
Please note:
Changes made as a result of publishing processes such as copy-editing, formatting and page numbers may not be reflected in this version. For the definitive version of this publication, please refer to the published source. You are advised to consult the publisher’s version if you wish to cite this paper.

This version is being made available in accordance with publisher policies. See http://orca.cf.ac.uk/policies.html for usage policies. Copyright and moral rights for publications made available in ORCA are retained by the copyright holders.
An Analysis of Two Genome-wide Association Meta-analyses Identifies a New Locus for Broad Depression Phenotype


ABSTRACT

BACKGROUND: The genetics of depression has been explored in genome-wide association studies that focused on either major depressive disorder or depressive symptoms with mostly negative findings. A broad depression phenotype including both phenotypes has not been tested previously using a genome-wide association approach. We aimed to identify genetic polymorphisms significantly associated with a broad phenotype from depressive symptoms to major depressive disorder.

METHODS: We analyzed two prior studies of 70,017 participants of European ancestry from general and clinical populations in the discovery stage. We performed a replication meta-analysis of 28,328 participants. Single nucleotide polymorphism (SNP)-based heritability and genetic correlations were calculated using linkage disequilibrium score regression. Discovery and replication analyses were performed using a p-value-based meta-analysis. Lifetime major depressive disorder and depressive symptom scores were used as the outcome measures. RESULTS: The SNP-based heritability of major depressive disorder was 0.21 (SE 0.02), the SNP-based heritability of depressive symptoms was 0.04 (SE 0.01), and their genetic correlation was 1.001 (SE 0.2). We found one genome-wide significant locus related to the broad depression phenotype (rs9825823, chromosome 3: 61,082,153, p 5 8.2 3 10–9) located in an intron of the FHIT gene. We replicated this SNP in independent samples (p 5 .02) and the overall meta-analysis of the discovery and replication cohorts (1.0 3 10–9).

CONCLUSIONS: This large study identified a new locus for depression. Our results support a continuum between depressive symptoms and major depressive disorder. A phenotypically more
inclusive approach may help to achieve the large sample sizes needed to detect susceptibility loci for depression.

The etiology of depression—a worldwide leading cause of disability (1)—is not well understood. As indicated by family, twin, and adoption studies, genetic factors mediate part of vulnerability to major depressive disorder (MDD) with a modest heritability of around 40% (2). However, we understand little of the specific genetic architecture of MDD. Multiple genome-wide association studies (GWASs) for MDD have been published (3–10). The largest MDD GWAS was the mega-analysis by the MDD Working Group of the Psychiatric Genomics Consortium (PGC). In that study, more than 9000 MDD cases and 9500 control subjects were analyzed, but no association with MDD reached genome-wide significance (7). Recently, the CONVERGE (China, Oxford, and VCU Experimental Research on Genetic Epidemiology) consortium identified two genome-wide significant associations in 5303 Chinese women with severe and recurrent MDD (near the SIRT1 gene, p  2.53 3 10–10, and in an intron of the LHPP gene, p  6.45 3 10–12) (11). A GWAS of depressive symptoms (23%–29% heritability) (12,13) in the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) consortium in approximately 50,000 people from the general population found no genome-wide significant associations (14). Owing to the relatively small sample sizes, the previous GWASs of depressive disorders and depressive symptoms were arguably underpowered to detect small genetic effects (15,16).

Depression can be conceptualized along a continuum of severity from subthreshold or minor depression to MDD of varying severity (e.g., mild, moderate, severe) (17). Using a continuum approach may augment statistical power because sample size can be increased substantially and patients who fall into the gray area can be assessed. Several lines of evidence support a depression continuum. In longitudinal studies, there is an increased risk of MDD in patients with minor depression and subthreshold depression (18,19). Statistical studies of disorder classification (taxometric) suggested that severity of depression is continuously distributed and that there is no discontinuity in the latent structure of depression (19,20). Family studies report that relatives of probands with milder forms of depression have greater risk of MDD compared with relatives of probands without any mood disorders (21–24). A higher number of depressive symptoms is related to greater disability, worse quality of life, and higher mortality risk (18,25–29). MDD and continuous measures of depression are highly correlated, and severity of depressive symptoms along the continuum is linear (30,31).

