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TITLE: Predicting alcohol use from genome-wide polygenic scores, environmental factors, and their interactions.

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KEYWORDS: polygenic, GxE, alcohol use, AUDIT-C, emerging adulthood

ABSTRACT:

Background:

Alcohol use in emerging adulthood is associated with adverse life outcomes but its risk factors are not well known. Genome-wide polygenic scores (GPS) based on a number of genome-wide association (GWA) studies for alcohol consumption have been able to predict alcohol use, although variance accounted for is rather low (~2.5%) [1]. Identifying environments that help reducing alcohol consumption among people with greater genetic propensities for alcohol use is important for developing effective interventions. Here, we tested if genetic influences on alcohol consumption change across environmental contexts, i.e., gene-environment (GxE) interactions.

Methods:

We predicted alcohol use in 3153 adults aged 22 years from the Twins Early Development Study (TEDS) using (a) GPS based on genome-wide association studies for the target phenotypes number of drinks per week [1] and Alcohol Use Disorders Identification Test (AUDIT-C) scores [2], (b) 30 environmental factors, and (c) their interactions (i.e. GxE effects).

Results:

The GPS accounted for up to 1.9% of the variance in alcohol use (i.e. AUDIT-C score), while the 30 measures of environmental factors together accounted for 21%. The 30 GPS-environment interaction terms accounted for an additional 0.3% variance, but none of the interactions survived multiple testing threshold.

Discussion:

We found that both genetic and environmental factors predict alcohol use in young adults, but we did not find support for GxE interaction effects on alcohol use. Our findings suggest that GPS and environmental factors have primarily direct, additive effects rather than interacting systematically.

References:
1.   Liu, M., et al., *Association studies of up to 1.2 million individuals yield new insights into the genetic etiology of tobacco and alcohol use.* Nat Genet, 2019. **51**(2): p. 237-244.
2.   Sanchez-Roige, S., et al., *Genome-Wide Association Study Meta-Analysis of the Alcohol Use Disorders Identification Test (AUDIT) in Two Population-Based Cohorts.* Am J Psychiatry, 2019. **176**(2): p. 107-118.