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Prevalence of HBV genotypes in Egypt among Hepatitis patients

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Abstract

Phylogenetic analysis has led to the classification of hepatitis B virus into eight genotypes, designated Ato H. The genotypes have differences in biological properties and show heterogeneity in their global distribution. These attributes of the genotypes may account not only for differences in the prevalence of hepatitis B virus mutantsin various geographic regions, but also makes them responsible for differences in the clinical outcome and response to antiviral treatment in different population groups.

Africa is one of the highly endemic regions of HBV with five genotypes (A-E) identified. Almost all patients in the Mediterranean area are infected with genotype D. However,there is little information of genotype distribution in Egypt. A total of 140 Egyptian patients with hepatitis B surface antigen (HBsAg) positive were enrolled in this study. Of the 140 patients, only100 patients were HBV DNA positive and only these were included in the study. They were classified in to 20 patients with acute hepatitis (AH), 75 patients with chronic active hepatitis (CAH) and 5 patients with hepatocellular carcinoma (HCC)]. HBV genotypes were determined using INNO-LiPA methodology which is based on the reversed hybridization principle. Results:

This study showed that genotype D constituted 87% of the total infections (75% CAH, 7% AH & 5% HCC). The other 13% showed mixed infections of D/F.

Conclusion:

These findings show that the most prevalent genotype in Egypt is genotype D especially in CAH and HCC patients while the mixed type D/F is mostly encountered in AH.

Keywords: Phylogenetic, Genotypes, and Hepatocellular