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Prevalence of hepatitis-B virus, genotypes and mutants in HBsAg positive patients in Meerut, India

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Objective: Genetic variability of hepatitis B virus (HBV) represents a challenge for the sensitivity of immunologic and molecular-based assays. Therefore, knowing the distribution of HBV genotypes & mutation, have considerable impacts on treatment strategies, vaccination program, diagnosis and prevention. The present study aimed to detect hepatitis-B virus genotypes & mutants in HBsAg positive patients.

Methods: The study conducted on 4927 patients in Meerut, India, which was performed in the central research station laboratory of microbiology at Netaji Subhash Chandra Bose Medical College and Hospital between March 2013 to April 2018. The serum samples were tested for HBsAg using ELISA kit then positive samples for HBsAg were tested for HBeAg ELISA kit and DNA isolation. Amplification HBV DNA of pre-S gene & precore, basal core region were performed by RT-PCR. Sequenced by the sequencer and analyzed for genotype & mutation.

Results: 245 were positive for HBsAg and 55 were for HBeAg positive. 16 sample were positive for PCR, 7(43.8%) were below 2000IU/mL HBV DNA levels, 4(25%) were between >2000IU/mL to 20000IU/mL HBV DNA levels and 5(3.25%) were >20000IU/mL HBV DNA levels. There were no mutation. Genotype B & A were detected. The prevalence of HBV genotype-B and genotype-A were 68.8% (n=11) & 31.25% (n=6) respectively.

Conclusions: Genotype-B was more prevalent in comparison to genotype A. The genetic diversity of HBV and distribution of its genotypes and mutation, improving current knowledge of epidemiological, clinical and virologic patterns of hepatitis B in this region which help physicians to prescribe proper antiviral/interferon therapy according to the current genotyping pattern.

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