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# Analysis of Single Nucleotide Polymorphisms in HLA-DRA, IL2RA, and HMGB1 Genes in Multiple Sclerosis

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#### **Abstract**

**Background:** Multiple sclerosis (MS) is a common demyelinating neurodegenerative disorder with significant heritability. Previous studies have associated genetic variants in human leukocyte antigen (*HLA*) complex, *IL2RA*, and *HMGB1* genes with the pathophysiology of MS.

**Methods:** In order to investigate the gene association in the Iranian population, we performed a genotyping study of 36 variants in the mentioned genes using Sanger sequencing in 102 MS patients and 113 healthy controls.

**Results:** Our results identified significant associations as well as significant allele frequency differences in some of the studied single-nucleotide polymorphisms including rs4935356, rs3177928, and rs7197 from HLA-DRA gene, and rs12722489 and rs12722490 variants from IL2RA gene (p<0.05). Moreover, the strong linkage disequilibrium of two common haplotypes was estimated from the HLA-DRA gene.

**Conclusions:** This association study may suggest the role of these polymorphisms in the genetic susceptibility of MS in the Iranian population and would facilitate the recognition of causative variants in this disease.

Keywords: HMGB1, HLA-DRA, IL2RA, Multiple sclerosis, Polymorphism.

#### Introduction

Multiple sclerosis (MS) is the most common autoimmune neurologic disease which affects approximately two million new cases worldwide, especially young adults (1). Three patterns of disease are seen in MS patients: relapsing-remitting (RRMS), in which episodic exacerbations are separated by periods of recovery; secondary progressive (SPMS), people diagnosed with

RRMS eventually develop progressive disability; and primary progressive (PPMS), in which disability progresses steadily from disease onset (2). Multiple sclerosis arises when a susceptible individual encounters environmental triggers that stimulate an inflammatory response against self-antigen in the central nervous system (CNS). The immunological studies have shown that dis-

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regulation of cellular and humoral immune responses elicit infiltration of lymphocytes and macrophages into the CNS along with anti-myelin antibodies and complement activation, which leads to episodes of inflammatory demyelination and a progressive neurodegenerative process with axonal transection and neuronal loss as an early event (3). An eruption of focal inflammation is responsible for the episodic RRMS phase, while axonal loss and neurodegeneration cause progressive accumulation of disability (4, 5).

Both environmental and genetic factors are involved in the etiology of MS. Vitamin D deficiency, smoking, Ultraviolet B (UVB)/ sunshine, and some pathogens are also considered as environmental risk factors for the development of MS (6).

Genetic factors are primarily responsible for the increased frequency of the disease in the relatives of affected individuals. Studies on twins and siblings suggest that multiple genes, each exerting different effects, play considerable roles in susceptibility to MS. Therefore, MS is considered as a mutagenic and complex disorder. Candidategene studies have validated the human leukocyte antigen (*HLA*) class II (*HLA-DRB1*) as the strongest susceptibility locus for MS. In 2011, the genome-wide association studies (GWAS) and ImmunoChip studies with more than 9,000 MS cases discovered 110 non-*HLA* genetic loci associated with MS (7).

Further studies have shown that genes encoding high mobility group box protein 1 (HMGB1) and the IL-2 receptor  $\alpha$  chain (IL-2R $\alpha$ ) exert critical functions regarding immune responses in the development of neurodegenerative diseases, such as Alzheimer's disease, Parkinson's disease, and MS (8). Elevation of peripheral blood mononuclear cells (PBMC), as well as upregulated serum and cerebrospinal fluid (CSF) levels of HMGB1, have been implicated in MS patients in several studies (9, 10). Large numbers of macrophages and microglia expressing the endogenous HMGB1 and its ligands as well as Toll-like receptor 2 (TLR2) and TLR4 are also found in MS patients (11). The cytokine interleukin-2 (IL-2 has a wide range of effects that are essential for the balance between immune response and tolerance. The IL-2 receptor α chain (IL-2Rα), also known as CD25, is a central

