Clinical relevance of mutations in the precore genome of the hepatitis B virus

H Tillmann, C Trautwein, D Walker, K Michitaka, S Kubicka, K Böker, M Manns

Abstract
A stop codon in the precore genome of the hepatitis B virus (HBV) in anti-HBe positive HBV carriers may be associated with a more progressive form of HBV infection. Earlier studies, however, were mainly performed in patients from the Mediterranean area who had severe infection. The aim of this study was to evaluate the prevalence of precore mutants in an unselected population living in northern Europe. Twenty of 42 of these patients are infected predominantly with a virus strain, which has the typical stop codon in the precore genome, characterised by a mutation at base 83. In six patients there was an additional G to A mutation at base 86 of the precore genome. Statistical analysis showed no difference between the patients with or without a stop codon in the precore genome. When patients with a double mutation at base 83 and 86 of the precore genome were compared with the other anti-HBe positive HBV carriers, however, the corresponding clinical data were worse. Therefore we suggest, that it is not the stop codon in the precore gene itself, but the occurrence of a double mutation at bases 83 and 86, which is associated with a more severe course of disease in anti-HBe positive HBV carriers.

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Keywords: hepatitis B, precore mutant, clinical relevance, epidemiology, replication.

Hepatitis B virus (HBV) infection can lead to a wide variety of clinical manifestations, ranging from acute self limited illness to different forms of chronic infection progressing to liver failure in some patients. The ordinary HBV induces production and secretion of HBsAg and HBeAg particles in the infected hepatocytes. HBeAg, derived from sequences in the core and precore region of the viral genome, is mainly produced during active replication and production of entire viral particles. Its determination is therefore used as an indirect marker of virus replication. Recently, however, it has been shown that high viral replication may occur without circulating HBeAg and even in the presence of circulating anti-HBe antibodies. This phenomenon was mainly seen in patients with a severe course of disease.1 When rapid sequencing methods became available, it was possible to show that this can be caused by mutations that prevent the HBV from producing HBeAg. ‘Stop codon’ and ‘frame shift’ mutations within the precore gene, or deletion of the precore initiation codon (ATG) have been described.2–17 The most commonly seen mutation is a G to A change at base 83 of the precore gene leading to the formation of a stop codon (TAG). Several reports suggested that this precore mutation is associated with a poor prognosis in chronic hepatitis B2–11 and may even be associated with an increased incidence of fulminant hepatic failure.12–14 However, this mutation was also found in asymptomatic carriers.15–17

The prevalence and clinical relevance of the base 83 precore HBV mutant seems to differ geographically. As most studies of precore HBV mutants originated in southern Europe we studied the prevalence of precore mutants in our regional population of northern Germany. We evaluated the clinical significance concerning the severity of liver disease in patients with the HBV precore mutation in a laboratory screened population, irrespective of their ethnic background and their disease activity. Additionally, we used a simple and quick method to detect mutations of base 83 of the precore genome, which may serve as a routine screening method.

Methods

Patients
A total of 2460 serum samples were screened for viral hepatitis between 1 January 1992 and 30 September 1992 in our laboratory, which serves as a reference laboratory. The patients were referred to our university hospital by their general practitioners or from smaller hospitals.

The prevalence of precore mutants was evaluated in the anti-HBe positive population of HBV carriers. The ethnic background was analysed for those patients whose samples could be sequenced.

Hepatitis virus serology
Serological diagnosis was performed for HBsAg, HBeAg, anti-HBs, anti-HBc, anti-HBe, anti-HDV, and anti-HCV (second generation) with commercial enzyme linked immunosorbent assay (ELISA) tests according to the instructions of the manufacturer (Abbott Laboratories, Chicago).

DNA extraction
DNA was digested with proteinase K for two
Mutations in the precore genome

Ordinary hepatitis virus; (**T**) = only; (B) = at the point of mutation.

Mutant BC-I primer: TGT GCC TTG GGT GGC TTT A

Sequence and corresponding either to the ordinary HBV (83G) or to the HBeAg-minus mutant (83A) and a common pre-C-antisense primer, which is also used in the routine PCR method. The PCR protocol differed in a very high annealing temperature of 75°C or 72°C depending on the primers' length (Table I).

Clinical data and statistical analysis

Laboratory data were obtained for all patients of whom HBV sequencing data had become available. The Wilcoxon's rank test was used for calculation of significant differences.

