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Hee Bok Chae  
College of Medicine and Medical Institute, Chungbuk National University, Cheongju

Hie-Won Hann  
Thomas Jefferson University, Hie-Won.Hann@jefferson.edu

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Recommended Citation
Chae, Hee Bok and Hann, Hie-Won, "Baseline HBV DNA level is the most important factor associated with virologic breakthrough in chronic hepatitis B treated with lamivudine." (2007). Division of Gastroenterology and Hepatology Faculty Papers. Paper 4.  
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Baseline HBV DNA level is the most important factor associated with virologic breakthrough in chronic hepatitis B treated with lamivudine

Hee Bok Chae, Hie-Won Hann

INTRODUCTION
A high incidence of virologic breakthrough (VBT) that results from viral resistance is a major disadvantage of lamivudine (LAM) treatment for patients with chronic hepatitis B (CHB). Data from a study of 592 patients who had undergone four years of LAM treatment indicated that resistance increased from 23% in year 1 to 71% in year 4[1,2]. The clinical consequences of viral resistance can be severe, but early studies suggest that median HBV DNA and ALT levels continue to improve even as resistance develops[3]. LAM is known to have long-term therapeutic effects, with well-known resistance and side effects. LAM therapy for CHB patients with advanced fibrosis significantly reduced the incidence of hepatic decompensation and hepatocellular carcinoma (HCC)[4]. In addition, it is becoming increasingly clear that CHB management requires a long-term therapy, thus making the cost of treatment an important consideration. The need for long-term therapy and the consequent financial burden become significant in the economically disadvantaged regions of the world which also happen to be the hyper-endemic areas for HBV. Furthermore, this cost issue presents a serious economic burden for CHB patients who immigrated to the US from the hyper-endemic regions. One study suggested that upfront LAM therapy may be highly cost-effective, assuming that patients who develop resistance begin a regimen of adefovir instead of continuing LAM treatment[5]. Our study sought to identify the factors associated with VBT in patients on LAM therapy and attempted to select a subgroup of patients who may respond well to LAM without developing VBT.

MATERIALS AND METHODS

Patients
We reviewed the medical records of 208 CHB patients who were treated at the Liver Disease Prevention Center,
HBsAg, HBeAg, anti-HBe, and HBV DNA quantification
All patients had been positive for hepatitis B surface antigen (HBsAg) for more than 6 mo. HBeAg/anti-HBe and anti-HDV were determined using ELISA (Abbott Laboratories, Chicago, IL), and anti-HCV antibodies were assayed using a third-generation enzyme immunoassay (Abbott Laboratories, North Chicago, IL). Between 2000 and 2002, a solution hybridization assay (Abbott Laboratories, North Chicago, IL) with a lower limit of detection (LLOD) of 1.6 pg/mL was used to measure HBV DNA levels. These values were converted to copies/mL by determining 283 000 copies/mL per 1 pg/mL of HBV DNA. From 2003 until the present, HBV DNA was assayed using a third-generation enzyme immunoassay (Abbott Laboratories, North Chicago, IL) and viral suppression was defined as the difference in HBV DNA levels between baseline and after 6 mo of treatment. Maximal virologic suppression was defined as HBV DNA levels between 3 and 5 log10 copies/mL. Based on earlier observations of 317 CHB patients[7], normal pre-therapy ALT was not considered a contraindication for beginning antiviral therapy in certain patients. These included patients who had normal ALT levels, high viral DNA, and a strong family history of HCC or patients who had previous ALT spikes but whose ALT levels were ≥3 0 log10 copies/mL. Treatment was initiated if HBV DNA levels were ≥3 0 log10 copies/mL. Eighteen patients had HBV DNA levels between 3 and 5 log10 copies/mL. Based on earlier observations of 317 CHB patients[7], normal pre-therapy ALT was not considered a contraindication for beginning antiviral therapy in certain patients. These included patients who had normal ALT levels, high viral DNA, and a strong family history of HCC or patients who had previous ALT spikes but whose ALT levels were ≥3 0 log10 copies/mL. Determination of HBV genotype, antiviral resistance, precore mutant, and core promoter mutant
HBV DNA was extracted using the QIAamp DNA Blood Mini Kit (Qiagen, Valencia, CA) according to the manufacturer’s instructions. The presence of HBV DNA polymerase gene mutations was determined using the InnoLiPA DR2 line probe assay (InnoGenetics, Ghent, Belgium) according to the manufacturer’s instructions. Line probe results were confirmed by bi-directional automated sequencing at the DNA sequencing core facility (Thomas Jefferson University’s nucleic acid facility, Philadelphia, PA) using the standard protocol for the Applied Biosystems DNA Sequencer 377 (Perkin Elmer Corp., Foster City, CA). This amplicon covers domains A, B, C, D, and E of the reverse transcriptase region of the HBV polymerase. The PCR protocol and primers for the surface/polymerase gene and core promoter/precore region used in this study were described previously[8].

