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Meta-Analyses of Genome-Wide Association Studies for Postpartum Depression

Corresponding Author: Jerry Guintivano (guinti@email.unc.edu)

Jerry Guintivano, PhD ¹; Enda M Byrne, PhD ^{2,3}; Jacqueline Kiewa ²; Shuyang Yao, PhD ⁴; Anna E Bauer, PhD ¹; Karolina A Aberg, PhD ⁵; Mark J Adams, PhD ⁶; Archie Campbell ^{7,8}; Megan L Campbell ^{9,10}; Karmel W Choi, PhD ^{11,12,13}; Elizabeth C Corfield, PhD ^{14,15}; Alexandra Havdahl, PhD ^{15,16,17}; Donald Hucks ¹⁸; Nastassja Koen, PhD ¹⁹; Yi Lu, PhD ⁴; Merete L Mægbæk, MSc ²⁰; Jimmy Mullaert, MD PhD ^{21,22}; Roseann E Peterson, PhD ^{23,24}; Laura M Raffield, PhD ²⁵; Hannah M Sallis, PhD ^{26,27}; Julia M Sealock, PhD ^{28,29}; Alicia Walker ³⁰; Hunna J Watson, PhD ^{1,31,32}; Ying Xiong ⁴; Jessica MK Yang ³³; Richard JL Anney, PhD ³⁴; Katherine Gordon-Smith, PhD ³⁵; Leon Hubbard, PhD ³⁶; Lisa A Jones, PhD ³⁵; Raluca Mihaescu, MD PhD ³⁷; Mette Nyegaard, PhD ³⁸; Antonio F Pardiñas, PhD ³⁶; Amy Perry, PhD ³⁵; Nazmus Saquib, PhD ³⁹; Aladdin H Shadyab, PhD ⁴⁰; Alexander Viktorin, PhD ⁴; Ole A Andreassen, MD PhD ^{41,42,43}; Tim B Bigdeli, PhD ^{44,45}; Lea K Davis, PhD ⁴⁶; Cindy-Lee Dennis, PhD ⁴⁷; Arianna Di Florio, MD PhD ³⁶; Caroline Dubertret, MD PhD ^{48,49}; Yen-Chen A Feng, PhD ^{11,12,13}; Benicio N Frey, MD PhD ^{50,51}; Sophie Grigoriadis, MD PhD ^{52,53}; Emilie Gloaguen ⁵⁴; Ian Jones, PhD ³⁶; James L Kennedy, MD PhD ^{53,55}; Holly Krohn ¹; Theodora Kunovac Kallak, PhD ⁵⁶; Yun Li, PhD ^{25,57}; Nick G Martin, PhD ⁵⁸; Andrew M McIntosh, MD ⁶; Jeannette Milgrom, PhD ^{59,60}; Trine Munk-Olsen, PhD ^{61,62}; Tim Oberlander, MD ^{63,64}; Catherine M Olsen, PhD ^{65,66}; Nicolas Ramoz, PhD ^{67,68}; Ted Reichborn-Kjennerud, MD PhD ^{14,69}; Emma Robertson Blackmore, PhD ⁷⁰; David Rubinow, MD ¹; Alkistis Skalkidou, PhD ⁵⁶; Jordan W Smoller, MD ^{11,12,13}; Dan J Stein, MD PhD ¹⁹; Zachary N Stowe, MD ⁷¹; Valerie Taylor, MD PhD ⁷²; Sarah Tebeka, MD PhD ^{49,73}; Martin Tesli, MD PhD ^{14,74}; Ryan J Van Lieshout, MD PhD ⁵⁰; Edwin JCG van den Oord, PhD ⁵; Simone N Vigod, MD ^{53,75}; Thomas Werge, PhD ^{76,77,78,79}; Lars T Westlye, PhD ^{80,81,82}; David C Whiteman, PhD ^{83,84}; Heather J Zar, MD PhD ^{85,86}; MDD Working Group; Naomi Wray, PhD ⁸⁷; Samantha Meltzer-Brody, MD ^{1,+}; Patrick Sullivan, MD FRANZCP ^{1,4,25,+}