constituent of the trimeric IL-2 receptor complex that binds to IL-2. It has been shown that singlenucleotide polymorphisms (SNPs) in or near HLA-DRA, IL2RA, and HMGB1 genes are associated with the increased risk of immune-mediated diseases including MS. The association of some SNPs in or near the mentioned genes has been studied extensively regarding increased risk of developing this disease. For instance, MSassociated IL2RA SNPs rs2104286 rs11256593 are associated with CD25 expression on CD4<sup>+</sup>T cells. Changes in CD25 expression may influence the immune and inflammation signaling cascades, thus affecting CD4<sup>+</sup>T cell differentiation and  $T_{Reg}$  cells suppressive activity (12).

The purpose of this study was to investigate the frequency of 36 SNPs in three known loci, *HLA-DRA*, *IL2RA*, and *HMGB1* in the Iranian population. A total of 102 MS patients and 112 control subjects were selected and genotyped using polymerase chain reaction (PCR) method and Sanger sequencing.

#### Materials and methods

#### Sample collection

A total of 102 MS patients and 112matched controls were selected from the individuals referred to Sina teaching Hospital in Tehran, Iran. The patients were diagnosed based on the McDonald criteria (4),clinical signs symptoms; all results were confirmed using brain magnetic resonance imaging (MRI). The control group was selected from patients who attended the hospital due to other causes and brain MRI was used to rule out MS. This group was age and sexmatched with the case group. The Ethics Committees of Sina teaching Hospital and Pasteur Institute of Iran approved the study. Written informed consent was taken from all participants.

#### DNA extraction

Five ml of peripheral blood from patients and healthy controls were collected in K3-EDTA tube and genomic DNA was extracted and purified from whole-blood lymphocytes by Mini QIAamp DNA Mini Kits (Cat. 51104; Qiagen GmbH, Hilden, Germany) according to the manufacturer's instructions. The DNA measurement and quality control were performed using spectrophotometry

observance at 260/280 and 260/230 respectively. The DNA integrity and fragmentation were investigated using 1% agarose electrophoresis.

# Polymerase chain reaction (PCR)

PCR was performed by using Step One Plus Realtime PCR system (Applied Biosystems, Foster City, USA) to detect the 36 polymorphisms. These SNPs, located in *HLA-DRA*, *IL2RA*, and *HMGB1* genes, were selected by Haploview 4.2 using genotype data from Genome Browser release #27

in the HapMap Project (http://www.hapmap.org). The chromosome location, dbSNP number, and gene annotation of selected polymorphisms are summarized in Table 1. The specific primer sequences for each gene were designed through the Primer3 online software (http://frodo.wi.mit.edu/primer3), and the primer specificity was checked out by Primer-BLAST and SNPCheck V3 tools. The physiochemical properties of primers were further evaluated using Gene Runner software. All primer sequences are shown in Table 2.

Table 1. The genomic properties of studied polymorphism of HMGB1, HLA-DRA, and IL2RA genes that were extracted from UCSC

genome browser for investigated genomic regions in this study.

