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CCR5, MCP-1 and VDR Gene Polymorphisms are Associated with the Outcome of Hepatitis B Virus Infection

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Abstract

Background and aim: Genetic variants of chemokine and regulatory cytokines play functional roles in chronic HBV infection. The objective of the study, was to evaluate the association between the CCR5D32, CCR5-2459A/G, MCP1-2518A/G, VDR-APa1A/a, VDR-Taq1T/t SNPs and HBV susceptibility, in a sample of Iranian.

Methods: The CCR5D32, CCR5-2459A/G, MCP1-2518A/G, VDR-APa1A/a, VDR-Taq1T/t polymorphisms were analyzed by polymerase chain reaction and 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 CCR5-2459A, MCP1-2518G and VDR-at alleles significantly increased risk of chronic HBV infection**.** In addition, WtAGat haplotype had a higher frequency in HBV patients than C and SR groups and might relate to the natural history of the infection. Statistical analysis indicated positive correlations between CCR5-2459A/G, MCP1-2518A/G, VDR-APa1A/a, VDR-Taq1T/t genotypes and serum levels of the CCR5, MCP-1 and VDR in HBV patients.

Conclusions: according to the statistical analysis, significant associations with susceptibility to chronic HBV infection was observed with CCR5-2459A/G, MCP1-2518A/G, VDR-APa1A/a, VDR-Taq1T/t polymorphisms. In addition, no association of CCR5D32 SNP with disease was found.

Keywords: Chemokine; HBV; Single nucleotide polymorphism.