THE GENETICS OF ALCOHOL DEPENDENCE:
HERITABILITY AND GENOME WIDE ASSOCIATION ANALYSES

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RESULTS

• Twin based heritability estimate of AD is 60% (55%-69%).
• GCTA shows that common SNPs jointly capture 33% (SE=0.12, p = 0.002) of this heritability.
• Top GWAS signals in 4q31.1, 2p16.1, 6q25.1, 7p14.1 with the strongest association for rs55768019 (P=7.58 ×10⁻⁷) (Fig. 1)
• Concordance of SNPs effects between our study and Gelernter et al, 2014 (permuted P=9.99×10⁻⁴ (95% CI: 5.12×10⁻⁵-0.0056).

CONCLUSIONS

• First GWAS of AD using the AUDIT measure found consistent results with previous genetic studies using DSM diagnosis.
• Concordance in heritability estimates and direction of SNPs effect and overlap with top hits from previous GWAS.
• The questionnaire based AUDIT may provide a useful, cost-effective alternative to DSM diagnosis when phenotyping large population-based cohorts or biobanks.

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