Variant ID	Chr:bp	Allele	MAF	Location	Gene
rs538493533	13:30460237	A/G	0.001	3'UTR	HMGB1
rs577524260	13:30460223	C/T	0.001	3'UTR	HMGB1
rs111892138	13:30460267	T/C	0.022	3'UTR	HMGB1
rs201945336	13:30460287-8	AA/A	-	3'UTR	HMGB1
rs182881863	13:30460196	T/G	0.001	3'UTR	HMGB1
rs149637108	13:30460189-94	CTTCCT/CT	-	3'UTR	HMGB1
rs61338778	13:30460263-5	TTT/TTTT	-	3'UTR	HMGB1
rs55642413	13:30460306-7	GG/G	-	3'UTR	HMGB1
Rs9281809	32444502 & 32444503	-/AACTAACT	0.344	intron	HLA-DRA
Rs4935356	6:32444611	T/A/G	0.341 (T)	Intron	HLA-DRA
Rs3135390	6:32444618	C/A	0.131 (C)	Intron	HLA-DRA
Rs4935354	6:32444621	C/G/T	0.341 (C)	Intron	HLA-DRA
Rs3177928	6:32444658	G/A	0.120(A)	3' UTR	HLA-DRA
Rs7194	6:32444703	G/A	0.341 (G)	3' UTR	HLA-DRA
rs7195	6:32444762	A/G	0.341 (A)	3' UTR	HLA-DRA
Rs1131541	6:32444789	T/A	0.120(A)	3' UTR	HLA-DRA
Rs7196	6:32444794	A/T	0.221 (A)	3' UTR	HLA-DRA
Rs7197	6:32444803	T/C/G	0.117(T)	3' UTR	HLA-DRA
Rs1051336	6:32444815	G/A/C	0.120(A)	3' UTR	HLA-DRA
Rs111471704	6:32444889	T/C	-	3' UTR	HLA-DRA
Rs1157343109	6:32444988	T/C	-	3' UTR	HLA-DRA
Rs1041885	6:32445032	T/A	0.119(A)	3' UTR	HLA-DRA
Rs12722489	10:6060049	C/T	0.091 (T)	Intron	IL2RA
Rs917751277	10:6060048	A/G	-	Intron	IL2RA
Rs992067421	10:6060043	C/A	-	Intron	IL2RA
Rs959264277	10:6060039	A/G	-	Intron	IL2RA
Rs11597542	10:6059981	T/C	0.001(C)	Intron	IL2RA
Rs140860467	10:6059935	T/C	0.007(C)	Intron	IL2RA
Rs17149458	10:6059897	T/A	0.029(A)	Intron	IL2RA
Rs12722490	10:6059828	C/T	0.010(T)	Intron	IL2RA
Rs3118470	10:6059750	T/A/C	0.319 (C)	Intron	IL2RA
Rs78556477	10:6059635	G/A	0.059(A)	Intron	IL2RA
Rs41294925	10:6059590	A/G	0.008(G)	Intron	IL2RA
Rs12722491	10:6059467	G/T	0.010(T)	Intron	IL2RA
Rs550805995	10:6059430	G/A	0.001 (A)	Intron	IL2RA
Rs12722621	10:6059210	C/A	0.041 (A)	Intron	IL2RA

**Table 2.** Sequence and amplicon size of primers.

Gene	Forward	Reverse	Length (bp)
IL2RA	ATGCTCTGCCTCTGGAAGACAC	TATCTCAATGGGTTTCCACACTGT	1472
HLA-DRA	TGCCTGCTTTTGCTTCTTTAGTCTC	AGGTGGTTTCAAGAATCAGTCAGAC	1173
HMGB1	AGAATGTATCCCCAAAAGCGTGAG	CACAGCACTGTAACTATCTTGGC	1366

DNA amplification was carried out by PCR with 3 µl of DNA in a 25 µl total reaction mixture containing 12.5 µl master mix (2x) and 0.5 µM of each primer. Thermal cycling conditions were as follows: denaturation at 94 °C for 5 min, followed by 35 cycles of denaturation at 94 °C for 30 s, annealing at 62 °C for 30 s, and extension at 72 °C for 30 s. The amplification was followed by the last extension step at 72 °C for 5 min. The PCR products were monitored after electrophoresis with agarose gel 1.5% using a gel documentation system.

## Sanger sequencing

The amplicons after gel purification were sent to the Macrogen Company (Seoul, South Korea) for Sanger sequencing. The results were trimmed and analyzed by BioEdit and Chromas software to ensure the quality and accuracy of the sequencing. Then, the extracted sequences were blasted against the non-redundant (NR) database to validate the annotated regions with sequences of interested genes.

