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Polygenic risk for Attention Deficit Hyperactivity Disorder: investigating the medical phenome across two genetic ancestries

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Introduction: Attention Deficit Hyperactivity Disorder (ADHD) is associated with numerous comorbid behavioral and physical problems. Electronic health records linked to genetic data provide an opportunity to test whether genetic liability for ADHD correlates with ADHD and additional health outcomes in a health care context across developmental epochs.

Methods: We generated polygenic scores (ADHD-PGS) trained on summary statistics from the latest genome-wide association study of ADHD (N=55,374) and applied them to genome-wide data from 12,383 unrelated individuals of African-American ancestry and 66,378 unrelated individuals of European ancestry from the Vanderbilt Biobank.

Results: Overall, only Tobacco use disorder (TUD) was associated with ADHD-PGS in the African-American ancestry group (Odds Ratio (95% Confidence Intervals) = 1.23(1.16 to 1.31), $p=9.3 \times 10^{-9}$). Eighty-six phenotypes were associated with ADHD-PGS in the European ancestry individuals, including ADHD (OR(95%CI)= 1.22(1.16 to 1.29), $p=3.6 \times 10^{-10}$), and TUD (OR(95%CI)= 1.22(1.19 to 1.25), $p=2.8 \times 10^{-46}$). We then stratified outcomes by developmental period (ages 0-11, 12-18, 19-25, 26-40, 41-60, 61-100).

Discussion: Our results suggest that genetic liability to ADHD is associated with ADHD early in life and with increasing burden of health conditions throughout the lifespan (even in the absence of ADHD diagnosis). This work reinforces the utility of applying trait-specific PGSs to biobank data, and performing exploratory sensitivity analyses, to probe relationships amongst clinical conditions.

Keywords:

Attention deficit hyperactivity disorder (ADHD), polygenic scores, Electronic health records