Seroprevalence Study of HCV Genotypes in Two Tertiary Hospitals and its Association with Risk Factors and Current Management Practice

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BACKGROUND
The distribution of hepatitis C virus (HCV) genotypes is well documented in many countries. However, reliable data are still lacking with respect to the frequency of the different HCV genotypes in Malaysia. This study aim to identify HCV genotypes and associated risk factors in a group of HCV infected patients from two tertiary hospitals.

MATERIALS AND METHODS
This is a seroprevalence study of HCV genotypes amongst infected patients in Hospital Tengku Ampuan Afzan, Kuantan, Pahang and Hospital Sultanah Nur Zahirah, Kuala Terengganu, Terengganu. Patients were screened using ELISA by detecting the anti-HCV in the sera. All negative first-round PCR products were re-tested by nested PCR. The base sequence of the PCR products was determined using the same primers as for the RT-PCR. By comparing the obtained nucleotide sequence data with sequences of known genotypes from the NCBI homepage, we deduced that our local isolates could be assigned to genotypes 1, 3, 4 and 6. We correlated the mode of transmission, basic demographic characteristics and current treatment strategy with the predominance of different genotypes.

RESULTS
Out of 171 patients diagnosed positive for anti-HCV by ELISA, 65 patients agreed for HCV genotypes evaluation. 32.3% (n=21) were of genotype 1, 58.5% (n=38) genotype 3, 6.1% (n=4) genotype 4 and 3.1% (n=2) genotype 6. There was no statistically significant difference between the risk factors analyzed and the acquisition of HCV infection. We also found out that only 53.8% (n=35) of these patients were treated and 27.8% (n=18) had liver biopsy. Interestingly we noted that out of four patients with genotype 4, one of them was an Egyptian and another two had exposure to risk factors on their travel to the Middle East countries.

CONCLUSION
Genotype 3 and 1 were the most prevalent genotypes (58.5% and 32.3% respectively) followed by genotype 1 and 6. Our study results are consistent with an unpublished data from the Malaysian Society of Gastroenterology and Hepatology [Genotype 3 (56%), genotype 1(39%)].