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Multiple Sclerosis Immune-genetic Characterization in Patients of Latvian Population

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Introduction. Multiple sclerosis (MS) is the most common neurological disease affecting young adults in Western part of the world. MS is the central nervous system (CNS) demyelinating disease associated with complex pathogenic autoimmunity against several CNS-myelin target antigens. Although the etiology of MS is yet unknown, numerous studies have confirmed a strong genetic component underlying its etiology. There is association with the HLA-DRB1*1501-DQB1*0602 haplotype which has been repeatedly demonstrated in high-risk (northern European) population, which also include the population of Latvia.

Aim. The purpose of this study is to determine of HLA-DRB1 alleles in patients with clinical, epidemiological and laboratory approved multiple sclerosis diagnosis in Latvian population.

Material and Methods. The study included 19 patients with MS (clinically and radiologically confirmed diagnosis) and 30 control (healthy) persons of Latvian population. The diagnosis was confirmed and imposed at Riga Eastern Clinical University Hospital, MS unit. Immunogenetic examinations were performed at Rīga Stradiņš University, Laboratory of Clinical Immunology and Immunogenetics. The HLA genotyping was performed with PCR method using mixture primers of DRB1 16 allele gene variants. The significance of differences in individual subtypes between patients and controls was assessed by Mantel-Haenszel test and Fisher exact correction for small numbers. The relative risk (RR), and 95% confidence intervals (CI) were computed by standard methods.

Results. Types of all sixteen DRB1 alleles were investigated. The frequency of HLA-DRB1 *15 (RR – 2.17 (1.07–4.40); p = 0.04) was significantly increased in the multiple sclerosis patients compared with the control group. HLA-DRB1*04 (RR 1.9 (0.6–6.13); p = 0.22) and –DRB1*11 (RR 0.9 (0.34–2.67); p = 0.57) were shown to be considerably increased in patients, although the difference was no longer significant when the p-value was no corrected for the number of alleles. Moreover, the allele DRB1*10 (RR 0.26 (0.03–2.01); p = 0.15) was smaller in Latvian multiple sclerosis patients and higher in controls group.

Conclusions. The predisposition to MS in Latvian population appears not to be limited of HLA-DR; some alleles also have a significant influence. In particular, HLA-DRB1*15 definitely contributes to a genetic predisposition of multiple sclerosis in Latvian population. To receive more reliable data on the prevalence of HLA alleles in Latvian population and their possible association with MS, further HLA alleles investigation is necessary including a larger number of multiple sclerosis patients and controls.