The Pre-S2 sequence mutations associated with HBV disease consequence among different patient groups

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Abstract :

Background: Sequence variation in Pre-s2 gene of Hepatitis B Virus (HBV) is enumerated as important viral factors contributed to infection outcome. While some studies indicated the role of Pre-S2 mutations in diseases progression when evaluated in B and C genotypes, the data supporting this idea on genotype D is limited.
Objectives: The aim of this study was to investigate if deletion mutation in Pre-S2 region attributed to disease progression. Here, the mutations in this region compared among patients with HCC, Liver cirrhosis and asymptomatic carriers.
Material methods and Patients: A total of 60 sera samples were collected from patients infected with HBV. They included 30 asymptomatic carrier (ASCs) individuals samples (22 male and 8 female, mid age: 51) and 30 HCC and Cirrhosis (20 HCC and 10 LC), (26 male and 4 female, mid age: 53). The viral DNA was extracted using DNA extraction kit, and then HBV Pre-s2 gene region were amplified by Nested-Polymerase Chain Reaction (Nested-PCR). Finally, DNA sequences of samples were qualified by Alignment tools (BLAST) then each group was compared with each other by Several Multiple Sequencing Aligment softwares.
Results: The results indicated higher rate of mutations among ASCs group than HCC/LC samples. In 26 ASCs samples (from total 30 samples) 13 critical point mutations in Pre-s2 was detected. Furthermore, in 7 ASCs, 7 deletion mutations were also revealed after analysis. In opposite, 5 point mutations and no sign of deletion mutation in LC/HCC group were confirmed after comparing their sequence with references.
Conclusions: The rate of deletion/point mutations in asymptomatic carriers was so higher than HCC and cirrhotic patients so it indicated that in HBV genotype D, Pre-s2 deletions are dispensable factors for HBV disease progression.

Keyword : HBV, genotype D, Pre-s2, Asymptomatic carrier, cirrhosis, HCC
Section : Young investigator