

The prevalence of hepatitis C virus genotypes in Mazandaran province, Iran Parisa Ebrahimzadeh¹, Mohammadreza Haghshenas*², Farhang Babamahmoodi³

¹MSc Student of Microbiology, Faculty of Medicine, Mazandaran University of Medical Sciences, Sari, Iran

² Corresponding Author: Associated Professor of Virology (PhD), Molecular and Cell Biology Research Center, Faculty of Medicine, Mazandaran University of Medical Sciences, Sari, Iran. haghshenas2001@yahoo.com

³Professor of Infectious Disease, Faculty of Medicine, Mazandaran University of Medical Sciences, Sari, Iran

Abstract

Background: Hepatitis C virus (HCV) infection is a major public health concern and the third most common cause of death from cancer, worldwide. This infection is the most common risk factor for the progression of chronic liver disease, chronic hepatitis, cirrhosis, and hepatocellular carcinoma. HCV infection has been classified into six major genotypes and multiple subtypes. The distribution of HCV genotypes seems to vary in different areas around the world.

Objectives: With this background in mind, in this study, we performed HCV-RNA positive testing and genotyping in anti-HCV-positive patients via polymerase chain reaction (PCR) and compared of this test with ELISA in Mazandaran province during 2015-2016.

Materials and Methods: A total of 157 patients with anti-HCV-positive specimens were enrolled in this study during 2015-2016. HCV-RNA was extracted from the plasma samples, using PureLink Viral RNA Mini Kit (Invitrogen). Detection of HCV nucleic acids were performed by using the plasma samples from anti-HCV positive specimens.

The genotypes of the HCV genome were determined by PCR, using the RNA-PCR kit (CinnaGen), Taq-DNA polymerase enzyme, and individual primers, according to the specified protocol. Also, the PCR products (RNA fragments) from the samples were run on 1.5% agarose gel and visualized on a UV analyzer. All the samples were examined at the virology laboratory of Mazandaran University of Medical Sciences, Sari, Iran.

Results: The mean age of the patients was 39±14.3 years (range: 20-68 years). In total, 110 (70.06%) and 47 (29.94%) anti-HCV-positive patients were male and female, respectively. HCV-RNA was detected in 84 (53.50%) out of 157 patients with positive HCV antibodies. Based on the findings, the majority of HCV-RNA-positive patients were intravenous drug users (46.43%). In this study, the 3a HCV genotype was predominant (59.52%), followed by the 1a/b genotype (40.48%).

Conclusion: The present findings indicate that the 3a genotype is the most frequent HCV genotype, followed by 1a/b in the study region. The prevalence and incidence of HCV genotypes seem to vary in different areas, with each genotype showing a different response to interferon therapy. Therefore, it is essential to determine the predominant subtypes of HCV.

Keywords: Hepatitis C virus, Genotyping, PCR