

Molecular assay and genotyping of hepatitis C virus among infected Egyptian and Saudi Arabian patients

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Hepatitis C virus (HCV) infection is a major health problem recognized globally. HCV is a common cause of liver fibrosis that may lead to liver cirrhosis or hepatocellular carcinoma. The aim of this study was to estimate the prevalence of HCV infection and genotyping among Egyptian and Saudi Arabian chronic patients using different molecular techniques. HCV RNA viral load was assessed by real-time polymerase chain reaction (RT-PCR) technology. For HCV genotyping, RT-PCR hybridization fluorescence-based method and reverse hybridization line probe assay (INNO-LiPA) were used. A total of 40 anti-HCV-positive patients with chronic hepatitis C were examined for HCV RNA, genotyping and different laboratory investigations. In the present study, HCV genotypes 4, mixed 4.1b and 1 were detected in patients of both countries, while genotype 2 was only detected in Saudi Arabian patients. Genotyping methods for HCV showed no difference in the classification at the genotype level. With regard to HCV subtypes, INNO-LiPA assay was a reliable test in HCV genotyping for the detection of major genotypes and subtypes while RT-PCR-based assay was a good test at the genotype level only. HCV genotype 4 was found to be the predominant genotype among Egyptian and Saudi Arabian chronic patients. In conclusion, data analysis for detecting and genotyping HCV was an important factor for understanding the epidemiology and treatment strategies of HCV among Egyptian and Saudi Arabian chronic patients.

Biography

Mohammad Rashad Mahmoud has completed his Master's degree from Alexandria University and PhD from Al-Azhar University, Egypt. He is currently a Lecturer of Microbiology in Medical Basic Science, Faculty of Dentistry, Majmaah University, KSA.

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