Distribution of MHC-DQ Haplotypes in Patients with Lyme Disease

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Introduction. Lyme disease is caused by infection with the tick-borne bacterium *Borrelia burgdorferi*. In order to initiate a specific immune response to an infectious agent, the immune system must be able to isolate particular protein products that will sharpen the efforts of host defence. The T-Cell Receptor (TCR) can recognize antigen only in the form of a peptide bound to an MHC molecule on a human cell surface. MHC-II molecules are composed of two non-covalently linked transmembrane chains, Alpha ƒn and Beta ƒn, and they are specialized for the presentation of extracellular antigens to the TCR of CD4+ T Cells. The genes encoding the DQ heterodimer of MHC molecules have been found to have the association with Lyme borreliosis risk.

Aim. The purpose of this study is to determine HLA-DQ haplotypes in patients with clinical, epidemiological and laboratory approved Lyme borreliosis diagnosis.

Material and Methods. The study included 109 patients with clinical stage – erythema migrans and 100 control (healthy) persons. The diagnosis was confirmed and imposed by Latvian Infectology Centre. Immunogenetic examinations were performed at RSU Clinical Immunology and Immunogenetic Laboratory with PCR-SSP method. This work was supported by the European Social Fund (ESF) project "Support for doctoral study program and acquiring scientific degree at Rīga Stradiņš University, agreement No. 2009/0147/1DP/1.1.2.1.2/09/IPIA/VIAA/009."

Results. The frequency of haplotypes: DQA1*02:01:01/DQB1*03:02:01 (OR – 3.27; $p < 0.040$); HLA-DQA1*05:01:01/DQB1*02:01:01 (OR – 2.54; $p < 0.048$) and HLA-DQA1*01:01:01/DQB1*02:01:01 (OR – 2.11; $p < 0.031$) were significantly increased in the Lyme *disease* patients compared with the control groups. But, the haplotypes of DQA1*01:02:01/DQB1*06:02:01(OR – 0.24; $p < 0.036$); DQA1*01:03:01/ DQB1*06:02:01 (OR – 0.27; $p < 0.046$) and DQA1*01:02:01/DQB1*06:02:01 (OR – 0.31; $p < 0.029$) were smaller in *Borreliosis* patients and significantly higher in controls.

Conclusions. This data suggest that HLA-DQ haplotypes may have a considerable effect on susceptibility/or protection to Lyme borreliosis. In particular, HLA-DQA1*02:01:01/DQB1*03:02:01, HLA-DQA1*05:01:01/DQB1*02:01:01, and HLA-DQA1*01:01:01/DQB1*02:01:01 haplotypes definitely contribute to a genetic predisposition to Borrelia burgdorferi infection in Latvian population, which may have implications in our understanding of pathogenesis of this disease.