

Poster

MM 24

**HEPATITIS C VIRUS INFECTION AMONG PATIENTS AT HOSPITAL TENGKU  
AMPUAN AFZAN, KUANTAN: GENOTYPES DISTRIBUTION, RNA SEQUENCE  
VARIATION, RISK FACTORS AND CO-MORBIDITIES**

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Hepatitis C virus (HCV) genotyping is very important for the clinical management of HCV-infected patients. HCV strains demonstrate a high degree of genetic heterogeneity. The 5' un-translated region (5'UTR) of HCV is the most highly conserved region of the virus genome, making this region ideal target for HCV RNA amplification-based detection assays. An additional target to determine the genotypes of HCV is the non-structural (NS) 5B region of the viral genome. The aim of this study was to determine HCV genotypes and identify sequence variations in common genotypes as well as their association with certain factors. Nucleotide sequence analysis of 5'UTR and NS5B region were performed to identify viral genotypes of 40 HCV infected patients attending Gastroenterology Clinic, HTAA Kuantan Pahang. Of the 40 samples, 39 (97.5%) tested positive for HCV RNA. RNA-positive isolates were subjected to direct sequencing and the results were compared with reference sequences from NCBI homepage. Based on the analysis of both of the above regions, 31 (77.5%) isolates were successfully classified into their genotypes and subtypes; 3a (57.5%), 1a (12.5%), 3b (2.5%) and 1b (2.5%). No genotype 2, 4, 5 and 6 were found in this study. However, there was one mixed-genotype (3a/1a) HCV infection. Sequence variations were analysed in both regions, NS5B region demonstrated greater genetic variability in its sequence than 5'UTR. No significant association was found between HCV genotypes with patient's demographic data, risk factors, alcohol consumption and co-infection with HBV or HIV. In conclusion, the use of the 5'UTR and NS5B-based assays proved to be a sensitive and reliable method for HCV RNA detection and genotyping. Genotype 3 followed by genotype 1 were the common HCV genotypes found in this study population. The base sequences of both genotypes varied at certain locations in both the 5'UTR and NS5B regions however NS5B region sequences displayed higher heterogeneity. Furthermore, no risk factors and co-morbidities were linked to HCV genotypes.