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Genome-wide association study of opioid dependence from the Psychiatric Genomics Consortium

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Opioid dependence (OD) is a growing problem affecting public health and social and economic welfare. Understanding its biology to develop more effective preventive strategies and treatments is a priority. The Substance Use Disorder workgroup of the Psychiatric Genomic Consortium completed the analysis of 3,402 OD cases and 2,846 exposed controls. Although no genome-wide significant (GWS) locus was observed in the single-variant association analysis, we identified two GWS signals in the gene-based analysis. *RNF157* (*Ring Finger Protein 157*) was observed in individuals of European descent (p = 1.7E-06); this gene is highly expressed in the brain and regulates dendrite growth and neuronal survival. *ITGB8* (*Integrin Subunit Beta 8*) was significant in the individuals of African descent (p = 1.1E-06); this gene is also expressed in the brain and plays a key role in maintaining normal cerebral angiogenesis. Although they did not survive multiple testing correction, OD-associated loci were particularly enriched with respect to transcriptomic regulation of cerebellar tissues in both African-American and European-American samples (p = 0.031 and p = 0.029, respectively). We are working on the integration of additional individual, aiming to a sample size for Freeze 1 of the PGC opioid GWAS of 4,800 OD cases and 4,600 exposed controls. With the larger sample size, we expect to see additional signals and to be able to examine genetic correlations with other disorders. There is a need for additional samples to understand the biology of opioid use and abuse. The findings expected will permit us to move opioid research forward.