after Bonferroni correction (p<8.25e-5). All of these were positively correlated with plasma mtDNA levels. These five miRNAs were significantly associated with the genes on TGF-beta signaling pathway, Glycosphingolipid biosynthesis - ganglio series, Thyroid hormone synthesis, Calcium signaling pathway and so on.
Discussion: Level of specific miRNAs and mtDNA were significantly associated and contributed common pathways in depressive patient. The results of this study may contribute to the new molecule of depression. We are continuing further analysis to identify genes and pathways associated with these detected miRNAs.

Disclosure: Nothing to disclose.

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S41
GENOMIC STRUCTURAL EQUATION MODELS OF MAJOR DEPRESSION SYMPTOMS

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Background: The standard diagnostic classification systems for depression specify a threshold number of symptoms to be present. While the operationalization into case/control status treats depression as a single disorder, the diagnostic criterion for depression can be met with any of the hundreds of possible combinations of symptoms. Twin studies have shown depression to be multidimensional, with three underlying genetic factors.
Methods: We conducted genome-wide association analyses of depression symptoms in UK and Australian population samples and in Psychiatric Genomics Consortium Major Depressive Disorder cohorts. We estimated Linkage Disequilibrium Score Regression (LDSC) genetic covariance matrices of symptoms and tested structural models using GenomicSEM. We conducted confirmatory factor analysis on common factor models and on three-factor models based on the twin literature.
Results: A common factor model and a three-factor model had acceptable fit in the UK population sample. An examination of the covariance matrices that included directional symptoms (increase or decrease in weight/appetite; insomnia or hypersomnia) suggested additional symptom heterogeneity. We will conduct exploratory factor analyses of depression symptoms in the samples and fit confirmatory models in GenomicSEM using a hold-out sample. We will conduct multivariate GWAS to identify genetic variants uniquely associated with symptom dimension.
Discussion: Structural equation modelling of genetic covariance matrices derived from genome-wide association summary statistics is a powerful tool to probe the genetic structure of depression symptoms. We will present results for alternative structural models.

Disclosure: Nothing to disclose.

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S42
EFFECTS OF PARENTAL GENOTYPES ON DEPRESSION

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Background: Twin studies have shown that Major Depressive Disorder (MDD) is a moderately genetic disorder with heritability estimates of 30-40% (Kessler et al., 2009). Environmental factors are clearly important; however, it is unclear to what extent parental genotypes contribute to this environment (Eichler et al., 2010; Kong et al., 2018). Exploring this using parental and offspring genotypes is possible; focusing on alleles transmitted from parent to offspring (direct genetic effects) and those not transmitted (indirect genetic effects) can help disentangle complex genetic and environmental pathways that influence MDD. This approach has been applied to educational attainment and shown that indirect genetic effects significantly influence the educational achievements of offspring (Bates et al., 2018; Kong et al., 2018). The aim of this study is to explore direct and indirect genetic effects associated with MDD using the available parent-offspring data within the Generation Scotland (GS) cohort.
Methods: The GS cohort is a family health based genetic epidemiology study with genetic, extensive sociodemographic and health data from 20,000+ individuals aged 18-98 across Scotland. There 2,689 parent-offspring trios available. In this study PRSs of MDD will be generated using the largest MDD GWAS available as the training dataset (Howard et al., 2019). The MDD PRSs will be generated from offspring and parental genotypes with separate PRSs for transmitted and non-transmitted alleles.
Results: The PRSs generated will then be analysed to identify the extent to which they predict offspring MDD.

The MDD PRSs of transmitted and non-transmitted alleles will be used to provide estimates of direct and indirect genetic effects as well as their significance in offspring MDD.

Further exploratory analyses will look into the effect of Neuroticism/Intelligence PRSs of non-transmitted alleles in traits that could influence MDD in offspring, such as parental personality

The PRSs are currently being generated - with a goal of completion in August 2019. Results will then be analysed and prepared for presentation at the WCPG conference in (late) October 2019.