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SEARCHING FOR THE GENETIC MARKERS CONNECTED WITH PARANOID SCHIZOPHRENIA AND CONDITIONING THE TREATMENT EFFICIENCY

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Aim: The aim of the study was to find genetic markers which can influence on susceptibility of paranoid schizophrenia and the treatment efficiency measured by the PANSS. We analyzed genes polymorphisms: DRD2 (Taq 1A, in egzon 8, - 141 C ins/del), DAT, GRIK3, SERT, 5HT2A, MAO-A, COMT.

Method: One hundred and ninety one patients with the diagnosis of paranoid schizophrenia were recruited as study group. To obtain the diagnosis meeting the criteria to ICD-10 we used the polish version of CIDI - Composite International Diagnostic Interview. Exclusion criteria included serious neurological disorders, major somatic disorders impairing cognitive functions and diagnosed mental impairment. The intensity of psychopathological symptoms was examined using the PANSS. Genomic DNA was extracted from leucocytes using the Miller's salting method. Polymorphisms were studied by the PCR method.

Statistical analyses were performed by the Statistica computer program, specifically Pearson's chi-square test. Associations between the treatment progress and the genotype were studied by analysis of variance (ANOVA).

Results: We didn't find associations between investigated genes polymorphisms and susceptibility of paranoid schizophrenia. Probably, there is no influence of studied polymorphisms on the treatment efficiency.

Conclusions: No differences were found in the genotypes distribution in investigated genes polymorphisms between the whole schizophrenics and the control group. No association was found between any particular genotype and the effect of antipsychotic treatment.

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