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Metro task. Left angular activity, also linked to social cognition [4], was reduced in patients with more IOR. The results suggest that referential thinking in psychotic patients is associated with abnormal brain activity in brain regions with a role in social cognition.

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P.605 The risk prediction of development of neuroleptic hyperprolactinemia based on genetic markers

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Background: The main method to treatment of schizophrenia is long-term antipsychotic therapy, which not only improves the long-term prognosis of the disease and facilitates its transition to remission, but unfortunately also has a wide range of side effects such as hyperprolactinemia (HP) [1,2]. The main goal of pharmacogenetics is the search for predictors of response to therapy, as well as determining the probability of developing side effects [3]. The target genes of the clinical effects of antipsychotic drugs are genes determining activity of neurotransmitter systems and genes of biotransformation of xenobiotics.

The present study aimed to investigate the most significant socio-demographic, clinical and genetic indicators that significantly contribute to the development of HP.

Methods: Four hundred and forty-six Russian patients with schizophrenia were examined. The average age of patients was 41.5 ± 13.4 years. Clinical symptomatology was assessed with Positive and Negative Syndrome Scale (PANSS), the Clinical Global Impression (CGI) scale, the scale of side

effect assessment (UKU). Evaluation of serum prolactin level was performed by ELISA using reagents set PRL of Test System (USA). Regression analysis was performed with HP as a dependent dichotomous variable and polymorphisms as factors. After calculation of the regression model was performed mixed discriminant analysis followed by cross-validation for the selected predictors. For the final model sensitivity, specificity, AUC (Area Under Curve), positive and negative predictive values were calculated.

Results: We studied 88 neurotransmitter polymorphic genes variants including HTR2C, HTR3A, HTR3B, HTR6, HTR2A, HTR1A, HTR1B, DRD1, DRD2, DRD2/ANKK1, DRD3, DRD4, SLC6A3, SLC6A2, COMT and genes of biotransformation of xenobiotics CYP1A2*1F, CYP2D6*3, CYP2D6*4, CYP2C19*3, CYP2C19*17, CYP2C19*2, GSTP1. In patients without HP, the average level of the hormone was 12.9 [8.12; 16.85] ng/ml, and in patients with HP: 49.66 [32.47; 76.39] ng/ml. In the analysis of the distribution of patients by sex, the prevalence of patients of female gender was revealed in the group with HP (63.8%), and in the group without HP male sex was most prevalent (70.0%). This indicates that the female gender is a factor determining vulnerability regarding the development of this side effect on the background of antipsychotic therapy ($p=0.006$).

Based on the results of a pharmacogenetic research a molecular-genetic panel for the development of neuroendocrine side effects of antipsychotic therapy in patients with schizophrenia was developed, which includes both genetic variants and as other signs: age, sex, daily average antipsychotics doses (expressed in chlorpromazine equivalents), "rs1176744" (HTR3B), "rs10042486" (HTR1A), "rs936461" (DRD4), "rs134655" (DRD2), "rs179997" (ATXN1), "rs1076562" (DRD2), "rs3773678" (DRD3), "rs167771" (DRD3), "rs1587756" (DRD3), "rs3892097" (CYP2D6*4), "rs1341239" (PRL), "rs4975646" (SLC6A3), "rs13333066" (SLC6A2).

Conclusion: This molecular-genetic panel can be used to predict the risk of developing HP even before the start of treatment of patients with schizophrenia for purposeful individual therapeutic treatment in this category of patients.

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