

Molecular Genetic Characteristic Patients with *Borrelia Burgdorferi* Infection

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Introduction. The MHC II genes encode the polymorphic -DR and -DQ molecules, which are expressed as α and β chain heterodimers on the cell surface. MHC II molecules are central in the initiation of cellular and humoral immune responses, but they have also been indicated as contributing factors for a variety of immune disorders. The constitutive expression of MHC II molecules is tissue specific and is restricted to professional antigen presenting cells (APCs) of the immune system. Because of their crucial role in the adaptive immune response, the genes encoding MHC II molecules are tightly regulated by genetic and epigenetic mechanisms at the transcriptional level to provide an effective immune response against pathogens.

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

Material and methods. The study included 78 patients with clinical stage – erythema migrans and 100 control (healthy) persons. The diagnosis was confirmed and imposed by the Latvian Infectology Center. Immunogenetic examinations were performed at RSU Clinical Immunology and Immunogenetic Laboratory. MHC genotyping was performed by PCR with sequence-specific primers (SSP). The statistical analysis of data was performed by Microsoft Office Excel 2003 and ARLEQUIN 3.11 software. Odds ratio and 95 % confidence intervals were computed by standard methods.

Results. The frequency of the following groups MHC haplotypes: - DRB1*15:01:01/DQA1*01:02:01/DQB1*03:02:01, (odds ratio (OR) = 8.34 p < 0.013); -DRB1*01:01:01/DQA1*03:01:01/DQB1*03:02:01, (OR = 6.17 p < 0.027); and -DRB1*03:01:01/DQA1*01:01:01/DQB1*05:01:01, (OR = 2.66 p < 0.032), were significantly increased in the Lyme disease patients compared with the control groups.

Conclusions. These results suggest that the inflammatory events of the subacute arthritis can set the stage for the development of chronic disease in individuals possessing risk haplotypes. In particular, the haplotypes -DRB1*15:01:01/DQA1*01:02:01/DQB1*03:02:01, (OR = 8.34); and DRB1*01:01:01/DQA1*03:01:01/DQB1*03:02:01, (OR = 6.17) contribute definitely to a genetic predisposition to *Borrelia burgdorferi* infection in Latvian population, which may have implications in our understanding of pathogenesis of the respective disease.