

Higher baseline viral diversity correlates with lower HBsAg decline following PEGylated interferon-alpha therapy in patients with HBeAg-positive chronic hepatitis B

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Background: Viral diversity seems to predict treatment outcomes in certain viral infections. The aim of this study was to evaluate the association between baseline intra-patient viral diversity and hepatitis B surface antigen (HBsAg) decline following PEGylated interferon-alpha (Peg-IFN- α) therapy.

Patients and methods: Twenty-six HBeAg-positive patients who were treated with Peg-IFN- α were enrolled. Nested polymerase chain reaction (PCR), cloning, and sequencing of the hepatitis B virus *S* gene were performed on baseline samples, and normalized Shannon entropy (Sn) was calculated as a measure of small hepatitis B surface protein (SHBs) diversity. Multiple regression analysis was used to estimate the association between baseline Sn and HBsAg decline.

Results: Of the 26 patients enrolled in the study, 65.4% were male and 61.5% were infected with hepatitis B virus genotype B. The median HBsAg level at baseline was 4.5 log₁₀ IU/mL (interquartile range: 4.1–4.9) and declined to 3.0 log₁₀ IU/mL (interquartile range: 1.7–3.9) after 48 weeks of Peg-IFN- α treatment. In models adjusted for baseline alanine aminotransferase (ALT) and HBsAg, the adjusted coefficients (95% CI) for Δ HBsAg and relative percentage HBsAg decrease were -1.3 ($-2.5, -0.2$) log₁₀ IU/mL for higher SHBs diversity (Sn \geq 0.58) patients and -26.4% ($-50.2\%, -2.5\%$) for lower diversity (Sn $<$ 0.58) patients. Further analysis showed that the “a” determinant upstream flanking region and the first loop of the “a” determinant (nucleotides 341–359, 371–389, and 381–399) were the main sources of higher SHBs diversity.

Conclusion: Baseline intra-patient SHBs diversity was inverse to HBsAg decline in HBeAg-positive chronic hepatitis B (CHB) patients receiving Peg-IFN- α monotherapy. Also, more sequence variations within the “a” determinant upstream flanking region and the first loop of the “a” determinant were the main sources of the higher SHBs diversity.

Keywords: HBsAg decline, viral diversity, Shannon entropy, interferon, chronic hepatitis B

Introduction

Chronic hepatitis B (CHB) is a serious infectious disease affecting ~250,000,000 people and resulting in an estimated 800,000 deaths annually worldwide.¹ Current CHB treatment guidelines recommend nucleot(s)ide analogs (NAs) or PEGylated interferon (Peg-IFN) therapy for CHB patients; highlighted hepatitis B surface antigen (HBsAg) loss is the ideal end point of treatment.^{2–4} However, the HBsAg loss is rare with either NAs or Peg-IFN therapy.

Significantly different treatment-induced HBsAg outcomes can be found in CHB patients with the same disease status.^{5,6} A number of studies have demonstrated that

certain clinical and patient factors are associated with serum HBsAg decline during antiviral therapy, such as HBeAg status, early pronounced HBsAg decline ($>1 \log_{10}$ decline by week 12 or 24), high pretreatment serum interleukin-23 levels, and genotype.⁷⁻⁹ Patients with genotypes A and D had more pronounced HBsAg decline and higher proportions of HBsAg loss than those with genotypes B and C during NA treatment.^{6,10-13} In addition to these aforementioned factors, the nature of small hepatitis B surface protein (SHBs), which is a part of HBsAg, has a significant impact on serum HBsAg levels.^{14,15} Xiang et al found that SHBs mutations were negatively correlated with serum HBsAg levels both in vivo and in vitro.¹⁶ Recently, a global ultra-deep sequencing-based genotyping study revealed that mutations in SHBs have an extremely high prevalence and that the majority of these amino acid mutations are found in the hepatitis B virus (HBV) B and C genotype population.¹⁷

Viral diversity within patients can be assessed using the measurement normalized Shannon entropy (Sn), which takes into account the diversity and frequency of amino acid substitutions at different genomic positions.¹⁸ Previous studies have reported that baseline viral diversity was associated with virological outcomes in hepatitis C virus (HCV),¹⁸⁻²² human immunodeficiency virus,²³⁻²⁵ human papillomavirus,²⁶ cytomegalovirus,²⁷ and hepatitis B e antigen seroconversion in CHB.^{18,28} Although these studies differ in pathogenic agents, medications, and clinical end points, there appears to be a universal feature present in all of the study results: high baseline intra-patient viral diversity is associated with poor treatment outcomes. Therefore, a hypothesis that baseline SHBs diversity may affect HBsAg decline during Peg-IFN therapy was proposed.

To date, little is known about the relationship between baseline SHBs diversity and serum HBsAg level. Thus, the aim of this study was to investigate whether baseline SHBs diversity affects HBsAg decline following Peg-IFN- α monotherapy in HBeAg-positive CHB patients.

