Replicative Activity of Hepatitis B Virus Is Negatively Associated with Methylation of Covalently Closed Circular DNA in Advanced Hepatitis B Virus Infection

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Introduction

The hepatitis B virus (HBV) has a 3.2-kb partially double-stranded relaxed circular DNA (rcDNA) genome that is converted into a covalently closed circular DNA (cccDNA) in the nuclei of infected hepatocytes. HBV cccDNA is clinically important because (1) it serves as a template for viral transcription and (2) it is responsible for failure of viral clearance after antiviral therapy. Recent reports have shown that the replicative activity of intrahepatic HBV cccDNA varies widely in chronic hepatitis B (CHB) [3, 4]. The host immune response and viral mutations have been proposed as the factors regulating the transcriptional activity of the cccDNA, but the exact mechanisms of transcriptional control of cccDNA are poorly understood [5].

The HBV genome that is integrated into the host DNA can be methylated [6], and previous studies demonstrated regulation of gene expression by methylation of integrat-
ed HBV DNA [7–10]. In contrast, the methylation status of episomal HBV cccDNA was not known until recently, when two independent groups reported the presence of methylation in the HBV cccDNA [11, 12]. These reports also showed an association between methylation and suppressed HBV replication in CHB. However, the impact of cccDNA methylation on the regulation of HBV gene expression has not yet been established.

Patients with HBV-related liver cirrhosis (HBV-LC), an end result of long-standing CHB, show wide variability of HBV levels in serum and liver [13]. However, it is not known whether the replicative activity of cccDNA is also variable in HBV-LC. Nor has the methylation of cccDNA been reported in HBV-LC. In this study, we studied the methylation status of intrahepatic HBV cccDNA in patients with HBV-LC by bisulfite sequencing, and assessed the association between cccDNA methylation and the replicative activity of HBV in these patients. We also tried to elucidate the effect of methylation on the transcriptional activity of HBV cccDNA molecules by in vitro transcription assay.

**Patients and Methods**

**Subjects**

The protocol of this study was approved by our hospital’s institutional review board, and written informed consent was obtained from all patients. Twelve consecutive HBsAg-positive patients with well-compensated (Child-Pugh class A) liver cirrhosis who underwent surgical resection of combined hepatocellular carcinoma were enrolled in this study. The characteristics of the patients are summarized in table 1. No patient had a prior history of antiviral therapy for HBV or chemotherapy for hepatocellular carcinoma. Fresh nonneoplastic liver tissue was obtained from the hepatectomy specimens in the operating room and was immediately processed as described below for the study of HBV cccDNA.

**Cell Lines and Culture Conditions**

The HepAD38 cell line, which produces HBV pregenomic RNA under the control of the tetracycline-responsive CMV-IE promoter (a generous gift from professor C. Seeger, Fox Chase Cancer Center, Philadelphia, Pa., USA), was maintained as described elsewhere [14]. To explore the effect of inhibition of de novo methylation, 5-aza-2’-deoxycytidine (5-aza; Sigma A3656) was replenished daily in the culture medium (final concentration of 2 μM).

**Isolation of HBV cccDNA and rcDNA**

HBV cccDNA was extracted by using a modified Hirt extraction procedure [15, 16]. Briefly, approximately 50 μg of each fresh nonneoplastic hepatocyte specimen was homogenized in a Potter-Elvehjem tissue grinder with 2 ml of cell lysis buffer [50 mM Tris–HCl (pH 8.0), 1 mM EDTA, 0.2% NP-40, 150 mM NaCl] at 4°C. The homogenate was centrifuged at 16,000 g at 4°C for 10 min to isolate the nuclei, and the supernatant was saved for extraction of cytoplasmic HBV rcDNA and HBV RNA. The nuclear pellet was then treated with the same volume of nuclear lysis buffer (6% SDS, 0.1 N NaOH), neutralized by the addition of 1/4 volume of 3 M potassium acetate (pH 5) and centrifuged. The supernatant was extracted twice with phenol and the cccDNA fraction was recovered by ethanol precipitation. Potential contaminating genomic DNA was further removed by treatment with Plasmid-Safe DNase (Epigenetic Biotechnologies, Madison, Wisc., USA), and the absence of contaminating genomic DNA was confirmed by the negative PCR results obtained with a primer pair for β-globin [17]. For isolation of HBV cccDNA from the HepAD38 cell line, cells that were grown in a 60-mm tissue culture dish were lysed by the addition of 0.4 ml of cell lysis buffer and incubated for 5–10 min on ice, and the lysate was centrifuged as described above.

