

## **Naturally occurring hepatitis B virus surface antigen mutant variants in Malaysian blood donors and vaccines**

### **ABSTRACT**

Hepatitis B virus surface mutants are of enormous importance because they are capable of escaping detection by serology and can infect both vaccinated and unvaccinated populations, thus putting the whole population at risk. This study aimed to detect and characterise hepatitis B-escaped mutants among blood donors and vaccinees. One thousand serum samples were collected for this study from blood donors and vaccinees. Hepatitis B surface antigen, antibodies and core antibodies were tested using a commercial enzyme-linked immunosorbent assay (ELISA) kit. DNA detection was performed via nested polymerase chain reaction (PCR), and the S gene was sequenced and analysed using bioinformatics. Of the 1,000 samples that were screened, 5.5 % (55/1,000) were found to be HBsAg-negative and anti-HBc- and HBV DNA-positive. All 55 isolates were found to belong to genotype B. Several mutations were found across all the sequences from synonymous and non-synonymous mutations, with the most nucleotide mutations occurring at position 342, where adenine was replaced by guanine, and cytosine at position 46 was replaced by adenine in 96.4 % and 98 % of the isolates, respectively. Mutation at position 16 of the amino acid sequence was found to be common to all the Malaysian isolates, with 85.7 % of the mutations occurring outside the major hydrophilic region. This study revealed a prevalence of 5.5 % for hepatitis B-escaped mutations among blood donors and vaccinated undergraduates, with the most common mutation being found at position 16, where glutamine was substituted with lysine.