Patients and methods

Patients

This was a longitudinal study conducted using prospectively collected serum samples from 26 eligible patients who were HBeAg-positive and treated with Peg-IFN- α monotherapy (180 μ g per week) for 48 weeks between May and December 2013 at the outpatient service of the Second Affiliated Hospital, Chongqing Medical University. The inclusion criteria were as follows: age 18–65 years; serum HBsAg-positive for at least 6 months; not been previously treated with NAs

or interferon (including conventional or Peg-IFN- α) within 6 months prior to Peg-IFN- α therapy; and completed full therapy course. The exclusion criteria included coinfection with hepatitis A virus, HCV, hepatitis D virus, hepatitis E virus, or HIV; liver cirrhosis, hepatocellular carcinoma; or a history of antiviral therapy within 6 months. This study was approved by the ethical committee of the Second Affiliated Hospital of Chongqing Medical University, and written informed consent was obtained from each study participant.

Variables

HBsAg quantification

Serum HBsAg levels were quantified using the electrochemiluminescence immunoassay Elecsys[®] HBsAgII (Roche Diagnostic, Mannheim, Germany) according to the manufacturer's instructions. The dynamic range of quantification of this assay is 0.05–52,000 IU/mL. In highly concentrated samples above the upper limit, a further dilution step was necessary to achieve results within the measuring range; these results were later multiplied by the dilution factor. HBsAg loss was defined as HBsAg-positive at baseline and HBsAg-negative at the end of treatment (EOT).

HBV DNA load, HBV markers, and biochemical index

Serum HBV DNA levels were measured using the Roche COBAS[®] AmpliPrep/COBAS TaqMan HBV test v2.0 (Roche Molecular Diagnostics, Pleasanton, CA, USA). The results were expressed in international units per milliliter (IU/mL). The lower limit of detection of the assay is 20 IU/mL. Serum HBe status was determined using commercial enzyme immunoassays (Roche Diagnostics, Mannheim, Germany) and were expressed as ratios of signal OD to cutoff. Serum levels of alanine aminotransferase (ALT) and aspartate aminotransferase were detected using an Automatic Biochemistry Analyzer (Beckman LX-20, Beckman, Brea, CA, USA), with a normal range of 0–40 U/L and 0–50 U/L, respectively.

SHBs diversity

SHBs diversity was assessed at baseline using clone-based sequencing (25–30 clones per patient) and was determined by calculating the Sn using the following formula: $Sn = -\sum_i (p_i \ln p_i) / \ln N$, where p_i is the frequency of each species, and N is the total number of clones analyzed within each subject. The process and performance of this assay was described in detail in our previous study.²⁹ Briefly, after the extraction of viral DNA from 200 μ L of serum using the QIAamp Ultrasens Virus Kit (Qiagen NV, Venlo, the

Netherlands), a nested polymerase chain reaction (PCR) was used to amplify the entire *S gene* fragment. PCR products were then cloned into the pEASY-T5 zero vectors (TransGen Biotech, Beijing, China) and transformed into *Escherichia coli* JM109 competent cells growing on ampicillin plates. Finally, ~25–30 individual clones per sample were randomly chosen for further sequencing. The protein sequences were analyzed using BioEdit 7.2.5 (<http://www.mbio.ncsu.edu/bioedit/bioedit.html>) and MEGA 7.0.³⁰

Viral genotype

The HBV genotypes were determined using the National Center for Biotechnology Information (NCBI) viral genotyping tool (<http://www.ncbi.nlm.nih.gov/projects/genotyping/formpage.cgi>).

Study outcomes

The outcomes of this study were Δ HBsAg and relative percentage HBsAg decrease. Δ HBsAg was defined as the difference in HBsAg between baseline and EOT. Relative percentage HBsAg decrease was defined as Δ HBsAg divided by baseline HBsAg.

Statistical analysis

Data are presented as mean \pm SD or median (interquartile range [IQR]) for continuous variables and proportions for categorical variables. Continuous variables were compared using Student's *t*-test. Categorical variables were compared using Fisher's exact test. Baseline SHBs diversity (*S_n*) was tested as both a continuous and a binary variable stratified by the turning point (0.58) obtained through piecewise regression. The kinetics of HBsAg decline was then assessed using mixed models with a random intercept and a random slope per subject and with a covariance structure depending on the different degree of baseline *S_n* (<0.58 or \geq 0.58). To further explore the independent association of baseline *S_n* and HBsAg decline, multiple linear regression was used to estimate coefficients (95% CIs) with adjustment for baseline level of ALT and HBsAg. Statistical analyses were performed using EmpowerStats (<http://www.empowerstats.com>, X&Y Solutions, Inc., Boston, MA, USA) and R (<http://www.R-project.org>, The R Foundation). A 2-sided significance level of 0.05 was used to evaluate statistical significance.

