Scott Vrieze on behalf of the GWAS and Sequencing Consortium of Alcohol and Nicotine use

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Abstract: Tobacco and alcohol use are modifiable addictive behaviors that strongly influence risk for a wide range of common complex disease. They are partially influenced by environmental circumstance but also moderately heritable. The handful of genetic variants discovered to be robustly associated with these behaviors have largely been limited to genes involved in nicotine and alcohol metabolism, and nicotinic acetylcholine receptor genes. To expand the catalogue of associated genetic variants, we conducted a genome-wide association meta-analysis of five related tobacco and alcohol use behaviors: smoking initiation, cigarettes smoked per day in smokers, age when began smoking regularly, smoking cessation (former versus current smokers), and alcoholic drinks per week. These sample sizes range from 350,000 to 1.2 million, and are an order of magnitude larger than previous genome-wide association analyses of these behaviors. Across all phenotypes, we discovered 533 independently associated variants in 414 independent loci, with 60 loci harboring variants associated with more than one phenotype at genome-wide significant levels. Discovered loci show strong enrichment in central nervous system cell types, implicate longstanding candidate genes for these addictive behaviors, and provide new biological insights into the etiology of alcohol and nicotine use.