

Serological Assay and Genotyping of Hepatitis C Virus in Infected Patients in Zanzan Province

Authors : Abdolreza Esmaeilzadeh, Maryam Erfanmanesh, Sousan Ghasemi, Farzaneh Mohammadi

Abstract : Background: Hepatitis C Virus (HCV), a public health problem, is an enveloped, single-stranded RNA virus and a member of the Hepacivirus genus of the Flaviviridae family. Liver cancer, cirrhosis, and end-stage liver are the outcomes of chronic infection with HCV. HCV isolates show significant heterogeneity in genetics around the world. Therefore, determining HCV genotypes is a vital step in determining prognosis and planning therapeutic strategies. Materials and Methods: Serum samples of 136 patients were collected and analyzed for anti-HCV antibodies using ELISA (The enzyme-linked immunosorbent assay) method. Then, positive samples were exposed to RT-PCR, which was performed under standard condition. Afterwards, they investigated for genotyping using allele-specific PCR (AS-PCR), and HCV genotype 2.0 line probe assay (LiPA). Results: Samples indicated 216 bp bands on 2% agarose gel. Analyses of the results demonstrated that the most dominant subtype was 3a with frequency of 38.26% in Zanzan Province followed by subtypes of 1b, 1a, 2, and 4 with frequencies of 25.73%, 22.05%, 5.14%, and 4.41%, respectively. The frequency of unknown HCV genotypes was 4.41%. Conclusions: According to the results, it was found that HCV high prevalent genotype in Zanzan is subtype 3a. Analysis of the results provides identification of certain HCV genotypes, and these valuable findings could affect the type and duration of the treatment.

Keywords : anti-HCV antibody, Hepatitis C Virus (HCV), genotype, RT-PCR, AS-PCR

Conference Title : ICMBB 2015 : International Conference on Molecular Biology and Biomedicine

Conference Location : Tokyo, Japan

Conference Dates : May 28-29, 2015