Results

Patient characteristics

Twenty-six HBV-infected HBeAg-positive patients receiving a 48-week course of antiviral therapy with Peg-IFN- α were

included in the study. Subjects' characteristics are presented in Table 1. Of the 26 patients evaluated, 17 (65.4%) were male and 9 were female, and the mean (SD) age and body mass index were 37.3 years (5.6) and 21.2 kg/m² (2.5), respectively. At baseline, the median HBV DNA level was 8.1 log₁₀ IU/mL (IQR: 7.8–8.5 log₁₀ IU/mL), and the median HBsAg level was 4.5 log₁₀ IU/mL (IQR: 4.1–4.9 log₁₀ IU/mL). At the EOT, the median HBsAg level was 3.0 log₁₀ IU/mL (IQR: 1.7–3.9 log₁₀ IU/mL). Of the entire study population at baseline, 14 patients (53.8%) achieved a >1 log₁₀ IU/mL decline of HBsAg, and 2 (7.7%) achieved HBsAg loss at EOT. After 2 years of follow-up, 2 patients were lost to follow-up and 4 received new treatment regimens. The follow-up of remaining patients was well documented. At 2 years of follow-up, the median HBsAg level was 3.2 log₁₀ IU/mL (IQR: 1.7–3.9 log₁₀ IU/mL), the Δ HBsAg was 1.5 log₁₀ IU/mL (IQR: 0.5–2.6 log₁₀ IU/mL), and the relative percentage of HBsAg decrease at 2 years of follow-up was

Table 1 Demographic, biochemical and virological characteristics of the study population

Characteristics	Total (N=26)
Baseline	
Male, n (%)	17 (65.4)
Age, years, mean (SD)	37.3 (5.6)
BMI, kg/m ² , mean (SD)	21.2 (2.5)
ALT, U/L, median (IQR)	119 (88–167)
AST, U/L, median (IQR)	65 (45–97)
HBV DNA, log ₁₀ IU/mL, median (IQR)	8.1 (7.8–8.5)
HBsAg, log ₁₀ IU/mL, median (IQR)	4.5 (4.1–4.9)
Genotype	
B	16 (61.5)
C	10 (38.5)
Cirrhosis, ^a n (%)	0
Fibrosis-4 score, n (%)	
<1.45	21 (80.8)
1.45–3.25	5 (19.2)
End of treatment (EOT)	
HBsAg, log ₁₀ IU/mL, median (IQR)	3.0 (1.7–3.9)
Δ HBsAg, ^b log ₁₀ IU/mL, median (IQR)	1.9 (0.5–2.8)
Relative percentage HBsAg decrease, ^c %	40.0 (10.8–62.9)
HBsAg loss, n (%)	2 (7.7)
Follow-up ^d (2 years)	
HBsAg, log ₁₀ IU/mL, median (IQR)	3.2 (1.2–3.8)
Δ HBsAg, ^b log ₁₀ IU/mL, median (IQR)	1.5 (0.5–2.6)
Relative percentage HBsAg decrease, ^c %	32.1 (12.0–69.5)

Notes: ^aCirrhosis was diagnosed by an ultrasound of the liver. ^b Δ HBsAg = HBsAg at baseline – HBsAg at EOT. ^cRelative percentage of HBsAg decrease = Δ HBsAg/HBsAg at baseline. ^dTwenty patients were included in analysis. The 2 patients who were lost of follow-up and 4 who received new treatment regimens were not included.

Abbreviations: ALT, alanine aminotransferase; AST, aspartate aminotransferase; BMI, body mass index; HBV, hepatitis B virus; HBsAg, hepatitis B surface antigen; IQR, interquartile range.

32.1% (IQR: 12.0%–69.5%). Of the entire study population at 2 years of follow-up, 2 patients achieved HBsAg loss and 1 obtained HBsAg seroconversion.

Non-linear negative relationship between baseline SHBs diversity (S_n) with HBsAg decline at EOT

There was a non-linear negative relationship between baseline SHBs diversity and Δ HBsAg at EOT (Figure 1A). Similar to Δ HBsAg, this relationship was also found between baseline S_n and the relative percentage of HBsAg decrease at EOT (Figure 1B). Next, we took advantage of piecewise regression to examine the threshold effect of baseline SHBs diversity on HBsAg decline. The HBsAg decline degree decreased with the baseline SHBs diversity levels up to the turning point (0.58) ($p < 0.01$ for both Δ HBsAg and relative percentage HBsAg decrease). When the SHBs diversity level was ≥ 0.58 , it was not associated with Δ HBsAg and relative percentage HBsAg decrease at EOT (both $p > 0.05$). These results indicate that intra-patient SHBs diversity might have different effects on HBsAg decline in patients treated with Peg-IFN- α .

Kinetics of HBsAg decline differ between patients with higher and lower baseline SHBs diversity (S_n)

We further analyzed the change in HBsAg kinetics in patients with different SHBs diversity. The decline in serum HBsAg levels during 48 weeks of treatment with Peg-IFN- α in HBeAg-positive patients is displayed in Figure 2. Both the

magnitude of HBsAg decline (mean decline 2.44 versus 1.03 \log_{10} IU/mL, $p = 0.02$, Figure 2A) and relative percentage of HBsAg decrease (mean decline 51.6% versus 23.6%, $p = 0.03$, Figure 2B) were larger in the patients who had lower SHBs diversity ($S_n < 0.58$) compared with patients who had higher diversity ($S_n \geq 0.58$) at EOT. During the Peg-IFN- α treatment, the kinetics of HBsAg decline was also significantly stronger in the lower diversity patients than in higher diversity patients ($p < 0.001$ for comparison of the slope of HBsAg decline; Figure 2C). At 2 years of follow-up, the median of serum HBsAg level rose slightly in both groups with higher ($n = 9$) and lower ($n = 11$) baseline SHBs diversity. However, the magnitude of HBsAg decline (mean decline 2.14 versus 0.80 \log_{10} IU/mL) and relative percentage of HBsAg decrease (mean decline 47.9% versus 18.7%) were still markedly stronger in the patients who had lower SHBs diversity compared with patients who had higher diversity.

