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Dissecting the Association Between Inflammation, Metabolic Dysregulation, and Specific Depressive Symptoms

A Genetic Correlation and 2-Sample Mendelian Randomization Study

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IMPORTANCE Observational studies highlight associations of C-reactive protein (CRP), a general marker of inflammation, and interleukin 6 (IL-6), a cytokine-stimulating CRP production, with individual depressive symptoms. However, it is unclear whether inflammatory activity is associated with individual depressive symptoms and to what extent metabolic dysregulation underlies the reported associations.

OBJECTIVE To explore the genetic overlap and associations between inflammatory activity, metabolic dysregulation, and individual depressive symptoms.

GWAS DATA SOURCES Genome-wide association study (GWAS) summary data of European individuals, including the following: CRP levels (204 402 individuals); 9 individual depressive symptoms (3 of which did not differentiate between underlying diametrically opposite symptoms [eg, insomnia and hypersomnia]) as measured with the Patient Health Questionnaire 9 (up to 117 907 individuals); summary statistics for major depression, including and excluding UK Biobank participants, resulting in sample sizes of 500 199 and up to 230 214 individuals, respectively; insomnia (up to 386 533 individuals); body mass index (BMI) (up to 322 154 individuals); and height (up to 253 280 individuals).

DESIGN In this genetic correlation and 2-sample mendelian randomization (MR) study, linkage disequilibrium score (LDSC) regression was applied to infer single-nucleotide variant–based heritability and genetic correlation estimates. Two-sample MR tested potential causal associations of genetic variants associated with CRP levels, IL-6 signaling, and BMI with depressive symptoms. The study dates were November 2019 to April 2020.

RESULTS Based on large GWAS data sources, genetic correlation analyses revealed consistent false discovery rate (FDR)–controlled associations (genetic correlation range, 0.152-0.362; FDR $P = .006$ to $P < .001$) between CRP levels and depressive symptoms that were similar in size to genetic correlations of BMI with depressive symptoms. Two-sample MR analyses suggested that genetic upregulation of IL-6 signaling was associated with suicidality (estimate [SE], 0.035 [0.010]; FDR plus Bonferroni correction $P = .01$), a finding that remained stable across statistical models and sensitivity analyses using alternative instrument selection strategies. Mendelian randomization analyses did not consistently show associations of higher CRP levels or IL-6 signaling with other depressive symptoms, but higher BMI was associated with anhedonia, tiredness, changes in appetite, and feelings of inadequacy.

CONCLUSIONS AND RELEVANCE This study reports coheritability between CRP levels and individual depressive symptoms, which may result from the potentially causal association of metabolic dysregulation with anhedonia, tiredness, changes in appetite, and feelings of inadequacy. The study also found that IL-6 signaling is associated with suicidality. These findings may have clinical implications, highlighting the potential of anti-inflammatory approaches, especially IL-6 blockade, as a putative strategy for suicide prevention.

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Supplemental content

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Accumulating evidence implicates the immune system in the pathogenesis of major depression (MD).[1] Low-grade inflammation, as indicated by higher (>0.3 mg/dL [>3 mg/L]) C-reactive protein (CRP) levels, is present in about one-quarter of patients with MD and longitudinally predicts occurrence of depressive symptoms.[2,3] Results of studies[4-9] have suggested specificity of the association of inflammation and depression to a subset of depressive symptoms. C-reactive protein and the proinflammatory cytokine interleukin 6 (IL-6), an upstream stimulator of CRP production, have been reported to be associated with increased appetite, sleep problems, loss of energy, diurnal variation in mood, and concentration difficulties. However, findings vary with regard to which inflammatory markers and depressive symptoms were assessed and which findings were replicated.[6] There is also debate on the robustness of the reported associations after adjustment for metabolic traits, such as body mass index (BMI), which attenuates inflammation-symptom associations.[6] Such attenuation corresponds to recent suggestions of a combined immune-metabolic subtype of depression[10] and warrants further research to disentangle immune from metabolic associations with depressive symptoms.

Associations of inflammation with specific depressive symptom profiles may be clinically relevant. Research suggests that anti-inflammatory drugs may improve depressive symptoms in patients with chronic inflammatory physical illness independent of improvements in physical illness.[11-14] In MD, it has been reported that immunotherapies may be helpful for those patients with evidence of low-grade inflammation or inflammation-associated risk factors.[15,16] Informed by these reports, several ongoing randomized clinical trials (RCTs) are selecting patients with evidence of elevated levels of inflammatory proteins or based on neuroimaging markers of inflammation or inflammation-related symptoms (eg, work by Khandaker et al[17] and 2 other clinical trials[18,19]). Therefore, identification of depressive symptoms that are associated with inflammation is key information that may aid patient selection in future RCTs.

Genetic approaches and increasing availability of genome-wide association study (GWAS) data may enable more fine-grained dissection of inflammation-depressive symptom associations. Genome-wide association studies have highlighted a polygenic architecture underlying both MD and serum CRP levels with many single-nucleotide variants (SNVs) exhibiting small associations.[20,21] Such polygenic associations can be summarized using polygenic risk scores (PRSs),[22] which sum the presence of risk alleles in individuals to create a single score. Milaneschi and colleagues[23,24] have reported that PRSs for both increased CRP levels and BMI are associated with symptom profiles characteristic of atypical (increased appetite or weight) but not typical (decreased appetite or weight) MD. However, it remains unclear from these analyses if symptoms other than changes in appetite or weight underlie the CRP-atypical MD association and whether this association is potentially causal or arising from metabolic factors.

Linkage disequilibrium score (LDSC) regression[25,26] and mendelian randomization (MR)[27] analyses could further dissect the associations between inflammation, metabolic factors, and depressive symptoms. Linkage disequilibrium score regression allows assessment of SNV-based phenotype heritability and coheritability between 2 traits. Mendelian randomization analyses enable an assessment of potential causal association between 2 traits based on the Mendel law that genetic variants are inherited independently, thus providing a natural RCT.[28,29] Initial studies[21,30,31] using LDSC regression and MR analyses reported mixed findings on associations of inflammatory markers and MD. None of these studies examined whether inflammation was associated with specific depressive symptoms.

Using large-scale GWAS data sources, the present study applied a combination of LDSC regression and MR analyses on measures of inflammation, as indicated by CRP levels and IL-6 signaling or activity, BMI, as an index of metabolic dysregulation, and 9 specific depressive symptoms. We tested 2 hypotheses. First, are the associations between inflammation and specific depressive symptoms underpinned by a common genetic basis (ie, coinherited)? Second, is inflammation potentially causally associated with specific depressive symptoms?

Key Points

Question Do inflammatory pathways share a genetic background with individual depressive symptoms, and do they potentially causally contribute to them?

Findings Based on large genome-wide association study data sources, this genetic correlation and 2-sample mendelian randomization study found genetic overlap between a higher C-reactive protein (CRP) level, a broad marker of inflammation, and 9 depressive symptoms; upregulated interleukin-6 signaling, a major stimulator of CRP, emerged as a potential causal risk factor for suicidality. Body mass index, but not interleukin 6 or CRP, was potentially causally associated with 4 other depressive symptoms.

Meaning Interleukin 6 overactivity could be associated with suicidality; interleukin-6 blockade may be a novel treatment target that warrants future research.

Methods

GWAS Data Sources

This genetic correlation and 2-sample MR study was performed from November 2019 to April 2020. Sample sizes and characteristics of GWAS data sources[20,21,32-39] are listed in **Table 1**. They are described in detail in the eMethods in the Supplement.

