Piddubna, A. Cytokines genotypes as predictors of disease outcomes in HIV-1 infected Ukrainians [Text] / A. Pidduban // Abstract book of the Conference of European Society of Human Genetics 2015, 6-9 June 2015, Glasgow, UK. – J07.3.

Cytokines genotypes as predictors of disease outcomes in HIV-1 infected Ukrainians

Background. Cytokines genes single nucleotide polymorphisms (SNPs) influence clinical course of HIV infection in different population groups. The objective of the research was to determine cytokines genotypes association with outcomes of the disease in Ukrainians with HIV-1.

Methods. We examined promoter SNPs in IL-4 (rs 2243250), IL-10 (rs 1800872), TNF-α (rs 1800629) among 78 naive HIV-1 infected European Ukrainians (68 % male, 32 % female; age at diagnosis (33,35±0,76) years) and 100 healthy controls using PCR-RFLP. Patients with HIV-1 were distributed into groups depending on implications of bacterial, viral, fungal and parasitic infections.

Results. All detected cytokines SNPs showed no significant deviation from the Hardy-Weinberg equilibrium in controls ($p \geq 0.1$). The dissimilarity in cytokines genotypes frequencies among HIV-1 infected persons with different clinical course of the disease was determined. We found the association of C/A IL-10 with bacterial (OR=0.74, $p \leq 0.05$), C/C IL-10 and G/A TNF-α - viral (OR=0.65, $p \leq 0.05$; OR=0.53, $p \leq 0.05$ appropriately), C/T IL-4 - fungal (OR=0.44, $p \leq 0.05$) infections. Cytokines genes variants played a protective role in patients with HIV-1: A/A IL-10 genotype in fungal (OR=3.98, $p \leq 0.05$), C/A IL-10 in viral (OR=1.93, $p \leq 0.05$), G/G TNF-α in viral and parasitic opportunistic infections (OR=1.83, $p \leq 0.05$, OR=1.79, $p \leq 0.05$ appropriately).

Conclusions. Our results demonstrate that cytokines genes polymorphisms may be used as clinical markers to predict outcomes of HIV-1 infection and warrant further studies in the host genetic factors sphere.