HLA Genetic Polymorphisms' Inheritance Associated with Rapid Progression of Human Immunodeficiency Virus Type 1 Infection

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Introduction. The most important functions of Human Leukocyte Antigens (HLA) are genetic control of immunity response and preservation of homeostasis of immune system in humans. Mutations in HLA genes may be linked to autoimmune diseases such as type 1 diabetes or coeliac disease. Gene polymorphisms can also be inherited, and some of them are related to infectious diseases. One of the HIV genesis hypotheses explains the greater inclination to the given pathology by the presence of particular HLA alleles, associated with the higher reactivity of immune system. This fact confirms that the information about the influence of genetic factors on the progress of disease of HIV infected patients is of very current interest.

The aim. Genetic inheritance of HLA gene polymorphisms, during viral infection, influences function of the immune response. The aim of this study was to determine HLA II class haplotypes – DRB1*/DQA1*/ DQB1* in HIV infected patients and to identify the possible connection with the effectiveness of therapy.

Materials and methods. 500 HIV infected patients and 200 healthy controls (healthy persons) were enrolled in the study. The clinical diagnosis was confirmed in the Infectology Center of Latvia. Immunogenetic examinations were performed in Rīga Stradiņš University (RSU) and in the Laboratory of Clinical Immunology and Immunogenetics. The Ethics Committee approval was obtained. For HLA typing, DNA was extracted from buffy coat cells by the DNA extraction, using Qiagen Ampli blood kits (UK), to yield highly pure DNA. HLA typing for DRB1*/DQA1*/ DQB1* was performed by Real Time Polymerase Chain Reaction (RT-PCR) with sequence-specific primers (SSP). The statistical analysis of data was performed using Microsoft Office Excel and ARLEQUIN software.

Results. This study revealed that high risk of HIV infection was associated with the following groups of haplotypes: HLA-DRB1*15:01/DQA1*03:01/DQB1*03:01 (OR = 7, p = 0.027); DRB1*15:01/DQA1*05:02/DQB1*02:01; (OR = 8.34, p = 0.013); DRB1*17:01/DQA1*03:01/DQB1*05:01 (OR = 2.66, p = 0.032); DRB1*07:01/DQA1*03:01/DQB1*02:01 (OR = 2.66, p = 0.032); DRB1*05:01/DQA1*03:01/DQB1*05:01 (OR = 2.66, p = 0.032).

These haplotypes in HIV positive patients were significantly increased in comparison with the control group. A possible protective haplotypes of DRB1*06:01/DQA1*01:02/DQB1*06:02-06:08 (OR = 0.24, p = 0.0001); DRB1* 01:01/DQA1*01:03/DQB1*06:02-06:08 (OR = 0.31, p = 0.0030); DRB1* 01:01/DQA1*01:02/DQB1*06:02-06:08 (OR = 0.27, p = 0.0008) were detected, the frequencies of these haplotypes were lower in all HIV patients than in the control group.

Conclusions. This study indicated that some of HLA class II haplotypes could increase the risk of HIV disease under the influence of viral infection. Our study confirmed the association of HLA class II haplotypes with predisposition or resistance to HIV infection.