Mutation Frequency of the rtA181T/sW172* mutants among Iranian chronic HBV patients who partially responded to nucleoside analogues therapy

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Abstract

Introduction & Aim: Hepatitis B virus (HBV) is the leading cause of cirrhosis and hepatocellular carcinoma (HCC) in the world. The main goal of therapy in chronic hepatitis B (CHB) patients includes the driving viral replication to the lowest possible level in order to halt the progression of chronic hepatitis to prevent the development of liver failure, due to subsequent liver cirrhosis, and the emergence of HCC. The aim of this study was the detection of rtA181T/sW172* mutant frequency among chronic HBV patients who show incomplete response to antiviral therapy.

Methods: We selected 30 patients who partially responded to nucleoside analogues regimen after 48 weeks of therapy. Genotyping was done for all sequences according to amino acid variants specifying HBV genotypes A to H within overlapped surface proteins using real time PCR and direct sequencing. Amino acid variations within polymerase protein were compared with reference sequences obtained from different HBV genotypes and sequences from Iranian isolates obtained from Gen Bank.

Results: The results of the phylogenetic analysis tree reveled that all isolates were of genotype D. among patients, 16.5% rtA181T/P in RT domain and 6.6% (sW172C/stop) in surface genes.

Conclusions: Of clinical significance is the recent observation that NA therapy selects for HBV mutants that encode truncated surface proteins and therefore could theoretically accelerate the progression to HCC. Emergence of the rtA181T/sW172* mutant in patients increased the risk of HCC development in the subsequent courses of antiviral therapy. Detection of this mutation is benefit to prevention of HCC.

Key words: Hepatitis B virus, hepatocellular carcinoma, rtA181T/sW172* mutant