Alcohol misuse is moderately heritable, with ~50% of the variance attributable to additive genetic influences (Verhulst et al. 2015). However, genetic influences on alcohol misuse are weaker among those in a committed relationship (Barr et al. 2015). However, genetic influences on alcohol misuse are weaker among those in a committed relationship (Barr et al. 2015; Heath et al. 1989), likely due to increased social control (Umberston et al. 2010). Men to over benefit from romantic partnerships in terms of health (Kiecolt-Glaser and Newton 2001). In the current analyses, we replicate findings from twin models using genome-wide polygenic scores (GPS) derived from a GWAS of drinks per week in ~1.3 million individuals (GSCAN, Nature, Forthcoming).

We answer the following research questions:

1. Do polygenic scores from a large scale GWAS (GSCAN PGS) predict various levels of severity in alcohol misuse (from consumption to problems)?
2. Does relationship status moderate the association between GSCAN PGS and alcohol misuse?
3. Are there sex differences in GxE?

Overall, Polygenic Scores for alcohol consumption from a large scale GWAS predicted all levels of alcohol misuse, from drinking frequency to alcohol dependence symptoms.

PGS show a stronger association in those not in a relationship compared to those in a relationship (top row). A significant 3-way interaction reveals this effect is driven primarily by males (bottom row).

**References**


