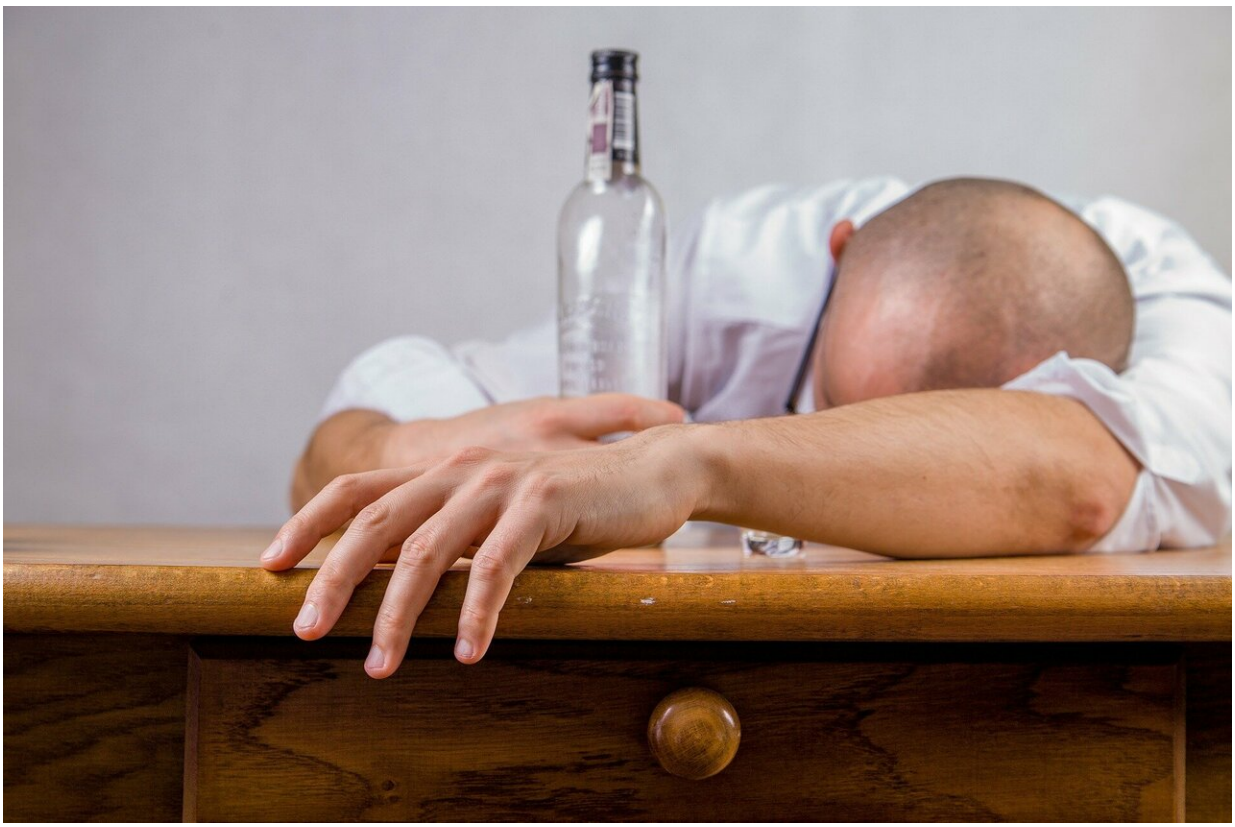
Medical Xpress

Study reveals genes associated with heavy drinking and alcoholism

April 2 2019



Credit: CC0 Public Domain

A large genomic study of nearly 275,000 people led by Penn Medicine researchers revealed new insights into genetic drivers of heavy drinking and alcohol use disorder (AUD), the uncontrollable pattern of alcohol

use commonly referred to as alcoholism. In the largest-ever genome-wide association study (GWAS) of both traits in the same population, a team of researchers found 18 genetic variants of significance associated with either heavy alcohol consumption, AUD, or both. Interestingly, while five of the variants overlapped, eight were only associated with consumption and five with AUD only.

