A Frequent, Naturally Occurring Mutation (P130T) of Human Hepatitis B Virus Core Antigen Is Compensatory for Immature Secretion Phenotype of Another Frequent Variant (I97L)

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A frequent mutation at codon 97 of human hepatitis B virus core antigen has been shown to cause an “immature secretion” phenotype, featuring nonselective and excessive secretions of virions containing immature viral genome. Our current study demonstrates that this abnormality can be efficiently offset by another frequent core mutation, P130T.

Hotspot mutations of the human hepatitis B virus (HBV) core antigen gene (HBcAg) have been identified in HBV chronic carriers, such as mutations at codons 5, 13, 59, 60, 87, 97, 130, and 182 (1, 13). Among these hotspots, codon 97 has the highest mutation frequency (1, 3, 6–8, 11–15, 20, 22–24, 26, 28–31), changing from a phenylalanine (F) or isoleucine (I) into a leucine (L). From earlier studies, it has been observed that the wild-type hepadnavirus DNA replicative intermediates can be enveloped and secreted as virions only after completion of the minus-strand DNA synthesis or initiation of plus-strand synthesis (10, 25). However, we recently reported that the acquisition of a leucine residue at codon 97 (97L) of HBcAg enabled the virus to secrete an excessive amount of immature genome with nascent incomplete single-strand DNA (ssDNA) in an envelope-dependent manner (33, 34). This immature secretion phenomenon is subtype independent, since it can occur in the genetic context of either ayw or adr subtypes, as long as the core gene contains a leucine residue at amino acid 97 (34).

Hepadnavirus immature secretion does not appear to be limited to the tissue culture system. For example, it was observed in vivo in woodchuck hepatitis B virus in one woodchuck treated with acyclovir (27). The mechanism of such drug-induced immature secretion remains unclear. Most recently, virion-like particles containing an abundant level of immature ssDNA were also found in sera containing snow goose hepatitis B viruses (SGHBV) (4), suggesting that immature secretion could also be found in avian hepadnaviruses in vivo. Whether such an immature secretion phenotype of SGHBV is simply a species-specific feature or is caused by naturally occurring mutations remains unclear. As demonstrated in HBV, it could be encoded entirely by a single missense mutation within the core gene (33, 34) or equally likely by mutations within the envelope or polymerase genes. So far, immature secretion of virions has been observed in several different hepadnaviruses in vivo and in culture.

Besides the 97L mutation, another frequent missense mutation occurs at codon 130 of HBcAg in patients (1, 3, 6–8, 11–15, 20, 22–24, 26, 28–31). According to the published data compiled from 19 independent studies with 96 reported HBcAg sequences from 66 hepatitis B patients, the proline-to-threonine change (P130T) is the most frequent mutation at codon 130 (67 of 96 [70%]). Approximately 30% (29 of 96) of mutations at codon 130 of HBcAg in chronic carriers change from proline (P) to amino acids other than threonine (T). At a closer examination, we noted that the P130T mutation is frequently associated with the occurrence of mutation I97L (50 of 67 [75%]), although it also can occur by itself (17 of 67 [25%]). Note that in some reports, direct sequencing of total HBV

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DNA without cloning was used. In that case, only one HBV sequence was obtained from one patient. Because HBV variant populations often exist as a mixture in the same individual, we chose to best present the association between these two mutations quantitatively by the number of independent clones rather than by the number of patients. To date, the functional significance of mutation P130T, alone or in association with the mutation 97L, remains unclear. In this study, we examined the capability of DNA replication and virion secretion of the naturally occurring single (P130T) and double (I97L/P130T) mutants.

We introduced a P-to-T change to a wild-type HBV (subtype adr) at codon 130 of HBcAg (Altered Sites II In Vitro Mutagenesis Systems; Promega) (17). The P130T mutation was created by using the oligonucleotide 5′-TCG CAC TCC TAC CGC TTA CAG-3′. The mutant P130T monomer was subsequently dimerized (pP130T) as described elsewhere (34). To test the effects of the mutation P130T in association with the mutation I97L, the double mutant pI97L/P130T was created by introducing the P130T mutation into mutant I97L (34).