The goal of the current study was to combine the results of the largest GWAS using categorical lifetime MDD and continuous measures of depression to identify genetic variants underlying the entire depression continuum.

METHODS AND MATERIALS

Study Design and Samples

This study was a collaboration between investigators on the PGC MDD and CHARGE genome-wide association meta-analyses (GWAMA). In the discovery phase, we aggregated two GWAMAs published in 2013 (7,14). Basic descriptive features and phenotype definitions of the contributing samples are provided in Supplemental Table S1. The mega-analysis of MDD consisted of nine studies of 9240 cases meeting international criteria for lifetime MDD and 9519 healthy control subjects. The CHARGE meta-analysis of depressive symptoms included 22 cohorts and comprised 51,258 persons. Each cohort contributing to the GWAMA of the PGC and CHARGE was distinct. In the replication analyses, 16 case-control studies with DSM-IV MDD (6718 cases and 13,453 control subjects) were
included along with 8157 subjects from the general population with assessment of depressive symptoms. All subjects were of European ancestry. Institutional review boards approved all studies, and all participants provided written informed consent.

**Phenotype Characteristics**

In the PGC GWAMA, MDD was established with structured clinical interviews (e.g., Clinical Interview Schedule–Revised, Diagnostic Interview for Genetic Studies, and Structured Clinical Interview for DSM-IV). All clinical evaluations were made by experienced clinicians or interviewers. Most cases were ascertained from clinical sources. Control subjects were screened in most of the studies to require the absence of MDD and were recruited from the general population. Full details about the PGC samples can be found in the previous publication (7). In the CHARGE GWAMA, depressive symptoms were assessed with validated questionnaires. Measures include the Center for Epidemiological Studies–Depression scale, Geriatric Depression Scale, Patient Health Questionnaire-9, and Beck Depression Inventory-II, mostly assessing depressive symptoms during previous weeks rather than lifetime MDD (14). Persons with schizophrenia, bipolar disorder, or dementia were excluded. Persons aged 40 years or older with genotype data and depressive symptom scores were included.

The 16 MDD case-control replication samples were part of an expanded but unpublished PGC MDD analysis. MDD was diagnosed with interviews. In the depressive symptom replication cohort, the Health and Retirement Study, the 8-item Center for Epidemiological Studies–Depression scale was applied. Respondents were excluded if they were under 40 years of age or displayed evidence of cognitive impairment.

**Genotyping and Imputation**

In the PGC samples (Supplemental Table S1), individual genotypes were assembled, processed through a central quality control pipeline, and imputed using the CEU (Central Europe) and TSI (Toscani in Italy) HapMap3 reference panels. Quality control procedures were extensive (7). In the CHARGE cohorts, genotype quality control and imputation were conducted in each study separately. The imputation reference was the HapMap2 CEU panel (14). In the MDD replication cohorts (Supplemental Table S3), imputation was performed using IMPUTE2 or SHAPEIT (chunk size of 3 Mb and default parameters). The imputation reference set consisted of 2186 phased haplotypes from the 1000 Genomes Project. In the Health and Retirement Study, imputation was performed using the HapMap2 CEU reference panel.

**Statistical Analyses**

Linkage disequilibrium score regression was used to compute the single nucleotide polymorphism (SNP)-based heritability and the genetic correlation using the 1000 Genomes CEU reference panel (32).

