

Abstract

Multiple Sclerosis (MS) is an autoimmune demyelinating disease of the central nervous system (CNS) with an unknown etiology. The prevalence of MS in various geographical and ethnical groups is very different and Iran is located in low range of MS. Unfortunately in recent years, the rate of MS increased in Iran. Many reports proposed that in the future, Iran have many new cases of MS and will be located in moderate rate of MS. Signal transducer and activator of transcription 3 (*STAT3*) gene located on chromosome 17q21.1, codes a nuclear transcription factor and was identified as a putative new multiple sclerosis (MS) susceptibility locus in Genome wide association studies. *STAT3* codes for a transcription factor that is involved in multiple pathways and functions, including the Jak-STAT pathway, neuron axonal guidance, apoptosis, activation of immune responses, and Th17 cell differentiation. In this study we tried to find the association of rs744166 SNP polymorphisms in *STAT3* gene with MS susceptibility in eastern parts of Iran. A case-control study was handled with 204 MS patients and 202 age and gender matched controls using PCR-RFLP strategy for (rs744166) SNP of *STAT3* gene. Statistical analysis was done using SPSS 19 for Windows (SPSS Inc., Chicago, IL). Genotypic and allelic frequencies were compared between patients and controls using the Chi-Square Tests. Results showed significant association between rs744166 SNP located in intron 1 of *STAT3* gene and MS disease in this study.

Key words: Multiple sclerosis, *STAT3*, Polymorphism, rs744166, SNP.



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The Thesis Submitted for the Degree of M.Sc

**Association study of rs744166 SNP in
STAT3 gene with multiple sclerosis in
East of Iran**

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September 2014