The intracellular core-associated HBV DNA was purified 7 days posttransfection and assayed by Southern blot analysis (Fig. 1). The total HBV DNA migrating near the 4.0-kb position, which is predominantly the near-full-length relaxed-
circle (RC) form, is more enriched in mutant P130T than the other three genotypes. Although the increase in the degree of intracellular genome maturity is small in mutant P130T, it is reproducible from experiment to experiment. We compared the intensity on the X-ray film between the RC and double-strand linear (DL) forms versus the intensity of full-length ssDNA at the 1.5-kb position (33). Our measurement revealed an increased proportion of the near-full-length RC DNA of mutant P130T at the 4.0-kb position by two- to threefold (2.5 ± 0.6; an average of three independent experiments).

The media of each of the transfected cultures were collected and examined for their respective secretion profiles of virion particles, according to their buoyant density, by cesium chloride gradient centrifugation. Each fraction was assayed for its immunoreactivity by enzyme-linked immunosorbent assay specific for HBV surface antigen (HBsAg) and e or core antigen (HBcAg or HBeAg, respectively) (Fig. 2A) as well as for its degree of genome maturity by Southern blot analysis (Fig. 2B). The gradient distributions of HBsAg and HBeAg or HBcAg are similar among these four different genotypes (Fig. 2A). Likewise, the HBV DNA profiles of the naked core particle fractions are similar among these four different genotypes (Fig. 2B). Consistent with the intracellular results in Fig. 1, secreted mutant P130T viruses have a more enriched full-length RC form DNA at the 4.0-kb position than the wild-type control. Perhaps, the most surprising finding to us is that the immature secretion pattern of mutant I97L appeared to be “cured” by the second mutation, P130T, in the genotype 197L/P130T (Fig. 2B).

As described previously (33), the maturity of the HBV DNA genome can be operationally defined as the ratio of RC-form DNA (the signals from the 4.0-kb position to the position right above the 1.5-kb ssDNA form) to ssDNA (the signals at and below the 1.5-kb position). As shown in Fig. 2B, the degree of genome maturity (RC/ssDNA ratio) of the wild type is 14-fold higher than that of mutant I97L (9.7/0.7). When mutation I97L is accompanied by mutation P130T in double mutant 197L/P130T, the RC/ssDNA ratio increased by about 10-fold more than that of the single mutant I97L (8.0/0.7), which is nearly 83% (8.0/9.7) of the level of the wild type (77% ± 6% of the wild-type level in three independent experiments) (Fig. 2B).

Our current study focused on the adw subtype, since few mutations at HBcAg codon 130 have been reported in the ayw subtype. Interestingly, in one longitudinal study of two chronic active hepatitis patients, the viral genomes in the sera acquired mutation I97L before the P130T mutation (i.e., mutant I97L emerged before mutant 197L/P130T) (14). It is conceivable that mutation P130T probably occurred later in patients to offset the immature secretion effect of the I97L mutation, which could have been acquired earlier through an independent mechanism such as immune escape. At present, it remains unclear if additional amino acid changes of HBeAg, other than at positions 97 and 130, could affect the compensatory property of the 130T mutation: e.g., mutants with double mutations at both codons 97 and 130 reported in references 1, 3, 6–8, 11–15, 20, 22–24, 26, and 28–31 might contain additional mutations. Note that the mutations at codon 97 often change from an isoleucine to a leucine (L) in the adw subtype or from a phenylalanine to a leucine in the ayw subtype.

Artificially created compensatory mutations, which can restore the stem-loop structure of HBV encapsidation signal and thus the replication activity, have been reported (16, 18, 21, 32). Most recently, compensatory mutations for the replication of 3TC drug-resistant polymerase variants have been reported (2, 5, 9, 19). To the best of our knowledge, this double mutation, 197L/P130T, is the first example of a naturally occurring compensatory mutation of the human HBV without any drug treatment. Further studies of the intramolecular compensatory mutations, such as I97L/P130T, could lead to a better understanding of the factors involved in plus-strand DNA synthesis and genome maturation, in addition to viral evolution and the structure-function relationship of HBeAg in virion secretion.

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