Briefly, we included GWAS data sources to maximize sample sizes yet avoid sample overlap. These data sources included the following information: serum CRP levels from 204 402 individuals included in the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Inflammation Working Group[21]; depressive symptoms from the Neale laboratory[39]; summary statistics for MD from a subset (ie, excluding 23andMe participants) of 2 prior Psychiatric Genomics Consortium (PGC) reports[20,32] that respectively include and

Table 1. GWAS Data Sources

Phenotype	GWAS data source	Sample size	Study or population	Covariates and exclusions	Objective	Reported genome-wide statistically significant hits
CRP levels	Ligthart et al,[21] 2018	204 402	GWAS meta-analysis of 88 studies of European individuals	Covariates: age, sex, population substructure, relatedness. Exclusions: >4 SD above the mean, autoimmune disease, immunotherapy	Primary exposure (LDSC regression and MR)	48 Independent loci
Depressive symptoms	Neale laboratory,[39] 2020	Up to 117 907[a]	UK Biobank study	Covariates: age, age^2, sex, age by sex, age^2 by sex, 20 principal components	Primary outcome	NA
MD	PGC; Wray et al,[32] 2018	Up to 230 214 (45 396 cases and 97 250 controls)[a]	Meta-analysis of PGC studies without UK Biobank and 23andMe samples	Covariates using RICOPILI[38]: age, sex, principal components	Secondary outcome (LDSC regression and MR) and positive control (LDSC regression)	44 Independent loci
MD[b]	PGC; Howard et al,[20] 2019	500 199 (170 756 Cases and 329 443 controls)	Meta-analysis of PGC studies and UK Biobank without 23andMe samples	Covariates in UK Biobank: age, sex, genotyping array, 8 principal components. Covariates in PGC studies using RICOPILI[38]: age, sex, principal components	Secondary outcome (LDSC regression and MR)	101 Independent loci
BMI	GIANT consortium; Locke et al,[33] 2015	Up to 322 154[a]	Meta-analysis of 80 GWAS data in European adults	Covariates: age, age^2, sex, study-specific covariates (eg, genotype-derived principal components)	Secondary exposure (LDSC regression and MR)	97 Independent loci
Insomnia	Jansen et al,[36] 2019	Up to 386 533[a]	UK Biobank without 23andMe sample	Covariates: age, sex, genotype array, 10 genetic principal components	Secondary outcome (LDSC regression and MR)	202 Independent loci
Height	GIANT consortium; Wood et al,[34] 2014	Up to 253 280[a]	Meta-analysis of 79 GWAS data	Covariates: age, sex, study-specific covariates (eg, genotype-derived principal components)	Negative control (LDSC regression)	423 Independent loci
sIL-6R plasma levels	Rosa et al,[37] 2019; Sun et al,[35] 2018	2994	INTERVAL study in the United Kingdom	Covariates: sex, age, duration between blood draw and processing, 3 principal components	Secondary exposure (MR)	NA

Abbreviations: BMI, body mass index; CRP, C-reactive protein; GIANT, Genetic Investigation of Anthropometric Traits; GWAS, genome-wide association study; LDSC, linkage disequilibrium score; MD, major depression; MR, mendelian randomization; NA, not applicable; PGC, Psychiatric Genomics Consortium; RICOPILI, Rapid Imputation for Consortias Pipeline; sIL-6R, soluble interleukin 6 receptor.

[a] Exact sample sizes vary per depressive symptom phenotype (minimum, 117 177; median, 117 822; maximum, 117 907) and per single-nucleotide variant for MD (Wray et al,[32] 2018) (minimum, 55 795; median, 142 646; maximum, 230 241), BMI (minimum, 50 005; median, 233 524; maximum, 322 154), insomnia (minimum, 366 461; median, 385 989; maximum, 386 533), and height (minimum, 50 003; median, 251 631; maximum, 253 280).

[b] Note that depression was characterized differently among samples in the study by Howard et al,[20] including definitions of broad depression, probable MD, and MD diagnosis ascertained from hospital records.

exclude UK Biobank participants, resulting in final sample sizes of 500 199 and up to 230 214 individuals (details are given in the eMethods in the Supplement); BMI (up to 322 154 individuals) and height (up to 253 280 individuals) from the Genetic Investigation of Anthropometric Traits (GIANT) consortium[33,34]; and soluble IL-6 receptor (sIL-6R) protein levels from the INTERVAL study.[35] Genome-wide association studies on depressive symptoms were based on UK Biobank data as assessed in an online follow-up survey using the self-report Patient Health Questionnaire 9 (PHQ-9) (up to 117 907 individuals).[40,41] The PHQ-9 asks about the presence of 9 depressive symptoms, as defined in the *DSM-IV* (Fourth Edition),[42] over the past 2 weeks (eTable 1 and eTable 2 in the Supplement list symptom descriptions and frequency statistics in the UK Biobank sample). Three PHQ-9 symptoms (sleep problems, changes in appetite, and psychomotor changes) do not differentiate between underlying diametrically opposite symptoms (eg, insomnia and hypersomnia). Although these symptoms are included for comprehensiveness of analyses, we emphasize that any associations specific to one (but not the other) underlying symptom are likely obscured in analyses. We have included GWAS data for insomnia[36] (up to 386 533 individuals) to disentangle associations with sleep problems to some extent but could not identify GWAS data for other underlying symptoms.

All original GWAS investigations were conducted with ethics committee approval. The UK Biobank study received approval from the National Health Service National Research Ethics Service. Written informed consent was obtained from participants.

LDSC Regression Analysis

Linkage disequilibrium score regression regresses SNV GWAS χ^2 statistics for 1 phenotype (to infer SNV-based heritability) or χ^2 statistics cross products for 2 phenotypes (to infer SNV-based coheritability) on LDSCs (ie, the sum of a SNV pairwise squared correlation with other SNVs in a 1cM window[43]). Genetic correlations between 2 phenotypes can be inferred by the regression slope.[25,26]

We used LDSC regression to assess the SNV-based heritability (h^2) of all phenotypes and the genetic correlations of CRP levels, MD, BMI, and height with depressive symptoms. For

Table 2. Genetic Instruments for MR Analyses

Exposure	GWAS data source	SNV *F* statistics[a]	SNV location	No. of SNVs: Used in present report[b]	No. of SNVs: Used in prior MR report	Prior MR report
Main MR analyses						
↑CRP levels	CRP GWAS meta-analysis[21]	Minimum, 32.2; median, 89.7; mean, 256.5; maximum, 1829.1	*CRP* gene (within 300-kb region of GRCh37/hg19 coordinates: chr1:159 382 079-159 984 379)	17	24	Georgakis et al,[51] 2020
↑IL-6 signaling	CRP GWAS meta-analysis[21]	Minimum, 48.6; median, 73.8; mean, 144.5; maximum, 458.2	*IL6R* gene (GRCh37/hg19 coordinates: chr1:154 077 669-154 741 926)	6	7	Georgakis et al,[51] 2020
Additional MR analyses						
↑CRP levels (alternative approach)	CRP GWAS meta-analysis[21]	Minimum, 30.0; median, 50.2; mean, 86.5; maximum, 987.2	Genome-wide	139	NA	NA
↑IL-6 signaling (alternative approach)	sIL-6R plasma-level GWAS[35]	Minimum, 16.8; median, 72.2; mean, 271.4; maximum, 5041.9	Within 250-kb region around *IL6R* gene (GRCh37/hg19 coordinates: chr1:154 077 669-154 741 926)	29	34	Rosa et al,[37] 2019
↑BMI	BMI GWAS meta-analysis of Locke et al,[33] 2015	Minimum, 29.0, median, 39.6; mean, 54.7; maximum, 238.5	Genome-wide	95	NA	NA

Abbreviations: BMI, body mass index; chr1, chromosome 1; CRP, C-reactive protein; GWAS, genome-wide association study; IL-6, interleukin 6; kb, kilobase; MR, mendelian randomization; NA, not applicable; sIL-6R, soluble interleukin 6 receptor; SNV, single-nucleotide variant; ↑, increasing.

