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Association of the IFNAR1-17470 and IL-10-592 cytokine variants with susceptibility to chronic hepatitis B viral infections in a Chinese population

Y. Xiang[1], S.F. Huang[1], J.R. Xia[1], D.Q. Ye[1], P. Chen[1], S.S. Yang[1], S. Sun[1], X.F. Lai[1] and L.P. Zhang[1,2]

[1]Department of Laboratory Medicine,
The First Affiliated Hospital of Chongqing Medical University,
Yuzhong District, Chongqing, China
[2]Department of Clinical Laboratory,
The First Affiliated Hospital of Chongqing Medical University,
Yuzhong District, Chongqing, China

Corresponding author: L.P. Zhang
E-mail: lipingzhang723@163.com

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ABSTRACT. An association between the sequence variants of cytokine genes and various clinical outcomes in subjects infected with the hepatitis B virus (HBV) has been demonstrated. However, the results are inconsistent and inconclusive. Further studies in other populations and the evaluation of a greater number of individuals may contribute to a better understanding of the influence of the cytokine genetic variants on the evolution of HBV infections. This study was performed to explore the relationships between the sequence variants of *TNF-A*-308, *IFNAR1*-17470, and *IL-10*-592 and the susceptibility to chronic hepatitis B (CHB) in a Chinese population. A total of 160 patients with CHB and 124 individuals who had spontaneously

recovered (SR) from hepatitis B were enrolled in the present study. The variants at *TNF-A*-308, *IFNAR1*-17470, and *IL-10*-592 were determined by PCR-restriction fragment length polymorphism analysis and were confirmed by bidirectional DNA sequencing. Significant differences were found between the CHB and the SR groups in the frequency and distribution of the genotypes of both *IFNAR1*-17470 and *IL-10*-592 genes. In comparison with the CHB patients with the *IFNAR1*-17470 G/G variant, the odds ratio (OR) of the CHB patients with the *IFNAR1*-17470 C/C variant developing chronic hepatitis was 2.06 (95%CI = 1.03-4.14). In addition, the OR of the patients with CHB having the IL-10-592 C/C variant developing chronic hepatitis was 2.77 (95%CI = 1.13-4.57) when compared with that of the patients with the *IL-10*-592 A/A variant. In conclusion, sequence variants of both the *IFNAR1*-17470 and *IL-10*-592 genes were correlated with susceptibility to CHB.

Key words: Hepatitis B virus; Chronic hepatitis B; Sequence variants; IFNAR1-17470; IL-10-592