## Statistical analysis

The calculated findings were illustrated via reporting odds ratio (OR) and 95% confidence intervals (CI) for each SNP. The differences in allelic and genotypic distribution between the groups were considered as studied two significant if the computed p value was less than 0.05. The Hardy-Weinberg equilibrium (HWE) was evaluated through the Chi-square  $(\chi 2)$ goodness-of-fit test, and allele frequencies and genotype distributions were analyzed using the Pairwise, Chi-square  $(\chi 2)$ test. disequilibrium (LD) of HLA-DRA, IL2RA, and HMGB1 SNPs was operated using Haploview 4.1 software and the obtained data were reported by describing the D' and  $r^2$  parameters. Moreover, 10.000 permutations were conducted to address significant levels in haplotypes.

#### **Results**

In this study, 102 MS patients, (17.6% men and 82.4% women) with a mean age of  $35.29\pm14.66$  years and 113 healthy controls (24.8% men and 75.2% women) were compared regarding totally 36 polymorphisms within the *HLA-DRA*, *IL2R*, and *HMGB1* genes, 14, 14 and, 8, respectively, by PCR-sequencing method. The association between various polymorphisms of these three genes and MS disease was evaluated by the chi-square test. Thus, the frequency of related genotypes in each polymorphism was computed in MS patients and control groups, separately. No deviation from HWE was identified in both MS patients and control groups for all SNPs (p> 0.05) (data not shown).

Based on our results, in the polymorphisms of the HLA-DRA gene, the rs4935356 (p= 0.001), rs3177928 (p= 0.002), and rs7197 (p= 0.002) SNPs were significantly associated with the risk of MS disease. Moreover, the frequencies of the A allele of rs3135390 (p= 0.026), an allele in rs3177928 (p= 0.027), and C allele in rs7197 (p= 0.001) were significantly altered in our MS patients. The findings of association analysis between HLA-DRA SNPs and the risk of MS are exhibited in Table 3.

Results of variants of IL2RA revealed that there was a statistically significant association between rs12722489 (p= 0.007) and rs12722490 (p=0.03) SNPs and the risk of MS; however, polymorphisms other of IL2RA gene (rs917751277, rs992067421, rs959264277, rs11597542, rs140860467, rs17149458, rs3118470, rs78556477, rs41294925, rs12722491, rs550805995, and rs12722621) had no significant differences between the two studied groups (p > 0.05). The frequency of T allele in rs12722489 showed significant discrepancies in MS patients compared to healthy controls. Differences in other SNPs of this gene did not

reach a level of significance (Table 4). Upon analysis of the polymorphisms of *HMGB1* gene, genotype and allele frequencies rs146076135, rs201945336, rs111892138, rs200308321, rs149637108, rs538493533, rs577524260, and rs182881863 SNPs were calculated and, finally no significant difference was observed in allele and genotype frequencies in both groups (p > 0.05) (Table 5). Finally, the linkage disequilibrium (LD) patterns of *HLA-DRA*, *IL2RA*,

and *HMGB1* SNPs were analyzed. Figure 1 illustrates the strong patterns of LD found in patients of this study. As shown, two haplotype blocks as following were significant predictors of MS disease in the *HLA-DRA* gene: one block of rs7194 and rs7195 SNPs; and another block consisting of rs4935356, rs3135390, rs4935354, rs3177928, rs7194, rs7195, rs1131541, rs7196, and rs7197 SNPs.

Table 3. The frequency of HLA-DRA alleles and genotypes in Iranian multiple sclerosis (MS) patients and controls.

