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# Investigation HLA class II alleles in patients with *Borrelia burgdorferi* infection in Latvia

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**Introduction:** *Lyme borreliosis* in recent years is very actual disease, and a disease level of Latvian is one of the highest in Europe. There are some similarities between the bacterial agents, and HLA molecules, because in organism develops one way or another immune response to infection. There are many hypotheses about the direct role of HLA molecules in the pathogenesis of infection. Clarifying the polymorphism of HLA immunogenetic molecular markers to identify regularities in the development and pathology to develop a new approach to treating these diseases.

**Objective:** To determine HLA-DR,-DQ molecules in patients with clinical, epidemiological and laboratory approved *Lyme borreliosis* diagnosis.

**Materials and Methods**: The study included 20 patients with clinical stage – *erythema migrans* and 25 control (healthy) persons. HLA genotyping was performed through PCR-SSP method.

**Results**: Typing of all sixteen alleles DRB1were investigated. The predisposition to the *Lyme disease* is associated with the HLA-DRB1 *17(03) (OR 7,5; p<0,044) and HLA-DRB1 *15 (OR 5,21; p<0,132). For the -DRB1 *18(03) allele, the evidence is controversial. Although DRB1 *18(03) allele presence in our healthy persons and among *Borreliosis* patients suggests that is not associated with the disease. However, this should be interpreted carefully because of the small number of studied individuals. The distribution of alleles in the patients included in this study follows the world tendency: DRB1 *17(03) was the most frequent allele in Caucasian population. Typing of all sixteen -DQ alleles were also studied. The HLA-DQA1*0201, -DQA1*0501 and DQB1*0201 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. And, the allele DRB1*13 (OR 0,18; p<0,091) was smaller in *Borreliosis* patients and significantly higher in controls. This data suggest that HLA-DR, -DQ molecules may have a considerable effect on susceptibility/or protection to *Lyme borreliosis*.

**Conclusions:** HLA predisposition to *Lyme borreliosis* appears not to be limited to HLA-DR or -DQ, but some alleles also have a significant influence. In particular, HLA-DRB1*17(03) 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 *Borreliosis* it is necessary to continue the investigation, detecting HLA alleles in the rest these patients and taking the control group of healthy individuals. The definitive conclusion of the disease-associated subtypes requires different ethnic group studies. And finally, it is a further step towards improving our understanding of the role of HLA molecules in this severe infectious disease.