Multiple linear regression reveals that baseline SHBs diversity affects HBsAg decline

In the crude model, the estimated coefficients of Δ HBsAg and relative percentage of HBsAg decrease comparing subjects with higher baseline S_n to those with lower S_n were -1.4 ($-2.5, -0.3$) and -28.0 ($-51.5, -4.5$), respectively (Table 2). The negative association was virtually unchanged in multiple linear regression models after adjusting for baseline ALT and baseline HBsAg ($\beta = -1.3$, 95% CI $[-2.5, -0.2]$, $p = 0.04$ for Δ HBsAg; $\beta = -26.4$, 95% CI $[-50.2, -2.5]$, $p = 0.04$ for

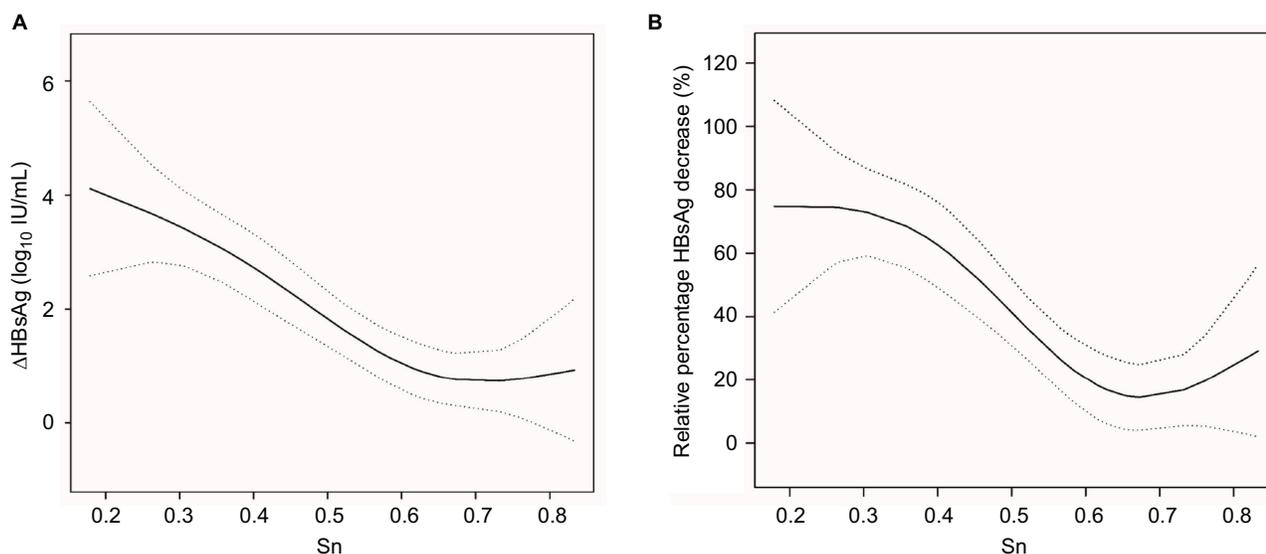


Figure 1 The non-linear negative relationship between baseline SHBs diversity (S_n) and Δ HBsAg (A), relative percentage of HBsAg decrease (B).

Notes: The black solid line represents the fitted line and the black dotted line represents the 95% CI of the fitted line.

Abbreviations: HBsAg, hepatitis B surface antigen; SHBs, small hepatitis B surface protein; S_n , normalized Shannon entropy.

relative percentage HBsAg decrease; Table 2). Our results suggest that baseline Sn appears to be an independent determinant of the decrease in HBsAg level following Peg-IFN- α therapy.

Sliding window analysis reveals multiple areas account for the differences in baseline Sn

As the aforementioned results demonstrated that SHBs diversity contributed to differences in HBsAg outcomes for Peg-IFN- α therapy, we carried out a sliding window analysis to determine if the Sn difference was driven by specific sub-regions (Figure 3). The sliding window analysis was used with a window size of 19 base pair (bp) nucleotide length segments migrating every 10 bp spanning the entire small *HBs gene* (678 bp) as described previously.¹⁴ In this analysis, 70.6% (48/68) of the 19-bp segments across the small *HBs gene* had lower mean SHBs diversity in the lower Sn group (<0.58) compared with those in the higher Sn group (\geq 0.58). Interestingly, differences in mean Sn between the

2 groups exceeded the significant threshold in only 3 regions, nucleotides 341–359, 371–389, and 381–399, corresponding to the “a” determinant upstream flanking region and the first loop of the “a” determinant (Figure 3). In contrast, transmembrane regions (nucleotides 21–84, 240–291, 510–573, and 606–669) were relatively conservative in the 2 groups.