Polymorphism	Status		(Frequency of Patients) Percent	(Frequency of Control) Percent	P-value	
		G	(143) 70.8	(136) 65.4		
	allele	T	(49) 24.25	(53) 25.5	0.219	
	aneie	A	(10) 4.95	(19) 9.1	_ 0.219	
-		A/A		(0) 0.0		
m 1025256		G/A	(1) 1.0 (6) 5.9		<del>-</del> -	
rs4935356		G/A G/G		(15) 14.4		
	genotype	G/G G/T	(52) 51.5 (33) 32.7	(50) 48.1	- <0.001 -	
		T/A	` /	(21) 20.2		
			(2) 2.0	(4) 3.8	_	
		T/T	(7) 6.9	(14) 13.5	<del></del> :	
	.11 . 1 .	A	(170)84.15	(191) 91.8	_ 0.026	
	allele	C	(31)15.35	(17) 8.2	_ 0.026	
2125200		T	(1) 0.5	(0) 0.0		
rs3135390		A/A	(74)73.3	(89) 85.6		
	genotype	C/A	(21) 20.8	(13) 12.5	- 0.049	
	0 11	C/C	(5) 5.0	(2) 1.9	_	
		T/A	(1) 1.0	(0) 0.0		
	allele	<u>C</u>	(49) 24.26	(55) 26.4	- 0.611	
,	uncic	T	(153) 75.74	(153) 73.6	0.011	
rs4935354	genotype	C/C	(7) 6.9	(15) 14.4	0.17	
		C/T	(35) 34.7	(25) 24.1		
		T/T	(59) 58.4	(64) 61.5		
	allele	G	(191) 94.55	(184) 88.5	- 0.027	
		A	(11) 5.45	(24) 11.5	0.027	
rs3177928		A/A	(1) 1.0	(0) 0.0	_	
	genotype	G/A	(9) 8.9	(24) 23.1	0.002	
		G/G	(91) 90.1	(80) 76.9		
	allele	G	(49) 24.26	(51) 24.5	_ 0.051	
		A	(153) 75.74	(157) 75.5	- 0.951	
rs7194		A/A	(59) 58.4	(66) 63.5	<del></del>	
	genotype	G/A	(35) 34.7	(25) 24.0	0.24	
	8 171	G/G	(7) 6.9	(13) 12.5		
	11 1	G	(153) 75.74	(159) 76.4	0.0.70	
	allele	A	(49) 24.26	(49) 23.6	- 0.868	
rs7195		A/A	(7) 6.9	(10) 9.6		
10,170	genotype	G/A	(35) 34.7	(29) 27.8	0.63	
	Schotype	G/G	(59) 58.4	(65) 62.0	_	
		T	(189) 93.56	(189) 90.9	0.000	
	allele	A	(13) 6.44	(19) 9.1	- 0.308	
rs1131541		A/A	(0) 0.0	(1) 1.0		
101101011	genotype	T/A	(13) 12.0	(17) 16.4	0.49	
	genotype	T/T	(88) 87.1	(86) 82.7		
s7196	allele	T	(165) 81.7	(171) 82.2	0.889	

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		A	(37) 18.3	(37) 17.8		
		A/A	(5) 5.0	(6) 5.8		
	genotype	T/A	(27) 26.7	(25) 24.0	0.87	
		T/T	(69) 68.3	(73) 70.2		
	allele	С	(172) 85.1	(198) 95.2	0.001	
	aneie	T	(30) 14.9	(10) 4.8	0.001	
rs7197		C/C	(75) 74.3	(95) 91.3	<u>.</u>	
	genotype	C/T	(22) 21.3	(8) 7.6	0.001	
		T/T	(4) 4.0	(1) 1.0		
	allele	G	(189) 93.56	(191) 91.8	0.490	
m1051226		A	(13) 6.44	(17) 8.2		
rs1051336	aan atr ma	G/A	(13) 12.9	(17) 16.3	0.57	
	genotype	G/G	(88) 87.1	(87) 83.7	<del></del> 0.57	
	allala	Т	(201) 99.5	(208) 100	0.402	
rs111471704	allele	A	(1) 0.5	(0) 0.0	0.493	
181114/1/04	an at ma	T/A	(1) 1.0	(1) 1.0	0.00	
	genotype	T/T	(99) 99.0	(103) 99.0	0.99	
rs1157343109	allele	T	(202) 100	(208) 100		
	genotype	T/T	(101) 100	(104) 100		
rs1041885	allele	T	(202) 100	(208) 100		
181041883	genotype	T/T	(101) 100	(104) 100		

