

Large genomewide association study of cannabis dependence: updates from the Substance Use Disorders working group of the Psychiatric Genomics Consortium

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There is some evidence that cannabis dependence has increased in the past decade. Despite this, only a small proportion of dependent individuals participate in treatment. Twin and family studies have consistently produced moderate heritability estimates for cannabis use phenotypes (50-60%). Two prior genomewide association studies have identified loci associated with cannabis dependence but results have been inconsistent. In addition, there have been few conclusive findings regarding the genetic relationships between cannabis dependence and other substance use disorders, psychiatric phenotypes, and health behaviors. The current study is a meta-analysis of over 7,000 cannabis dependent cases (EA+AA) and over 10,000 cannabis exposed controls. In addition to performing the association analysis, ongoing analyses will (a) estimate the heritability explained by genome-wide SNPs in the unrelated cases and controls, (b) partition the heritability according to functional categories and biological networks and pathways, and (c) estimate the genetic correlation between cannabis dependence and other phenotypes using LDHub. Against the backdrop of legislative change related to recreational cannabis use, to our knowledge, this is the largest GWAS of cannabis dependence performed to date, and is an important next step in better understanding the genetic etiology of this substance use disorder.