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Genomic influences on self-reported childhood maltreatment

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Background: Childhood maltreatment is highly prevalent and a major risk factor for the development of psychopathology in adulthood. Retrospective reports of childhood maltreatment has a twin-based heritability of 6%.
Rationale: While a number of key risk factors for childhood maltreatment have been investigated, studies have seldom focused on associated genetic variation. The few genetic association studies of childhood maltreatment have only considered variants in candidate genes and have had insufficient power to detect the small polygenic effect sizes typically associated with behavioral phenotypes.
Hypothesis: Using data from well-powered studies such as PGC-PTSD and the UK Biobank, we will identify genetic variation that has an association with self-reported childhood maltreatment.
Results: SNP-based heritability of childhood maltreatment was estimated to be ~6%. Two genome-wide significant loci associated with childhood maltreatment (rs142346759, $p=4.35 \times 10^{-8}$, *FOXP1*; rs10262462, $p=3.24 \times 10^{-8}$, *FOXP2*) were identified in the discovery dataset (UK Biobank) but were not replicated in PGC-PTSD. The most significant genetic correlation of childhood maltreatment was with depressive symptoms ($rg=0.70$, $p=4.65 \times 10^{-40}$).
Discussion: This is the first large-scale genetic study to identify specific variants associated with self-reported childhood maltreatment. Speculatively, *FOXP* genes might influence externalizing traits and so be relevant to childhood maltreatment. Alternatively, these variants may be associated with a greater likelihood of reporting maltreatment. A clearer understanding of the genetic relationships of childhood maltreatment with a range of phenotypes, may ultimately be useful in in developing targeted treatment and prevention strategies.