Original Paper

Prevalence of IL18 -607A/C polymorphism in patients with visceral leishmaniasis

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Abstract

Background and Objective: Visceral leishmaniasis (VL) is a parasitic disease caused by a protozoan of Leishmania genus and in Iran by Leishmania infantum. The protective immune response against VL is cellular immunity through Th1 CD4+, which dominant chemokiens are IL12, IFN- γ and IL18 and lead to Th1 response. Single nucleotide polymorphism (SNP) on IL-18 gene and its relation to IL18 levels in blood and IL18 function have been studied in many inflammatory diseases such as Behcect's disease and tuberculosis. According to the important role of IL-18 in immunity against visceral leishmaniasis, this study was conducted to demonstrate the prevalence of genotypes on -607A/C in promoter region of IL-18 gene.

Materials and Methods: This descriptive and cross-sectional study was done on 91 pateints with confirmed VL, 105 healthy sero-negative controls and 78 seropositive controls during 1999-2009. Salting out method was used to extract DNA and ARMS-PCR was used to determine the genotype of -607A/C allele of individuals. Statistical analysis of genotypes was performed using Chi-Square test.

Results: According to the results, -607C/C was the dominant genotype among the groups (35.8%). Distribution of genotypes among groups had not any significant difference. The lowest genotype among healthy sero-positive and patients were -607A/C and -607A/A, respectively. Statistical analysis of distribution of genotypes, did not reveal any significant difference among groups.

Conclusion: The dominant genotypes of VL patients, healthy sero-negatives and healthy sero-positives were -607C/C (38.5%), -607A/C (37.1%) and -607C/C (35.9%) respectively.

Keywords: Visceral leishmaniasis, Interlukin-18, Polymorphism, ARMS-PCR

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