In addition, previous studies reported the significant correlation between amino acid substitutions in HBV surface protein and lower HBsAg synthesis and/or secretion both in vitro and in vivo.^{16,31} We conducted a detailed and systematic inventory of the published literature (Table S1). Among these patients, at least 1 related mutation was detected in 16 (61.5%) patients (Figure 4; Table S2). In 14 of 16 (87.5%) patients, the related mutations occurred with an intra-patient prevalence of <35% (mean: 10.3%, range: 3.6%–33.3%; Figure 4), suggesting their fixation in the viral population as a non-predominant species. As expected, the influence on HBsAg decline was not significantly different (Figure 5A and B). The related mutation of sL98V and sT126S was detected in the remaining 2 patients who belonged to dif-

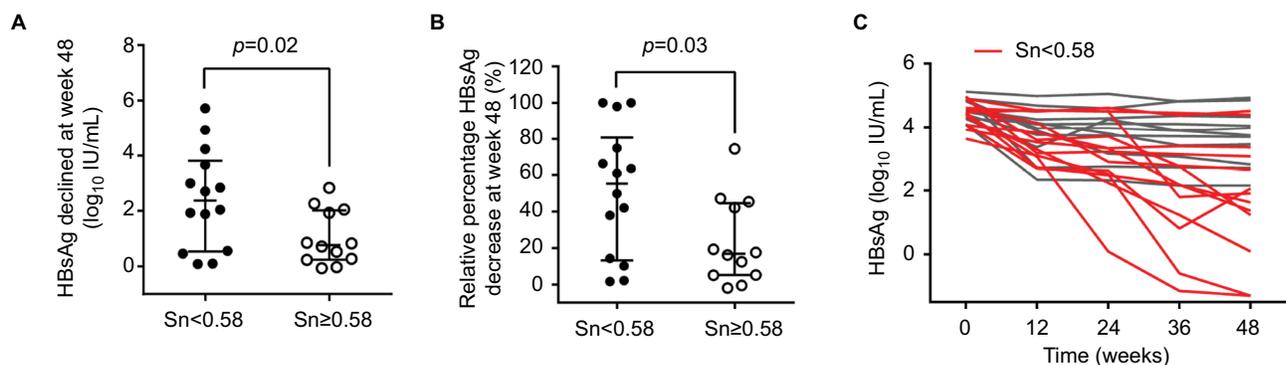


Figure 2 The change in HBsAg kinetics in patients with different degrees of SHBs diversity (Sn <0.58 versus \geq 0.58).

Notes: Comparison of HBsAg decline (A) and relative percentage HBsAg decrease (B) between the Sn <0.58 (n=14) and \geq 0.58 (n=12) groups at EOT. (C). The serum level of HBsAg in every patient in the Sn <0.58 (n=14) and the Sn \geq 0.58 (n=12) groups during Peg-IFN- α treatment. Patients with Sn <0.58 tended to have a steeper HBsAg decline than patients with Sn \geq 0.58 ($p < 0.001$ for the comparison of the slope of HBsAg decline determined using a linear mixed model).

Abbreviations: EOT, end of treatment; HBsAg, hepatitis B surface antigen; Peg-IFN, PEGylated interferon; SHBs, small hepatitis B surface protein; Sn, normalized Shannon entropy.

Table 2 Multiple linear regression models examining the impact of baseline SHBs diversity (Sn) on HBsAg decline following Peg-IFN- α therapy

Variables	Crude model	Model I	Model II
Δ HBsAg			
Sn <0.58	Reference	Reference	Reference
Sn \geq 0.58	-1.4 (-2.5 to -0.3) 0.02	-1.4 (-2.5 to -0.2) 0.03	-1.3 (-2.5 to -0.2) 0.04
Relative percentage HBsAg decrease			
Sn <0.58	Reference	Reference	Reference
Sn \geq 0.58	-28.0 (-51.5 to -4.5) 0.03	-26.7 (-50.5 to -3.2) 0.04	-26.4 (-50.2 to -2.5) 0.04

Notes: Data are presented as β , 95% CI, and p -values. The crude model did not adjust for any variables; Model I adjusted for baseline ALT; and Model II adjusted for Model I + baseline HBsAg.

Abbreviations: ALT, alanine aminotransferase; HBsAg, hepatitis B surface antigen; Peg-IFN, PEGylated interferon; SHBs, small hepatitis B surface protein; Sn, normalized Shannon entropy.

