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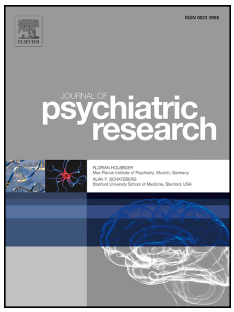

Genome-wide association study of depressive symptoms in the Hispanic Community Health Study/Study of Latinos

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Abstract

Although genome-wide association studies (GWAS) have identified several variants linked to depression, few GWAS of non-European populations have been performed. We conducted a genome-wide analysis of depression in a large, population-based sample of Hispanics/Latinos. Data came from 12,310 adults in the Hispanic Community Health Study/Study of Latinos (HCHS/SOL). Past-week depressive symptoms were assessed using the 10-item Center for Epidemiological Studies of Depression scale. Three phenotypes were examined: a total depression score, a total score modified to account for psychiatric medication use, and a score excluding medication users. We estimated heritability due to common variants (h^2_{SNP}), and performed a GWAS of the three phenotypes. Replication was attempted in three independent Hispanic/Latino cohorts. We also performed sex-stratified analyses, analyzed a binary trait indicating probable depression, and conducted three trans-ethnic analyses. The three phenotypes exhibited significant heritability (h^2_{SNP}=6.3-6.9%; p=0.002) in the total sample. No SNPs were genome-wide significant in analyses of the three phenotypes or the binary indicator of probable depression. In sex-stratified analyses, seven genome-wide significant SNPs (one in females; six in males) were identified, though none was supported through replication. Four out of 24 loci identified in prior GWAS were nominally associated in HCHS/SOL. There was no evidence of overlap in genetic risk factors across ancestry groups, though this may have been due to low power. We conducted the largest GWAS of depression-related phenotypes in Hispanic/Latino adults. Results underscore the genetic complexity of depressive symptoms as a phenotype in this population and suggest the need for much larger samples.