In the PGC GWAMA, a logistic regression analysis was used to test the association between MDD and imputed SNP dosages under an additive model and adjusting for study indicators and five principal components (7). In the CHARGE GWAMA, a linear regression analysis was applied to test the association of depressive symptom score on imputed SNP dosages in the contributing studies adjusting for age and sex. Analyses were adjusted for principal components for most, but not all, cohorts in the CHARGE GWAMA. A p-value-based meta-analysis was applied in the CHARGE GWAMA (14). Effect size estimates were based on a dichotomous outcome in the PGC and on a continuous outcome in the CHARGE GWAMA. To combine these effect estimates, a p-value-based meta-analysis weighted by sample size with METAL (http://www.sph.umich.edu/csg/abecasis/metal/) was used.
This method allows different weights for each study and takes into account the direction of effect at each SNP (33). To specify the direction of the effect, the PGC used the logistic regression coefficient beta and the CHARGE used z scores. Weights were based on the number of MDD cases in the PGC study (n = 9240), and the number of individuals in the CHARGE with clinically significant depressive symptoms (n = 5976) using population-specific cutoff scores of the questionnaires was considered for weighting. To test whether the results are affected by different sample size weightings, equal weights per study, or no weight as suggested by Stouffer et al. (34), we carried out a series of sensitivity analyses.

We selected the genome-wide significant SNPs in two loci from the discovery stage for replication. After analyzing these data, we performed a p-value-based meta-analysis combining all replication samples. Furthermore, we analyzed the results of the discovery and all replication samples weighting for number of cases.

RESULTS

In the discovery stage, we performed a GWAMA in 70,017 participants of European ancestry by combining the PGC MDD (7) and CHARGE GWAMA (14). We applied a linkage disequilibrium score regression to the summary statistics from each study to compute the SNP-based heritabilities and the genetic correlation. As reported previously (35), the SNP-based liability scale heritability of MDD was 0.2 (SE = 0.02) for 20% of prevalence. The lambda was 1.1 and the regression intercept was 1.0 (SE = 0.01). The SNP-based heritability of depressive symptoms was 0.04 (SE = 0.01). The lambda was 1.1 and the regression intercept was 1.0 (SE = 0.01). The SNP-based heritability of the broad depression phenotype was 0.3 (SE = 0.04). MDD and depressive symptoms showed significant coheritability (1.001, SE = 0.2, z score = 4.6, p = 4.6 \times 10^{-6}). This result supports the contention of a continuum between depressive symptoms and MDD. However, the genetic correlation should be interpreted carefully because linkage disequilibrium regression is quite sensitive to environmental confounding and, like twin studies, often lacks precision. In addition, different evaluation methods of the depression phenotypes might cause different genetic correlation estimates that cannot easily be compared.

We conducted a meta-analysis of the PGC MDD and the CHARGE depressive symptoms GWAMA using a weighted, p-value-based meta-analysis. The results are summarized in Figure 1 and Supplemental Figures S1 to S3. The combined meta-analysis was conducted for 918,921 SNPs. Two loci were genome-wide significant: an SNP in an intron of the FHIT gene (rs9825823, chromosome 3: 61,082,153, p = 5.82 \times 10^{-9}) and an SNP in an intron of PLEK2 (rs9323497, chr14: 67,873,128, p = 3.33 \times 10^{-8})(Table 1). All SNPs with a p value of association, p < 5 \times 10^{-5} are presented in Supplemental Table S2. Using different weights or Stouffer’s unweighted method had only slight effects on the results (data not shown). Supplemental Figures S4 and S5 show forest plots for two SNPs shown in Table 1.

Table 2 presents the replication analyses and the meta-analysis of discovery and replication results. One of the genome-wide significant variants within the FHIT gene (rs9825823) was associated with the depression continuum in the replication cohorts (z score = 2.4, p = 5.02). The result of the final meta-analysis of discovery and replication samples also indicated a positive replication as indexed by a lower p value (z score = 5.61, p = 5.10 \times 10^{-9}). This SNP had a positive association with depressive symptoms in the CHARGE study (p = 5.53 \times 10^{-4}), and a similar pattern was observed in the PGC study (p = 4.13 \times 10^{-6}). The SNP in an intron of PLEK2 (rs9323497) was not related to the depression continuum significantly (z score = 5.2, p = 5.90).
We performed an additional replication analysis of our two genome-wide significant SNPs using the publicly available data of the recently published GWAMA of depressive disorders in a sample of Chinese women (the CONVERGE study) (11). In CONVERGE, rs9825823 (odds ratio 5 1.01, p 5 .12) and rs9323497 (odds ratio 5 0.97, p 5 .0002, with a different direction of association than in our discovery sample) were not related to depression at the genome-wide significance level, although the latter reached nominal significance. However, in the joint meta-analysis of the Health and Retirement Study, the PGC MDD study, and CONVERGE study, we found that the association between rs9825823 and the depression continuum (z score 5 2.85, p 5 .004) was slightly stronger than our initial replication analysis. When these replication and discovery samples were combined, the association with our top hit also became stronger (analysis without the CONVERGE data: z score 5 6.1, p 5 1 3 10–9; analysis with the CONVERGE data: z score 5 6.2, p 5 6.8 3 10–10). Results of additional replication analyses are given in Supplemental Table S4.