[a] *F* statistics were computed using the following approximation: $F = \beta^2 \div SE$.[2,37,52]

[b] Available number of SNVs used is reported here for Patient Health Questionnaire 9 depressive symptom outcome; however, these differ per outcome, and exact numbers are listed in eTable 7 in the Supplement.

genetic correlations with depressive symptoms, MD and height served as positive and negative control variables showing strong and absent associations with depressive symptoms, respectively. European ancestry information from the 1000 Genomes Project was used as the linkage disequilibrium reference panel, aligning with European origin of GWAS samples.[44] We used the Benjamini-Hochberg method[45] to control the false discovery rate (FDR) across PHQ-9 symptoms for each phenotype.

2-Sample Mendelian Randomization Analyses

Genetic Instruments

Mendelian randomization uses genetic variants associated with an exposure as instruments to test for potential causal association of this exposure with an outcome. Genetic instruments were based on functional knowledge of the inflammatory pathway underlying CRP production. C-reactive protein is produced in the liver as a consequence of upstream IL-6 signaling via membrane-bound IL-6 receptors (IL-6Rs) on hepatocytes.[46] The IL-6Rs also exist in soluble form in the plasma (sIL-6Rs), but IL-6–sIL-6R complexes are neutralized under physiological conditions.[46-49] Therefore, lower sIL-6R plasma levels constitute an indirect index of IL-6 signaling.[37,49]

We used genome-wide statistically significant, independent ($R^2 < 0.1$), and strong (*F* statistics >10)[50] genetic instruments for higher CRP levels, IL-6 signaling, and BMI[21,33,35,37,51,52] as summarized in **Table 2.** In the eMethods in the Supplement, we describe details for genetic instrument selection, clumping procedure, comparison with previous work,[31] a functional description of included SNVs, and the number of SNVs across instruments and analyses (eTables 3-7 and eFigure 1 in the Supplement). Briefly, we defined 2 main genetic instruments for upregulated CRP levels and IL-6 signaling using SNVs around *CRP* (GenBank 1401) and *IL6R* (GenBank 3570) genes, respectively, that were associated with CRP levels based on CRP GWAS summary statistics.[21,51]

As alternative approaches and to demarcate associations of inflammatory activity from those of metabolic dysregulation,[53] we defined further genetic instruments for CRP levels, IL-6 signaling, and BMI. We used SNVs associated with CRP levels and BMI throughout the genome and SNVs in the *IL6R* gene associated with sIL-6R plasma levels, which were inversed to reflect an indirect marker of IL-6 signaling.

Statistical Analyses

Two-sample MR analyses were performed using *R,* version 3.6.0 (R Foundation for Statistical Computing) and the TwoSampleMR package.[54,55] Exposure and outcome GWAS summary statistics were harmonized by aligning summary statistics to the forward strand if the forward strand was known or could be inferred. Ambiguous SNVs and SNVs with a noninferable forward strand were excluded from analyses.

We first performed fixed-effects meta-analysis of genetic instruments using inverse-variance weighting (IVW).[56] Standard errors were computed with the Wald estimator and delta weighting to account for uncertainty in genetic association with the exposure.[57] To assess the robustness of our findings, the weighted median MR approach was performed, which provides valid estimates if at least 50% of the MR instrument weights on the exposure are valid.[56,58,59]

To assess horizontal pleiotropy (ie, an association of the genetic instrument with the outcome independent of the exposure), we tested for the presence of statistically significant ($P < .05$) heterogeneity in IVW MR analyses using the Cochran *Q* statistic.[60] We also performed more restrictive MR analyses focusing on SNVs within *CRP* and *IL6R* genes (compare gene loci in Table 2) using MR-Egger estimation for genetic instruments including SNVs throughout the genome, leave-one-out, and single-SNV MR analyses.[58,61,62] Details are available in the eMethods in the Supplement.

All MR analyses were FDR controlled across PHQ-9 symptoms using the Benjamini-Hochberg method.[45] Because main IVW MR analyses for CRP levels and IL-6 signaling focused on 2 genetic instruments, we also corrected these comparisons with the Bonferroni method.

Availability of Data and Materials

Genome-wide association study data sources are openly available as GWAS summary statistics and by request for CRP levels from the CHARGE Inflammation Working Group.[21] Genetic instrument files and analysis scripts are available on the Open Science Framework.[63]

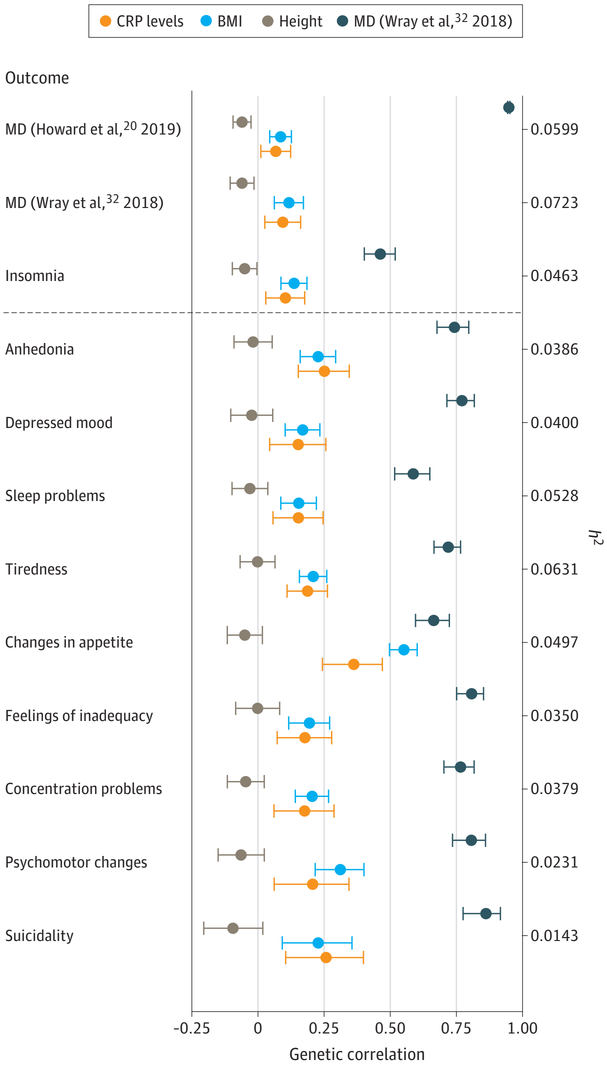
Results

LDSC Regression Analyses

Using LDSC regression, we estimated SNV-based heritability (h^2) and genetic correlations of CRP levels,[21] BMI,[33] MD (based on work by Wray et al[32] as positive control), and height (negative control)[34] with depressive symptoms, MD,[20,32] and insomnia[36] (**Figure 1**). Exact values are listed in eTables 8, 9, and 10 in the Supplement.

