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Hepatitis B virus: a study of genotypes in an infected Saudi cohort

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Hepatitis B virus (HBV) is a small non-cytopathic virus with a circular DNA genome that contains four genes (*C*, *S*, *X* and *P*).[1] The *S* gene codes for the surface antigen (HBsAg). Hepatitis B virus is polymorphic and is classified into eight genotypes (A–H).[2–4] Hepatitis B virus genotypes differ by 8%,[5] while subgenotypes differ by at least 4%.[6] Genotypes and subgenotypes show a distinct geographical distribution,[7] with the former appearing to correlate with disease progression[8–10] and response to treatment.[11–13]

In Saudi Arabia, HBV infection is declining, and this is due mainly to the introduction of a successful vaccination programme. The authors have observed this decreasing rate of HBV infection in Saudi blood donors,[14] and the aim of the present study is discover which HBV genotypes are present in Saudi patients with acute HBV infection.

A total of 65 Saudi patients (mean age: 30.2 years + 15.3; 62 males, three females) with a positive HBeAg marker were recruited to the study. Extracted DNA was obtained using AmpliPrep sample processing. Hepatitis B virus DNA was extracted from plasma using the CAP instrument and TNAI kit, according to the manufacturer's instructions.

Genotyping was performed using INNO-LiPA HBV genotyping (Innogenetics, Ghent, Belgium). This is a line probe assay designed to identify all eight of the hepatitis B virus genotypes[15] by detecting type-specific sequences in the HBV polymerase gene domain (B to C). Table 1 shows the genotyping results obtained.

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Table 1. Hepatitis B virus genotype distribution in 65 infected Saudi patients.

Genotype	Number	%
B	3	4.6
C	1	1.5
D	61	93.9

Several studies have evaluated the molecular epidemiology and the relevance of HBV genotypes to clinical outcome. In the present study, it was found that HBV genotype D is the predominant genotype in Saudi Arabia. Other genotypes are present at much lower frequencies.

The results present here support those of Abdo *et al.*,[16] who published a study of the frequency of HBV genotypes in Saudi Arabia. They found genotype D to be the most common (81.4%), with a few instances of genotypes A, C and E, but not a single case of genotype B.

Saudi Arabia is home to foreign workers from different parts of the world. The largest communities comprise peoples mainly from Indonesia and the Philippines. The most prevalent HBV genotypes in these countries are genotypes B and C.

Hepatitis B virus genotypes have a geographical distribution.[7] Genotype D is found mainly in Mediterranean countries; in Albania, the Middle East, Turkey and Iran. Genotype B is found mainly in south-east Asia, Taiwan, Japan, Indonesia, China, Hong Kong, Vietnam and Thailand. Genotype C is found mainly in eastern Asia, Taiwan, Japan, Korea, China, Hong Kong, Thailand, Indonesia, Vietnam, the USA and Brazil.

It is now well established that HBV genotypes influence the severity of liver disease and its response to interferon and lamivudine. Genotype C appears to carry a higher risk for chronic disease and a lower response to treatment.[17]

In a prospective study, Thakur *et al.*[18] examined the prevalence and clinical significance of HBV genotypes A and D in Indian patients with chronic HBV infection. They found that genotype D is associated with more severe liver disease and that it may predict the occurrence of hepatocellular carcinoma (HCC) in young Indian patients.

Further studies are needed to investigate the effect of HBV genotypes on acute versus chronic infection, on response to treatment and on the risk of HCC in Saudi patients.

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