DISCUSSION

We report the results of a combined GWAMA of the depression continuum including MDD (18,759 cases and control subjects) and depressive symptoms (51,258 participants). In the discovery stage, we found genome-wide significant associations in the FHIT and PLEK2 genes. One SNP in the intron of the FHIT gene showed a significant association in the combined analysis of discovery and replication samples of MDD and depressive symptoms samples, and it exceeded a genome-wide significance threshold.

The significant locus (rs9825823, chr3: 61,082,153) maps to the intronic region of the FHIT gene, a tumor suppressor protein implicated in several cancers (36). FHIT is expressed in multiple brain regions (amygdala, anterior cingulate cortex, caudate nucleus, prefrontal cortex, hippocampus, and hypothalamus; http://www.gtexportal.org/home/gene/FHIT). It plays an important role in oxidative stress and level of DNA damage (37), biological processes implicated in MDD (38,39).

FHIT is a circadian clock modifier gene (40) and has been related to daytime sleepiness (41), which may be salient to the etiology of depression.

In a GWAS of recurrent, early-onset MDD, three SNPs located in the FHIT gene were among the strongest associations in the overall and sex-stratified analyses (8), although none had genome-wide significance. Genetic variants located in FHIT have been reported in genetic studies of anxiety (42),
autism (43), mental stress (44), comorbid depressive syndromes and alcohol dependence (45),
citalopram-induced side effects (46), and a latent class analysis of MDD symptoms (7), but none has
met genome-wide significance.

Several methodological aspects should be discussed. First, we evaluated the depression continuum
by combining cases from clinical populations diagnosed with MDD and participants from the general
population who had been assessed for depressive symptoms. Such an inclusive approach may
increase heterogeneity of the phenotype especially because lifetime MDD was evaluated, whereas
depressive symptoms indicate past weeks only. If anything, such an approach would cause an
underestimation of the effects because less information on depressive symptoms was obtained.
However, the advantages of a large sample can outweigh the disadvantages of a less precisely
defined phenotype. This has been observed in the GWAS of educational attainment that was
successfully used as a proxy for intelligence (47). Our additional replication analysis showed that
increasing the sample size yielded a stronger association of the top hit with the depression
continuum. It is complex to calculate statistical power of the current analysis because quantitative
and qualitative measures were combined. In the current study, a genetic association with the
depression continuum may reflect an effect on broad depressive phenotypes but could also be
accounted for by an association with low levels of general well-being (12%–18% heritability) that co-
occur with depressive symptoms (48). Second, we used a p-value-based meta-analysis because
effect estimates could not be directly evaluated in a straight-forward manner. Third, the
heterogeneity of the imputation methods used in the PGC and CHARGE discovery samples might
reduce the statistical power. However, different imputation references did not change the results in
the published PGC MDD study (7).

In conclusion, in this large GWAMA of a broad depression phenotype, we detected a locus
associated with depression in clinical and general population samples. Our results suggest the
importance of a broader depression phenotype to identify genetic variants underlying depression.
Large samples with different depression phenotypes may also help to disentangle the genetic
background of different forms of depression.