- 1 Department of Psychiatry, University of North Carolina at Chapel Hill, Chapel Hill, NC, USA
- 2 Child Health Research Centre, The University of Queensland, Brisbane, Queensland, Australia
- 3 Institute for Molecular Bioscience, The University of Queensland, Brisbane, Queensland, Australia
- 4 Department of Medical Epidemiology and Biostatistics, Karolinska Institutet, Stockholm, Sweden
- 5 Center for Biomarker Research and Precision Medicine, Virginia Commonwealth University, Richmond, VA, USA
- 6 Division of Psychiatry, University of Edinburgh, Edinburgh, UK
- 7 Centre for Genomic and Experimental Medicine, Institute of Genetics and Cancer, University of Edinburgh, Edinburgh, UK
- 8 Usher Institute for Population Health Sciences and Informatics, University of Edinburgh, Edinburgh, UK
- 9 MRC Genomic and Precision Medicine Research Unit, Division of Human Genetics. Institute for Infectious Diseases and Molecular Medicine, University of Cape Town, Cape Town, South Africa
- 10 Global Initiative for Neuropsychiatric Genetics Education in Research, Broad Institute, Cambridge, MA, USA
- 11 Center for Precision Psychiatry, Department of Psychiatry, Massachusetts General Hospital, Boston, MA, USA
- 12 Department of Psychiatry, Harvard Medical School, Boston, MA, USA
- 13 Psychiatric & Neurodevelopmental Genetics Unit, Center for Genomic Medicine, Massachusetts General Hospital, Boston, MA, USA
- 14 Department of Mental Disorders, Norwegian Institute of Public Health, Oslo, Norway
- 15 Nic Waals Institute, Lovisenberg Diaconal Hospital, Oslo, Norway
- 16 Center for Genetic Epidemiology and Mental Health, Norwegian Institute of Public Health, Oslo, Norway
- 17 Department of Psychology, PROMENTA Research Center, University of Oslo, Oslo, Norway

- 18 Department of Medicine, Division of Genetic Medicine, Vanderbilt Genetics Institute, Vanderbilt University Medical Center, Nashville, TN, USA
- 19 SAMRC Unit on Risk & Resilience in Mental Disorders, Dept of Psychiatry & Neuroscience Institute, University of Cape Town, Cape Town, Western Cape, South Africa
- 20 National Centre for Register-based Research, Department of Economics and Business Economics, Aarhus University, BSS, Aarhus, Denmark
- 21 Department of Epidemiology, Biostatistics and Clinical Research, AP-HP.Nord – Université Paris Cité, Paris, France
- 22 UMR 1137 IAME, INSERM, Paris, France
- 23 Department of Psychiatry and Behavioral Sciences, SUNY Downstate Health Sciences University, Brooklyn, NY, USA
- 24 Institute for Genomics in Health, SUNY Downstate Health Sciences University, Brooklyn, NY, USA
- 25 Department of Genetics, University of North Carolina at Chapel Hill, Chapel Hill, NC, USA
- 26 Centre for Academic Mental Health, Population Health Sciences, Bristol Medical School, University of Bristol, Bristol, UK
- 27 MRC Integrative Epidemiology Unit, University of Bristol, Bristol, UK
- 28 Analytic & Translational Genetics Unit, Massachusetts General Hospital, Boston, MA, USA
- 29 Stanley Center for Psychiatric Research, Broad Institute, Cambridge, MA, USA
- 30 Institute for Molecular Bioscience, University of Queensland, Brisbane, Queensland, Australia
- 31 Discipline of Psychology, Curtin University, Perth, Western Australia, Australia
- 32 Division of Paediatrics, The University of Western Australia, Perth, Western Australia, Australia
- 33 MRC Centre for Neuropsychiatric Genetics and Genomics, Division of Psychological Medicine and Clinical Neurosciences, Cardiff University, Cardiff, UK
- 34 Division of Psychological Medicine & Clinical Neurosciences, MRC Centre for Neuropsychiatric Genetics & Genomics, Cardiff University, Cardiff, UK
- 35 Psychological Medicine, University of Worcester, Worcester, UK