The SNV-based heritability was low for depressive symptoms (h^2 range = 0.0143-0.0631), MD (h^2 range = 0.0599-0.0723), and CRP levels (h^2 = 0.0941), whereas BMI (h^2 = 0.1297) and height (h^2 = 0.3120) displayed relatively higher levels. Of note, h^2 for suicidality was slightly below the suggested threshold of $z > 4$ (h^2 z = 3.97), which could reflect a potential unreliability of genetic correlation estimates.[26] There was evidence for genetic correlations of CRP levels with all depressive symptoms after FDR correction (genetic correlation range, 0.152-0.362), with the lowest correlation seen for depressed mood (genetic correlation [SE] = 0.152 [0.056]; FDR P = .006) and the highest for changes in appetite (genetic correlation [SE] = 0.362 [0.067]; FDR P < .001). C-reactive protein levels showed small genetic correlations with MD and insomnia (eTable 10 in the Supplement). Body mass index showed a similar pattern of genetic correlations in that the BMI–depressive symptom estimates were associated with CRP–depressive symptom estimates (Pearson r = 0.89, P = .001; Spearman ρ = 0.92, P = .001).

Figure 1. Single-Nucleotide Variant (SNV)–Based Heritability and Genetic Correlation Estimates for MD and Depressive Symptoms



The SNV-based heritability coefficients (h^2) for major depression (MD) and depressive symptoms (y-axis) are shown on the z-axis. Sleep problems, changes in appetite, and psychomotor changes reflect composite symptoms, which may obscure associations specific to one but not the other underlying symptom (psychomotor retardation or agitation, increased or decreased weight or appetite, and insomnia or hypersomnia). The error bars indicate 95% CIs, which were calculated using Fisher z transformation. Outcomes below the dashed line are the Patient Health Questionnaire 9 depressive symptoms.

MR Analyses

Mendelian randomization analyses allowed testing of potential causal association between proinflammatory activity and depressive symptoms. **Figure 2** shows MR analyses for CRP levels, IL-6 signaling, and BMI instruments using IVW meta-analysis[20,32] (exact values are listed in eTable 11 in the Supplement).

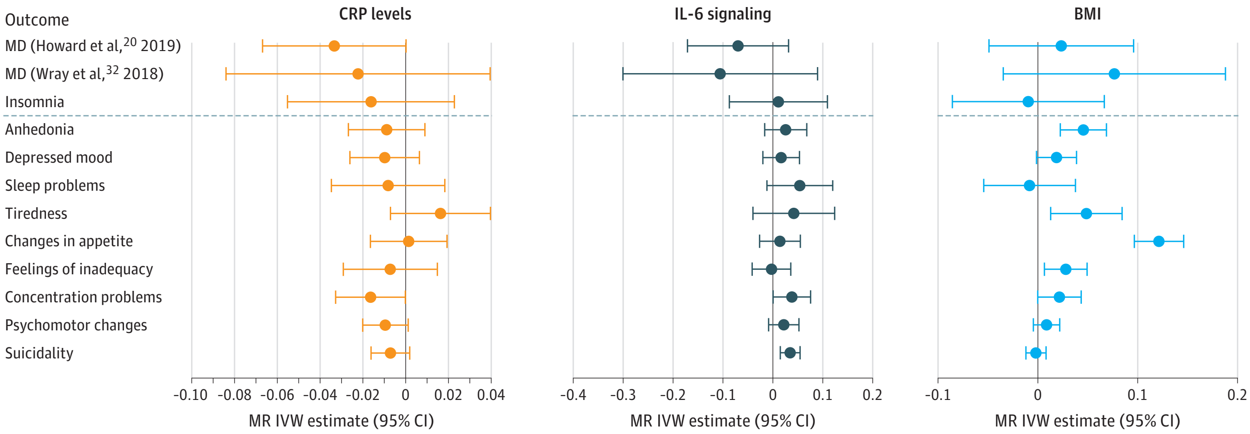
Findings for CRP Levels

Mendelian randomization analyses of the CRP levels instrument did not show evidence for associations with depressive symptoms, MD, or insomnia (eTable 11 and eTable 12 in the Supplement). Using the alternative CRP instrument, there was some evidence for associations of increased CRP levels with tiredness, changes in appetite, and psychomotor changes (**Table 3**),[20,32,45] but none of these associations replicated in weighted median MR (eTable 13 in the Supplement).

Findings for IL-6 Signaling

We observed an association of upregulated IL-6 signaling with suicidality even after conservative FDR and Bonferroni corrections (estimate [SE], 0.035 [0.010]; FDR plus Bonferroni

Figure 2. Mendelian Randomization Inverse-Variance Weighted (IVW) Associations of Genetic Instruments for Upregulated C-Reactive Protein (CRP) Levels, Interleukin 6 (IL-6) Signaling, and Higher Body Mass Index (BMI) With Major Depression (MD) and Depressive Symptoms



Sleep problems, changes in appetite, and psychomotor changes reflect composite symptoms, which may obscure associations specific to one but not the other underlying symptom (psychomotor retardation or agitation, increased or decreased weight or appetite, and insomnia or hypersomnia). The error bars indicate 95% CIs. Outcomes below the dashed line are the Patient Health Questionnaire 9 depressive symptoms.

Table 3. MR IVW Estimates of Alternative Genetic Instruments for Upregulated CRP Levels and IL-6 Signaling

	CRP levels (genome-wide)			IL-6 signaling (indirect)		
Outcome	Estimate (SE)	*P* value	FDR *P* value[a]	Estimate (SE)	*P* value	FDR *P* value[a]
MD (Howard et al,[20] 2019)	−0.021 (0.011)	.06	NA	−0.002 (0.003)	.53	NA
MD (Wray et al,[32] 2018)	0.020 (0.020)	.33	NA	−0.012 (0.007)	.09	NA
Insomnia	−0.010 (0.013)	.42	NA	0.004 (0.003)	.25	NA
Anhedonia	0.002 (0.005)	.64	.64	0.000 (0.002)	.80	.80
Depressed mood	−0.004 (0.005)	.45	.58	0.000 (0.001)	.72	.80
Sleep problems[b]	0.012 (0.008)	.16	.29	0.005 (0.002)	.01[c]	.06
Tiredness	0.021 (0.007)	.002[c]	.02[c]	0.002 (0.002)	.26	.40
Changes in appetite[b]	0.012 (0.006)	.048[c]	.14	0.001 (0.002)	.46	.59
Feelings of inadequacy	−0.003 (0.006)	.63	.64	−0.002 (0.002)	.14	.30
Concentration problems	−0.005 (0.005)	.34	.51	0.003 (0.002)	.06	.19
Psychomotor changes[b]	−0.006 (0.003)	.046[c]	.14	0.001 (0.001)	.24	.40
Suicidality	0.004 (0.003)	.15	.29	0.002 (0.001)	.005[c]	.049[c]

Abbreviations: CRP, C-reactive protein; FDR, false discovery rate; IL-6, interleukin 6; IVW, inverse-variance weighting; MD, major depression; MR, mendelian randomization; NA, not applicable.

[a] *P* values were FDR controlled across depressive symptoms of each outcome using the Benjamini-Hochberg method.[45]

[b] Sleep problems, changes in appetite, and psychomotor changes reflect composite symptoms, which may obscure associations specific to one but not the other underlying symptom.

[c] $P < .05$ for nominal and FDR-controlled statistically significant results.

