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.