- 36 MRC Centre for Neuropsychiatric Genetics and Genomics, Cardiff University, Cardiff, UK
- 37 Department of Psychiatry, Catharina Hospital, Eindhoven, Netherlands
- 38 Department of Health Science and Technology, Aalborg University, Aalborg, Nordjylland, Denmark
- 39 Clinical Sciences, Sulaiman AlRajhi University, Bukairiyah, Saudi Arabia
- 40 Department of Epidemiology, Herbert Wertheim School of Public Health and Human Longevity Science, University of California, San Diego, La Jolla, CA, USA
- 41 NORMENT Centre, University of Oslo, Oslo, Norway
- 42 Division of Mental Health and Addiction, Oslo University Hospital, Oslo, Norway
- 43 KG Jebsen Centre of Neurodevelopment Research, University of Oslo, Oslo, Norway
- 44 Psychiatry and Behavioral Sciences, SUNY Downstate Health Sciences University, Brooklyn, NY, USA
- 45 Research Service, Department of Veterans Affairs New York Harbor Healthcare System, New York, NY, USA
- 46 Department of Medicine, Division of Genetic Medicine, Vanderbilt University Medical Center, Nashville, TN, USA
- 47 Lawrence S Bloomberg Faculty of Nursing, University of Toronto, Toronto, Ontario, Canada
- 48 INSERM U1266, Université de Paris, Paris, France
- 49 Department of Psychiatry, AP-HP, Louis Mourier Hospital, Colombes, France
- 50 Department of Psychiatry and Behavioural Neurosciences, McMaster University, Hamilton, Ontario, Canada
- 51 Women's Health Concerns Clinic, St. Joseph's Healthcare Hamilton, Hamilton, Ontario, Canada
- 52 Department of Psychiatry, Sunnybrook Health Science Centre and Research Institute, Toronto, Ontario, Canada
- 53 Department of Psychiatry, University of Toronto, Toronto, Ontario, Canada
- 54 Hôpital Bichat, Department of Epidemiology Biostatistics and Clinical Research, AP-HP, Paris, France

- 55 Molecular Brain Science Dept, Centre for Addiction and Mental Health, Toronto, Ontario, Canada
- 56 Department of Women's and Children's Health, Uppsala University, Uppsala, Sweden
- 57 Department of Biostatistics, University of North Carolina at Chapel Hill, Chapel Hill, NC, USA
- 58 Genetic Epidemiology, QIMR Berghofer Medical Research Institute, Brisbane, Queensland, Australia
- 59 Parent-Infant Research Institute, Heidelberg Heights, Victoria, Australia
- 60 University of Melbourne, Melbourne, Victoria, Australia
- 61 The National Center for Register-based Research, Aarhus University, Aarhus, Denmark
- 62 Department of Clinical Research, Psychiatric Research Unit, University of Southern Denmark, Odense, Denmark
- 63 BC Children's Hospital, Vancouver, British Columbia, Canada
- 64 Department of Pediatrics, Faculty of Medicine, University of British Columbia, Vancouver, British Columbia, Canada
- 65 Population Health Department, QIMR Berghofer Medical Research Institute, Brisbane, Queensland, Australia
- 66 The Frazer Institute, The University of Queensland, Brisbane, Queensland, Australia
- 67 Institute of Psychiatry and Neuroscience of Paris, INSERM U1266, Paris, France
- 68 Faculty of Medicine, University Paris Cite, Paris, France
- 69 Institute of Clinical Medicine, University of Oslo, Oslo, Norway
- 70 Behavioral Sciences & Social Medicine, Florida State University, Daytona Beach, FL, USA
- 71 Department of Psychiatry, University of Wisconsin at Madison, Madison, WI, USA
- 72 Department of Psychiatry, University of Calgary, Calgary, Alberta, Canada
- 73 INSERM U1266, Université Paris Cité, Paris, France
- 74 Centre for Research and Education in Forensic Psychiatry, Department of Mental Health and Addiction, Oslo University Hospital, Oslo, Norway
- 75 Department of Psychiatry, Women's College Hospital, Toronto, Ontario, Canada
- 76 Institute of Biological Psychiatry, Mental Health Services, Copenhagen University Hospital, Copenhagen, Denmark