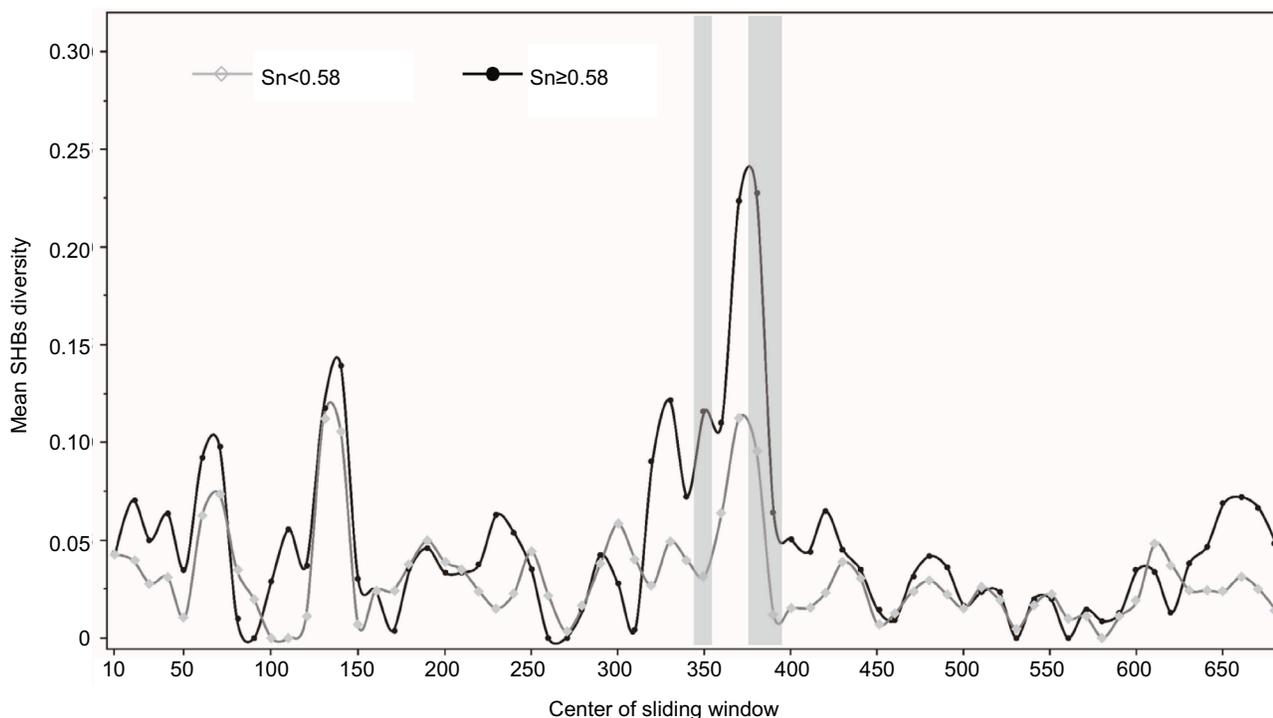


Figure 3 A sliding window analysis with overlapping 19-nucleotide segments migrating every 10 nucleotides for the small HBs gene.
Notes: The gray line represents the $S_n < 0.58$ group, and the black line represents the $S_n \geq 0.58$ group. Grayed out segments correspond to statistically significant differences.
Abbreviations: HBs, hepatitis B surface; SHBs, small hepatitis B surface protein; S_n , normalized Shannon entropy.

