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SYMPTOM DIMENSIONS OF SCHIZOPHRENIA IN THE CONTEXT OF MTHFR GENE POLYMORPHISM

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Introduction. Clinical polymorphism of schizophrenia, defined by Liddle in three classic psychopathological dimensions (psychotic symptoms, disorganization, negative symptoms) is based on factor analysis strategy and casts doubt on the idea of common nature of disease's classical symptoms within a single specific process. The search for biological determinants (endophenotypes, risk alleles) of psychopathological dimensions of schizophrenia represents an actual task, nevertheless the system of gene expression regulation (DNA methylation) is still underinvestigated in this aspect.

Aim. To explore the association between C677T polymorphism of MTHFR gene – the key enzyme for methionine synthesis – and psychopathological dimensions of schizophrenia in repetitive episode of illness relapse.

Methods. SAPS\SANS questionnaires were used for clinical assessment of patients, many years suffering from schizophrenia (mean illness duration 16,4±9,9 years); PCR genotyping strategy was used to identify allelic variants of MTHFR.

Results. Mean score of dimension 'disorganization' was almost twice higher (18,26 vs.10,91, $p<0,05$) in group of T-allele carriers with lower enzymatic activity of MTHFR (mostly due to such symptoms as derailment, tangentiality, incoherence, circumstantiality, logorrhea, distractibility, also SANS sign 'inappropriate affect').

Conclusion. Genetically determined dysregulation of methylation patterns in brain can mediate specific biochemical and electrophysiological 'shifts' and result in specific abnormalities of thinking and behavior in schizophrenia. Neurocognitive and neurophysiological dysfunction underlying such linkage is under further investigation

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