

Association of core promoter mutations of hepatitis B virus and viral load is different in HBeAg(+) and HBeAg(-) patients

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Abstract

AIM: To identify the prevalence of hepatitis B e antigen (HBeAg) and to assess the association of hepatitis B virus (HBV) core promoter mutations and viral load in Indonesian patients.

METHODS: Sixty-four patients with chronic hepatitis, 65 with liver cirrhosis and 50 with hepatocellular carcinoma were included in this study. HBeAg and hepatitis B e antibody (HBeAb) tests were performed using enzyme-linked immunosorbent assay and the mutations were analyzed by sequencing. Viral load was measured by real-time polymerase chain reaction.

RESULTS: Of 179 patients, 108 (60.3%) were HBeAg(-) and 86 (79.6%) of these HBeAg(-) patients had been seroconverted. The A1896 mutation was not found in HBeAg(+) patients, however, this mutation was detected in 70.7% of HBeAg(-) patients. This mutation was frequently found when HBeAg was not expressed (87.7%), compared to that found in HBeAg seroconverted patients (65.1%). The A1899 mutation was also more prevalent in HBeAg(-) than in HBeAg(+) patients ($P = 0.004$). The T1762/A1764 mutation was frequently found in both HBeAg(+) and HBeAg(-) patients, however, the prevalence of this mutation did not significantly differ among the two groups ($P = 0.054$). In HBeAg(+) patients, the T1762/A1764 mutation was correlated with lower HBV DNA ($P < 0.001$). The A1899 mutation did not correlate with HBV DNA ($P = 0.609$). In HBeAg(-) patients, the T1762/A1764 mutation alone was not correlated with HBV DNA ($P = 0.095$), however, the presence of either the T1762/A1764 or A1896 mutations was associated with increased HBV DNA ($P < 0.001$).

CONCLUSION: The percentage of HBeAg(-) patients is high in Indonesia, and most of the HBeAg(-) patients