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► **COVER:** 'Acid trip' by Patrick Morgan, inspired by the Review on p541.



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As complex traits go, psychiatric conditions are about as complicated as you get, characterized as they are by many distinct biological mechanisms, genetic, allelic and phenotypic heterogeneity, and environmental influences. The nature of this beast means that we must proceed with caution when applying genome-wide association (GWA) studies, which are the present 'answer' to complex traits.

Our current, still rather unclear, picture of the genetics of psychiatric conditions is the result of a string of failed or irreproducible attempts at identifying variants using linkage, candidate and association studies. But there are signs that the field has turned a corner — convincingly replicated findings have emerged by incorporating endophenotypes and environmental risk factors into analyses. We also have stricter standards for GWA studies — increasing sample sizes and sharpening phenotypic boundaries should iron out many of the current statistical limitations. Or will it?

As Burmeister and colleagues point out on page 527, the best strategy will be determined by the degree of heterogeneity. If variants are common and each makes only a marginal contribution to risk for any disorder, then GWA studies using vastly larger sample sizes might be fruitful, as was the case for type 2 diabetes. But recent publications highlight the importance of rare structural mutations in autism (see the Review by Abrahams and Geschwind in our May issue) and schizophrenia (Walsh, T. *et al. Science* **320**, 539–543 (2008); Xu, B. *et al. Nature Genet.* 30 May 2008 (doi:10.1038/ng.162)). If many risk alleles are rare then we need to throw efforts into high-throughput resequencing instead. And these are just the extreme scenarios.

Reproducible results will be hard won but hugely valuable — perhaps unusually for complex disorders, new biological information is expected to be incorporated quickly into clinical practice, primarily in diagnosis.

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