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PREDICTION OF CLINICAL SYMPTOMS OF SCHIZOPHRENIA BASED ON COMT METHYLATION MARKER

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Introduction: The dopamine hypothesis of schizophrenia is based on the fact that hyper-dopaminergic state is involved in causing psychosis and antipsychotic drugs block the dopamine receptor. *COMT* regulates the homeostatic levels of neurotransmitter dopamine in the synapses and plays a role in the neurocognitive function. The dysregulation of dopamine in the prefrontal cortex influences the cognitive function and the severity of the psychotic symptoms in schizophrenia. During epigenetic event, methylated *COMT* gene may cause reduction in its expression and contribute to the clinical presentation of schizophrenia. Therefore, the aim of this study was to assess the feasibility of using *COMT* DNA methylation for the prediction of specific psychotic presentation of schizophrenia.

Materials and method: In this study, 138 schizophrenia patients were recruited from the Psychiatry Clinic, Hospital Tengku Ampuan Afzan, Kuantan Pahang. Genomic DNA from peripheral blood was subjected to the Methylight Taqman® analysis for quantitative measurement of the *COMT* DNA methylation. The psychopathological symptoms were assessed using the Positive and Negative Syndrome Scale (PANSS).

Results: The regression analysis showed that the Positive and Excited subdomains of PANSS were significant predictors of *COMT* hypomethylation (ß= -0.288, p= -0.031; ß= -0.288, p= -0.031). The Excited subdomain of PANSS was negatively correlated with *COMT* DNA methylation (r^2= -0.380, p= 0.000) as well as the Depressed subdomain (r^2= -0.288, p= 0.001).

Conclusion: The relationship between DNA methylation of *COMT* with the positive, excited and depressed symptoms might indicate the epigenetic role of *COMT* gene in the manifestation of schizophrenia.