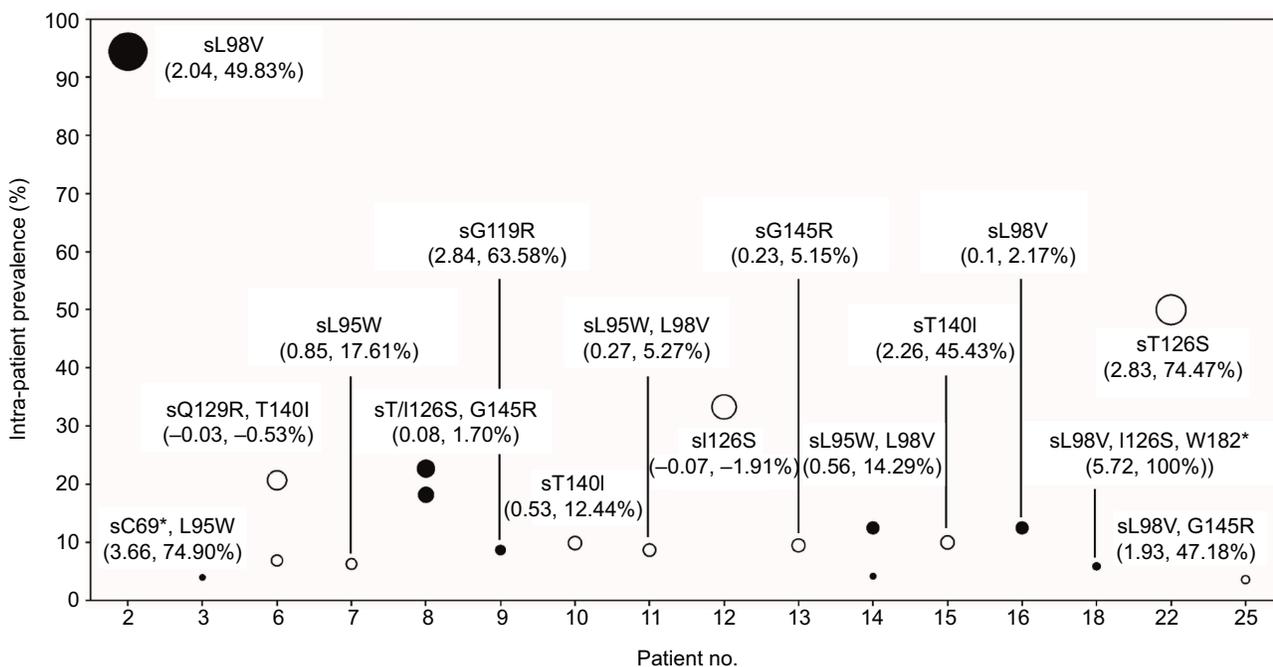


Figure 4 Intra-patient prevalence of HBs mutations was associated with lower HBsAg synthesis/secretion in this study.
Notes: Intra-patient prevalence was expressed as percent of clones with the specific mutation. At least 1 related mutation was detected in 16 (61.5%) patients. Of these, 14 (87.5%) patients' prevalence of related HBs mutation was $< 35\%$ (mean: 10.3%, range: 3.6%–33.3%). The relative dimension of black ($S_n < 0.58$, $n=7$) and white ($S_n \geq 0.58$, $n=9$) dots represents the intra-patient prevalence of related HBs mutations. The numbers indicate the Δ HBsAg and the relative percentage of HBsAg decrease. *Indicates the stop codon.
Abbreviations: HBs, hepatitis B surface; HBsAg, hepatitis B surface antigen; S_n , normalized Shannon entropy.

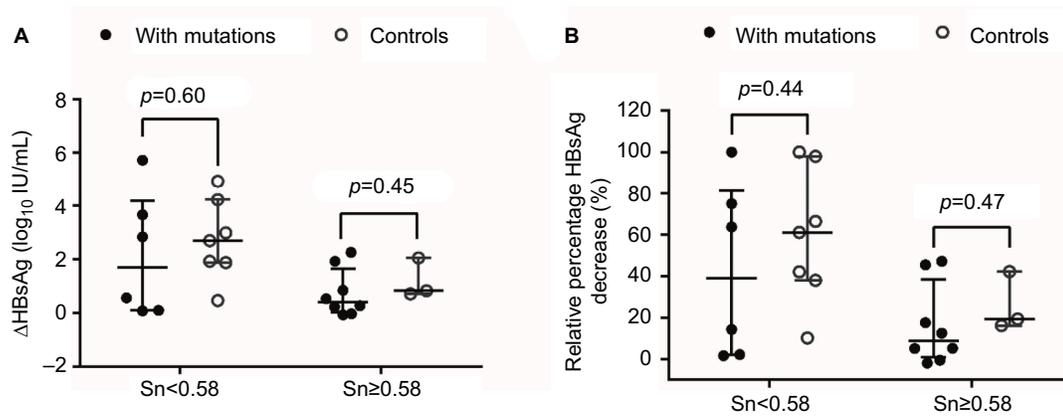


Figure 5 Effect of HBs-specific mutations on the Δ HBsAg (A) and the relative percentage of HBsAg decrease (B) both in the Sn < 0.58 and \geq 0.58 groups. **Abbreviations:** HBs, hepatitis B surface; HBsAg, hepatitis B surface antigen; Sn, normalized Shannon entropy.

ferent 2 groups, with an intra-patient prevalence of \geq 50% (94.4% and 50%, respectively). Although the 2 mutations were characterized by a high HBsAg decline (2.04 \log_{10} IU/mL and 2.83 \log_{10} IU/mL), the Sn did not change if left out these 2 mutations. It seems unlikely that HBsAg-related mutation is the main source of the differences in baseline Sn.

Discussion

In this study, we evaluated the relationship between baseline SHBs diversity and HBsAg decline in HBeAg-positive patients treated with Peg-IFN- α . Our results show that the presence of higher baseline SHBs diversity was associated with lower HBsAg reduction in response to Peg-IFN- α therapy. Moreover, the differences in the “a” determinant upstream flanking region and the first loop of the “a” determinant (nucleotides 341–359, 371–389, and 381–399) were the main source for the higher baseline SHBs diversity.

Charuworn et al examined baseline interpatient hepatitis B viral diversity using mean genetic distance in tenofovir-treated patients who lost HBsAg and compared it with that of control patients with high HBsAg levels.¹⁴ Their results suggested that patients with HBsAg loss have less interpatient viral diversity within the *HBs gene*. Although we used Sn in the present study, we also obtained the similar result that the patients with lower baseline SHBs diversity has more HBsAg decline compared with those with higher baseline SHBs diversity in Peg-IFN- α therapy. Both the mean genetic distances and Sn are ways to evaluate viral diversity. In previous studies, we evaluated the HBV diversity using both methods and found that the results were consistent. This demonstrates that the bias from the evaluation method is minimal and can be ignored. In addition, similar results have also been demonstrated in patients infected with HCV in Peg-IFN- α

therapy.^{21,22} These results suggest that the high viral diversity of pretreatment was associated with poor treatment outcomes, although studies did differ in pathogenic agents (HBV and HCV), medications (NA and Peg-IFN- α), and clinical end points (degree of HBsAg decline and virological response).

However, several studies reported the distinct results that increased viral diversity within the HBV X/pre-core/core regions contributes to HBeAg seroconversion in genotypes B and C patients during Peg-IFN or NA therapy.^{18,28} This discrepancy might be because of several differences between those studies and ours. First, in the aforementioned studies, the X/pre-core/core regions were analyzed, whereas the SHBs region was evaluated in our study. There is no doubt that the patterns of HBV genetic variability are significantly different between different regions, particularly those that locate in structural-coding areas with rich immune epitopes.^{32,33} Indeed, Charuworn et al confirmed that HBV X and pre-core/core regions generally displayed higher viral diversity than other regions.^{14,32} Second, only 10 clones per sample were used to evaluate viral diversity, whereas this study used 25–30 clones per sample. The number of clones is too small to well reflect the complexity of the intra-patient virus population and can, therefore, cause bias when calculating viral diversity.