Statistical analysis
Statistical testing was performed using SPSS version 13.0 (SPSS Inc., Chicago IL). Results were expressed as mean ± SD or median (minimum-maximum). HBV DNA levels were logarithmically transformed for analysis. Continuous variables were compared using the two-tailed student’s t-test, and categorical data were compared using the two-tailed χ2 test. Factors associated with an initial virologic response and LAM resistance were analyzed by univariate analysis. Clinical, biochemical and virologic factors that could influence LAM resistance, including gender, route of infection, baseline ALT level, baseline HBV DNA level, were analyzed by binary logistic regression. The cumulative probability of lamivudine resistance was estimated by Kaplan-Meier analysis. P < 0.05 was considered statistically significant.

RESULTS

Baseline characteristics of patients prior to beginning lamivudine treatment
Seventy-nine patients (54 males) met eligibility criteria. All were Asian Americans, with a mean age of 47 ± 12 years. Thirty-seven (45%) had been infected at birth by vertical transmission from their mothers. Twenty-four patients (30%) had liver cirrhosis and two (2%) had liver cancer prior to starting LAM therapy. The mean duration of therapy was 26 ± 10 mo. At baseline, the ALT was 66 (11-3395) IU/L and the mean log HBV DNA level was 6.0 ± 1.6. The baseline HBV DNA level in the 34 HBeAg-positive patients was 6.6 ± 1.5, and the baseline DNA level in the 45 HBeAg-negative patients was 5.6 ± 1.5 log10 copies/mL. Treatment was initiated if HBV DNA levels were > 3 0 log10 copies/mL. Eighteen patients had HBV DNA levels between 3 and 5 log10 copies/mL. Based on earlier observations of 317 CHB patients[7], normal pre-therapy ALT was not considered a contraindication for beginning antiviral therapy in certain patients. These included patients who had normal ALT levels, high viral DNA, and a strong family history of HCC or patients who had previous ALT spikes but whose ALT levels were ≥3 0 log10 copies/mL. Treatment was initiated if HBV DNA levels were > 3 0 log10 copies/mL. Eighteen patients had HBV DNA levels between 3 and 5 log10 copies/mL. Based on earlier observations of 317 CHB patients[7], normal pre-therapy ALT was not considered a contraindication for beginning antiviral therapy in certain patients. These included patients who had normal ALT levels, high viral DNA, and a strong family history of HCC or patients who had previous ALT spikes but whose ALT levels were ≥3 0 log10 copies/mL.
HBV DNA sequences were examined in nine patients’ sera HBV genotype, precore mutant, and core promoter mutant. As shown in Table 3, YMDD mutants were observed in six of the nine individuals in the VBT group and none were observed in the non-VBT group (67% vs 0%, *P < 0.01). All patients had HBV genotype C. The frequency of precore and core promoter variants did not differ significantly between VBT and non-VBT groups.

Patient 6 in the VBT group had a precore mutation in the 1896 position and was HBeAg-positive (Table 3). Patients 3 and 8 also had smaller A peaks than G peaks at the 1896 position, but were classified as wild-type (Table 3).

