Genotype diversity of hepatitis C virus (HCV) in HCV-associated liver disease patients in Indonesia

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Abstract
Background: Hepatitis C virus (HCV) genotype distribution in Indonesia has been reported. However, the identification of HCV genotype was based on 5'-UTR or NS5B sequence.

Aims: This study was aimed to observe HCV core sequence variation among HCV-associated liver disease patients in Jakarta, and to analyse the HCV genotype diversity based on the core sequence.

Methods: Sixty-eight chronic hepatitis (CH) and 48 liver cirrhosis (LC) and 34 hepatocellular carcinoma (HCC) patients were included in this study. HCV core variation was analysed by direct sequencing.

Results: Alignment of HCV core sequences demonstrated that the core sequence was relatively varied among the genotype. Indeed, 237 bases of the core sequence could classify the HCV subtype; however, 236 bases failed to differentiate several subtypes. Based on 237 bases of the core sequences, the HCV strains were classified into genotypes 1 (subtypes 1a, 1b and 1c), 2 (subtypes 2a, 2e and 2f) and 3 (subtypes 3a and 3k). HCV 1b (47.3%) was the most prevalent, followed by subtypes 1c (18.7%), 3k (10.7%), 2a (10.0%), 1a (6.7%), 2e (5.3%), 2f (0.7%) and 3a (0.7%).

Conclusion: Hepatitis C virus core sequence (237 bases) could identify the HCV subtype and the prevalence of HCV subtype based on core sequence was similar to those based on the NS5B region.