Submitter Name: Gretchen Saunders
Submitted email: saund247@umn.edu
PI Name (if different): Scott Vrieze
PI email (if different): vrieze@umn.edu

Trans-ancestry GWAS meta-analysis of tobacco and alcohol use

Gretchen Saunders[1], GWAS & Sequencing Consortium of Alcohol and Nicotine Use (GSCAN)

[1]Psychology, University of Minnesota, Minneapolis, MN

Despite the global nature of alcohol and nicotine use, the vast majority of genome-wide association studies thus far have been restricted to European only samples. To better understand genetic influences on nicotine and alcohol use behaviors we conducted a trans-ancestry GWAS meta-analysis in up to 3.4 million individuals of diverse ancestries from the four major ancestral groups: African (up to N = 121,858), American (up to N = 285,155), East Asian (up to N = 298,624), and European (up to N = 2,669,029). For the phenotype indexing whether an individual had ever been a regular smoker (N = 3,377,408 from 75 studies) we identified 916 loci; for age of initiation of regular smoking (N = 731,870; 64 studies) we identified 33 loci; for cigarettes per day, a measure of heaviness of use (N = 782,790; 81 studies) we identified 140 loci; for a measure of smoking cessation (N = 1,400,906; 74 studies) we identified 132 loci; and finally for a measure of alcohol use, drinks per week (N = 2,896,131; 62 studies), we identified 426 loci. Our results suggested that the majority of these loci show homogeneous effect sizes across ancestry, with only a minority providing evidence for allelic heterogeneity. Finally, we report ancestry-specific heritability estimates, genetic correlations, and polygenic prediction and bias across ancestries.