$P = .01$) (eFigure 2 in the Supplement), but there were no associations with MD, insomnia, or other depressive symptoms. The IL-6-suicidality association was replicated with the (indirect) IL-6 signaling instrument and across IVW and weighted median MR analyses (main IL-6 signaling weighted median estimate [SE], 0.030 [0.011]; $P = .006$; alternative IL-6 signaling IVW estimate [SE], 0.002 [0.001]; $P = .005$; and alternative IL-6 signaling weighted median estimate [SE], 0.002 [0.001]; $P = .047$) (Table 3 and eTable 12 and eTable 13 in the Supplement). There was also some evidence in IVW but not weighted median MR analysis for associations of (indirect) IL-6 signaling with sleep problems, but not with insomnia, suggesting potential association specificity to hypersomnia (Table 3).

Findings for BMI

In IVW MR analyses, the instrument used for BMI indicated that higher BMI was associated with anhedonia, tiredness, changes in appetite, and feelings of inadequacy (estimate [SE], 0.046 [0.012]; FDR $P = .001$ for anhedonia; estimate [SE], 0.049 [0.018]; FDR $P = .02$ for tiredness; estimate [SE], 0.121 [0.013]; FDR $P < .001$ for changes in appetite; and estimate [SE], 0.028 [0.011]; FDR $P = .02$ for feelings of inadequacy) (Figure 2 and eTable 11 and eFigure 3 in the Supplement). Except for feelings of inadequacy, these associations persisted in weighted median MR analyses (estimate [SE], 0.042 [0.016]; $P = .007$ for anhedonia; estimate [SE], 0.057 [0.023]; $P = .01$ for tiredness; estimate [SE], 0.141 [0.017]; $P < .001$ for changes in appetite; and estimate [SE], 0.031

[0.016]; *P* = .06 for feelings of inadequacy) (eTable 12 in the Supplement).

Assessment of Horizontal Pleiotropy

Assessing if SNV-outcome associations are mediated via the exposure and not via other mechanisms (ie, horizontal pleiotropy) is a key prerequisite for validity of causal inference from MR analysis. As detailed in the eResults in the Supplement, we assessed horizontal pleiotropy by measuring between-SNV heterogeneity (eTable 14 and eTable 15 in the Supplement), and we performed sensitivity analyses that are more robust to pleiotropy, including gene-restricted MR, MR-Egger regression, and MR analyses excluding outlying pleiotropic SNVs (eFigure 4 and eTables 16-20 in the Supplement). The association of IL-6 signaling with suicidality was robust across sensitivity analyses (main IL-6 signaling Cochran *Q* = 5.77; *P* = .33; gene-restricted IVW estimate [SE], 0.027 [0.011]; *P* = .01). The associations of higher BMI with anhedonia, tiredness, changes in appetite, and feelings of inadequacy were directionally consistent in all sensitivity analyses (MR-Egger slope [SE], 0.028 [0.036]; *P* = .44 for anhedonia; MR-Egger slope [SE], 0.043 [0.056]; *P* = .45 for tiredness; MR-Egger slope [SE], 0.183 [0.038]; *P* < .001 for changes in appetite; and MR-Egger slope [SE], 0.050 [0.033]; *P* = .14) for feelings of inadequacy.

Discussion

We tested SNV-based genetic correlation and potential MR association between proinflammatory activity and individual depressive symptoms. Using LDSC regression, we showed consistent genetic correlations between CRP levels, a sensitive index of inflammatory activity, and depressive symptoms as assessed with the PHQ-9. Genetic correlations between CRP levels and each specific depressive symptom were small and similar in size (genetic correlation range, 0.152-0.362). Mendelian randomization analyses for specific depressive symptoms showed consistent evidence for associations between higher IL-6 activity and suicidality. Findings of increased CRP levels and IL-6 overactivity with other PHQ-9 symptoms were inconsistent, but there were some indications that IL-6 signaling could be associated with hypersomnia, which requires replication in future work. Regarding metabolic dysregulation and depressive symptoms, we found consistent MR associations of higher BMI with anhedonia, tiredness, changes in appetite, and feelings of inadequacy. However, our MR analyses did not replicate prior research showing MR associations of CRP levels or IL-6 signaling with MD[31] (eDiscussion in the Supplement).

Inflammation and Suicidality

Suicidality and suicidal behavior have a multifactorial origin, and identification of causal markers is critical to advance prevention and treatment efforts.[64,65] Increased levels of inflammatory markers, and IL-6 in particular, have been found to be associated with suicidality or suicidal behavior, and patients with chronic inflammatory illnesses, such as inflammatory bowel disease, exhibit increased suicide rates.[66-69] We provide evidence for an association between higher IL-6 signaling and suicidality. Findings of this association were consistent across LDSC regression and MR analyses using different genetic proxies for IL-6 signaling.

An association between IL-6 signaling and suicidality may have important clinical implications. First, suicidality may become a useful symptom (characteristic of inflammatory activity beyond CRP levels) for stratification efforts in RCTs of immunotherapy in depression. Second, it may be informative to evaluate the symptom-specific effectiveness of immunotherapies for depression and for treating suicidality in particular. Raison and colleagues[15] demonstrated the symptom-specific effectiveness of the tumor necrosis factor α inhibitor infliximab for suicidality (among 4 other symptoms) in patients with MD with high CRP levels before treatment. Data from available RCTs of immunotherapies for chronic inflammatory illnesses and from RCTs of anti–IL-6 and anti–IL-6R drugs in MD[17] may be valuable to further examine symptom-specific immunotherapy outcomes. Therefore, our findings emphasize the need for considering suicidality in immunopsychiatry research and highlight the clinical potential of immunotherapies, and specifically IL-6R blockade, for treatment of suicidality.

Inflammation, Metabolic Dysregulation, and Depressive Symptoms

Apart from suicidality and preliminary indications for hypersomnia, results for inflammation and other PHQ-9 depressive symptoms were divergent between LDSC regression, in which robust genetic correlations between CRP levels and depressive symptoms were found, and MR analyses, in which inconsistent associations that did not replicate across instruments or statistical models were found (Table 3 and eTables 11-17 in the Supplement). This dissociation of genetic correlation and MR results for other PHQ-9 depressive symptoms may offer important new insights into the interrelationship between low-grade inflammation, metabolic dysregulation, and depression.

Mendelian randomization associations of higher BMI, but not of increased inflammatory markers, with anhedonia, tiredness, changes in appetite, and feelings of inadequacy suggest that metabolic dysregulation may underlie the coheritability of inflammatory activity with these symptoms. In the context of previous results,[4,70-72] it is likely that associations with changes in appetite are specific to increased appetite or hyperphagia. Taken together, these results suggest immune and metabolic factors may constitute separate, symptom-specific risk factors in depression.

Because depressive symptoms themselves could promote proinflammatory lifestyle choices, such as an unhealthy diet and reduced physical activity,[73,74] reverse causal inference needs to be assessed as an alternative or additional explanation. Future studies need to replicate our results and should further investigate pleiotropic or residual confounding factors that could explain genetic correlations between CRP levels and BMI with depressed mood, concentration problems, and psychomotor changes. In these studies, symptoms should ideally be assessed without composite items and based on multiple symptom indicators.

Strengths and Limitations

We report genetic analyses of inflammatory activity, metabolic dysregulation, and depressive symptoms based on large GWAS data sources. Our sample size maximizes power for genetic analyses.

