

Basic Health Sciences

Poster

Abstract ID: 29

Distribution of Hepatitis C virus genotypes among chronic Hepatitis C patients in Kuantan Pahang

Siti Nurul Fazlin Abdul Rahman^a | Hairul Aini Hamzah^a | Mohamed Hadzri Hasmoni^b | Mohammed Imad Mustafa^a

^a*Department of Basic Medical Sciences, Kulliyah of Medicine, International Islamic University Malaysia*

^b*Department of Internal Medicine, Kulliyah of Medicine, International Islamic University Malaysia*

Introduction: Hepatitis C virus (HCV) has been classified into seven genotypes with more than 80 subtypes isolated worldwide. HCV genotypes are an important parameter in determining the right antiviral dosage, duration and monitoring the response of that treatment. The main aim of this study was to determine the distribution of HCV genotypes, their association with demographic variables and to investigate the presence of uncommon mixed-genotype infection case. **Methods:** This cross sectional study was performed in Hospital Tengku Ampuan Afzan, Kuantan, Pahang from January to July 2014. The sera samples from 40 HCV seropositive patients were analyzed using reverse-transcription PCR (RT-PCR) and direct DNA sequencing assays. **Results:** More than half of study patients were from male patients (32/40; 80%), below the age of 45 (27/40; 67.5%) and Malays (34/40; 77.5%). Thirty one out 40 (77.5%) samples were successfully sequenced for genotyping with genotype 3 (24/31; 77.4%) predominate the study, followed by genotype 1 (6/31; 19.3%). There is no significant association established between the demographic factors and HCV genotypes. Majority of the HCV RNA positive samples were identified as mono genotype HCV infection. There was one isolate with mixed-genotype infection. **Conclusions:** The findings of the study showed that genotype 3 and 1 are still the commonest genotypes found among the study population. No association can be established from HCV genotypes and basic demographic factors. The finding of mixed HCV genotype infection from this study requires further investigation to evaluate the clinical role of this type of infection in treatment outcome.

KEYWORDS: Hepatitis C, HCV, genotyping, RT-PCR, direct sequencing