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

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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 = 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.