D29

Huseyin Gedik Advisor(s): Roseann Peterson

Examining Polygenic Risk for Psychiatric Disorders in Ancestrally Diverse College Student Population

Genome-wide association studies (GWAS) have uncovered numerous genetic risk loci associated with complex traits, providing the opportunity to aggregate them to estimate polygenic risk and improve clinical risk prediction. However, most of the published genetic research findings are from populations with European ancestry which hinders the transferability of Polygenic Scores (PGS) across populations. To address this, we employed PGS techniques within an ancestrally diverse college cohort. Our aim was elucidating the associations between polygenic risk profiles and psychiatric outcomes, thereby advancing our understanding of the interplay between genetic predispositions and mental health across populations.The data was from the Spit for Science (S4S) study, college student population, where participants reported on behavioral health (N=9,588; ancestry: 21.3% African [AFR], 12.5% Admixed Americas [AMR], 9.6% East Asian [EAS], 48.1% European [EUR], 8.6% South Asian [SAS]). Using GWAS summary statistics from multiple ancestries weighted by PRS-CSx, we performed trans-ancestry PGS. We tested associations between PGS and psychiatric outcomes. Principal components and sex were covariates. Results were meta-analyzed using METASOFT. This study was approved by the ethics review board at Virginia Commonwealth University. The largest available GWAS summary statistics for common psychiatric disorders were: major depression, PTSD (Million Veterans Program - MVP), problematic alcohol use disorder (AUD) (MVP) and alcohol consumption (AC) (MVP and GSCAN). Significant associations were observed between PGS, AUD and AC. Of all participants 30.3% met the AUD diagnostic criteria. No significant difference in AUD prevalence was observed among sexes. Consumption in males was greater than females (P = 1.07x10-6). Significant associations of alcohol-PGSs with AC (P = 3.97x10-3) and AUD (P = 1.17x10-3) were observed. This study is an extension of polygenic risk prediction among populations.