NEWS

Genetics: Large analysis pins down schizophrenia regions

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A large association study links five new genetic regions to schizophrenia and implicates MIR137, a regulatory RNA that plays a role in neuron development, in the disorder. The results were published 18 September in *Nature Genetics*[1].

Genome-wide association studies can identify genetic regions that are more likely to be mutated in individuals with a disorder than in controls. However, these studies **need a large number of participants** to achieve significance.

A large international collaboration, called the **Psychiatric GWAS Consortium**, aims to **resolve this issue** by combining data from several individual studies.

In the new study, researchers from the schizophrenia arm of the consortium looked at more than a million single nucleotide polymorphisms (SNPs) — genetic variants that alter a single base pair — in 9,394 individuals with schizophrenia compared with 12,462 controls.

They then reexamined any SNP that had a genome-wide association in this dataset in another group of 8,442 individuals with schizophrenia and 21,397 controls.

Together, the two steps identified five new chromosomal regions associated with schizophrenia at the level of genome-wide significance: 1p21.3, 2q32.3, 8p23.2, 8q21.3 and 10q24.32-q24.33. They also identified an association between schizophrenia and two regions already associated with the disorder: 6p21.32-p22.1 and 18q21.2.

The most significant association is a SNP within MIR137, a microRNA that regulates the generation of new neurons. Four of the regions associated with schizophrenia overlap with genes that are predicted to be regulated by MIR137, the study found.

MicroRNAs, which control gene expression by inactivating the RNA transcript that codes for protein, are emerging as important players **in neurodevelopmental disorders**.

References:

1: Ripke S. *et al. Nat. Genet.* Epub ahead of print (2011) **Abstract**