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PHYLOGENETIC ANALYSES OF HEPATITIS B VIRUS ISOLATED IN PEKANBARU, INDONESIA

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ABSTRACT

Background: Hepatitis B virus (HBV) infection is the main cause of hepatocellular carcinoma in Asia. HBV genotypes and subtypes have a distinct geographic and ethnic distribution. Additionally, HBV genotypes may influence the clinical manifestation of chronic hepatitis B infection, development of HCC and treatment outcome.

Objective: This study aimed to determine the HBV genotypes and subtypes among chronic hepatitis B-infected patients in Pekanbaru city, Indonesia.

Methods: HBV DNA was amplified and sequenced from 30 HBV chronically infected subjects. Phylogenetic analysis was performed on partial nucleotide sequences of HBV S gene fragment. Phylogenetic tree was constructed using Neighbor-Joining (NJ) method with software program of Mega version 4.1. HBV subtypes was determined based of amino acid sequences at position 122 and 160.

Results: This study included 7 asymptomatic carriers, 9 patients with liver cirrhosis and 14 with hepatoma. Of the 30 HBV DNA analyzed, 19 (63,7 %) were classified as HBV genotype C and 11 (37,3 %) belonged to genotype B. Patients with liver cirrhosis and hepatoma were more frequently infected with HBV genotype C than genotype B. Moreover, phylogenetic analyses revealed that all HBV genotype Bs were clustered with subgenotype B3, whereas genotype Cs were predominantly grouped with subgenotype C1 (63.2 %). While C1 was the most common HBV subgenotype in hepatoma patients, subgenotype B3 and C1 predominated in patients with liver cirrhosis. The majority of isolates belonged to serological subtype adr (63.3 %) followed by subtype adw (36.7 %).

Conclusion: These findings suggest that infection with HBV genotype C resulted into more severe forms of chronic hepatitis B infection, including liver cirrhosis and hepatoma.

Reference: Arfianti, E., Djojogugito, F.A., Endriani, R., Zainal, A., & Bird, S.P. (2018, January 23-24). Phylogenetic analyses of hepatitis B virus isolated in Pekanbaru, Indonesia. Paper presented at the APDP International Conference on Research for Impact: Advancing Australian and Indonesian Research Collaboration, Jakarta, Indonesia.

