Table 1 Analysis of the signalling lymphocytic activation molecule family member 1 single-nucleotide polymorphisms by affected family-based control, transmission disequilibrium and genotype relative risk tests in 100 French families with rheumatoid arthritis

SNP alleles	Allele frequencies		p Value	TDT		p Value	p Value
	Frequency transmitted	Frequency untransmitted		Transmitted	Untransmitted		
rs 2295612_C	0.79	0.83	0.30	28	36	0.31	0.31
rs 2295612_A	0.21	0.17		36	28	0.31	
rs 1809963_C	0.99	0.995	0.31	1	3	0.31	0.62
rs 1809963_G	0.01	0.005		3	1	0.31	
rs 3796504_C	0.89	0.9	0.74	17	19	0.73	0.08
rs 3796504_A	0.11	0.1		19	17	0.73	

GRR, genotype relative risk; SNP, single-nucleotide polymorphism; TDT, transmission disequilibrium test.

obtained using genotype relative risk and affected family-based control tests (table 1).

Moreover, our results showed the same distribution of *SLAMF1* alleles and genotypes between Tunisian patients and controls ($p>0.05$).

Three different haplotypes (CCC, CCA, ACC) were identified at the *SLAMF1* gene, with a frequency $>5\%$ in the French and Tunisian populations. Neither a significant disequilibrium of transmission to patients with rheumatoid arthritis nor a significant difference in distribution of these haplotypes between Tunisian patients with rheumatoid arthritis and controls was found.

Our study is the first report to examine the potential role of the *SLAMF1* gene in the susceptibility to rheumatoid arthritis in both the French and Tunisian populations, which indicates that *SLAMF1* polymorphisms do not contribute to susceptibility to rheumatoid arthritis in the studied populations. Our study should be replicated in other populations to confirm our preliminary results. Genotypes are available at <http://www.GenHotel.com>.

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Palindromic rheumatism: different genetic background implies a distinct disease entity

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Palindromic rheumatism is characterised by multiple, episodic and recurrent attacks of arthritis, accompanied by periarticular inflammation without residual joint damage, occurring at irregular intervals and lasting from a few hours to several days.^{1–3}

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The definite pathogenesis and disease entity of palindromic rheumatism has not been clarified until now. We investigated the association of rheumatoid arthritis and palindromic

Abbreviation: HLA, human leucocyte antigen

Table 1 Susceptibility to palindromic rheumatism (PR) based on human leucocyte antigen-DRB1 genotypes between patients with PR (n = 110) and controls (n = 392)

Genotype	Patients with PR, n (%)†	Controls, n (%)†	OR (95% CI)	p Values
*0803/X	63 (59.4)	47 (12.2)	10.54 (6.43 to 17.26)	<0.001
*1302/X	4 (3.8)	73 (19.0)	0.17 (0.06 to 0.47)	<0.001
X/X*	39 (36.8)	265 (68.8)	1	—

PR, palindromic rheumatism.

X, all alleles except an allele susceptible to PR (DRB1*0803) and an allele protective against PR (DRB1*1302). The p values were estimated by Fisher's exact test.

†In genotypic analysis of susceptibility to PR, 4 of the 110 patients with PR (one *0803/*0803 and three *0803/*1302) and 7 of the 392 controls (four *0803/*1302 and three *1302/*1302 genotypes) were excluded. p<0.05 was considered to be significant.

rheumatism with regard to genotype by identifying the distribution of human leucocyte antigen (HLA)-DRB1 alleles in patients with palindromic rheumatism and controls in the Korean population.

In all, 110 eligible patients with palindromic rheumatism (53 men and 57 women) were recruited. All enrolled patients met our inclusion criteria, which were based on diagnostic features previously described in the literature.²⁻⁵ Only those who did not develop rheumatic arthritis after 2 years were included. A total of 392 healthy participants without any evidence of autoimmune disease were included as a control group.

HLA-DRB1 genotyping was carried out as previously described.⁶ The susceptibility to palindromic rheumatism of HLA-DR alleles and genotypes between the controls and patients with palindromic rheumatism was assessed using Fisher's exact test.

A total of 33 HLA-DRB1 alleles were genotyped. Although there were significant differences in the frequencies of the *0406, *0803, *1101 and *1302 alleles in patients, compared with controls, HLA-DRB1 *0803 and *1302 had a significant association with the development of palindromic rheumatism by multivariate logistic regression analysis ($p^{\text{adj}} < 0.001$, odds ratio (OR) = 6.32, 95% confidence intervals (CI) 3.74 to 10.66 and $p^{\text{adj}} = 0.002$, OR = 0.22, 95% CI 0.09 to 0.57, respectively). In the genotypic analysis, patients with the *0803 or *1302 alleles had increased or decreased risk of developing palindromic rheumatism, respectively, compared with those without these alleles ($p < 0.001$, OR = 10.54, 95% CI 6.43 to 17.26 and $p < 0.001$, OR = 0.17, 95% CI 0.06 to 0.47; table 1).

Our study showed that HLA-DRB1 allele *0803 may be a genetic marker for the development of palindromic rheumatism in the Korean population. Several clinical and immunological studies have failed to find definitive evidence for either similarities or differences between palindromic rheumatism and rheumatoid arthritis.⁴⁻⁷ Stastny⁸ described an association of the B cell alloantigen DRw4 in patients with rheumatoid arthritis. The gene dosage of HLA-DRB1 *0401 and *0404 in palindromic rheumatism encoding the shared epitope suggested an immunogenetic similarity to the pathogenesis of palindromic rheumatism, and was a genetic risk factor for progression from palindromic rheumatism to rheumatoid arthritis.⁵⁻⁹⁻¹⁰ In contrast with previous studies, we identified marked differences in allele frequencies for only two alleles (DRB1 *0803 and *1302) in patients with palindromic rheumatism compared with controls. No evidence for correlation of HLA-DRB1 *0803 with inflammatory arthritis such as rheumatoid arthritis has been found in the literature, including the previous study by our group, in which HLA-DRB1 *0405 and *0901 were associated with increased susceptibility to rheumatoid arthritis in Koreans.⁶

In summary, HLA-DRB1 *0803 was identified in a large proportion of patients with palindromic rheumatism and is probably a useful genetic marker for susceptibility to palindromic rheumatism in the Korean population. These findings suggest that the disease entity of palindromic rheumatism may be independent of rheumatoid arthritis on the basis of genetic susceptibility.

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