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The Influence of IL-10 Gene Polymorphisms on the Susceptibility to Hepatitis B Virus Infection: a Meta-Analysis

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Abstract:

Background and Objective: Interleukin 10 (IL-10) is a cytokine with anti-inflammatory functions. The results of the different studies vary in the roles of the IL-10 SNPs in the susceptibility to the hepatitis B virus infection. In particular, the -1082A/G, -819 C/T and -592 A/C polymorphisms have most often been implicated. We have performed a meta-analysis including 31 case-control studies to summarize the data on the association between IL-10 SNPs and susceptibility to HBV infection. This study aimed at evaluating the relationship between polymorphisms in the IL-10 promoter region and HBV infection.

Search Method: All the relevant studies in NCBI PubMed, EMBASE, Medline and Web of Science were searched and poor qualified studies were excluded. Thirty one studies were included. Data are presented as the odds ratio (OR) with a 95% confidence interval (CI). Investigation of heterogeneity among individual studies and the publication bias were also evaluated.

Findings: This study revealed a significant association between the IL-10-819 C/T polymorphism and HBV infection susceptibility in the Asian population. Our results indicated that the presence of the IL-10 -819 C allele significantly increased the risk for persistent HBV infection. In our meta-analysis, sensitivity analysis showed that the combined result was not associated with the worldwide population. In contrast, the IL-10 -1082A/G and -592A/C polymorphisms were not associated with an increased susceptibility to HBV infection.

Conclusion: Our meta-analysis supports the growing body of evidence that the presence of the IL-10-819 C/T SNP is associated with persistent HBV infection in Asians. In addition, IL-10-819 C/T polymorphism might be a risk factor for HBV in Asians but not in Europeans.

Keywords: interleukin-10, polymorphism, hepatitis B virus, meta-analysis

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