Genotype 3 is the predominant hepatitis C genotype in a multi-ethnic Asian population in Malaysia

Shiaw-Hooi Ho, Kee-Peng Ng, Harvinder Kaur and Khean-Lee Goh

Kuala Lumpur, Malaysia

BACKGROUND: Genotypes of hepatitis C virus (HCV) are distributed differently across the world. There is a paucity of such data in a multi-ethnic Asian population like Malaysia. The objectives of this study were to determine the distribution of HCV genotypes between major ethnic groups and to ascertain their association with basic demographic variables like age and gender.

METHODS: This was a cross-sectional prospective study conducted from September 2007 to September 2013. Consecutive patients who were detected to have anti-HCV antibodies in the University of Malaya Medical Centre were included and tested for the presence of HCV RNA using Roche Cobas Amplicor Analyzer and HCV genotype using Roche single Linear Array HCV Genotyping strip.

RESULTS: Five hundred and ninety-six subjects were found to have positive anti-HCV antibodies during this period of time. However, only 396 (66.4%) were HCV RNA positive and included in the final analysis. Our results showed that HCV genotype 3 was the predominant genotype with overall frequency of 61.9% followed by genotypes 1 (35.9%), 2 (1.8%) and 6 (0.5%). There was a slightly higher prevalence of HCV genotype 3 among the Malays when compared to the Chinese ($P=0.043$). No other statistical significant differences were observed in the distribution of HCV genotypes among the major ethnic groups. There was also no association between the predominant genotypes and basic demographic variables.

CONCLUSIONS: In a multi-ethnic Asian society in Malaysia, genotype 3 is the predominant genotype among all the major ethnic groups with genotype 1 as the second commonest genotype. Both genotypes 2 and 6 are uncommon. Neither genotype 4 nor 5 was detected. There is no identification of HCV genotype according to ethnic origin, age and gender.

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KEY WORDS: Asian; genotype; hepatitis C; Malaysia; multi-ethnic

Introduction

Hepatitis C infection is a global disease. The pathogen, hepatitis C virus (HCV), with its vast genetic diversity, shows distinct genotypic distribution according to geographical region. About 60%-80% of acute HCV infections fail to resolve leading to chronic hepatitis, frequently progressing to cirrhosis and hepatocellular carcinoma (HCC).[1] It has been estimated that 20% of patients with chronic hepatitis C progress to cirrhosis within 10 to 20 years and in this group of cirrhotic patients, 1% to 4% develop HCC per year.[1,2] In our local setting, Qua and Goh reported that up to 18.5% of patients with cirrhosis were attributable to chronic hepatitis C.[3] In Western countries and Japan, hepatitis C is known as the most common cause of cirrhosis and liver cancer.[4,5] So, being a common cause of chronic liver disease worldwide, it is not surprising that HCV infection accounts for most of patients with HCC and liver transplantation.

Fortunately, hepatitis C infection can be effectively treated with pegylated interferon and oral ribavirin combination which was first approved for use by FDA in 2001. However, its efficacy varies considerably between different genotypes of the virus, which is now considered the strongest predictive factor for sustained viral response (SVR) after treatment.[7-9] Other important predictive factors are host factors such as IL28B allele, liver...