

Single nucleotide polymorphisms in cytokines genes promoters are associated with the susceptibility to HIV-1 infection in the Ukrainians

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Background. Cytokines genes single nucleotide polymorphisms (SNPs) involved in the vulnerability to HIV infection in different population groups. We aimed to determine whether the carriage of cytokines genes allele variants influence the risk HIV-1 infection in Caucasian Ukrainians.

Methods. We examined promoter SNPs in IL-4 (rs 2243250), IL-10 (rs 1800872), TNF- α (rs 1800629) among 78 HIV-1 infected European Ukrainians (68 % male, 32 % female; age at diagnosis (33,35 \pm 0,76) years), 22 HIV-negative persons from the high risk infection group and 100 healthy controls using PCR-RFLP.

Results. The dominant cytokines genes variants among HIV-1 infected Ukrainians were major allele homozygotes that correspond to controls and the high risk infection group (C/C IL-4 - 62.82 %, C/C IL-10 - 53.85 %, G/G TNF- α - 62.82 %). T/T IL-4 and G/A TNF- α genotype variants significantly overrepresented in people with HIV-1 ($p \leq 0.01-0.05$); susceptibility to HIV-1 infection does not depend on gender. IL-10 minor allele distribution showed the difference among study groups: A/A variant was associated with the disease in men ($p \leq 0.05$). We found that carriage of IL-10 homozygous major allele genotype had protector effect on risk of HIV-1 infection among male population ($p \leq 0.05$).

Conclusions. The first report of cytokines genes allele frequencies in Ukrainian population shows their association with susceptibility to HIV-1 infection and suggests further research in the field of host genetic risk factors.

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