Association of CTLA-4 gene with the familial diabetes mellitus

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The work was initiated to study role of CTLA4 gene in the onset of familial diabetes mellitus (DM).

Materials and methods. The samples of peripheral blood taken from children (mean age 12.5 years) of patients with type 1 DM and their blood relatives, such as parents and siblings, and apparently healthy subjects were used in the study. Among the recruits, there were 56.5% of boys and 43.5% of girls.

Results. The findings from the genotyping of CTLA4 gene 49A/G polymorphism demonstrated no significant deviations of the genotypes observed from the expected ones in the group of apparently healthy subjects and the diabetics.

The frequencies of A and G alleles in the control group were 57.7% and 42.6%, respectively. The frequencies of A/A and G/G homozygous genotypes were 32.7% and 17.3%, respectively, the one of A/G heterozygous type was 50%.

The study on distribution of CTLA4 gene polymorphism among the patients with the hereditary burden of DM demonstrated that the frequencies of A and G alleles in the control group were 38.6% and 61.4%, respectively. The frequencies of A/A and G/G homozygous genotypes were 4.5% and 27.3%, respectively, the one of A/G heterozygous type was 68.2%.

Conclusions. The association of G allele and heterozygous genotype of CTLA4 gene A49G polymorphism registered in the children of patients with type 1 DM and their blood relatives could be implicated in DM risk and used as a marker in the development of a complex for early diagnosis of the disease.