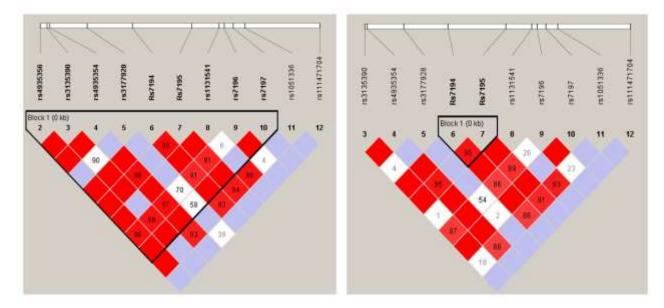
Table 4. The frequency of IL2RA allele and genotype in Iranian multiple sclerosis (MS) patients and controls.

Polymorphism	olymorphism Stat		(Frequency of Patients) Percent	(Frequency of Control) Percent	P-value	
rs12722489	.11.1.	A	(28) 13.7	(13) 5.8	- 0.005	
	allele -	G	(176) 86.3	(211) 94.2		
		AA	(5) 4.9	(3)2.8		
	genotype	G/A	(18) 17.6	(5)4.7	0.007	
		G/G	(79) 77.5	(99) 92.5	•	
rs917751277	allele	T	(204) 100	(224) 100	-	
18917731277	genotype	TT	(102)100	(107)100	-	
rs992067421	allele	G	(204) 100	(224) 100	-	
18992007421	genotype	GG	(102)100	(107)100	-	
rs959264277	allele	T	(204) 100	(224) 100	-	
18939204211	genotype	TT	(102)100	(107) 100	-	
rs11597542	allele	A	(204) 100	(224) 100	-	
1811397342	genotype	AA	(102)100	(107) 100	-	
m140960467	allele	A	(204) 100	(224) 100	-	
rs140860467	genotype	AA	(102)100	(107) 100	-	
rs17149458	allele	A	(204) 100	(224) 100	-	
181/149438	genotype	AA	(102)100	(107) 100	-	
	allele -	A	(12) 5.9	(7) 3.1	- 0.167	
		G	(192) 94.1	(217) 96.9		
rs12722490	_	AA	(0) 0.0	(1) 0.9	0.03	
	genotype	GA	(12) 11.8	(5) 4.7		
		GG	(90) 88.2	(101)94.4		
	allele -	A	(130) 63.7	(150) 67.0	0.482	
	anele	G	(74) 36.3	(74) 33.0	0.462	
rs3118470	_	AA	(45) 44.1	(52) 48.6		
	genotype	GA	(40)39.2	(39)36.4	0.83	
		GG	(17)16.7	(16) 15.0		
rs78556477	allele	C	(204) 100	(224) 100	-	
15/03304//	genotype	CC	(102) 100	(107) 100	-	
	allele -	T	(201) 98.5	(224) 100	- 0.107	
rs41294925	ancie	C	(3) 1.5	(0)  0.0		
	genotype	TC	(3) 2.9	(0) 0.0	0.114	

		TT	(99) 97.1	(107) 100	
rs12722491	allele	С	(204) 100	(224) 100	-
	genotype	CC	(102) 100	(107) 100	
rs550805995	allele	С	(204) 100	(224) 100	-
	genotype	CC	(102) 100	(107) 100	-
rs12722621	allele	G	(204) 100	(224) 100	-
	genotype	GG	(102) 100	(107) 100	-