- 77 Department of Clinical Medicine, University of Copenhagen, Copenhagen, Denmark
- 78 LF Center for Geogenetics, Globe Institute, University of Copenhagen, Copenhagen, Denmark
- 79 iPSYCH, The Lundbeck Foundation Initiative for Integrative Psychiatric Research, Copenhagen, Denmark
- 80 Department of Psychology, University of Oslo, Oslo, Norway
- 81 NORMENT, Division for Mental Health and Addiction, Oslo University Hospital, Oslo, Norway
- 82 K.G. Jebsen Centre for Neurodevelopmental Disorders, University of Oslo, Oslo, Norway
- 83 Population Health Program, QIMR Berghofer Medical Research Institute, Brisbane, Queensland, Australia
- 84 School of Public Health, The University of Queensland, Brisbane, Queensland, Australia
- 85 Department of Paediatrics & Child Health, University of Cape Town, Cape Town, Western Cape, South Africa
- 86 SA-MRC Unit on Child & Adolescent Health, University of Cape Town, Cape Town, Western Cape, South Africa
- 87 Queensland Brain Institute, University of Queensland, Brisbane, Queensland, Australia,
- + Contributed equally to this work

ABSTRACT

Objective: Postpartum depression (PPD) is a common subtype of major depressive disorder (MDD) that is more heritable, yet understudied in psychiatric genetics. Meta-analyses of genome-wide association studies (GWAS) were conducted to investigate the genetic architecture of PPD.

Method: Meta-analyses were conducted on 18 cohorts of European ancestry (17,339 PPD cases and 53,426 controls), one cohort of East Asian ancestry (975 cases and 3,780 controls), and one cohort of African ancestry (456 cases and 1,255 controls) totaling 18,770 PPD cases and 58,461 controls. Post-GWAS analyses included: 1) single-nucleotide polymorphism (SNP)-based heritability (h_{SNP}^2), 2) genetic correlations between PPD and other phenotypes, and 3) enrichment of the PPD GWAS findings in 27 human tissues and 265 cell types from the mouse central and peripheral nervous system.

Results: No SNP achieved genome-wide significance in the European or the trans-ancestry meta-analyses. The h_{SNP}^2 of PPD was 0.14 (s.e. = 0.02). Significant genetic correlations were estimated for PPD with MDD, bipolar disorder, anxiety disorders, post-traumatic stress disorder, insomnia, age of menarche, and polycystic ovary syndrome. Cell type enrichment analyses implicate inhibitory neurons in the thalamus and cholinergic neurons within septal nuclei of the hypothalamus, a pattern that differs from MDD.

Conclusions: While more samples are needed to reach genome-wide levels of significance, the results presented confirm PPD as a polygenic and heritable phenotype. There is also evidence that despite a high correlation with MDD, PPD may have unique genetic components. Cell enrichment results suggest GABAergic neurons, which converge on a common mechanism with the only FDA approved medication for PPD (brexanolone).

INTRODUCTION

Postpartum depression (PPD) is a perinatal form of major depressive disorder (MDD) with a global prevalence of 17% (1-3). PPD is one of the most frequent complications of childbirth (4-7) and is associated with many adverse outcomes including maternal morbidity and mortality (1, 2), increased risk for infanticide (8), poorer maternal-infant attachment, and impaired parenting behaviors (6, 9). Despite these negative impacts, PPD is understudied in psychiatric genomics and its genetic risk factors are largely unknown. Smaller GWAS have been performed (10, 11), but no large GWAS meta-analyses have been done.

