Immunogenetic Markers in Latvian Patients with *Borrelia burgdorferi* Infection

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Introduction. Lyme disease (Lyme borreliosis) is caused by infection with the tick-borne bacterium *Borrelia burgdorferi*. Human pathogen, *B. burgdorferi* causes a multisystem disease that may affect skin, nervous system, heart, or joints. The disease incidence in Latvia is one of the highest in Europe. Over last 10 years (2003–2012) 6772 cases of Lyme borreliosis were reported with the highest number (866) in 2011. In 2012, 724 cases of Lyme disease were notified composing the incidence rate 35.5 per 100,000 of population.

The aim. The purpose of this study was to determine -DR,-DQ alleles HLA in patients with clinical, epidemiological and laboratory approved Lyme borreliosis diagnosis.

Materials and methods. The study included 38 patients with clinical stage – *erythema migrans* and 100 control (healthy) persons. The diagnosis was confirmed at Infectology Center of Latvia. Immunogenetic examinations were performed in the RSU, Laboratory of Clinical Immunology and Immunogenetics. HLA genotyping performed with PCR method using primers. The significance of differences in individual subtypes between patients and controls was assessed by Fisher exact test. Odds ratios and 95% confidence intervals were computed by standard methods.

Results. The frequency HLA -DRB1 *17(03) (OR = 4.06; p = 0.002) and -DRB1*04 (OR = 3.22; p = 0.011) was significantly higher in the Lyme disease patients compared with the control groups. However, the frequency of allele DRB1*10 (OR = 0.16; p = 0.036) was lower in Lyme borreliosis patients and significantly higher in controls. We did not detect significant differences in frequencies of HLA-DQ alleles. Although, the frequencies of HLA-DQA1*0201, -DQA1*0501, and DQB1*0201 were higher in patients in comparison with the control group, but the difference was no longer significant.

Conclusions. These results suggest that inflammatory events of the subacute arthritis can set the stage for development of chronic disease in individuals possessing an HLA susceptibility allele. In particular, immunogenetic markers -DRB1*17(03) and -DRB1*04 contributes definitely to a genetic predisposition to *Borrelia burgdorferi* infection in Latvian population, which may have implications in our understanding of pathogenesis of this disease. To receive more reliable data on the prevalence of HLA alleles in Latvian population and their possible relationship with Lyme borreliosis, it is necessary to continue the investigation and extend the range of persons under investigation.