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Evaluation of SNP rs763361 on Gly307Ser gene in multiple sclerosis patients compared to healthy subjects

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Introduction: The prevalence of MS 20–60/100,000 in Iran and 73/100,000 in Isfahan. Isfahan is considered as an area with high risk of MS. The patients affected MS interface with physical, psychological, family, occupation, societal, and family problems. MS is a multifaceted gene–environment interactions. Recently, there has been increasing evidence shown that a non-synonymous exchange (Gly307Ser/rs763361) of the CD226 gene on chromosome 18q22 is linked to some autoimmune diseases such as multiple sclerosis (MS). On the other hand MS has an increasing rate in our area and we know that the genetical model of the disease would be varied in different ethnic and geographic areas, we decided to study the polymorphism of the Gly307Ser gene in Relapsing Remit- ting Multiple Sclerosis (RRMS) patients in order to identify some disease susceptibility gene variants

Materials and methods: After written consent, blood samples from 200 patients with RRMS (180 females and 20 male; mean age=31.6578.3) with clinically and MRI defined RRMS who had recruited to MS research center (Isfahan, Iran), and 200 age and sex matched healthy subjects of blood donors (160 females and 40 male; mean age=31.7477.75) with no history of neurological disorders were included in the study. DNA was extracted from whole blood using a commercially available kit (Qiagene) and stored at – 20 1C until used for genotyping. SNP analysis was performed using Highy Resolution Melt (HRM) Real Time PCR (Corbett). Differences in allele and genotype frequencies among the respective groups were evaluated by chi square calculation.

Result: According to our findings frequency of the T allele for rs763361 in case group comparing with control group showed different ($P=0.035$) and genotype frequency was CC (25%), CT (43%), TT (32%) in patient group. **Conclusion:** This Case-Control study provided evidence that rs763361 SNP is not correlated to RRMS susceptibility in studied population.