ACKNOWLEDGMENTS AND DISCLOSURES

We acknowledge the essential role of the CHARGE consortium in development and support of this
manuscript. CHARGE members include the Netherlands’ Rotterdam Study; the National Heart, Lung,
and Blood Institute’s Framingham Heart Study, Cardiovascular Health Study, and Atherosclerosis Risk
in Communities Study; and the National Institute on Aging’s (NIA) Iceland Age, Gene/Environment
Susceptibility Study. Core funding for the PGC is from the U.S. National Institute of Mental Health
(U01MH094421). The PGC was supported by the National Institute of Mental Health (NIMH R01
MH094421 and NIMH R01 MH094421). The Health and Retirement Study is supported by the NIA (NIA U01AG009740). The genotyping was funded separately by the NIA (RC2 AG036495 and RC4 AG039029). Our genotyping was conducted by the National Institutes of Health (NIH) Center for Inherited Disease Research at Johns Hopkins University. Genotyping quality control and final preparation of the data were performed by the Genetics Coordinating Center at the University of Washington. The CoLaus|PsyCoLaus study was and is supported by research grants from GlaxoSmithKline, the Faculty of Biology and Medicine of Lausanne, and the Swiss National Science Foundation (3200B0-105993, 3200B0-118308, 33CSCO-122661, 33CS30-139468, and 33CS30-148401). Framingham, Massachusetts; Rush Alzheimer’s Disease Center & Department of Neurological Sciences (DAB, JY), Rush University Medical Center; and Department of Preventive Medicine (MCC), Northwestern University Feinberg School of Medicine, Chicago, Illinois; Department of Psychiatry (PM, ACH, MLP, JPR), Washington University, St. Louis, Missouri; Department of Medicine (THM Jr), University of Mississippi Medical Center, Jackson, Mississippi; Translational Gerontology Branch (LF, TT), National Institute on Aging, Baltimore, Maryland; Brown Foundation Institute of Molecular Medicine (MF), University of Texas Health Science Center at Houston, Houston, Texas; Department of Psychiatry (SPH), Kaiser Permanente San Francisco Medical Center, San Francisco; and Department of Psychiatry and Behavioral Sciences (DFL), Stanford University, Stanford, California; Department of Epidemiology (KK), Mailman School of Public Health, Columbia University; College of Physicians and Surgeons (MMW), Columbia University and New York State Psychiatric Institute; and Division of Psychiatric Genomics (SMP), Department of Psychiatry, Icahn School of Medicine at Mount Sinai, New York, New York; Janssen Research & Development LLC (QSL), New Brunswick, New Jersey; Charles E. Schmidt College of Medicine (MLP), Florida Atlantic University, Boca Raton, Florida; Department of Psychiatry (JBP), University of Iowa Carver College of Medicine, Iowa City, Iowa; Division of Cancer Epidemiology and Genetics (JS), National Cancer Institute, National Institutes of Health, Bethesda, Maryland; Group Health (SS), Seattle, Washington. Department of Psychiatry (UD), University of Marburg, Marburg; Department of Psychiatry and Psychotherapy (SR), Charité, Campus Mitte, Berlin; Institute of Human Genetics (SC, MMN), University of Bonn, and Department of Genomics (SC, MMN), Life & Brain Center, Bonn; Institute of Neuroscience and Medicine (SC), Research Centre Jülich, Jülich; Department of Psychiatry and Psychotherapy (UD), University of Münster, Münster; Department of Psychiatry and Psychotherapy (HJG), Helios Hospital Stralsund; Department of Psychiatry and Psychotherapy (HJG, SVDa), University Medicine Greifswald; German Center for Neurodegenerative Diseases (HJG, SVDa), Site Rostock/Greifswald; Interfaculty Institute for Genetics and Functional Genomics (GH), University of Greifswald; Institute for Community Medicine (AT), University Medicine Greifswald, Greifswald; Max Planck Institute of Psychiatry (SK, SL, BM-M); Institute of Psychiatric Phenomics and Genomics (TGS), LudwigMaximilians-University; Department