Unlocking the genetic code of schizophrenia

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A comprehensive mapping of the genes and biological pathways involved in schizophrenia reveals new targets for treatment as well as methods for disease risk prediction, according to a study published online this week in Molecular Psychiatry. The findings suggest that there is much more consistency in the genes and biological pathways involved in schizophrenia across populations than previously appreciated, in contrast to the marked variability at the level of single-nucleotide polymorphisms (SNPs).

To identify and prioritize the genes involved in schizophrenia, Alexander B. Niculescu and colleagues combined genome-wide association data with gene expression and other genetic data from independent
human and animal model studies. This approach, called Convergent Functional Genomics, focuses on gene-level reproducibility across independent studies, identifying and prioritizing specific genes. The investigators then demonstrated that a panel of genes thus prioritized can distinguish between schizophrenic individuals and healthy controls, in four independent cohorts of two different ethnicities. This provides a prototype for how genetic risk can be assessed in individuals before the disease manifests itself.

The work also identified new targets for drug development, and the possible repositioning of existing drugs currently used for other indications for the treatment of schizophrenia. Lastly, the investigators compared the genomic landscape of schizophrenia with that of other psychiatric disorders, showing significant overlap and pinpointing areas of future progress in terms of a better, more biologically-based classification, of psychiatric disorders.

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