Objectives: Hepatitis C virus (HCV) genotyping is important for treatment and epidemiological purposes. The objective was to determine HCV genotype and their associations with certain risk factors at University Kebangsaan Malaysia Medical Centre (UKMMC). Methods: A total of 89 samples were collected from December 2009 to January 2011. Demographic data of patients were collected from medical record. Reverse Transcriptase Polymerase chain reaction (RT PCR) was performed and sixty-four samples yielded positive for HCV. Sequencing was performed and analyzed based on sequence information in GenBank. Statistical analysis were done using SPSS version 15. Results: HCV genotype 3 (73%) was the most frequent genotype, followed by genotype 1(27%). The distribution of HCV genotype/subtype was as follows: 3a (64.8%), 1a (13.5%), 1 (10.8%), 3 (8.1%) and 1b (2.7%). Conclusions: HCV subtypes 3a, 1a, and 1b were identified in patients at UKMMC, Malaysia with subtype 3a being the most prevalent. No significant association was found between HCV genotypes and patients' demographic data.

Subject: RT-PCR; HCV Genotype; HCV Subtype; Phylogenetic Analysis; Risk Factors

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