Genetic Associations with Depression in Ancestrally Diverse Populations

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The majority of previous genome-wide association studies of depression have used samples with European ancestry, raising questions about the genetic factors that shape risk for depression in non-European populations and whether genetic factors are the same across populations. Our goal was to address these gaps by performing a trans-ethnic analysis and constructing the largest mega-analysis of individuals with and without major depressive disorder (MDD). The rising numbers of biobanks and cohorts with health record linkage – coupled with a high prevalence of MDD in the general population worldwide (8-16%) - provide a unique opportunity to build a resource of diverse ancestry samples.

We used mental health questionnaires and screened electronic health records to identify individuals with a depressive symptoms or a clinical diagnosis of MDD. Using data from 241,740 samples (21,300 cases), we carried out joint and ancestry-specific association analyses and meta-analysed the results across studies. We evaluated the evidence for shared causal genetic architecture by estimating trans-ethnic genetic correlations.

Results from this study will fill a critical gap in the field and help to address the underrepresentation of racial/ethnic minorities in psychiatric genetics work.