PPD is a strong candidate for genomic studies. PPD is a more homogenous form of MDD: only females affected, reproductive age-banded, and with exposure to the same biopsychosocial event. Moreover, the twin heritability of PPD (54%) is higher than that of MDD (32%) (12). With sample sizes increasing in number and diversity, clinically relevant results can begin to be uncovered and the genomic basis for PPD will become better understood. Not only could successful genomic analyses of PPD allow stratification of a specific presentation of MDD, but it may also allow delineation of the role genetic risk plays in the presentation of PPD features (i.e., onset, duration, symptom severity, recurrence) which could guide more effective treatment selection. This is critical given there is currently only one approved medicine with a specific indication for PPD, brexanolone (Zulresso) (13-15).

Discerning the biological basis of psychiatric disorders has been difficult. Most likely PPD is impacted by many genetic loci, each with small effects (16), similar to other psychiatric disorders (17-19). Although early GWAS for MDD were negative (20, 21), increases in sample size have made considerable progress (22, 23). The major lesson from MDD and other psychiatric GWAS is that progress is possible, but genetic approaches for higher prevalence/lower heritability diseases like PPD and MDD are challenging and require large sample sizes.

Therefore, we conducted the first large GWAS meta-analyses for PPD across 20 international cohorts (18 European ancestry, one east Asian, and one African). The results from these meta-

analyses enabled us to: 1) estimate the SNP-based heritability (h_{SNP}^2) of PPD, 2) calculate genetic correlations (r_g) to identify potentially pleiotropic relationships between PPD and other psychiatric disorders, medical diseases, and biomedical traits, and 3) identify specific cell types that may underlie PPD etiology.

RESULTS

Cohort Comparability

We identified 18 cohorts of European ancestry (EUR) that used a range of methods to ascertain cases with PPD (**Table S1** and **Supplemental Material**). The methods used by these cohorts were thoroughly reviewed and we assessed the comparability of the cohorts using summary-level data. We evaluated the comparability of these cohorts in two ways: 1) directly comparing our three largest cohorts (sample size greater than 5,000) and 2) meta-analyzing cohorts with the same ascertainment methods. For each of these comparisons we estimate the common variant genetic correlations (r_g) and perform targeted replication using a leave-one-out (LOO) approach (Cohort Comparability in **Supplemental Methods**).

Among our three largest cohorts (agds, pact, ukb) the weighted mean r_g was 0.73 (s.e. = 0.14), supporting their comparability (**Table S2**). This estimate can be benchmarked against the weighted mean r_g between MDD GWAS cohorts of 0.76 (s.e. = 0.03) (23). For LOO targeted replication, , we meta-analyzed 17 EUR cohorts (leaving out one of the three cohorts listed above), using the left-out cohort as a replication sample. LD independent SNPs from each meta-analysis were identified and used for replication. Sign tests were significant ($p < 0.05$) for two of the three LOO analyses (agds LOO $p = 2.93 \times 10^{-3}$; pact LOO $p = 5.45 \times 10^{-2}$; ukb LOO $p = 2.70 \times 10^{-2}$; **Table S2**), indicating consistent directions of effect across cohorts.

Next, we compared meta-analyzed cohorts with similar ascertainment methods (clinical interview/ICD code, Edinburgh Postnatal Depression Scale [EPDS], minimal self-report). The weighted mean r_g was 0.56 (s.e. = 0.10). For LOO target replication, sign tests were significant for two of the three LOO analyses (clinical/icd LOO $p = 0.601$; epds LOO $p = 1.97E-59$; minimal

LOO $p = 6.63\text{E-}61$; **Table S2**), indicating consistent direction of effect across ascertainment methods.