**Table 5.** The frequency of *HMGB* allele and genotype in Iranian multiple sclerosis patients and controls.

Polymorphism	Status		(Frequency of Patients) Percent	(Frequency of Control) Percent	P-value
	allele	С	(183) 97.0	(195) 70.0	
DEL INICO140076125		C-/-	(0) 0.0	(1) 0.9	
DELINSCrs146076135	genotype	C/-	(21) 20.6	(27)24.1	0.51
		C/C	(81) 79.4	(84) 75.0	
DEI INICT (2010/5226	allele	T	(204) 100		-
DELINSTrs201945336	genotype	T/T	(102) 100	(112) 100	-
rs111892138	allele	A	(204) 100		-
18111092130	genotype	A/A	(102) 100	(112)100	-
DELING A 100200221	allele	A	(204) 100	(214) 100	
DELINSArs200308321	genotype	A-/A-	(102) 100	(107)100	-
DEL D. 1997 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	allele	GAAG	(204) 100	(222) 91.0	
DELINSGAAGrs14963710 8	anot ma	GAAG/-	(0)0.0	(1) 0.9	0.00
O	genotype	GAAG/GAAG	(102) 100	(111)99.1	0.98
529.402522	allele	T	(204) 100	(224)100	
rs538493533	genotype	TT	(102) 100	(112)100	· -
	allele	G	(204) 100	(224)100	-
rs577524260	genotype	GG	(102) 100	(112)100	-
102001072	allele	A	(204) 100	(224)100	-
rs182881863	genotype	AA	(102) 100	(112)100	=



**Fig. 1.** Linkage disequilibrium (LD) of *HLA-DRA* SNPs using D' (left, red color) and  $r^2$  (right, gray color) values for patient (left) and control (right) group. High levels of LD are depicted via increasing scale intensity from 0 to 100, as exhibited by the bars.

## **Discussion**

In the present study, we investigated the associations between 36 SNPs and the risk of MS in a population in Iran. A significant association (p< 0.05) among certain SNPs from *HLA-DRA* and *IL2RA* genes were found. Although a number of non-*HLA* genes have recently been recognized to contribute to susceptibility to MS with a modest effect, the *HLA* region is generally identified as being the strongest risk contributor. Meta-analysis studies suggest that *HLA-DR2*, and specifically the *DRB1\*15* allele, are significant risk determinants in Chinese MS patients, nonetheless less strong correlations were revealed in Western MS populations; whereas, *HLA-DR9* alleles appeared to confer the resistance to disease in this population (13).

This study showed significant associations as well as significant allele frequency differences in some of the studied SNPs including rs4935356, rs3177928, and rs7197 from the *HLA-DRA* gene and rs12722489 and rs12722490 variants from the *IL2RA* gene.

The rs4935356 variant from the HLA-DRA gene was previously reported to be involved in alcoholism and addiction disorders through influencing the brain, behavior, and immune system (5). Here, by observing significant associations, we found a novel relationship and possibly new disease-related function rs4935356 at risk of MS condition. In addition, the SNP variant rs3177928, significantly related to increased risk of MS, is reported in novel HLA-DRA downstream variants that were independent of HLA-DRB1 alleles which are associated with non-Löfgren sarcoidosis (NL Sarcoidosis) as a multiorgan inflammatory disorder. Recent nonsarcoidosis studies showed that rs3177928 was associated with lipoprotein metabolism and connected with inflammatory mechanisms (14). Moreover, recently it was discovered that rs7197 SNP is strongly associated with antibody response against viral elements such as Epstein-Barr virus (EBV) capsid antigen. Our results are consistent with this finding and suggest that rs7197 genetic variation might have a role in developing MS disease through immune-mediated and particular microbial genes and susceptibility (15). In addition, the results of LD analysis demonstrated a strong linkage between rs7195 and rs7194, which was

confirmed by findings showing almost the same level of non-significance for their genotypes and allele frequencies.

