

Evaluation of common hepatitis C virus genotypes in anti-HCV positive individuals in Guilan province

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Abstract: Introduction & Objective: Hepatitis C virus is one of the viruses transmitted through the blood. The virus has 6 main genotypes and several subgroups. Although it is classified the component of the flaviviridae family (flavivirus), but it is different the full range of known viruses and Hepacivirus viruses, and is therefore classified as the sole member of the Hepacivirus family of of the flaviviridae family. The virus is one of the six common Hepatotrop that has been called nonA-non-B until recently. The disease is transmitted through contaminated blood and there is more to be seen in patients with a history of injecting drug use, contaminated blood transfusions, tattooed and infected needles. Other forms of transmission are sexual intercourses which account for less. Often carcinoma in the liver cells is the consequence of this hepatitis. In this study, the frequency of HCV genotypes in patients referring to medical diagnostic laboratories in Rasht was studied. **Materials and Methods:** The blood plasma of patients with anti-HCV positive patients was extracted genomic RNA and amplified by region-wide RT-PCR, in length 234 bp the 5UTR gen region and in order to genotyping , it determines the Sequencing and genotype of the virus was determined by sequencing analysis using Blast software. **Results:** Of the 225 plasma samples studied, 142 samples were negative during the molecular study of hepatitis C virus (63.2%) and 83 samples (36.8%) were positive. Of the 83 positive samples, 29 genotype a1 (34.94%), 5 genotype 1b (6.33%), 3 samples of genotype 1c (62.2%), 44 samples of genotype a3 (53.01%), 2 samples of genotype a3 and a1 were combined (2.4%). The results of this study indicate that genotype a3 is the most common genotype of hepatitis C virus in Guilan.

Keywords : Keywords: Hepatitis C Virus, Molecular Identification, Genotyping

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