Results

Stop codon and frame shift mutations in the precore genome of the anti-HBe positive HBV carriers

Two hundred and forty one of all patients screened for viral hepatitis in a nine month period were HBsAg positive and of these 127 patients were anti-HBe positive. HBV-DNA was detected by PCR in the serum in only 68 (54%) of 127 anti-HBe positive carriers. In 26 of 68 patients the amount of HBV-DNA was too low for the less sensitive allele specific PCR or a sequencing reaction. Therefore results were available for allele specific PCR and sequencing reactions in 42 of 68 patients. Nineteen (45%) patients were predominantly infected with the HBV mutant at base 83 of the pre-C-genome, while 22 (52%) patients were infected predominantly with the ordinary HBV. One patient had the mutant and ordinary HBV in almost equal amounts, shown by similarly strong bands for G (guanine) and A (adenine) in the sequencing reaction at base 83 of the pre-C-genome (Fig 1). Ten of 30 patients of German origin exhibited the mutated HBV while 10 of 12 patients of foreign origin showed the mutation at base 83. Five of 10 immigrants with this mutation came from Turkey, one from Saudi Arabia, one from Russia, one from Greece, one from former Yugoslavia, and one from Italy. Among the 22 patients who were infected with the ordinary HBV at position 83, one patient of Polish origin showed a C to T mutation at the 4th base of the precore genome, which leads to a stop codon at the second codon. Therefore 21 (50%) of all patients had a stop codon in the precore open reading frame of their predominant or codominant HBV strain. Two patients of German origin had an insertion of an A (adenine) between base 24 and 27 (TA(A)AT) of the precore gene leading to a frame shift mutation. Thus 23 of 42 (54%) patients had precore genome sequences unable to produce HBeAg. The only patient of foreign origin with no mutation preventing HBeAg secretion was a dentist, who probably became infected while working as a dentist in Germany.

Other mutations in the precore genome of anti-HBe positive HBV carriers

Beside the mutations preventing the HBV from producing HBeAg, seven other mutations

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**Table 1: Primers for routine PCR, allele specific PCR, and sequencing**

<table>
<thead>
<tr>
<th>Primer</th>
<th>Sequence</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pre-C-sense primer</td>
<td>GGA GCC TGT AGG CAT AAA TTG GTC</td>
</tr>
<tr>
<td>Pre-C-sense primer</td>
<td>GAT CTT CTG GGA GCC GCC GAT TGA GA</td>
</tr>
<tr>
<td>Pre-C-sense primer</td>
<td>CCA AGC TGT GCC TTG GGT GCC TTT A</td>
</tr>
<tr>
<td>Mutant primer</td>
<td>GGA GCC TGT AGG CAT AAA TTG GTC</td>
</tr>
<tr>
<td>BC-I</td>
<td>GGA GCC TGT AGG CAT AAA TTG GTC</td>
</tr>
</tbody>
</table>

Parentheses show the eight bases that were different between the long and the short primer for the PCR.

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**Figure 1:** Sequence at base of the potential stop mutation of the precore genome. (A) Mutant virus only; (B) codominant infection with mutation at base 83 and ordinary HBV; (C) mutation of base 83 and 86; (D) ordinary HBV infection only. C = cytosine; T = thymine; A = adenine; G = guanine.
were found in the precore genome sequence (Fig 2). Among these mutations, a G to A mutation at base 86 was seen in two patients of German origin and in four patients of foreign origin. This mutation only occurred in association with the stop codon at base 83. Furthermore, homology over the whole pre-C-genome was found in these patients. Another more frequent mutation was found at codon 13 in nine patients, all of German origin except one who was from Turkey. Beside these mutations the remaining five mutations were infrequent and located between base 24 and 34 (Fig 2). Furthermore, according to the precore sequence 14 patients' HBV strains were of the HBV genotype A, characterised by a CCC triplet at bases 43 to 45 instead of CCT found in all other known HBV genotypes.19 None of these 14 patients were of foreign ethnic background. Interestingly the HBeAg-minus mutant, caused by a G to A mutation at position 83, is never found in patients with the HBV genotype A as dominant circulating virus strain.19 The patients with HBV genotype A had better liver function test than those with another genotype (Table II). No mutation occurred within the codons 16 to 27.

Allele specific PCR for G to A mutation at precore base 83

As it is known that a high percentage of all the anti-HBe positive HBsAg positive patients have a stop codon at the position 83 of the HBV precore genome, we wanted to establish a PCR method that could detect the mutation at this position without sequencing. As there is no restriction site at this base, an allele specific PCR approach was used with two different sets of sense primers and a common antisense primer. The end of the two different sense primers was placed at base 83. The primer had either the corresponding sequence of the ordinary HBV sequence (83G) or the mutant genome (83A). The sample from each patient was amplified by the different sense primers in two reaction mixtures. A specific annealing temperature was found where either the ordinary hepatitis B or the mutant PCR reaction became positive according to whether an A or a G was found in the sequencing reaction at base 83. Because of the high annealing temperature (75°C for the 25mer primer and 72°C for the 19mer primer), which was necessary for specific amplification, the allele specific PCR had a lower detection rate; amplification products were found in 42 of 68 samples positive in our standard reaction. Both reactions were always positive in all allele specific PCR, when the HBV-DNA of the patient showing the ordinary hepatitis B and the mutant sequence at base 83 was amplified. In one patient the ordinary HBV and the mutant at base 83 were found in equal amounts showing similarly strong reaction for both sets of primers in the allele specific PCR and similarly strong bands in the sequencing gel.