Detection of HBV cccDNA was performed by selective PCR amplification with HBV cccDNA-specific primers as described elsewhere [18, 19]. The cytoplasmic HBV rcDNA fraction was treated with proteinase K, phenol extracted and ethanol precipitated. Quantification of HBV rcDNA and cccDNA was conducted using the Applied Biosystems 7500 Real-Time PCR System (Applied Biosystems, Foster City, Calif., USA) as described elsewhere [20, 21]. To confirm the absence of contaminating rcDNA in the cccDNA fraction, Southern blot was performed as reported elsewhere, with minor modifications [22]. Briefly, HBV DNA from HepAD38 cells was subjected to electrophoresis in a 1.5% agarose gel and transferred onto Nylon membrane (Roche Applied Science). The 462-bp HBV DNA was amplified by using the sense primer HB7F and antisense primer HB7R as reported elsewhere [23–25]. The PCR product was amplified again by using the single sense primer to generate single-stranded digoxigenin-labeled probes for hybridization [24]. Hybridization and detection were performed by using the DIG high prime DNA labeling and detection starter kit II (Roche Applied Science) according to the manufacturer’s instructions.

### Table 1. Characteristics of the patients and status of HBV cccDNA methylation

<table>
<thead>
<tr>
<th>Patient</th>
<th>Age (years)</th>
<th>Sex</th>
<th>HBeAg</th>
<th>HBeAb</th>
<th>Serum HBV DNA ( \log_{10} \text{copies/ml} )</th>
<th>HBV cccDNA methylation, %</th>
</tr>
</thead>
<tbody>
<tr>
<td>P1</td>
<td>65</td>
<td>M</td>
<td>+</td>
<td>–</td>
<td>6.12</td>
<td>44.4</td>
</tr>
<tr>
<td>P2</td>
<td>47</td>
<td>M</td>
<td>+</td>
<td>–</td>
<td>6.74</td>
<td>20.0</td>
</tr>
<tr>
<td>P3</td>
<td>59</td>
<td>M</td>
<td>+</td>
<td>–</td>
<td>7.43</td>
<td>50.0</td>
</tr>
<tr>
<td>P4</td>
<td>40</td>
<td>M</td>
<td>+</td>
<td>–</td>
<td>7.47</td>
<td>15.4</td>
</tr>
<tr>
<td>P5</td>
<td>39</td>
<td>M</td>
<td>+</td>
<td>–</td>
<td>7.77</td>
<td>13.3</td>
</tr>
<tr>
<td>P6</td>
<td>55</td>
<td>M</td>
<td>–</td>
<td>+</td>
<td>ND</td>
<td>38.5</td>
</tr>
<tr>
<td>P7</td>
<td>59</td>
<td>M</td>
<td>–</td>
<td>+</td>
<td>ND</td>
<td>50.0</td>
</tr>
<tr>
<td>P8</td>
<td>64</td>
<td>M</td>
<td>–</td>
<td>+</td>
<td>ND</td>
<td>55.6</td>
</tr>
<tr>
<td>P9</td>
<td>48</td>
<td>M</td>
<td>–</td>
<td>+</td>
<td>4.56</td>
<td>0</td>
</tr>
<tr>
<td>P10</td>
<td>48</td>
<td>F</td>
<td>–</td>
<td>+</td>
<td>5.63</td>
<td>26.7</td>
</tr>
<tr>
<td>P11</td>
<td>42</td>
<td>M</td>
<td>–</td>
<td>+</td>
<td>7.09</td>
<td>0</td>
</tr>
<tr>
<td>P12</td>
<td>34</td>
<td>M</td>
<td>–</td>
<td>+</td>
<td>7.99</td>
<td>0</td>
</tr>
</tbody>
</table>

ND = Not detectable.
Fig. 1. Bisulfite sequencing of HBV cccDNA from patients with HBV-LC. a Southern blotting confirmed the absence of rcDNA (RC), double-stranded linear DNA (DSL) and single-stranded DNA (SS) in the Plasmid-Safe DNase-treated cccDNA fraction that was used for bisulfite sequencing. b CpG dinucleotides on the HBX region (1319–1670) are marked in bold. Fig. 1. c–e Alignment of the HBX sequences from HBeAg-positive patients (c), HBeAg-negative patients (d) and a negative control (e). Filled and open circles correspond to methylated and unmethylated CpG dinucleotides, respectively.
Quantitation of Hepatic HBV RNA

Total RNA was extracted from the cytoplasmic fraction of liver tissues using Trizol (Invitrogen). Transcript-specific quantitative RT-PCR was performed using the Pgp (5’-CAACCTCT-GCCTAATCATC-3’) and BCI (5’-GGGAAGAAGTCAAGGGC-3’) primer pair to measure the HBV RNA [3]. The RNA levels were compared by the relative comparative threshold method with glyceraldehyde-3-phosphate dehydrogenase as an internal loading control. The transcriptional activity of cccDNA was estimated by the relative amount of HBV RNA synthesized per HBV cccDNA molecule [3, 4].

