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Molecular genetic characteristics patients with *Borrelia burgdorferi* infection

The MHC II genes encode the polymorphic-DR and DQ molecules, Lyme disease (Lyme borreliosis) is infectious vector-borne diseases which has a large polymorphism of clinical manifestations and caused at least three species of bacteria of the genus *Borrelia*: *Borrelia burgdorferi sensu stricto* dominated as the causative agent of Lyme disease in the United States, whereas *Borrelia afzelii* and *Borrelia garinii* in Latvia and Europe. One of the major unsolved problems of today is the study of the interactions of organism and pathogens genospecies *Borrelia burgdorferi* (Bb). In this connection particular interest is the analysis of one of the major systems of the body controlled by the immune response-complex HLA including the identification of possible associations of HLA genotypes with clinical features of Lyme disease. Although various factors participate in the immune response to infection (e.g., intensity of the infection and T-cell functioning), the interaction of these mechanisms with genetic factors seems to be important in determining the evolution of the disease. Furthermore, the immune response to infections varies from one individual to another, on account of the polymorphism of the genes that influence this response. HLA antigens may act alone or in combination with other genes, conferring susceptibility to, or protection against infectious diseases. The obtained results suggest that the inflammatory events of the sub acute arthritis can set the stage for development of chronic disease in individuals possessing a risk haplotypes. In particular, the haplotypes HLA-DRB1*15:01:01/DQA1*01:02:01/DQB1*03:02:01, (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) 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. Knowledge of the mechanisms of genetic protection against and susceptibility to infectious diseases is one of the important steps towards controlling them in endemic areas and contributes to our understanding of both the pathogenic and protective mechanisms of these processes. The mechanisms of immune response to infection that are influenced by the HLA genes may be the key to future vaccines using the peptides of organisms that mimic the HLA antigens.

Biography

Angelika Krumina is a leading Researcher in Infectology field in Riga East Clinical University Hospital. She is a Scientific Expert of Latvian Academy of Sciences, Board Member of Latvian Medical Association and Member of European Society of Clinical Microbiology and Infectious Diseases. During 2011-2012, she was a Project Coordinator in State Program of Latvian Academy of Sciences. Currently she is a Work Package 6 Leader in Latvia of Baltinfect project of the Seventh Framework Program (FP7) of the European Commission.

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