Our data revealed that the “a” determinant upstream flanking region and the first loop of the “a” determinant (nucleotides 341–359, 371–389, and 381–399) were the main sources for higher baseline SHBs diversity. These regions included critical epitopes for humoral and cellular immunity.³⁴ A possible explanation was that more sequence variations within these regions perturb host immune control, resulting in the survival of more viral variants. Finally, HBsAg levels declined more slowly in these patients.³⁵ Further studies are needed to confirm this hypothesis.

There were certain limitations to this study. First, the HBsAg decline was chosen as the study outcome but not hard end points, including HBsAg loss or seroconversion. However, HBsAg loss or seroconversion, whether spontaneous or treatment-induced, is still a rare event in CHB patients. From this point of view, it seems more reasonable to choose HBsAg decline as the end point in the current study. In addition, considering the individual differences in baseline HBsAg levels, we included the Δ HBsAg and the relative percentage HBsAg decrease in the HBsAg decline as study end points. Second, the sample size for the study was small, and all participants were HBeAg-positive. Thus, the generalizability of the study results is constrained to HBeAg-positive patients for those receiving Peg-IFN- α therapy.

Conclusion

This study showed that the higher SHBs diversity was associated with lower HBsAg reduction in response to 48-week Peg-IFN- α therapy. Moreover, more sequence variations within the “a” determinant upstream flanking region and the first loop of the “a” determinant were the main sources for the higher of baseline SHBs diversity. The evaluation of SHBs diversity at baseline could be used to guide patient screening and inform both patients and clinicians of the likelihood of HBsAg reduction in the setting of Peg-IFN- α therapy. Whether this observation extends to an HBeAg-negative population and other treatment strategies remains to be determined in further studies. However, our findings suggest that consideration should be given to the SHBs diversity at the time of therapy initiation, especially when we seek to achieve functional HBV cure (HBsAg loss) in the setting of CHB therapy.

Acknowledgments

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Disclosure

The authors report no conflicts of interest in this work.

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Supplementary materials

Table S1 Summary of known mutations associated with lower HBsAg synthesis/secretion in vivo and in vitro

Mutation	Source		Intracellular HBsAg	Extracellular HBsAg
E2G	CHB	HepG2	↓	↓
C69*	CHB	HepG2	↓	↓
W74*	CHB	Huh7	↓	↓
L95W	CHB	HepG2	↓	↓
L98V	CHB	HepG2	↓	↓
G119R	OBI	Huh7/mice	↑	↓
T125A	CHB	Huh7	–	↓
I/T126S	OBI	Huh7/mice	↑	↓
Q129R	OBI	Huh7/mice	↑	↓
S136P	OBI	Huh7/mice	↑	↓
T140I	OBI	Huh7/mice	↑	↓
K141E	OBI	Huh7/mice	↑	↓
D144A/G	OBI	Huh7/mice	↑	↓
G145R/A	OBI	Huh7/HepG2/mice	↓	↓
W182*	CHB	HepG2	↓	↓
M103I+G145A	OBI	Huh7/HepG2	↓	↓
R122K+G145A	OBI	Huh7/HepG2	↓	↓
M103I+R122K+G145A	OBI	Huh7/HepG2	↓	↓

Notes: *Stop codon mutation. ↑, increase; ↓, decrease.

Abbreviations: CHB, chronic hepatitis B; HBsAg, hepatitis B surface antigen; OBI, occult hepatitis B infection.

Table S2 Intra-patient prevalence of mutations associated with lower HBsAg synthesis/secretion in this study

Group	Patient	C69*	L95W	L98V	G119R	T/I126S	Q129R	T140I	G145R	W182*
1	2	0	0	94.4	0	0	0	0	0	0
1	3	4	4	0	0	0	0	0	0	0
1	8	0	0	0	0	18.2	0	0	22.7	0
1	9	0	0	0	8.7	0	0	0	0	0
1	14	0	12.5	4.2	0	0	0	0	0	0
1	16	0	0	12.5	0	0	0	0	0	0
1	18	0	0	5.9	0	5.9	0	0	0	5.9
2	6	0	0	0	0	0	20.7	6.9	0	0
2	7	0	6.3	0	0	0	0	0	0	0
2	10	0	0	0	0	0	0	9.9	0	0
2	11	0	8.7	8.7	0	0	0	0	0	0
2	12	0	0	0	0	33.3	0	0	0	0
2	13	0	0	0	0	0	0	0	9.5	0
2	15	0	0	0	0	0	0	10	0	0
2	22	0	0	0	0	50	0	0	0	0
2	25	0	0	3.6	0	0	0	0	3.6	0

Notes: Data are presented as percentage (%). Group 1: Sn <0.58; Group 2: Sn ≥0.58. *Indicates the stop codon.

Abbreviations: HBsAg, hepatitis B surface antigen; Sn, normalized Shannon entropy.

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