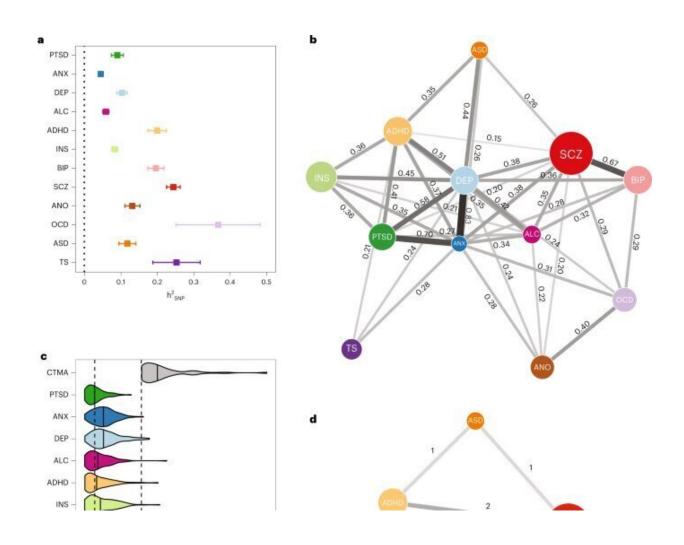


A genome-wide association study for overlap of 12 psychiatric disorders

December 6 2022, by Bob Yirka



SNP-based heritability, genetic correlations and cross-trait meta-analysis lead SNP P values of the 12 psychiatric disorders. Credit: *Nature Genetics* (2022). DOI: 10.1038/s41588-022-01245-2



A team of researchers from Vrije Universiteit Amsterdam in the Netherlands and the Veterans Administration in the U.S. has conducted a genome-wide association study looking into genetic overlap between 12 common psychiatric disorders. The group describes profiling pleiotropic genetic incidences to 12 common psychiatric disorders in their paper published in the journal *Nature Genetics*.

Many years ago, psychiatrists and other <u>medical professionals</u> preferred to think of psychiatric conditions as separate diseases, unrelated to one another. More recently, genetics findings involved in psychiatric disorders have suggested that not only are some of them related, but some have overlap, which suggests that illnesses such as <u>autism</u> might have multiple forms, giving rise to a spectrum of diseases.

In this new effort, the research team conducted a cross-examination of 12 psychiatric disorders, looking specifically for genetic overlap. Their work involved conducting a cross-trait meta-analysis to study the impact of single-nucleotide polymorphisms (SNPs), genes in general, cells, pathways and tissue types that might be shared by the 12 disorders ADHD, alcoholism, anorexia, anxiety disorder, autism, bipolarism, depression, OCD, PTSD, schizophrenia and Tourette syndrome.

The analysis was conducted using publicly available statistics on the disorders under study and resulted in discovery of a wide variation in genetic strength of signals associated with the disorders.

The researchers also used software provided by the University of Queensland/QIMR Berghofer Medical Research Institute's Complex Trait Genetics Virtual Lab to look for genetic overlap in the disorders. Additionally, they conducted functional mapping and annotation to search for loci associated with SNPs discovered in the cross-trait analysis.



The researchers found over three-dozen genes and multiple genomic risk loci that seemed to coincide with overlapping associations between disorders. They also found associations that were not overlapping but shared pathways and multiple neuronal cell types.

Still, they were not able to find any SNPs or loci that could definitively be associated with more than two of the 12 disorders—and just two genes. They also found that schizophrenia-related associations were the most common—they were involved in almost half of all those discovered.

More information: Cato Romero et al, Exploring the genetic overlap between twelve psychiatric disorders, *Nature Genetics* (2022). DOI: 10.1038/s41588-022-01245-2

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