



CD24 as a genetic modifier of disease progression in multiple sclerosis in Argentinean patients

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ABSTRACT

Introduction: Previous reports have shown that CD24 gene polymorphisms have an important role in the risk of development and progression of multiple sclerosis (MS).

Objective: To investigate the association between P226 polymorphisms (T/C), P105G (A/G), P1527 (TG/del) and P1626 (A/G) of the CD24 gene and MS, comparing allele and genotype frequencies of patients versus controls.

Materials and methods: We analyzed DNA samples from 102 MS patients and from 205 unrelated healthy individuals. DNA was extracted from peripheral blood and polymorphic regions were amplified by nested PCR. Genotyping was performed by restriction fragments length polymorphisms. Time from disease onset to reach EDSS 6 and time to conversion to secondary progressive phase (SP) were used as variables of survival as well as percentage of patients that reached those endpoints. We used the log Rank test for data comparison (significant $p \leq 0.05$).

Results: We found no differences between cases and controls in frequency of polymorphisms at the CD24 gene. 44.6% of patients with the AA genotype (P1626) reached an EDSS 6 vs 16% of patients with other genotypes ($p < 0.001$, HR 3.2, 95% CI 1.4 to 7.4). 45.8% of patients with the AA genotype reached SPMS vs 16.7% without this genotype ($p < 0.001$, HR 3.4, 95% CI 1.5 to 7.8).

Conclusions: This study showed a strong association between the presence of AA genotype in the 1626 polymorphism of the CD24 gene and the risk of disease progression in MS patients.

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