This study also has some limitations. First is a lack of granular information on some depressive symptoms assessed by the PHQ-9, which does not differentiate between diametrically opposite symptoms. Although inclusion of insomnia summary data helped in providing some preliminary suggestions on associations between IL-6 and hypersomnia, more detailed investigations disentangling composite symptoms are needed.

Second, depressive symptoms in the general population and in patients with MD are likely to exist on a continuum, but they could also be different with regard to their origin and implications, especially because depressive symptoms are common and may arise in the general population owing to a variety of reasons other than depression.[75] In future work, MR analysis of symptoms in patients with MD is required to assess the relevance of our findings for depressive symptoms occurring in the context of MD.

Third, inferences on causality should ideally rely on multiple types of studies because MR analyses rely on 3 key assumptions that are not always met or completely testable.[57,76] Ohlsson and Kendler[77] have advocated triangulation of causality using different study designs, such as MR and RCTs, which we also support.

Fourth, our IL-6 signaling instrument was weighted on downstream associations with CRP levels, and it is debatable if this approach captures an independent association of IL-6 signaling. However, the fact that we replicated our results using an sIL-6R–based instrument supports this interpretation.

Conclusions

This genetic correlation and 2-sample MR study reports a detailed investigation of inflammatory activity, metabolic dysregulation, and specific depressive symptoms using LDSC regression and 2-sample MR analyses of large GWAS data. The findings suggest small but robust genetic correlations of BMI and CRP levels with depressive symptoms, and MR associations show that higher BMI could be a causal risk factor for anhedonia, tiredness, changes in appetite, and feelings of inadequacy. Regarding proinflammatory processes, IL-6 signaling may be potentially causally associated with suicidality. This hypothesis is clinically relevant because symptom expression of suicidality could help identify patients who will respond to immunotherapy. The findings also suggest that pharmacological approaches targeting IL-6 signaling may be valuable for treatment of suicidality, which requires further research.

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Correction: This article was corrected on December 2, 2020, to fix the CRP level axis in Figure 2.

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REFERENCES

1. Dantzer R, O'Connor JC, Freund GG, Johnson RW, Kelley KW. From inflammation to sickness and depression: when the immune system subjugates the brain. *Nat Rev Neurosci*. 2008;9(1):46-56. doi:10.1038/nrn2297

2. Khandaker GM, Pearson RM, Zammit S, Lewis G, Jones PB. Association of serum interleukin 6 and C-reactive protein in childhood with depression and psychosis in young adult life: a population-based longitudinal study. *JAMA Psychiatry*. 2014;71(10):1121-1128. doi:10.1001/jamapsychiatry.2014.1332

3. Osimo EF, Baxter LJ, Lewis G, Jones PB, Khandaker GM. Prevalence of low-grade inflammation in depression: a systematic review and meta-analysis of CRP levels. *Psychol Med*. 2019;49(12):1958-1970. doi:10.1017/S0033291719001454

4. Lamers F, Milaneschi Y, de Jonge P, Giltay EJ, Penninx BWJH. Metabolic and inflammatory markers: associations with individual depressive symptoms. *Psychol Med*. 2018;48(7):1102-1110. doi:10.1017/S0033291717002483

5. Jokela M, Virtanen M, Batty GD, Kivimäki M. Inflammation and specific symptoms of depression. *JAMA Psychiatry*. 2016;73(1):87-88. doi:10.1001/jamapsychiatry.2015.1977

6. Fried EI, von Stockert S, Haslbeck JMB, Lamers F, Schoevers RA, Penninx BWJH. Using network analysis to examine links between individual depressive symptoms, inflammatory markers, and covariates. *Psychol Med*. Published online October 28, 2019. doi:10.1017/S0033291719002770

7. Chu AL, Stochl J, Lewis G, Zammit S, Jones PB, Khandaker GM. Longitudinal association between inflammatory markers and specific symptoms of depression in a prospective birth cohort. *Brain Behav Immun*. 2019;76:74-81. doi:10.1016/j.bbi.2018.11.007

8. Moriarity DP, Giollabhui NM, Ellman LM, et al. Inflammatory proteins predict change in depressive symptoms in male and female adolescents. *Clin Psychol Sci*. 2019;7(4):754-767. doi:10.1177/2167702619826586

9. Duivis HE, Vogelzangs N, Kupper N, de Jonge P, Penninx BWJH. Differential association of somatic and cognitive symptoms of depression and anxiety with inflammation: findings from the Netherlands Study of Depression and Anxiety (NESDA). *Psychoneuroendocrinology*. 2013;38(9):1573-1585. doi:10.1016/j.psyneuen.2013.01.002

10. Milaneschi Y, Lamers F, Berk M, Penninx BWJH. Depression heterogeneity and its biological underpinnings: toward immunometabolic depression. *Biol Psychiatry*. 2020;88(5):369-380. doi:10.1016/j.biopsych.2020.01.014

11. Wittenberg GM, Stylianou A, Zhang Y, et al. Effects of immunomodulatory drugs on depressive symptoms: a mega-analysis of randomized, placebo-controlled clinical trials in inflammatory disorders. *Mol Psychiatry*. 2020;25(6):1275-1285. doi:10.1038/s41380-019-0471-8

12. Kappelmann N, Lewis G, Dantzer R, Jones PB, Khandaker GM. Antidepressant activity of anti-cytokine treatment: a systematic review and meta-analysis of clinical trials of chronic inflammatory conditions. *Mol Psychiatry*. 2018;23(2):335-343. doi:10.1038/mp.2016.167

13. Köhler O, Benros ME, Nordentoft M, et al. Effect of anti-inflammatory treatment on depression, depressive symptoms, and adverse effects: a systematic review and meta-analysis of randomized clinical trials. *JAMA Psychiatry*. 2014;71(12):1381-1391. doi:10.1001/jamapsychiatry.2014.1611

14. Köhler-Forsberg O, Lydholm CN, Hjorthøj C, Nordentoft M, Mors O, Benros ME. Efficacy of anti-inflammatory treatment on major depressive disorder or depressive symptoms: meta-analysis of clinical trials. *Acta Psychiatr Scand*. 2019;139(5):404-419. doi:10.1111/acps.13016

15. Raison CL, Rutherford RE, Woolwine BJ, et al. A randomized controlled trial of the tumor necrosis factor antagonist infliximab for treatment-resistant depression: the role of baseline inflammatory biomarkers. *JAMA Psychiatry*. 2013;70(1):31-41. doi:10.1001/2013.jamapsychiatry.4

16. McIntyre RS, Subramaniapillai M, Lee Y, et al. Efficacy of adjunctive infliximab vs placebo in the treatment of adults with bipolar I/II depression: a randomized clinical trial. *JAMA Psychiatry*. 2019;76(8):783-790. doi:10.1001/jamapsychiatry.2019.0779

17. Khandaker GM, Oltean BP, Kaser M, et al. Protocol for the INSIGHT study: a randomised controlled trial of single-dose tocilizumab in patients with depression and low-grade inflammation. *BMJ Open*. 2018;8(9):e025333. doi:10.1136/bmjopen-2018-025333

18. An efficacy and safety study of sirukumab in participants with major depressive disorder. ClinicalTrials.gov identifier: NCT02473289. Updated June 11, 2019. Accessed September 14, 2020. https://clinicaltrials.gov/ct2/show/NCT02473289

19. Biomarkers of neuroinflammation and anti-inflammatory treatments in major depressive disorder. ClinicalTrials.gov identifier: NCT02362529. Updated May 23, 2019. Accessed September 14, 2020. https://clinicaltrials.gov/ct2/show/NCT02362529