The findings, published this week in *Nature Communications*, suggest that, although heavy drinking is a prerequisite for AUD, variants in several genes—DRD2 and SIX3, for example—may need to be present for people to develop AUD.

"This study has revealed an important genetic independence of these two traits that we haven't seen as clearly before," said Henry R. Kranzler, MD, a professor of Psychiatry in the Perelman School of Medicine at the University of Pennsylvania, and first author of the study. "Focusing on variants only linked to AUD may help identify people at risk and find targets for the development of medications to treat it. The same applies to alcohol consumption, as those variants could inform interventions to help reduce consumption in heavy drinkers, who face their own set of adverse effects."

An estimated 16 million people in the United States suffer from AUD, according to the National Institute on Alcohol Abuse and Alcoholism (NIAAA). Excessive drinking is associated with a host of adverse medical, psychiatric, and social consequences—and an estimated 88,000 Americans die every year from alcohol-related causes. What's more, alcohol misuse costs the United States nearly $300 billion a year, according to the most recent stats from the NIAAA.

Environmental, hereditary, and genetic factors all play a role in AUD; however, many of the variants across the genome believed to be associated with the disorder remain to be identified.

For the study, the researchers used genetic data from the multi-ethnic Million Veteran Program (MVP), a national, voluntary research program sponsored by the Department of Veterans Affairs, which includes white, African-American, Latino, and Asian participants. The diverse study sample is notable, in that it included more than 50,000 African-Americans, one of the largest genome-wide studies of this population. Scores from the Alcohol Use Disorder Identification Test-Consumption (AUDIT-C) screenings and AUD diagnoses were obtained from the same population (a total of 274,424 people) to conduct the GWAS for the two traits. The researchers also analyzed other data from health records to look for correlations between genes and diseases, as well as other non-alcohol related traits.

A strength of this study is the size of the study sample. Large-scale biobanks, such as the MVP, offer the potential to link genes to health-related traits documented in electronic health records with greater statistical power than can ordinarily be achieved in genome-wide studies.

The researchers identified 13 independent genetic variants associated with alcohol consumption, eight of which had not been previously reported, including VRK2, DCLK2, ISL1, FTO, IGF2BP1, PPR1R3B, BRAP, and RBX1. Ten variants were associated with AUD, including seven that had not been previously associated with it: GCKR, SIX3, SLC39A8, DRD2 (rs4936277 and rs61902812), chr10q25.1, and FTO. The five variants associated with both heavy drinking and AUD were ADH1B, ADH1C, FTO, GCKR, and SLC39A8.

They also discovered 188 different genetic correlations to health outcomes among the study group, some in opposite directions. Notably, heavy drinking was associated with lower risk of coronary artery disease and glycemic traits, including type 2 diabetes, but positively correlated with overall health rating, HDL or "good" cholesterol concentration, and years of education. AUD was significantly correlated with 111 traits or

diseases, including lower intelligence and likelihood of quitting smoking and greater risk of insomnia and most psychiatric disorders. The genetic differences between the two alcohol-related conditions and the observed opposite correlations point to potentially important differences in comorbidity and prognosis. That underscores the need to identify the effects of the risk variants in future, especially where they diverge by traits, to better understand and treat them, the authors said.

More information: Henry R. Kranzler et al, Genome-wide association study of alcohol consumption and use disorder in 274,424 individuals from multiple populations, *Nature Communications* (2019). DOI: 10.1038/s41467-019-09480-8

Provided by Perelman School of Medicine at the University of Pennsylvania

Citation: Study reveals genes associated with heavy drinking and alcoholism (2019, April 2) retrieved 25 April 2024 from https://medicalxpress.com/news/2019-04-reveals-genes-heavy-alcoholism.html

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.