

## A Preliminary Report of HBV Full Genome Sequencing Derived from Iranian Intravenous Drug Users

**Authors :** Maryam Vaezjalali, Koroush Rahimian, Maryam Asli, Tahmineh Kandelouei, Foad Davoodbeglou, Amir H. Kashi

**Abstract :** Objectives: The present study was conducted to assess the HBV molecular profiles including genotypes, subgenotypes, subtypes & mutations in hepatitis B genes. Materials/Patients and Methods: This study was conducted on 229 intravenous drug users who referred to three Drop- in-Centers and a hospital in Tehran. HBV DNA was extracted from HBsAg positive serum samples and amplified by Nested PCR. HBV genotype, subgenotypes, subtype and genes mutation were determined by direct sequencing. Phylogenetic tree was constructed using neighbor- joining (NJ) method. Statistical analyses were carried out by SPSS 20. Results: HBV DNA was found in 3 HBsAg positive cases. Phylogenetic tree of derived HBV DNAs showed the existence of genotype D (subgenotype D1, subtype ayw2). Also immune escape mutations were determined in S gene. Conclusion: There were a few variations and genotypes and subtypes among infected intravenous drug users. This study showed the predominance of genotype D among intravenous drug users. Our study concurs with other reports from Iran, that all showing currently only genotype D is the only detectable genotype in Iran.

**Keywords :** drug users, genotype, HBV, phylogenetic tree

**Conference Title :** ICMVM 2015 : International Conference on Molecular Virology and Microbiology

**Conference Location :** Bangkok, Thailand

**Conference Dates :** December 17-18, 2015