

# Identification of Genes for Schizophrenia Susceptibility

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## Abstract

**Introduction:** Advances in genotyping, mapping and genome analysis methods over the last few years offer great promise towards the discovery of genes involved in the pathogenesis of schizophrenia, a mental disorder with a high degree of heritability. **Methods:** This article draws on published reports in major international journals in the field of schizophrenia and human genetics. **Results:** We summarise the major findings from family linkage studies, genome scan with microsatellite markers and association studies with polymorphisms in candidate genes. However, although recent developments in the technology for genotyping and gene identification have provided new leads to genetic abnormalities underlying schizophrenia, they have yet to result in the identification of any disease gene. There are both positive and negative data for reported linkages to specific chromosomal regions and candidate gene polymorphisms. **Conclusions:** Conflicting data and nonreplication of association and linkage studies are problems that need to be addressed. One solution might be clearer and narrower definition of subphenotypes and use of only a specific phenotypic marker in linkage and association studies. When successful, identification of susceptibility genes will lead to better understanding of cognitive functions and socio-emotional behaviour and also help in the formulation of preventive strategies for those found to be at high risk.

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**Key words:** Candidate genes, Genome scan, Linkage, Psychiatric disorder

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