Bisulfite Sequencing

Cytosine methylation of HBV cccDNA was assessed by bisulfite modification of HBV cccDNA as described elsewhere [25, 26], followed by bisulfite sequencing PCR analysis [27]. The PCR primers were designed using MethPrimers [27] (forward (1327–1352), 5’-GGGATTGATAATTTTGTTGTTTTTT-3’; reverse (1642–1670), 5’-TCCAAAATCCTTATATAAACCTTA-3’) to amplify the bisulfite-modified HBX gene region (nucleotide position 1327–1670), which corresponds to CpG island 2 of Vivelad [27]). The PCR amplicon was sequenced using the PGP (5’-CATTGCAGAGAGTCCAAGAGTCCTC-3’/reverse primer, 5’-GCAAGGAGTCTGGAGCAACAA-3’) primer pair to measure the HBV RNA transcript with glyceraldehyde-3-phosphate dehydrogenase as an internal control. The HBV RNA transcript was quantified by real-time PCR with the PPG (5’-GGAAAGAAGTCAGAAG-3’/3’). The PCR products were digested with HpaII and amplified by HBV cccDNA-specific primers and cloned into pDrive TA cloning vector (Qiagen). The cloned plasmid (pDrive-HBX) was propagated in E. coli (New England Biolabs, Ipswich, Mass., USA), bisulfite modified and sequenced as described above.

In vitro Transcription Assay

Nuclear extracts were prepared from Huh7 cells exactly as described previously [29]. The run-off transcription assay was set up as reported previously [29, 30]. Final concentrations for the reaction included 7 mg/ml Huh7 nuclear extract and 5 X 10^6 copies/ml HBV cccDNA. The transcription reaction was performed for 45 min at 30°C and was treated with DNase I for 30 min at 37°C to remove template cccDNAs. The RNA was reverse transcribed using random hexamers and amplified by HBV cccDNA-specific primers as described above.

Chromatin Immunoprecipitation

The presence of methyl-CpG-binding proteins (MBPs) on HBV cccDNA was studied by chromatin immunoprecipitation as described elsewhere [31–33]. Anti-methyl-CpG-binding domain protein 1 (MBD1; sc-9395) and anti-DNA methyltransferase 3a (DNMT3a; sc-10232) antibodies were purchased from Santa Cruz Biotechnology (Santa Cruz, Calif., USA). Anti-Mecp2 (ab2828) antibodies were purchased from Abcam (Cambridge, UK).

Statistical Analysis

Continuous variables were compared between different subgroups by Student’s t test. Fisher’s exact test was used for the analysis of categorical variables. Statistical calculations were performed with SPSS software package version 15 (SPSS Inc., Chicago, Ill., USA).

Results

Variable Degrees of Methylation Were Present in HBV cccDNA from HBV-LC

The results of bisulfite sequencing are summarized in figure 1. Among the 12 studied patients with HBV-LC, 9 patients showed methylation in HBV cccDNA isolated from liver cirrhosis tissues; methylated CpG dinucleotides were identified in all 5 HBeAg-positive patients (fig. 1c) and 4 of 7 HBeAg-negative patients (fig. 1d) by bisulfite sequencing. The possibility of false-positive results due to incomplete bisulfite conversion of HBV cccDNA was excluded by showing that methylation was absent in the pDrive-HBX plasmid that was propagated in dam/dcm E. coli (fig. 1e). The HBV cccDNA methylation ratio (the percentage of methyl CpG-positive cccDNA clones) varied widely among the patients, ranging from 0 to 55.6% (table 1). The average HBV cccDNA methylation ratios were not different between HBeAg-positive and HBeAg-negative patients (28.6 vs. 24.4%, respectively; p = 0.747). The sites of methylation were also variable, even in cccDNA molecules from the same patient. The methyl-CpGs were dispersed over the sequenced HBX area without a favored CpG site. These findings indicate that HBV cccDNA molecules are heterogeneous in terms of methylation in patients with HBV-LC.

Factors Associated with Methylation of HBV cccDNA

Next, we sought to identify clinical, biochemical and virologic factors which may be associated with methylation of HBV cccDNA. Older age and lower serum HBV DNA titers were significantly associated with increased HBV cccDNA methylation, whereas biochemical parameters were not different between the high- and low-methylation groups (table 2).

