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## **A genome-wide association study of methamphetamine use among people with HIV**

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**Background:** Amphetamine-like stimulants are the most used psychostimulants, of which methamphetamine has the greatest number of users worldwide. Use is especially prevalent among people with HIV (PWH). Prolonged methamphetamine use can cause lasting damage to the heart, gut, and brain, as well as auditory hallucinations and paranoid thinking. However, relatively little is known about methamphetamine dependence and its genetic contributors. In this study, we set out to identify genetic variants associated with methamphetamine use.

**Methods:** Using genetic information from the Centers for AIDS Research Network of Integrated Clinical Systems (CNICS) cohort, we conducted a multi-ancestry genome-wide association study (GWAS) for methamphetamine use among 5,946 PWH. Based on patient reported outcomes at their first study visit, we identified 1,196 individuals who reported ever using methamphetamine and 4,750 who reported no use in their lifetime. We conducted generalized linear mixed models treating methamphetamine use (never/ever) as the outcome, adjusting for age at visit, the first five genetic principal components and genotyping array as fixed effects and treating the genetic relatedness matrix as a random effect.

**Results:** No single nucleotide polymorphism (SNP) reached genome-wide significance ( $p < 5e10^{-8}$ ) in our study. Further, we compared our results to those reported in three previous GWAS for methamphetamine use. None of the previously reported SNPs reached  $p < 0.05$  in our analysis.

**Discussion:** Our study did not identify any genetic contributors to lifetime methamphetamine use in the CNICS cohort. Larger studies are warranted to better understand the genetic contributors to methamphetamine use.