**Viral replication and clinical parameters**

HBV-DNA concentration in the serum of HBsAg positive, anti-HBe positive patients predominantly infected with the ordinary HBV was 3.8 (4.8) pg/ml (mean (SD)) compared with 95.1 (228.7) pg/ml in the serum of the patients with the stop codon at bases 82–84 of the precore genome of their predominant virus strain (Fig 3). Both DNA values were much lower, however, compared with that found in the HBeAg positive HBV carriers 196 (252-5) pg/ml.

Clinical data were available from 39 of 42 patients where the precore genome was sequenced. Most published reports show that HBsAg positive, anti-HBe positive patients infected with the ordinary HBV have a better prognosis compared with patients with a stop codon at base 82 to 84 of the precore genome. In our study patients were not preselected by the clinical outcome and therefore we were interested in correlating our epidemiological data with the course of infection in these patients.

Prothrombin time, bilirubin, and cholinesterase were chosen as parameters for liver function, while aspartate aminotransferase and γ-glutamyltransferase served as parameters for liver cell necrosis and cholestasis. No significant difference was found when the different parameters were compared between the 'ordinary hepatitis B' and the 'mutant' patients (Table III). When only those patients were chosen, in which the additional mutation at base 86 was found, a difference became detectable (Table IV). All of the clinical data are worse in these patients and the difference reaches statistical significance for the prothrombin time value (p=0.0238 for the
patients with the double mutation vs patients with the ordinary HBV and the patients with the mutation at base 83 only. All patients of this group show signs of active liver disease compared with the other patients included in our study; those with a single mutation of base 83, or those belonging to HBV genotype A. Seven of 14 patients (50%) infected with the first and seven of 14 patients (50%) infected with the second virus type are asymptomatic carriers.

**Discussion**

In our study, the occurrence of HBeAg-minus mutations, characterised by the introduction of a stop codon at base 82–84 is less frequently found compared with Italian or eastern European studies where nearly all the patients who are anti-HBe positive seem to have this

<table>
<thead>
<tr>
<th>Base 83 mutant</th>
<th>Ordinary hepatitis B virus</th>
</tr>
</thead>
<tbody>
<tr>
<td>ALT</td>
<td>60-16 (66)</td>
</tr>
<tr>
<td>AST</td>
<td>36-47 (27-33)</td>
</tr>
<tr>
<td>α-Globulin</td>
<td>21-11 (9-06)</td>
</tr>
<tr>
<td>CHE</td>
<td>3-77 (1-84)</td>
</tr>
<tr>
<td>PTT</td>
<td>79-58 (20-21)</td>
</tr>
<tr>
<td>Bilirubin</td>
<td>30-52 (36-47)</td>
</tr>
</tbody>
</table>

Abbreviations as in Table II. Data shown as mean (SD).

**TABLE IV**

<table>
<thead>
<tr>
<th>Base 83 mutant without base 86 mutant</th>
<th>Base 83 and 86 mutation</th>
<th>Ordinary HBV</th>
</tr>
</thead>
<tbody>
<tr>
<td>ALT</td>
<td>54 (70-23)</td>
<td>NS 73-5 (59-43) p=0.08*</td>
</tr>
<tr>
<td>AST</td>
<td>29-31 (23-02)</td>
<td>NS 52 (31-55) p=0.07*</td>
</tr>
<tr>
<td>α-Globulin</td>
<td>18-08 (6-02)</td>
<td>NS 27-67 (11-52) p=0.043</td>
</tr>
<tr>
<td>CHE</td>
<td>4-24 (1-74)</td>
<td>NS 2-72 (1-77)</td>
</tr>
<tr>
<td>PTT</td>
<td>87-08 (13-80)</td>
<td>NS 63-53 (23-37) p=0.014*</td>
</tr>
<tr>
<td>Bilirubin</td>
<td>21-46 (24-64)</td>
<td>NS 50-17 (51-52) p=0.001*</td>
</tr>
</tbody>
</table>

Abbreviations as in Table II. Data presented as mean (SD). *Significance value for patients with the double mutation vs patients with the ordinary HBV and patients with the mutation of base 83.

