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Unusual HBV mixed genotype infections among hepatitis type B Iraqi patients in Wasit Province, Iraq

Sareaa Maseer Gatya Al-Mayahie[1], **Ali Shakir Kamil Al-Suraifi**[1] **Ahmed Darwish Jabbar Al-Rubaie**[1] and **Naeem Mohammed Mohsen Al-Abedy**[2]

[1]Wasit University, Iraq

[2]Alkarama Teaching Hospital, Iraq

Hepatitis B virus (HBV) is the leading cause to liver disease, cirrhosis and primary liver cancer. About 1 million people die from HBV each year, which equates to about 2 HBV related deaths each minute. Depending on the virus sequence homogeneity as a minimum 10 genotypes (A to J) and numerous sub-genotypes have been identified. Hepatitis B virus variants may be differing in their virulence, models of serologic reactivity, pathogenicity, response to treatment and global distribution. This study was carried out to detect HBV genotypes among Iraqi hepatitis type B patients in Wasit Province, Iraq using nested PCR protocol. A total of 105 outpatients (65 males and 40 females, aged 1-95 years) clinically suspected with viral hepatitis were included in this study. All the patients' sera (105 samples) were positive for HBV surface antigen (HBsAg) by ELISA screen test. Whereas, 72 (60.5%) and 33 (31.4%) of these samples were positive and negative for HBV DNA, respectively, by first PCR. Survey of DNA positive samples for HBV genotypes by nested PCR (second PCR) demonstrated unique results that no single genotype was found and all of these samples had mixed genotypes of which the pattern A+B+C+D+E was the most common (77.7%), followed by A+B+D+E (16.66%), A+B+C (2.77%), A+B+E (1.38%), and A+D+E (1.38%), whereas genotype F was not found in any patient. Statistically, there was non-significant difference in distribution of genotypes among males and females. The presence of mixed infection with about 5 HBV genotypes among most of our patients lead us to conclude that these patients are incurred to different sources of infection at different times and this required an epidemiological evaluation of HBV infection among our patients not only in Wasit Province but also all over Iraq to control this abnormal acquisition of these genotypes by Iraqi people.

sareaamaseer@gmail.com