of Psychosomatic Medicine and Psychotherapy (K-HL), Klinikum rechts der Isar, Technische Universität München; and Munich Cluster for Systems Neurology (BM-M), Munich; Institute of Epidemiology II (K-HL), Mental Health Research Unit, Helmholtz Zentrum München, German Research Center for Environmental Health, Neuherberg; Department of Genetic Epidemiology in Psychiatry (MRie), Central Institute of Mental Health, Medical Faculty Mannheim/Heidelberg University, Mannheim; and Department of Psychiatry and Psychotherapy (TGS), University of Göttingen, Göttingen, Germany. Discipline of Psychiatry (TA, AT, BTB), School of Medicine, University of Adelaide, Adelaide, South Australia; Queensland Brain Institute (EMB), University of Queensland, St. Lucia, Queensland; QIMR Berghofer Medical Research Institute (SDG, NGM, GWM, DRN), Brisbane, and Institute of Health and Biomedical Innovation (DRN), Queensland University of Technology, Brisbane, Queensland; and Department of Psychiatry and Psychiatric Neuroscience (GCS), School of Medicine and Dentistry, James Cook University, Townsville, Queensland, Australia. Division of Psychiatry (DHRB, T-KC, DJM, AMM), University of
Edinburgh, Edinburgh; MRC Social, Genetic & Developmental Psychiatry Centre Centre (GB, CML, MRiv, RU), Institute of Psychiatry, Psychology & Neuroscience, King’s College London; and Division of Psychiatry (GL), University College London, London; University of Exeter Medical School (DJL), Exeter; University of Liverpool (BM-M), Institute of Translational Medicine, Liverpool; and MRC Centre for Neuropsychiatric Genetics and Genomics (MCO, KET), Institute of Psyco-logical Medicine and Clinical Neurosciences, School of Medicine, Cardiff University, Cardiff, United Kingdom. Translational Neuropsychiatry Unit (HNB), Department of Clinical Medicine; Department of Biomedicine and Centre for Integrative Sequencing (ADB), Aarhus University; The Lundbeck Foundation Initiative for Integrative Psychiatric Research (HNB, ADB OM), Aarhus; and Research Department P (OM), Aarhus University Hospital, Risskov, Denmark. Department of Psychiatry (EC, MP), Lausanne University Hospital, and Institute of Social and Preventive Medicine (ZK), Centre Hospitalier Universitaire Vaudois, Lausanne; Division of Medical Genetics (SC), Department of Biomedicine, University of Basel; and Roche Pharmaceutical Research and Early Development (ED, CH, JAQ, DU), Neuroscience, Ophthalmology and Rare Diseases Discovery & Translational Medicine Area, Roche Innovation Center Basel, F Hoffman–La Roche Ltd., Basel, Switzerland. Centre for Integrative Biology (ED), University of Trento, Trento, Italy. National Institute for Health and Welfare (JGE), Department of Chronic Disease Prevention; Department of General Practice and Primary Health Care (JGE), University of Helsinki; Unit of General Practice (JGE), Helsinki University Central Hospital; Folkhalsan Research Centre (JGE, JL); Institute of Behavioural Sciences (JL, KR), University of Helsinki, Helsinki; and Vasa Central Hospital (JGE), Vasa, Finland. Estonian Genome Center (TE, AM) and Institute of Molecular and Cell Biology (AM), University of Tartu, Tartu, Estonia. Department of Psychiatry (MG), Trinity Centre for Health Science, Dublin, Ireland. CIBERSAM–Universidad de Granada (MRiv) and Instituto de Investigación Biosanitaria ibs.GRANADA (MRiv), Hospitales Universitarios de Granada/Universidad de Granada, Granada, Spain. Dal-housie University (RU), Halifax, Nova Scotia, Canada. Department of Medical Epidemiology and Biostatistics (PFS), Karolinska Institutet, Sweden.

ND and SW contributed equally to this work. HT and PFS contributed equally to this work.

Address correspondence to Henning Tiemeier, M.D., Ph.D., Department of Epidemiology, Erasmus University Medical Centre, P.O. Box 2040, 3000 CA Rotterdam, The Netherlands; E-mail: h.tiemeier@erasmusmc.nl.

REFERENCES


