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The relationship between tumour necrosis factor-a gene polymorphism and susceptibility hepatitis B virus infection in an Iranian population

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Abstract

Background and aim: The host genetic background regulates the natural history of chronic HBV infection. The aim of this study was to investigate the association between TNF-a gene polymorphism in the promoter region with susceptibility to chronic hepatitis B virus infection.

Methods: Four polymorphisms of TNF-a gene, -238 A/G, -308 A/G, -857C/T and -863 A/C were analyzed by RT-PCR using 100 chronic HBV infected patients, 40 spontaneously recovered HBVsubjects and 100 healthy controls. All participants were unrelated Iranians.

Results: The study showed that the existence of -308 G, -857C and -863 A alleles significantly increased risk of chronic HBV infection**.** In addition, GGCA haplotype had a higher frequency in HBV patients than C and SR groups and might relate to the natural history of the infection. Chronic HBV patients with -308GG, -857CC and -863AA genotypes had higher levels of TNF-a compared to the other genotypes.

Conclusions: The results indicate that there is a positive association between susceptibility to chronic HBV infection and TNF-a polymorphism.

Keywords: Tumor necrosis factor-a, Chronic hepatitis B virus**,** Polymorphism**.**