20. Howard DM, Adams MJ, Clarke TK, et al; 23andMe Research Team; Major Depressive Disorder Working Group of the Psychiatric Genomics Consortium. Genome-wide meta-analysis of depression identifies 102 independent variants and highlights the importance of the prefrontal brain regions. *Nat Neurosci*. 2019;22(3):343-352. doi:10.1038/s41593-018-0326-7

21. Ligthart S, Vaez A, Võsa U, et al; LifeLines Cohort Study; CHARGE Inflammation Working Group. Genome analyses of >200,000 individuals identify 58 loci for chronic inflammation and highlight pathways that link inflammation and complex disorders. *Am J Hum Genet*. 2018;103(5):691-706. doi:10.1016/j.ajhg.2018.09.009

22. Martin AR, Daly MJ, Robinson EB, Hyman SE, Neale BM. Predicting polygenic risk of psychiatric disorders. *Biol Psychiatry*. 2019;86(2):97-109. doi:10.1016/j.biopsych.2018.12.015

23. Milaneschi Y, Lamers F, Peyrot WJ, et al; CHARGE Inflammation Working Group and the Major Depressive Disorder Working Group of the Psychiatric Genomics Consortium. Genetic association of major depression with atypical features and obesity-related immunometabolic dysregulations. *JAMA Psychiatry*. 2017;74(12):1214-1225. doi:10.1001/jamapsychiatry.2017.3016

24. Milaneschi Y, Lamers F, Peyrot WJ, et al; CHARGE Inflammation Working Group. Polygenic dissection of major depression clinical heterogeneity. *Mol Psychiatry*. 2016;21(4):516-522. doi:10.1038/mp.2015.86

25. Bulik-Sullivan BK, Loh PR, Finucane HK, et al; Schizophrenia Working Group of the Psychiatric Genomics Consortium. LD Score regression distinguishes confounding from polygenicity in genome-wide association studies. *Nat Genet*. 2015;47(3):291-295. doi:10.1038/ng.3211

26. Bulik-Sullivan B, Finucane HK, Anttila V, et al; ReproGen Consortium; Psychiatric Genomics Consortium; Genetic Consortium for Anorexia Nervosa of the Wellcome Trust Case Control Consortium 3. An atlas of genetic correlations across human diseases and traits. *Nat Genet*. 2015;47(11):1236-1241. doi:10.1038/ng.3406

27. Smith GD, Ebrahim S. "Mendelian randomization": can genetic epidemiology contribute to understanding environmental determinants of disease? *Int J Epidemiol*. 2003;32(1):1-22. doi:10.1093/ije/dyg070

28. Davey Smith G, Ebrahim S. What can mendelian randomisation tell us about modifiable behavioural and environmental exposures? *BMJ*. 2005;330(7499):1076-1079. doi:10.1136/bmj.330.7499.1076

29. Hingorani A, Humphries S. Nature's randomised trials. *Lancet*. 2005;366(9501):1906-1908. doi:10.1016/S0140-6736(05)67767-7

30. Wium-Andersen MK, Ørsted DD, Nordestgaard BG. Elevated C-reactive protein, depression, somatic diseases, and all-cause mortality: a mendelian randomization study. *Biol Psychiatry*. 2014;76(3):249-257. doi:10.1016/j.biopsych.2013.10.009

31. Khandaker GM, Zuber V, Rees JMB, et al. Shared mechanisms between coronary heart disease and depression: findings from a large UK general population-based cohort. *Mol Psychiatry*. 2020;25(7):1477-1486. doi:10.1038/s41380-019-0395-3

32. Wray NR, Ripke S, Mattheisen M, et al; eQTLGen; 23andMe; Major Depressive Disorder Working Group of the Psychiatric Genomics Consortium. Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. *Nat Genet*. 2018;50(5):668-681. doi:10.1038/s41588-018-0090-3

33. Locke AE, Kahali B, Berndt SI, et al; LifeLines Cohort Study; ADIPOGen Consortium; AGEN-BMI Working Group; CARDIOGRAMplusC4D Consortium; CKDGen Consortium; GLGC; ICBP; MAGIC Investigators; MuTHER Consortium; MIGen Consortium; PAGE Consortium; ReproGen Consortium; GENIE Consortium; International Endogene Consortium. Genetic studies of body mass index yield new insights for obesity biology. *Nature*. 2015;518(7538):197-206. doi:10.1038/nature14177

34. Wood AR, Esko T, Yang J, et al; Electronic Medical Records and Genomics (eMEMERGEGE) Consortium; MIGen Consortium; PAGEGE Consortium; LifeLines Cohort Study. Defining the role of common variation in the genomic and biological architecture of adult human height. *Nat Genet*. 2014;46(11):1173-1186. doi:10.1038/ng.3097

35. Sun BB, Maranville JC, Peters JE, et al. Genomic atlas of the human plasma proteome. *Nature*. 2018;558(7708):73-79. doi:10.1038/s41586-018-0175-2

36. Jansen PR, Watanabe K, Stringer S, et al; 23andMe Research Team. Genome-wide analysis of insomnia in 1,331,010 individuals identifies new risk loci and functional pathways. *Nat Genet*. 2019;51(3):394-403. doi:10.1038/s41588-018-0333-3

37. Rosa M, Chignon A, Li Z, et al. A Mendelian randomization study of IL6 signaling in cardiovascular diseases, immune-related disorders and longevity. *NPJ Genom Med*. 2019;4(1):23. doi:10.1038/s41525-019-0097-4

38. Lam M, Awasthi S, Watson HJ, et al. RICOPILI: Rapid Imputation for COnsortias PIpeLIne. *Bioinformatics*. 2020;36(3):930-933. doi:10.1093/bioinformatics/btz633

39. Neale Lab UK Biobank. Accessed September 14, 2020. https://www.nealelab.is/uk-biobank/

40. Löwe B, Unützer J, Callahan CM, Perkins AJ, Kroenke K. Monitoring depression treatment outcomes with the Patient Health Questionnaire-9. *Med Care*. 2004;42(12):1194-1201. doi:10.1097/00005650-200412000-00006

41. Davis KAS, Coleman JRI, Adams M, et al. Mental health in UK Biobank: development, implementation and results from an online questionnaire completed by 157 366 participants:

a reanalysis. *BJPsych Open*. 2020;6(2):e18. doi:10.1192/bjo.2019.100

42. American Psychiatric Association. *Diagnostic and Statistical Manual of Mental Disorders*. 4th ed. American Psychiatric Association; 1994.

