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HBV genome analysis in the progression of HBV related chronic liver disease

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Abstract

Although HBV is a non-cytopathic virus, alteration of viral genome may also alter host immunity and may play a part in the pathogenesis LC and HCC. During the last decade, various studies have shown that mutations in the HBV genome may play a role in HCC pathogenesis. Here, we have analyzed HBV genome from patients with asymptomatic HBV carrier [ASC]), chronic hepatitis B (CHB), cirrhosis of liver (LC), and hepatocellular carcinoma (HCC) of Bangladeshi origin. A total of 225 patients tested positive for HBV with different stages of chronic HBV infection were enrolled in this study. The extent of liver damages were assayed by estimating serum levels of alanine aminotransferase (ALT), serum bilirubin and finally by abdominal ultrasonography and/or fine needle aspiration cytology. Wherever required, cancer marker like alpha fetoprotein (AFP) was assessed. HBV genotype was evaluated by immunoassays and sequenced. A total of 25 patients were ASC, 135 were CHB and 65 were LC and HCC. Among ASC patients, 5, 7 and 13 belonged to HBV genotype A, C, and D, respectively. On the other hand, HBV genotype C was most prevalent in CHB patients (about 42%), followed by HBV genotype D (36%). About 69% patients with LC and HCC also had genotype C. Full genomic analysis of sera of patients with progressive liver damages (LC and HCC) revealed mutations at HBeAg promoter regions in more than 80% patients. However, mutations in this region were mostly unseen in ASC and patients with less progressive liver diseases. HBV genotype was found quite different in Bangladeshi HBV patients which seem a mixture of Indian and Asia-Pacific region. This study also reveals that HBeAg promoter region mutation may have role in development of HBV related LC and HCC.

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