P-1331 - POPULATION-BASED AND FAMILY-BASED ASSOCIATION STUDIES OF ANK3 LOCUS AND SCHIZOPHRENIA

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Background: rs10761482 in ANK3 gene showed a significant association with schizophrenia in a genome-wide association study (GWAS). Another marker rs10994336 in ANK3 with the risk of bipolar disorder (BD) which might have more genetic overlap with schizophrenia, had been reported in two meta-analyses of GWAS.

Objective: In this study, we investigated the association between ANK3 polymorphisms and the susceptibility of schizophrenia in Chinese Han population.

Methods: Population-based (schizophrenia patients = 516 and controls = 400) and family based (trios of early onset schizophrenia= 81) study was performed through genotyping the most promising makers rs10761482, rs10994336, and two missenses rs3808942 and rs3808943 near promoter of ANK3. Particularly, we conducted an association analysis for the combined case-control and family samples.

Results: Our population-based study replicated the association between rs10761482 (P=0.0268 with C allele) and schizophrenia, and detected a novel association with rs10994336 (P=4.0×10^{-4} with T allele). Haplotype analysis revealed the higher frequencies of C-T, and T-C (rs10761482-10994336) in the cases than controls (P=0.0032 and P=0.0012, respectively). In the family study, the C allele of rs10761482 (P=0.0940) and T allele of rs10994336 (P=0.0832) were slightly over-transmitted, and T-C was significantly associated with schizophrenia (P=0.0304). The results from the combined samples analysis were consistent with independent analysis. rs10761482, rs10994336, C-T, and T-C were significantly associated with schizophrenia (P=3.3×10^{-6}~3.9×10^{-5}), whilst rs3808942 and rs3808943 did not reach normal significance.

Conclusions: Our data strongly support ANK3 gene is a schizophrenia susceptibility gene, and also provide further evidence for the shared susceptibility loci between schizophrenia and BD.