The IL-2/IL2Rsignaling stimulates proliferation and survival of activated T cells and has a paramount non-redundant role in the production of regulatory T cells (16). Our data showed significant associations of rs12722489 and rs12722490 SNPs in IL2RA and the risk of MS. Additionally, allele frequency differences were noted too. The rs12722489 polymorphism is linked with multiple autoimmune conditions such as rheumatoid arthritis, multiple sclerosis, Crohn's disease, and ulcerative colitis. In silico analysis suggested significant discrepancies in the affinity of estrogen receptor (ER) binding site between the alternative allelic variants, with a stronger predicted affinity for the risk (G) allele. Electrophoretic mobility shift assessment illustrated that purified human ERa only bound G variant of a 32-bp genomic sequence containing rs12722489 (17). Chromatin immunoprecipitation showed that endogenous ERa in humans interacted with rs12722489 genomic region in vivo and DNA pulldown assay confirmed differential allelic binding of amplified 189-bp genomic fragments containing rs12722489 with endogenous human ERα. In a luciferase reporter assay, a kb-long genomic part containing G but not A allele of rs12722489 demonstrated enhancer properties in MT-2 cell line, an HTLV-1 transformed human cell line with a regulatory T cell phenotype (17). Moreover, associations with various autoimmune disorders of polymorphisms in an LD block in which the IL2/IL21 genes map (4q27), and also in genes encoding the IL2RA and IL2RB subunits located in 10p15 and 22q13, respectively, were identified through GWAS. Polymorphisms in these three genes were studied in 430 MS patients and in 550 ethnically matched controls in Spain. Replication and meta-analysis with results from an independent cohort of 771 MS patients and 759 controls in Spain confirmed the association of polymorphisms in the IL2RA gene but did not verify the association for *IL2RB* (18). Regression analyses of the combined cohort in in Spain study revealed the independence of two IL2RA association signals: rs2104286 and rs11594656/rs35285258.

related role of the *IL2RA* gene on MS susceptibility is well in line with its common effect on autoimmune risk and the suggestive association of IL2/IL21 warrants further investigation (18).

The HMGB1 belongs to the classification of endogenous damage-associated molecular pattern molecules (DAMPs), also known as alarmins. HMGB1 is passively released from necrotic cells and it is actively secreted from activated immunocompetent cells, including macrophages (19). Nevertheless, extracellular HMGB1 has inhibitory effects on phagocytic activity of macrophages (efferocytosis), which is critical to the resolution of inflammation (20). Increasing evidence exists for the role of HMGB1 in autoimmune disorders. In this context, recent studies have shown associations between HMGB1 and rheumatoid arthritis, systemic erythematosus, psoriasis, and Sjögren's syndrome (21). Studies on *HMGB1* are scarce in MS. In this examination, we considered the SNPs of *HMGB1*; however, none of the studied polymorphisms was significantly associated with the risk of MS regarding both genotype and allele frequency. Zhen et al. examined HMGB1 levels of peripheral blood mononuclear cells (PBMC), serum, and CSF in MS patients and found a considerably higher HMGB1 level in serum, PBMC, and CSF compared to healthy individuals and noninflammatory neurological disorder controls (10). Andersson et al. demonstrated that HMGB1 and its receptors, RAGE (receptor for advanced glycation

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end-products), are highly expressed in active lesions of MS as well as in its counterpart animal model EAE (experimental autoimmune encephalomyelitis), while being expressed at normal levels in inactive lesions. This suggests a potential interaction of these molecules in the inflammatory process involved in pathogenesis (11). We might suggest that the reason behind not significant differences between the two groups could be the effect of sample size or the fact that simply this genetic variation is not notably altered among Iranian MS patients.

In conclusion, we studied 36 SNPs in *HLA-DRA*, *IL2RA*, and *HMGB1* genes in Iranian MS patients. Our results demonstrated significant associations of these genetic variants and MS disease. Further assessment of these SNPs in larger sample sizes along with other variants of mentioned genes would highly facilitate the recognition of causative variants in MS disease.

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