**Table 1 Baseline characteristics of patients (mean ± SD)**

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>All patients (n = 79)</th>
<th>Breakthrough (n = 24)</th>
<th>Non-breakthrough (n = 55)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age (yr)</td>
<td>47 ± 12</td>
<td>47 ± 13</td>
<td>47 ± 11</td>
</tr>
<tr>
<td>Female (%)</td>
<td>32</td>
<td>29</td>
<td>33</td>
</tr>
<tr>
<td>Family history of CHB (%)</td>
<td>47</td>
<td>46</td>
<td>46</td>
</tr>
<tr>
<td>ALT (IU/L)</td>
<td>149 ± 44</td>
<td>98 ± 20</td>
<td>171 ± 63</td>
</tr>
<tr>
<td>Total bilirubin (mg/dL)</td>
<td>1.1 ± 0.1</td>
<td>1.3 ± 1.4</td>
<td>1.0 ± 0.9</td>
</tr>
<tr>
<td>Albumin (g/dL)</td>
<td>4.4 ± 0.4</td>
<td>4.2 ± 0.5</td>
<td>4.3 ± 0.4</td>
</tr>
<tr>
<td>INR</td>
<td>1.07 ± 0.12</td>
<td>1.09 ± 0.15</td>
<td>1.06 ± 0.08</td>
</tr>
<tr>
<td>Cirrhosis (%)</td>
<td>30</td>
<td>36</td>
<td>24</td>
</tr>
<tr>
<td>HBeAg-positive (%)</td>
<td>43</td>
<td>36</td>
<td>36</td>
</tr>
<tr>
<td>HBV DNA log</td>
<td>6.0 ± 1.6</td>
<td>6.6 ± 1.5</td>
<td>5.7 ± 1.5</td>
</tr>
<tr>
<td>copies/mL *</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Mean duration of lamivudine treatment (mo)</td>
<td>26 ± 10</td>
<td>29 ± 11</td>
<td>25 ± 10</td>
</tr>
<tr>
<td>3 log &lt; HBV DNA &lt; 5 log (%)</td>
<td>19</td>
<td>3</td>
<td>16</td>
</tr>
<tr>
<td>HBV DNA ≥ 5 log (%)</td>
<td>60</td>
<td>21</td>
<td>39</td>
</tr>
</tbody>
</table>

*P < 0.05 breakthrough vs non-breakthrough group INR: International normalized ratio.

were normal at the beginning of the study. All baseline characteristics except HBV DNA level were similar between the VBT and non-VBT groups. Only ALT level was shown as mean ± SE (Table 1).

**Response to lamivudine treatment**

In HBeAg-positive patients (n = 34), the mean log reduction (copies/mL) in HBV DNA from baseline was 4.6 ± 1.4, 3.7 ± 2.4, and 2.7 ± 3.0 at 6 mo, 12 mo, and 24 mo, respectively. The less reduction in two years may be due to VBT in some patients. As shown in Table 2, initial viral suppression was 4.2 ± 2.0 and 4.3 ± 1.5 in VBT and non-VBT groups, respectively. The maximal viral suppression was 4.8 ± 1.7 and 4.6 ± 1.2 in VBT and non-VBT groups, respectively. Eighty percent of patients showed an initial anti-viral response at 6 mo post-treatment. HBeAg loss rate was 18, 26, and 29% at 1, 2, and 3 years, respectively. Excluding individuals with normal or absent ALT levels at baseline, ALT normalization was observed in 90% and 96% of patients after 6 mo and 12 mo, respectively. The mean time for VBT detection was 21 (9-36) mo. There was no viral or biochemical variable with a significant difference between VBT and non-VBT groups.

In HBeAg-negative patients (n = 45), the mean log reduction (copies/mL) in HBV DNA from baseline was 3.2 ± 2.0 at 6 mo, 4.2 ± 1.9 at one year, and 3.1 ± 3.0 at two years. Initial viral suppression was 2.8 ± 2.5 and 3.4 ± 1.9 in VBT and non-VBT groups, respectively. Maximal suppression was 4.3 ± 1.7 and 4.3 ± 1.6 in VBT and non-VBT groups, respectively. Eighty-one percent of patients showed an initial antiviral response at 6 mo post-treatment. Excluding individuals with normal or absent ALT levels at baseline, ALT normalization was observed in 84% and 82% of patients after 6 mo and 12 mo, respectively. The mean time for VBT detection was 22 (9-36) mo. Also, there was no viral or biochemical variable with a significant difference between VBT and non-VBT groups.

