Summary

The research of the way of participation of each transmitte system in pathology of ADHD can be of help, in the future, in the selection of the appropriate drug as substances with different mechanisms of functioning are used to treat the hyperkinetic syndrome. For our research the genes of dopominergic (DRD2, DRD3 a DAT1), noradrenergic (DBH) and serotoninergic (5-HTT) systems were selected. In these genes 11 polymorphisms were analysed by molecular-genetic methods based on association strategy „case-control". The presence of risk alleles was compared between the sample of 100 ADHD children and a control group of 100 subjects, in whom the ADHD symptoms were excluded by Conners´ test. The results of our research suggest the an association of the genes with ADHD. Specifically, after multiple testing correction, sex correction, and power analysis, it could be concluded:

1) the risk of ADHD is significantly increased in the presence of one risk allele in genes DRD2 (7,5-fold), 5-HTT (2,7-fold) and DAT1 (1,6-fold)
2) the risk of ADHD is significantly increased at homozygotes for risk alleles in genes DRD2 (54-fold), 5-HTT (6,7-fold) and DAT1 (6,6-fold)

For polymorphisms G444A and C1603T in DBH, which were detected by univariant analysis, haplotype analysis was performed and resulted in conclusion that:

3) the risk of ADHD is significantly increased in the presence of allele DBH +444A as well as in the presence of allele DBH +1603T (14,9-fold).

Genetic studies of ADHD have a fundamental importance not only from theoretical but also from practical point of view. They allow the choice of a convenient medicament according to genetic ethiology. Nowadays, the farmakological aproach is the most effective way of treatment of ADHD and its early application protects from the progress of secondary disorders.