Sirinadda Romporn 2014: The Role of Class II cytokine receptor Family in Disease Susceptibility and Progression of Chronic Hepatitis B Virus Infection in Thai Population. Master of Science (Microbiology), Major Field: Microbiology, Department of Microbiology. Thesis Advisor: Assistant Professor Ingorn Kimkong, Ph.D. 72 pages.

The hepatitis B virus infection is a major cause of acute liver diseaseand chronic hepatitis. More than 2000 million people around the world who have a history of infection or hepatitis B virus infection, approximately 90% of those infected with the disease cured. The other 10% cannot eliminate the virus and have developed a chronic hepatitis B. The majority of the population is in Asia and Africa. For Thailand is one country in Asia - Pacific is still an epidemic of hepatitis B. The causes of disease from several factors, including viral, environmental and genetic factors. Studies in family education China, Taiwan and the epidemiology of chronic hepatitis B in the community who are of different races have been suggested that genetic factor is important in the pathogenesis of chronic hepatitis B virus.Therefore, we investigated the effects of two functional polymorphisms, type I interferon receptor 2 gene (IFNAR2)-F8S and interleukin-10 receptor subunit beta gene (IL10RB)-K47E, on chronic hepatitis B virus (HBV) infection. We included 227 Thai patients with chronic HBV infection [100 with hepatocellular carcinoma (HCC) and 127 non- HCC], 170 individuals with self-limited HBV infection and 150 healthy controls. Polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) method was used to analyze these two single nucleotide polymorphisms (SNPs). In this study, the C allele of IFNAR2-F8S was found to be significantly increased in chronic HBV patients when compared with healthy controls [odds ratio, OR (95% confidence interval, CI) = 3.31 (2.11-5.21), $P = 6.214 \times 10^{-9}$ and corrected P-value, $P_c = 1.864 \times 10^{-8}$]. The effect of this allele was similar to that of an autosomal dominant gene in the presence of CC and CT genotype, when compared to TT with an OR of 4.02 ($P = 4.631 \times 10^{-9}$ and $P_c = 1.389 \times 10^{-8}$). Furthermore, AA genotype of IL10RB-K47E was found to be significantly decreased in chronic HBV patients compared with individuals with self-limited HBV infection ($P = 0.006$, $P_c = 0.018$ and OR = 0.45). For haplotype analysis, we found CA and CG haplotypes were associated with susceptibility to chronic HBV ($P = 0.014$, OR = 6.84 and $P = 0.002$, OR = 3.75, respectively) when compared with healthy individuals. This study suggests that IFNAR2-F8S polymorphisms might be involved in the susceptibility to chronic HBV infection. Moreover, AA genotype of IL10RB-K47E may provide a protective effect in this disease. However, an association study using a larger sample size should be performed to confirm these findings.

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