European Ancestry Genome-wide Association Study of PPD

Given the positive evidence for comparability of these cohorts, we performed a primary GWAS meta-analysis in women of European ancestry, comprising of 9,750,447 SNPs in 17,339 women with a history of PPD and 53,426 controls. No evidence of residual population stratification or systematic technical artifact was observed in the final meta-analysis ($\lambda = 1.04$, $\lambda_{1000} = 1.00$) (**Figure 1**) or in any of the individual data sets (**Table S1** and **Figures S1 - S2**). LD score regression (24) indicated that 87% of the observed test-statistic inflation was attributable to an underlying genome-wide polygenic signal. We estimated the h_{SNP}^2 to be 0.14 (s.e. = 0.02, liability scale, assuming lifetime risk of 0.10; **Figure S3**).

No SNP reached genome-wide significance ($p < 5.0 \times 10^{-8}$) in the EUR GWAS meta-analysis. The most significant SNP, rs3788305, is located on chromosome 22q11.21 ($\beta = -0.09$, $p = 2.09 \times 10^{-7}$) (**Table 1**; see also **Figure S4**). rs3788305 lies within an intron of *TXNRD2* (thioredoxin reductase 2). Across the genome, we identified 62 SNPs with a p -value $< 1\text{e-}6$, which segregate into seven LD-independent loci. These loci were identified by LD pruning ($r^2 < 0.1$) followed by conditional association analyses controlling for the most significant SNP within each 2-Mb window and manual inspection of regional association plots to confirm the presence of supporting statistical evidence of association from nearby SNPs. These top seven LD-independent index SNPs are presented in **Table 1** (**Figures S4 – S10**).

Trans-Ancestry Genome-wide Association Study of PPD

Next, we conducted a trans-ancestry random effects meta-analysis comprised of the 18 cohorts of European ancestry, one cohort of East Asian (EAS) ancestry (975 cases and 3,780 controls), and one cohort of African (AFR) ancestry (456 cases and 1,255 controls). No evidence of residual population stratification or systematic technical artifact was observed in any of these individual data sets (**Table S1** and **Figures S11 - S12**). The estimated h_{SNP}^2 for the EAS ($h_{SNP}^2 = 0.17$, s.e. = 0.15) and AFR ($h_{SNP}^2 = 0.36$, s.e. = 0.19) cohorts (both on the liability scale, assuming

lifetime risk of 0.10) were comparable to what was observed in our EUR meta-analysis. Among the seven LD independent loci and SNPs in strong LD with each ($r^2 > 0.8$) from the EUR meta-analysis, 59% of SNPs (111 out of 188 loci; binomial test $p < 2.2 \times 10^{-16}$) show consistent direction of effect in both AFR and EAS cohorts (**Table S3**). This trans-ancestry GWAS consisted of 9,129,923 SNPs in 18,770 women with a history of PPD and 58,461 controls. There was no evidence of residual population stratification ($\lambda = 0.94$, $\lambda_{1000} = 1.00$) (**Figure 1**).

No SNP reached genome-wide significance ($p < 5.0 \times 10^{-8}$) in the trans-ancestry analysis. The most significant SNP, rs10879002, is located on chromosome 12q15 ($\beta = 0.15$, $p = 7.26 \times 10^{-8}$) (**Figure S8**). This increases the significance of SNPs seen in the same region of the EUR only meta-analysis (chr12: 69847907 – 70000236). rs10879002 is an intronic variant of *FRS2*, which encodes fibroblast growth factor receptor substrate 2. In total, the trans-ancestry analysis increased the number of significant SNPs ($p < 1 \times 10^{-6}$) in three of the seven loci identified in the EUR ancestry analysis (**Figures S7, S8, and S10**).