Replicative Activity of HBV Is Negatively Associated with CpG Methylation of HBV cccDNA in HBV-LC

Since methylation of HBV cccDNA was associated with low serum HBV DNA titers, we wanted to know whether the methylation is associated with the amount or activity of intrahepatic HBV cccDNA. There was no correlation between HBV cccDNA methylation and the amount of intrahepatic cccDNA (fig. 2a), and the cccDNA levels were not different between the groups with low (≤0.2) and high (>0.2) methylation ratios (4.7 ± 0.9 and 5.2 ± 1.8 log_{10} copies/mg tissue, respectively; p = 0.628). In contrast, the virion productivity, an indicator of HBV replicative activity [4], was negatively cor-

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Table 2. Variables associated with the degree of HBV cccDNA methylation

<table>
<thead>
<tr>
<th>Variable</th>
<th>Low HBV cccDNA methylation ratio (≤0.2; n = 6)</th>
<th>High HBV cccDNA methylation ratio (&gt;0.2; n = 6)</th>
<th>p value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age, years</td>
<td>41.7 ± 5.2</td>
<td>58.3 ± 6.3</td>
<td>0.001</td>
</tr>
<tr>
<td>AST, IU/l</td>
<td>71 ± 53</td>
<td>40 ± 23</td>
<td>0.230</td>
</tr>
<tr>
<td>ALT, IU/l</td>
<td>72 ± 66</td>
<td>38 ± 29</td>
<td>0.278</td>
</tr>
<tr>
<td>Bilirubin, mg/dl</td>
<td>0.8 ± 0.1</td>
<td>0.8 ± 0.4</td>
<td>0.928</td>
</tr>
<tr>
<td>Albumin, g/dl</td>
<td>4.2 ± 0.5</td>
<td>4.2 ± 0.2</td>
<td>0.694</td>
</tr>
<tr>
<td>Prothrombin time, INR</td>
<td>1.09 ± 0.07</td>
<td>1.10 ± 0.11</td>
<td>0.905</td>
</tr>
<tr>
<td>HBeAg, positive/negative</td>
<td>3/3</td>
<td>4/2</td>
<td>0.558</td>
</tr>
<tr>
<td>Serum HBV DNA, log_{10} copies/ml</td>
<td>6.93 ± 1.25</td>
<td>4.84 ± 1.79</td>
<td>0.041</td>
</tr>
</tbody>
</table>

Quantitative variables are expressed as means ± SD. AST = Aspartate aminotransferase; ALT = alanine aminotransferase; INR = international normalized ratio.
related with the cccDNA methylation ratio ($r = -0.689$, $p = 0.013$; fig. 2b). The mean virion productivity tended to be lower in the high-methylation ratio group compared to the low-methylation ratio group, although the significance was marginal (3.0 vs. 11.4, respectively; $p = 0.05$).

The real-time RT-PCR assays showed significant correlation between the hepatic HBV RNA levels and the virion productivity (fig. 2c). The relative copy numbers of HBV RNA produced per cccDNA molecule, an estimate of the transcriptional activity of cccDNA, were significantly lower in the high-methylation ratio group compared to the low-methylation ratio group ($p = 0.049$; fig. 2d), again supporting the hypothesis that methylation of cccDNA suppresses replicative activity.

CpG Methylation Is Associated with Suppressed Transcriptional Activity of HBV cccDNA

The relationship between cccDNA methylation and the replicative activity of HBV was further examined by in vitro experiments. When HepAD38 cells were replenished with 5-aza, cccDNA methylation was suppressed (fig. 3a) and the virion productivity was increased (fig. 3b) compared to the control without 5-aza treatment. To exclude the possibility that HBV replication was directly affected by 5-aza, we performed an in vitro transcription assay using the HBV cccDNAs with known methylation status as templates (cccDNAs that were analyzed for methylation as shown in figure 3a). Indeed, cccDNAs with increased methylation showed suppressed transcriptional activity compared to cccDNAs with minimal
methylation (fig. 3c). In addition, an in vitro transcription assay using the cccDNAs from 2 HBeAg-negative patients also showed suppression of transcriptional activity by increased methylation (fig. 4).

**HBV cccDNA Is Bound by MBD1**

Finally, we examined whether the cccDNA recruited transcriptional repressor proteins (MBPs [34] and DNMT3a [35]) which may suppress viral transcription. Chromatin immunoprecipitation assays showed that MBD1 was bound to cccDNA in HepAD38 cells, whereas antibodies against MeCP2 and DNMT3a did not precipitate HBV cccDNA (fig. 5).

