

# The dominant prevalence of genotype D among different HBV infected patient groups, A study from referral center in south of Iran

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## Abstract :

**Background:** There are more than 7 well described Hepatitis B Virus (HBV) genotypes worldwide. This genetic diversity has been associated with differences in clinical outcomes. In Iran, genotype D was determined as the most common type of virus. In compare to others, Genotype D virus harbors a natural omission in Pre-s1, from aa 2 to 13.

**Objectives:** The aim of this study was to determine HBV genotype through survey in Pre-s1 region and phylogenetic analysis coincidentally.

**Material methods and Patients:** A total of 60 sera samples were collected from patients infected with HBV. They included 30 asymptomatic carriers (22 male and 8 female, mid age: 51), 20 HCC and 10 Cirrhotic patients (26 male and 4 female, mid age: 53). The viral DNA was extracted using DNA extraction kit, and then HBV Pre-s1 gene region was amplified by Nested-Polymerase Chain Reaction (Nested-PCR). The sequences of samples were qualified by Alignment tool (BLAST) then they were compared with other genotypes sequences from Genbank by Multiple Sequencing Alignment.

**Results:** The sequencing results showed that all of 60 samples were containing genotype D related deletions in Pre-s1 region, from aa2 to 13, which was indicative for the presence of this genotype in all of them. Blast analysis and phylogenetic survey was also supportive of this finding.

**Conclusions:** In our region, HBV genotype D is dominant among different patient groups in Shiraz-Iran.

**Keyword :**

**Section :** Young investigator