

Problems with alcohol? 29 gene variants may explain why

May 25 2020



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A genome-wide analysis of more than 435,000 people has identified 29 genetic variants linked to problematic drinking, researchers at Yale University School of Medicine and colleagues report May 25 in the



journal Nature Neuroscience.

"The new data triple the number of known genetic risk loci associated with problematic alcohol use," said Yale's Joel Gelernter, the Foundations Fund Professor of Psychiatry and professor of genetics and of neuroscience, who is the senior author of the multi-institutional study.

The study includes genome-wide analysis of people of European ancestry contained in four separate biobanks or datasets. The researchers looked for shared genetic variants among those who met criteria for problematic alcohol use, including <u>alcohol use disorder</u> and alcohol use with medical consequences. These disorders are major contributors to a wide variety of medical problems worldwide.

The analysis found 19 previously unknown independent genetic <u>risk</u> <u>factors</u> for problematic alcohol use, and confirmed 10 previously identified risk factors.

The meta-analysis of biobank data also included information on genetic risk factors for several <u>psychiatric disorders</u>. This information allowed researchers to study shared genetic associations between problematic drinking and disorders such as depression and anxiety.

They also found genetic heritability of these variants was enriched in the brain and in evolutionarily conserved regulatory regions of the genome, attesting to their importance in biological function. Using a technique called Mendelian randomization, they were able to investigate how one genetically influenced trait affects another genetically linked trait.

"This gives us ways to understand causal relations between problematic alcohol use traits such as psychiatric states, risk-taking behavior, and cognitive performance," said Yale's Hang Zhou, associate research scientist in psychiatry and lead author of the study.



"With these results, we are also in a better position to evaluate individuallevel risk for problematic <u>alcohol</u> use," Gelernter said.

More information: Genome-wide meta-analysis of problematic alcohol use in 435,563 individuals yields insights into biology and relationships with other traits, *Nature Neuroscience* (2020). DOI: 10.1038/s41593-020-0643-5, www.nature.com/articles/s41593-020-0643-5

Provided by Yale University

Citation: Problems with alcohol? 29 gene variants may explain why (2020, May 25) retrieved 23 May 2024 from <u>https://medicalxpress.com/news/2020-05-problems-alcohol-gene-variants.html</u>

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