

Prevalence of Mixed Mutation in Precore Region of Hepatitis B Virus in HBeAb Positive Patients

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Background & Objectives: More than two billion people in the world have been exposed to Hepatitis B virus. Furthermore, 400 million of them, 5% of the whole world population, are infected with chronic HBV infection (1, 2). HBeAg is coded from the core region of virus. Mutations in precore region prevent producing HBeAg. A1896 variants which consist 95% of mutations are able to replicate and are also infectious (3). The purpose of this study was to investigate prevalence of mutation in precore region of gene C in HBeAb positive patients.

Methods: 50 sera of patient infected with hepatitis B are used in this study. Serological markers of hepatitis B include, HBsAg, HBeAg, HBeAb, HBcAb were measured by ELISA (Enzyme Linked Immunosorbent Assay). HBV-DNA was extracted from the sera, and then PCR was performed on extracted HBV-DNA with the use of specific primer of gene C. HBV viral load was detected by Real-Time PCR. Line Probe Assay technique was done on 30 patients by using INNO-LiPA HBV Precore Kit (3, 4). The findings were analyzed by SPSS software, version 20.

Results: All 50 samples were HBsAg and anti-HBc positive and also HBV-DNA were detected in all the patients. 30 samples were examined among them with were respect to the mutations in precore region and 86.7% of them were HBeAb positive. 36.7% of the patients had the viral load of upper than 105 Copy/mL. Prevalence of mixed mutation in precore region among patients was 53.2% (16 Cases).

Conclusion: In patients with chronic hepatitis B Virus, there are spectrums of patients with a mixed population of wild-type virus and precore mutants after HBeAg seroconversion.

Keywords: Precore Mutation; Hepatitis B Virus; Viral Load