greater incidence of fulminant hepatitis might be associated with the high replication and protein production in the early phase, as was shown on the HBV/B1_PCm clone in this study. The defect of immunologic tolerance as a result of the absence of HBeAg may play an important role in the fulminant course of precore mutation in HBV infection.[42] This would concur with a previous report by Bocharov et al which proposed that enhanced HBV replication would efficiently stimulate immune responses, represented by the cytotoxic T-lymphocyte response,[43] suggesting that enhanced replication by HBV/B1 with G1896A mutation might lead to an extremely high cytotoxic T-lymphocyte response, resulting in fulminant hepatitis. But in this study, HBV/B1_PCm showed similar responses to HBV/C2 infection because chimeric mice did not have an immune system that was strong enough to invite strong cytotoxic T-lymphocyte response against viral infection. To uncover these unique characteristics of PC mutant, further study would be needed by using the infection model but not gene transfer.