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Abstract (poster session)

Evaluation of interleukin-10 gene promoter polymorphisms and hepatitis B virus infection outcome

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Objectives: Single nucleotide polymorphisms (SNP) in the promoter region of the interleukin (IL)-10 gene has been reported to have a role in determining of hepatitis B virus (HBV) infection outcome. The present study was undertaken to evaluate the association between HBV infection and SNP in the promoter region of the IL-10 gene in a central Iranian city. **Methods:** A total of 127 cases including 32 patients with chronic hepatitis B infection and 34 healthy carriers collapsed as persistent group, 30 subjects who had spontaneously recovered from HBV infection and 31 healthy controls were enrolled in this study. The three biallelic (-819,-592,-1082) polymorphisms in the IL-10 gene promoter were analyzed by polymerase chain reaction and direct sequencing. **Results:** No significant difference was found in frequencies of genotypes and haplotypes of IL-10 gene promoter region at position -1082, -819 and -592 among controls, individuals spontaneously recovering from HBV infection, carriers and patients with chronic hepatitis B infection. However, frequencies of A/A genotype at position -592 and T/T genotype at position -819 were higher in the HBV clearance group, while frequency of G/G genotype at position -1082 was higher in persistence group. GCC/GCC and GCC/ACC haplotypes were significantly more frequent in anti-HBe positive patients. **Conclusion:** It seems that genetic polymorphisms of IL-10 promoter region are not associated with HBV infection outcome. However, patients with high and intermediate producer haplotypes of IL-10 had more ability to produce anti-HBe than those with low producer haplotypes.