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A WEAK ASSOCIATION OF THE CLDN5 LOCUS WITH SCHIZOPHRENIA IN CHINESE CASE-CONTROL SAMPLES

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Background: An increasing number of studies have described the relationship between velo-cardio-facial syndrome (VCFS) and schizophrenia. In a family-based study, we found that rs10314, a single nucleotide polymorphism (SNP) present in the 3'-flanking region of the CLDN5 gene, was associated with schizophrenia among a Chinese population. High false positive rate is a common problem with the association study of human diseases. It is very important to replicate an initial finding with different samples and experimental designs.

Methods: A total of 749 patients with schizophrenia and 383 age and sex matched healthy control subjects in Chinese population were recruited. PCR-based RFLP protocol was applied to genotype rs10314 to see its disease association.

Results: The χ^2 goodness-of-fit test showed that the genotypic distributions of rs10314 were in Hardy-Weinberg equilibrium in both the patient group ($\chi^2=1.12$, $P=0.289$) and the control group ($\chi^2=0.22$, $P=0.639$). rs10314 was associated with schizophrenia with an odds ratio (OR) of 1.32 in the male subjects ($\chi^2=5.45$, $P=0.02$, 95% CI 1.05-1.67) but not in the female subjects ($\chi^2=0.64$, $P=0.425$, OR=1.14, 95% CI 0.83-1.57). The χ^2 test showed a genotypic association only for combined samples ($\chi^2=7.80$, $df=2$, $P=0.02$). SNP rs10314 is a G to C base change. Frequency of the genotypes containing the C allele was significantly higher in the patient group than in the control group.

Conclusions: The present work shows that the CLDN5 gene polymorphism is more likely to be involved in schizophrenic men than women, suggesting that this gene may contribute to the gender differences in schizophrenia.