

Prevalence Determination of Hepatitis D Virus Genotypes among HBsAg Positive Patients in Kerman Province of Iran

Authors : Khabat Barkhordari, Ali Mohammad Arabzadeh

Abstract : Hepatitis delta virus (HDV) is a RNA virus that needs the function of hepatitis B virus (HBV) for its propagation and assembly. Infection by HDV can occur spontaneously with HBV infection and cause acute hepatitis or develop as secondary infection in HBV suffering patients. Based on genome sequence analysis, HDV has several genotypes which show broad geographic and diverse clinical features. The aim of current study is determine the prevalence of hepatitis delta virus genotype in patients with positive HBsAg in Kerman province of Iran. This cross-sectional study a total of 400 patients with HBV infection attending the clinic center of Besat from 2012 to 2014 were included. We carried out ELISA to detect anti-HDV antibodies. Those testing positive were analyzed further for HDV-RNA and for genotyping using restriction fragment length polymorphism (RFLP) and RT-nested PCR- sequencing. Among 400 patients in this study, 67 cases (16.75 %) were containing anti-HDV antibody which we found HDV RNA in just 7 (1.75%) serum samples. Analysis of these 7 positive HDV showed that all of them have genotype I. According to current study the HDV prevalence in Kerman is higher than the reported prevalence of 6.6% for Iran as a whole and clade 1 (genotype 1) is the predominant clade of HDV in Kerman.

Keywords : genotyping, hepatitis delta virus, molecular epidemiology, Kerman, Iran

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