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TWO NOVEL LOCI ASSOCIATED WITH SCHIZOPHRENIA USING DMS AS ENDOPHENOTYPE

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Objective: To capture common variants of schizophrenia by using quantitative trait, DMS(delay matching to sample), as endophenotype of schizophrenia.

Method: 100 first-episode schizophrenia patients and 140 healthy controls were recruited for DMS test, linear regression model was built to associate interaction of genotyped markers and affect status with DMS test results.

Result: two SNPs reache P value of association significance(5×10^{-6}), rs17069969 located in MAML2 in chromosome 3 when associated with DMS_TC and rs555329 positioned in FHIT in chromosome 11 when associated with both DMS_PC_A and DMS_PEGC.

Conclusion: DMS was proved to be reasonable index as endophenotype to capture loci susceptible to schizophrenia. Pleiotropic effect of gene played an important role in genesis of schizophrenia.

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