Journal of Human Genetics (2013) 58, 182

www.nature.com/jhg

COMMENTARY

A commentary on DRD2 haplotype associated with negative symptoms and sustained attention deficits in Han Chinese with schizophrenia in Taiwan

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Journal of Human Genetics (2013) **58,** 182; doi:10.1038/jhg.2013.13; published online 28 February 2013

Schizophrenia (SZ) is a heterogeneous psychiatric disorder with a heritability of around 80%, caused by both genetic and environmental factors and their interactions.[1,2] Dopamine system dysfunction has been widely implicated in the pathogenesis of SZ.[3] Emerging evidence suggests that genetic factors, such as variations in the dopamine receptor D2 (DRD2) gene, may have a critical role in the development of SZ.[4,5] The human DRD2 gene is located on chromosome 11 at q22q23 and spans ~270 kb with a ~250-kb intron separating the first and second exons.[6] In this issue of *Journal of Human Genetics*, Chien *et al.*[7] evaluated the relationships between DRD2 genetic polymorphisms and clinical symptoms and neuropsychological function in SZ patients. In this family-based study of 2408 Han Chinese, including 1214 affected individuals from 616 families, seven single-nucleotide polymorphisms (SNPs) and two blocks were assessed to provide a comprehensive and reliable conclusion on the role of these genetic variants of DRD2 in the disease process of SZ. Their results indicated that the A allele of rs1079727, G allele of rs2283265, A allele of rs1124492 and the risk haplotype [rs1079727(A)–rs2440390(C)–rs2283265(G)] of block 3 were associated with more severe negative symptoms, and the risk haplotype [rs1801028(G)–rs1110977(A)–rs1124492(C)–rs2734841(T)] of block 4 was associated with poorer neuropsychological performance in the sustained attention task. Although the exact functions and effects of DRD2 genetic polymorphisms on clinical symptoms and neuropsychological function in SZ patients are not yet clear, a possible reason could be that inherited mutations in DRD2 may be associated with the changes in central nervous system noradrenergic and dopaminergic function and thereby could possibly explain inter-individual differences in symptom severity in SZ patients.[8] These relationships have the potential to provide functional profiling of the DRD2 gene involved in the development of SZ. It may also be a director for further studies in diagnosis and clinical therapy of SZ.

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