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The *MTHFR* gene predict weight change in drug-naïve patients with bipolar II disorder

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Objective: Patients with BP-II have a higher prevalence rate of metabolic disturbance and obesity than do the general population. Genetic variants of the methylene tetrahydrofolate reductase (*MTHFR*) gene have been regarded as predictors of weight gain in schizophrenia. In the present study, we investigated whether the *MTHFR* C677T polymorphism may predict changes in metabolic indices after 12 weeks of treatment in patients with BP-II.

Methods: First diagnosed patients (n=117) with BP-II according to DSM-IV criteria were recruited. Metabolic profiles (cholesterol, triglyceride, HbA1C, fasting serum glucose, body mass index (BMI)) were measured at baseline and 2, 8, and 12 weeks post-treatment. The genotype of the *MTHFR* polymorphism was determined using a polymerase chain reaction-restriction fragment length polymorphism analysis. Multiple linear regressions with generalized estimating equation methods were used for analysis of repeated assessments.

Results: Seventy-six (65.0%) patients completed the intervention. Significantly difference in BMI change was associated with the *MTHFR* C677T genotypes (P=0.005). Patients with the C/C genotypes had higher frequency of metabolic syndrome at baseline than those with the C/T+T/T genotypes; no significant difference in frequency of metabolic syndrome was found at between the two genotypes after 12 weeks of treatment.

Conclusion: We conclude that the *MTHFR* C677T polymorphism is associated with changes in BMI and metabolic syndrome in BP-II patients after 12 weeks of treatment.

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