**Discussion**

Recently, epigenetic modifications, especially the status of cccDNA-bound histones, were shown to influence cccDNA function [33, 36]. Since DNA methylation and histone deacetylation constitute two related epigenetic mechanisms of transcriptional repression in eukaryotic cells, it can be hypothesized that methylation of cccDNA may also influence HBV replication [37–39]. To our knowledge, only two previous papers have reported the presence of cccDNA methylation in CHB [11, 12]. These reports also suggested an association between cccDNA methylation and suppressed viral replication. The study by Guo et al. [12] included only patients with an HBV viral load of $>10^3$ copies/ml; since a significant proportion of HBeAg-negative patients may have undetectable serum HBV titers [40], these patients might have been systematically excluded in their study. The study by Vivekanandan et al. [11] included cccDNA samples from liver cancer tissues, and the frequencies of cccDNA methylation were not quantitatively correlated to the HBV viral loads. In both reports, the presence of combined liver cirrhosis was not specified. Considering the possible interactions between the HBV viral load and the presence of severe fibrosis (cirrhosis) [41, 42], we focused our study on HBV-LC regardless of HBV viral loads to elucidate the factors associated with cccDNA methylation in this population while minimizing the possible confounding interactions between the degree of liver fibrosis and HBV replication. Although small sample size is the main limitation of this study, our data may give a better insight into the methylation status of HBV cccDNA in liver cirrhosis patients.

Our bisulfite sequencing data show variable degrees of CpG methylation in the intrahepatic HBV cccDNA from HBV-LC patients. We also found that old age is associ-
ated with increased methylation. Considering the epidemiology of HBV infection in Korea, where perinatal infection is the main mode of transmission, a patient’s age may correspond to the duration of HBV infection [43]. Thus, it could be argued that methylation of cccDNA accumulates over time. Since HBV cccDNA is quite stable in quiescent hepatocytes [5], methylated cccDNA may be passed to daughter cells after mitotic division, and additional methylation on replenished cccDNA may increase the methylation frequency of the cccDNA population in chronic HBV infection.

The association between cccDNA methylation and suppressed serum HBV DNA titers in HBV-LC suggests that methylation regulates the replicative activity of cccDNA in these patients. This hypothesis is further supported by our data showing that (1) cccDNA methylation is negatively associated with the virion productivity in both HBV-LC and HepAD38 cells, (2) HBV RNA copy numbers generated per cccDNA, another indicator of the activity of cccDNA [3, 4], are suppressed in HBV-LC with elevated cccDNA methylation and (3) cccDNA methylation directly suppresses transcriptional activity in in vitro transcription assays using cccDNA templates from HepAD38 cells and HBV-LC patients. Taken together, these results suggest the possibility that increased HBV cccDNA methylation may contribute to suppressed viral productivity in HBV-LC.

Our data showed that increased cccDNA methylation was associated with older age and a low serum HBV DNA titer, and these factors are generally associated with HBeAg clearance [44]. Previous studies demonstrated suppressed replicative activity of cccDNA in HBeAg-negative CHB [3, 4]. Therefore, it can be postulated that HBeAg clearance is associated with increased cccDNA methylation, which in turn leads to suppressed viral productivity. Indeed, a recent study reported increased cccDNA methylation in HBeAg-negative CHB [12], but our results did not show a significant relation between HBeAg positivity and cccDNA methylation. The small sample size in our study may explain this discrepancy, but it is also possible that the methylation status of cccDNA may be similar regardless of HBeAg positivity in liver cirrhosis. As our study population was limited to patients with pathologically proven liver cirrhosis, and other factors such as host immunity may also affect viral productivity, the overall quantitative contribution of cccDNA methylation to the transcriptional regulation of HBV in chronic HBV infection needs validation in different stages of HBV infection in further studies.

Our study also gives clues to the mechanism of in vitro transcriptional block by cccDNA methylation. Methylation of mammalian DNA induces transcriptional silencing by recruiting MBPs which function as methylation-dependent transcriptional repressors [45]. MBPs are a major family of MBPs in vertebrates and include MBD1, MBD2, MBD3, MBD4 and MeCP2 [34, 45]. DNMT3a has also been reported to function as a corepressor of transcription [35]. Our ChIP data showed that MBD1 is bound to HBV cccDNA, suggesting that methylated CpG recruits MBD1, which might lead to transcriptional repression of methylated cccDNA. Further studies are warrant- ed to confirm the mechanism(s) of transcriptional suppression by cccDNA methylation in human specimens.

In conclusion, HBV cccDNA is variably methylated, and methylation of cccDNA is associated with suppressed viral replicative activity in HBV-LC.

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References


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