

Significance of polymorphism in 2',5'-oligoadenylate synthetase genes in HIV infection

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Abstract

© 2016, Nizhny Novgorod State Medical Academy. All rights reserved. The aim of the investigation was to assess the prognostic value of polymorphism of genes encoding 2',5'-oligoadenylate synthetase (OAS) synthesis in HIV infection. **Materials and Methods.** The DNA of 94 HIV infected patients have been sequenced using multiplex polymerase chain reaction. For molecular genetic testing we used DNA samples isolated from the scraping of oral epithelial cells. We studied interferon-induced genes, namely: OAS enzyme. It was a case-control study. Depending on the decrease rate of CD4-lymphocytes, the patients were divided into two groups: with typical disease progression and those with slow progression. We determined the frequencies of mutant alleles and genotypes in patients with different progression rates, and assessed genotype associations with different outcomes. **Results.** There have been found oligonucleotide polymorphisms of OAS genes of different enzyme forms: OAS2 rs2072137 (chr12:113440921) and OAS3 rs1859330 (chr12:113376388). The frequency of mutant allele C of OAS2 rs2072137 polymorphism appeared to be significantly higher in a group with a typical disease progression ($p=0.03$). The frequency of mutant allele A of OAS3 rs1859330 polymorphism had no difference in the groups. In a group with mutant genotypes TC and CC of OAS2 rs2072137 polymorphism, the frequency of typical disease progression was significantly higher than that in the group with the main ("wild") genotype TT ($p=0.0125$). Logistic regression revealed typical HIV infection progression in patients to be significantly associated with OAS2 rs2072137 polymorphism and age. **Conclusion.** OAS2 rs2072137 polymorphism is associated with typical progressive HIV infection, and, probably, presents a new genetic prognostic marker of the disease.

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Keywords

2',5'-OAS, 2',5'-Oligoadenylate synthetase, Gene polymorphism, HIV infection, OAS