43. Murray JC, Buetow KH, Weber JL, et al; Cooperative Human Linkage Center (CHLC). A comprehensive human linkage map with centimorgan density. *Science*. 1994;265(5181):2049-2054. doi:10.1126/science.8091227

44. Auton A, Brooks LD, Durbin RM, et al; 1000 Genomes Project Consortium. A global reference for human genetic variation. *Nature*. 2015;526(7571):68-74. doi:10.1038/nature15393

45. Benjamini Y, Hochberg Y. Controlling the false discovery rate: a practical and powerful approach to multiple testing. *J R Stat Soc Series B Stat Methodol*. 1995;57(1):289-300. doi:10.1111/j.2517-6161.1995.tb02031.x

46. Hunter CA, Jones SA. IL-6 as a keystone cytokine in health and disease. *Nat Immunol*. 2015;16(5):448-457. doi:10.1038/ni.3153

47. Del Giudice M, Gangestad SW. Rethinking IL-6 and CRP: why they are more than inflammatory biomarkers, and why it matters. *Brain Behav Immun*. 2018;70:61-75. doi:10.1016/j.bbi.2018.02.013

48. Ridker PM. From C-reactive protein to interleukin-6 to interleukin-1: moving upstream to identify novel targets for atheroprotection. *Circ Res*. 2016;118(1):145-156. doi:10.1161/CIRCRESAHA.115.306656

49. Calabrese LH, Rose-John S. IL-6 biology: implications for clinical targeting in rheumatic disease. *Nat Rev Rheumatol*. 2014;10(12):720-727. doi:10.1038/nrrheum.2014.127

50. Palmer TM, Lawlor DA, Harbord RM, et al. Using multiple genetic variants as instrumental variables for modifiable risk factors. *Stat Methods Med Res*. 2012;21(3):223-242. doi:10.1177/0962280210394459

51. Georgakis MK, Malik R, Gill D, Franceschini N, Sudlow CLM, Dichgans M; INVENT Consortium,CHARGE Inflammation Working Group. Interleukin-6 signaling effects on ischemic stroke and other cardiovascular outcomes: a Mendelian randomization study. *Circ Genom Precis Med*. 2020;13(3):e002872. doi:10.1161/CIRCGEN.119.002872

52. Pierce BL, Ahsan H, Vanderweele TJ. Power and instrument strength requirements for Mendelian Randomization studies using multiple genetic variants. *Int J Epidemiol*. 2011;40(3):740-752. doi:10.1093/ije/dyq151

53. Hartwig FP, Bowden J, Loret de Mola C, Tovo-Rodrigues L, Davey Smith G, Horta BL. Body mass index and psychiatric disorders: a Mendelian randomization study. *Sci Rep*. 2016;6(1):32730. doi:10.1038/srep32730

54. R Core Team. R: The R Project for Statistical Computing. Accessed September 14, 2020. https://www.r-project.org/

55. Hemani G, Zheng J, Elsworth B, et al. The MR-Base platform supports systematic causal inference across the human phenome. *eLife*. 2018;7:1-29. doi:10.7554/eLife.34408

56. Hemani G, Bowden J, Davey Smith G. Evaluating the potential role of pleiotropy in Mendelian randomization studies. *Hum Mol Genet*. 2018;27(R2):R195-R208. doi:10.1093/hmg/ddy163

57. Lawlor DA, Harbord RM, Sterne JAC, Timpson N, Davey Smith G. Mendelian randomization: using genes as instruments for making causal inferences in epidemiology. *Stat Med*. 2008;27(8):1133-1163. doi:10.1002/sim.3034

58. Burgess S, Small DS, Thompson SG. A review of instrumental variable estimators for Mendelian randomization. *Stat Methods Med Res*. 2017;26(5):2333-2355. doi:10.1177/0962280215597579

59. Bowden J, Davey Smith G, Haycock PC, Burgess S. Consistent estimation in Mendelian randomization with some invalid instruments using a weighted median estimator. *Genet Epidemiol*. 2016;40(4):304-314. doi:10.1002/gepi.21965

60. Greco M FD, Minelli C, Sheehan NA, Thompson JR, Thompson JR. Detecting pleiotropy in Mendelian randomisation studies with summary data and a continuous outcome. *Stat Med*. 2015;34(21):2926-2940. doi:10.1002/sim.6522

61. Burgess S, Thompson SG. Interpreting findings from Mendelian randomization using the MR-Egger method. *Eur J Epidemiol*. 2017;32(5):377-389. doi:10.1007/s10654-017-0255-x

62. Bowden J, Davey Smith G, Burgess S. Mendelian randomization with invalid instruments: effect estimation and bias detection through Egger regression. *Int J Epidemiol*. 2015;44(2):512-525. doi:10.1093/ije/dyv080

63. Open Science Framework. Dissecting the association between inflammation, metabolic dysregulation, and specific depressive symptoms. Last updated August 21, 2020. Accessed September 14, 2020. https://osf.io/ub83a/

64. Turecki G, Brent DA. Suicide and suicidal behaviour. *Lancet*. 2016;387(10024):1227-1239. doi:10.1016/S0140-6736(15)00234-2

65. Turecki G. The molecular bases of the suicidal brain. *Nat Rev Neurosci*. 2014;15(12):802-816. doi:10.1038/nrn3839

66. Black C, Miller BJ. Meta-analysis of cytokines and chemokines in suicidality: distinguishing suicidal versus nonsuicidal patients. *Biol Psychiatry*. 2015;78(1):28-37. doi:10.1016/j.biopsych.2014.10.014

67. Ganança L, Oquendo MA, Tyrka AR, Cisneros-Trujillo S, Mann JJ, Sublette ME. The role of cytokines in the pathophysiology of suicidal behavior. *Psychoneuroendocrinology*. 2016;63:296-310. doi:10.1016/j.psyneuen.2015.10.008

68. Brundin L, Erhardt S, Bryleva EY, Achtyes ED, Postolache TT. The role of inflammation in suicidal behaviour. *Acta Psychiatr Scand*. 2015;132(3):192-203. doi:10.1111/acps.12458

69. Gradus JL, Qin P, Lincoln AK, et al. Inflammatory bowel disease and completed suicide in Danish adults. *Inflamm Bowel Dis*. 2010;16(12):2158-2161. doi:10.1002/ibd.21298

70. Milaneschi Y, Lamers F, Bot M, Drent ML, Penninx BWJH. Leptin dysregulation is specifically associated with major depression with atypical features: evidence for a mechanism connecting obesity and depression. *Biol Psychiatry*. 2017;81(9):807-814. doi:10.1016/j.biopsych.2015.10.023

71. Lamers F, Milaneschi Y, Vinkers CH, Schoevers RA, Giltay EJ, Penninx BWJH. Depression profilers and immuno-metabolic dysregulation: longitudinal results from the NESDA study. *Brain Behav Immun*. 2020;88:174-183. doi:10.1016/j.bbi.2020.04.002

72. Simmons WK, Burrows K, Avery JA, et al. Appetite changes reveal depression subgroups with distinct endocrine, metabolic, and immune states. *Mol Psychiatry*. 2020;25(7):1457-1468. doi:10.1038/s41380-018-0093-6

73. Fedewa MV, Hathaway ED, Ward-Ritacco CL. Effect of exercise training on C reactive protein: a systematic review and meta-analysis of randomised and non-randomised controlled trials. *Br J Sports Med*. 2017;51(8):670-676. doi:10.1136/bjsports-2016-095999

74. Bauer ME, Teixeira AL. Inflammation in psychiatric disorders: what comes first? *Ann N Y Acad Sci*. 2019;1437(1):57-67. doi:10.1111/nyas.13712

75. Flett GL, Vredenburg K, Krames L. The continuity of depression in clinical and nonclinical samples. *Psychol Bull*. 1997;121(3):395-416. doi:10.1037/0033-2909.121.3.395

76. Haycock PC, Burgess S, Wade KH, Bowden J, Relton C, Davey Smith G. Best (but oft-forgotten) practices: the design, analysis, and interpretation of Mendelian randomization studies. *Am J Clin Nutr*. 2016;103(4):965-978. doi:10.3945/ajcn.115.118216

77. Ohlsson H, Kendler KS. Applying causal inference methods in psychiatric epidemiology: a review. *JAMA Psychiatry*. 2020;77(6):637-644. doi:10.1001/jamapsychiatry.2019.3758