

## **Genetic diversity of hepatitis B co-infection with hepatitis C, D and E viruses among Malaysian chronic hepatitis B patients**

### **ABSTRACT**

Background: Hepatitis B virus co-infection with other strains of viral hepatitis is associated with increased risk of liver cirrhosis and hepatic decompensation. Objectives: This is a prevalence study that assessed the genetic diversity of chronic hepatitis B patients and coinfection. Methods: Chronic hepatitis B patients enrolled in this study were tested for antibodies of other hepatitis viruses using ELISA kits. Patient clinical profiles were collected and partial genes of HBV, HCV, and HEV were amplified, sequenced, and analyzed using phylogenetic analysis. The associations between variables were determined using the chi-squared test. Results: Of the 82 patients recruited for this study, 53.7% were non-cirrhotic, 22.0% cirrhotic, 20.7% acute flare and 3.7% hepatocellular carcinoma. Majority (58%) of patients had a high level of ALT ( $\geq 34$  U/L). Sequence analysis showed HBV (63.9%) belonged to genotype B, HEV belonged to genotype 4 while HCV belonged to genotype 3a and the genotypes were found to be significantly associated with the clinical stage of the patients ( $\chi^2=56.632$ ;  $p<0.01$ ). Similarly, Hepatitis B e antigen was also found to be significantly associated with the clinical stage of infection ( $\chi^2=51.952$ ;  $p<0.01$ ). Conclusion: This study revealed that genetic diversity was found to have a significant impact on the severity of infection.

**Keyword:** Hepatitis co-infection; Hepatitis genetic diversity; Malaysia

