ABSTRACT

ANALYSIS SINGLE NUCLEOTIDE POLYMORPHISM OF HOST GENOME (TNF-α, TGF-β1, P53), HEPATITIS B VIRUS (HBV) X GENE MUTATION AND VIRAL LOAD ON CHRONIC LIVER DISEASE WITH HBV INFECTION IN SURABAYA, INDONESIA

Backgrounds. The progression of Hepatitis B Virus (HBV)-related Chronic Liver Disease (CLD) is related to high mortality in developing countries, including Indonesia. Pathogenesis of HBV infection is influenced by viral and host factors.

Aims. This study was aimed to determine potential associations of host nucleotide polymorphisms (TNF-α, TGF-β1, p53), HBV X gene mutation, and HBV viral load in patients with HBV-related CLD in Surabaya, Indonesia.

Methods. Sera were collected from 87 CLD patients with HBV infection. TNF-α, TGF-β1, p53 SNPs were genotyped by PCR-RFLP. HBV X gene was sequenced and compared to the reference strains to determine its mutations. Viral load was measured using Real-Time PCR.

Results. In Indonesian patients, no association was found between TNF-α, TGF-β1, p53 polymorphisms with CLD and X gene mutation. A total of 23% (20/87) samples had HBV X gene mutations with 10 types of substitutions, 1 deletion, and 1 insertion. There was a significant difference between the K130M+V131I mutations and the progression of CLD ($p < 0.05$). Significant differences in viral load levels were found in HBV-infected patients who had X gene mutations in general and K130M+V131I mutation ($p < 0.05$).

Conclusions. The presence of K130M+V131I mutations may serve as predictive factors for the progression of HBV-related liver diseases in Indonesia and other countries.

Keywords: Chronic Liver Disease, Hepatitis B Virus, Single Nucleotide Polymorphism, X Gene Mutation