**Figure 3:** HBV-DNA concentrations in relation to base 83 and anti-HBe status. Data shown as mean (SD).
disease. Thus our data do not support the hypothesis that the mutation of base 83 in the precore genome is directly responsible for the progressive course of the disease in anti-HBe positive HBV carriers. However, this phenomenon could also just be a marker of a more advanced disease. It may be that the double mutation at base 83 and 86 occurs in patients with longer duration of their disease as those exhibiting the double mutation tend to be of older age (Table V).

We analysed only those patients whose serum had adequate amounts of HBV-DNA for direct sequencing. We are aware that this could form some selection bias. It is known, however, that anti-HBe positive patients’ serum exhibiting the mutation at base 83 show higher amounts of DNA compared with patients’ serum with ordinary HBV and it is believed that the mutation at the base 83 is correlated with a worse prognosis.\(^2\)\(^-\)\(^11\) We realise that it would also be interesting to analyse the HBV-DNA in liver biopsy specimens of these patients. As there was no clinical necessity, however, no biopsy specimens were taken for scientific reason.

We would favour the hypothesis that the mutation at base 83 of the precore sequence is a marker for associated mutations such as the mutation of base 86 of the precore sequence, which are associated with a progressive form of disease. Base 86 already belongs to the Kozak sequence of the core gene m-RNA.\(^27\) The Kozak sequence is part of the sequence just upstream of the initiation codon and influences ribosomal translation of the specific mRNA.\(^27\) Although a G to A mutation in this Kozak sequence may influence the expression of the core gene, it could be speculated that a quantitative change in the presentation of the core peptides on the cell surface may lead to an increased attack of the immune system against the infected hepatocytes. Therefore further investigations are needed to support the hypothesis that additional mutations besides the stop codon at base 82–84 are responsible for the more progressive course of disease among these patients, and whether this may lead to an enhanced expression of the core protein.

There are 12 possible mutations in the precore region, which would create a stop codon by a single nucleotide change. However, only two of these mutations are found in our study. The mutation described in the second codon, a C to T mutation at the 4th base seems to be less important in our population as this variation was found in only one patient of Polish origin. The most frequent mutation, similar to many other studies, was the G to A change at base 83 of the pregenome. Beside these two mutations and the insertion of an adenine between base 24 and 27 in two additional patients, no other mutation disabling HBsAg secretion was found in our population. We did not find mutations of the initiation codon, although five different possibilities have been described.\(^15\)\(^-\)\(^29\) These mutations sometimes represent only minor virus populations,\(^15\)\(^-\)\(^29\) which may not be found by direct sequencing.

It is still unknown why the potential stop codons appear only in so few of the possible codons. As this region harbours different functions of the virus, however, such as nuclear encapsidation, viral replication, and binding sites for transcription factors it is also probable that these changes would interfere with the normal life cycle. The double repeat region 1 is essential for viral replication\(^30\) and spans base 10 to base 21 of the precore gene, therefore it is not surprising that mutations are not found in this region. The last 54 bases of the precore gene were shown to belong to the encapsidation signal.\(^21\)\(^-\)\(^31\) Tong et al were able to show that two possible mutations (TGC-to-TGA, bases 67–69; TGG-to-TGA, bases 76–78) within the encapsidation signal\(^30\) producing stop codons show a defect in RNA packaging and might therefore not exist in nature.\(^32\)

HBsAg is not found in some patients despite viral replication, although there is no mutation preventing the HBsAg production on the DNA level. In these patients additional mechanisms may exist – outside the precore region.

This work is dedicated to Professor Meyer zum Buschenfelde on the occasion of his 65th birthday. This work was supported by the Sonderforschungsbereich (SFB) 265, Project C5. Part of this work has been presented at the 48th meeting of the German society for digestive and metabolic diseases, 22–25 September 1993, Frankfurt/Main. Part of this work is taken from the thesis of H Tillmann.

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Table V: Patients’ age in relation to mutations of base 83 and base 86

<table>
<thead>
<tr>
<th>Patients with double mutant</th>
<th>49–83 (10–36) years</th>
</tr>
</thead>
<tbody>
<tr>
<td>Patients with ordinary HBV</td>
<td>44–86 (16–95) years</td>
</tr>
<tr>
<td>Patients with base 83 mutant</td>
<td>41–28 (11–42) years</td>
</tr>
</tbody>
</table>

Data shown as mean (SD).
Mutations in the precore genome


12 Carman WF, Fagan EA, Hadziyannis S, Tassopoulos NC, Williams R, Thomas HC. Association of a precore genomic variant of hepatitis B virus with fulminant hepato-


27 Kosa M. Point mutations define a sequence flanking the AUG initiator codon that modulates translation by eukaryotic ribosomes. Cell 1986; 44: 283-92.