**DISCUSSION**

Our study demonstrated that patients with lower HBV DNA levels had less VBT with LAM therapy. Other predictors of LAM-resistant mutations include male gender, Asian ethnicity, higher baseline HBV DNA, longer duration of lamivudine treatment, and higher BMI[2]. Our study clearly showed that the baseline HBV DNA level is the most significant predictor. However, it is true that the number of study subjects was relatively small (n = 79) and the median duration of follow-up was about 40 mo.

But, the findings of our study are contradictory to the observation of the Taiwanese study[8]. They reported that HBeAg status, HBV DNA, ALT levels and treatment duration were the major determinants for the YMDD mutation during lamivudine therapy. The most important difference between two studies is what they observed. We observed VBT, but they observed the genotypic resistance. Besides, there were several differences between two studies, such as study designs and the test for HBV DNA.
When the study criteria were set up, AGA (American Gastroenterology Association) expert panel recommendations were followed; HBeAg-positive patients were individuals with HBV DNA > 5 log_{10} copies/mL, while HBeAg-negative patients were individuals with HBV DNA > 4 log_{10} copies/mL. In this study, a lower HBV DNA cutoff, above 3 log, was used for starting antiviral treatment. Although we did not know the recent Taiwanese data when we started to treat our patients, but it shows that higher baseline serum DNA levels are associated with increased risk of HCC and liver cirrhosis independent of serum ALT level[9]. The AGA panel specifies that ALT levels should be abnormal, but this is not always helpful in determining who should be treated[10]. ALT levels do not serve as a good indicator of liver cirrhosis. In addition, revision of the normal limits for ALT levels was recommended in patients with chronic HCV infection or nonalcoholic fatty liver disease (NAFLD) since current standards for normal were defined using the populations that included individuals with subclinical disease[11,12]. Some patients experienced disease progression during follow-up because they had normal ALT levels and were not treated earlier. Thus, early antiviral treatment may be beneficial to reduce HBV DNA levels, HCC risk, and the frequency of liver transplantations[8,13]. LAM can reduce serum HBV DNA levels and normalize ALT level in cirrhotic patients[14,15].

As shown in Table 1, we noted that HBeAg-negative CHB have lesser LAM resistance than HBeAg-positive CHB, which is in agreement with previous studies[16,17].

We conducted genotypic resistance analysis on 15 patients who had serum samples harvested upon viral breakthrough or at the end of follow-up. Genotypic resistance occurred only in the VBT group and was not observed in the non-VBT group. However, three patients in the VBT group, and five in the non-VBT group had the wild-type. The most plausible explanation for the disparity between phenotypic and genotypic resistance is medication non-compliance. Possible solutions for this problem, like pill counts and nurse monitoring, were beyond the scope of our study. A blip in viral numbers is another potential explanation for the presence of wild-type virus in the VBT patients. The InnoLiPa assay could be used to define the mixed strains in six patients from the VBT group.

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we found the viral breakthrough in 25 patients, we recommended several options such as adefovir monotherapy, adefovir overlapped with lamivudine, and tenofovir monotherapy to our patients.

Two patients of suboptimal responders had YMDD mutants. They did not show VBT during treatment period. But we might have missed VBT in these patients because the test for HBV DNA had not been tested at the right time, or YMDD mutants may have existed even before the start of lamivudine because of low incidence of drug resistance. We investigated the factors associated with virologic breakthrough in patients on lamivudine therapy and identified a subgroup of patients who responded well to lamivudine without developing virologic breakthrough. Therefore, we believe that for this subgroup of CHB patients, lamivudine may still remain the most cost-effective drug among 4 currently available oral anti-HBV drugs.

ACKNOWLEDGMENTS

Dr. Hann is on the speaker’s bureau for Gilead, Bristol-Myers Squibb and GlaxoSmithKline, and has received research support from all three companies. The authors are grateful to Dr. Scott Fung at the University of Toronto for his valuable advice in preparing the manuscript, Ms. Munira Hussain at the University of Michigan for providing invaluable information about primers and the PCR protocol, and Dr. Mark Feltel for providing the laboratory facility to conduct the molecular biology.

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