Genetic Correlations with Postpartum Depression

Clinical studies have shown that PPD is associated with a wide range of other disorders and traits. To assess the shared genetic architecture between PPD and psychiatric disorders, medical diseases, and biomedical traits, r_g were calculated with our meta-analyzed summary statistics of EUR ancestry using LD score regression. **Table S4** contains the full results, and **Figure 2** shows the significant r_g values with false discovery rate (FDR) < 0.05 . First, the genetic correlation between PPD and the most recent MDD GWAS was indistinguishable from 1 ($r_g = 0.95$, s.e. = 0.05; $H_0: r_g = 0$, $p = 1.34 \times 10^{-80}$ $H_0: r_g = 1$, $p = 0.30$). Additionally, the genetic correlation of PPD with bipolar disorder type 2 ($r_g = 0.51$, s.e. = 0.09, $p = 3.38 \times 10^{-9}$) is greater than ($p = 1.24 \times 10^{-142}$) for bipolar disorder type 1 ($r_g = 0.25$, s.e. = 0.05, $p = 1.89 \times 10^{-6}$).

Second, we observed significant positive genetic correlations between PPD and anxiety disorders ($r_g = 0.91$, s.e. = 0.22, $p = 3.43 \times 10^{-5}$), specifically post-traumatic stress disorder ($r_g = 0.70$, s.e. = 0.12, $p = 2.98 \times 10^{-9}$) and panic disorder ($r_g = 0.46$, s.e. = 0.13, $p = 2.00 \times 10^{-4}$).

Furthermore, there were significant genetic correlations across many psychiatric disorders

including attention deficit hyperactivity disorder ($r_g = 0.44$, s.e. = 0.07, $p = 6.70 \times 10^{-11}$) and schizophrenia ($r_g = 0.28$, s.e. = 0.05, $p = 9.87 \times 10^{-9}$).

Lastly, the common variant genetic architecture of PPD was correlated with insomnia ($r_g = 0.41$, s.e. = 0.05, $p = 9.83 \times 10^{-15}$). In addition, we also saw significant correlations with reproductive hormone related traits age of menarche ($r_g = -0.11$, s.e. = 0.04, $p = 5.40 \times 10^{-3}$) and polycystic ovary syndrome (PCOS) ($r_g = 0.23$, s.e. = 0.10, $p = 2.12 \times 10^{-2}$).

Tissue and Cell Type Enrichment Analyses

Integrating GWAS results with data from RNA-sequencing studies characterizing specific tissues and cell types aid in understanding the biological implications of PPD associated loci. We used partitioned LD score regression to evaluate the enrichment of the PPD GWAS findings in 27 human tissues (Genotype-Tissue Expression project; GTEx, **Table S5**) (25) and 39 cell types (**Table S6**) that consists of 265 more refined cell types (**Table S7**) in the mouse central and peripheral nervous system (26). We did not find clear enrichment for any bulk tissue RNA-seq GTEx tissues. For cell types, the strongest signals identified were for inhibitory neurons in the thalamus (DEINH4; $p = 4.50 \times 10^{-4}$; q-value = 5.64×10^{-2}) and cholinergic neurons within septal nuclei of the hypothalamus (DECHO1; $p = 7.64 \times 10^{-3}$; q-value = 0.205, indicating we should expect 20.5% of all the results with q-value less than this [$n = 35$] to be false positives). Analyses of single-cell data more broadly implicate peptidergic neurons ($p = 5.84 \times 10^{-3}$; q-value = 0.114). Together these cell types can be characterized by their shared role as GABAergic neurons (26). These patterns differ from those seen in either the first MDD GWAS (MDD1) (20), which has a similar sample size to our PPD analysis, or the most recent MDD GWAS (MDD2) (23) (**Figure 3**). Comparing the enrichment ratios for these cell types (DEINH4 and DECHO1) between PPD and MDD2, we observe significant differences (DEINH4: PPD enrichment = 2.19, MDD2 enrichment = 1.03, $p = 3.50 \times 10^{-3}$; DECHO1: PPD enrichment = 1.79, MDD2 enrichment = 1.02, $p = 0.02$). The nominally significant cell type enrichments for PPD were more modest in both prior MDD analyses, suggesting unique targets for PPD.

DISCUSSION

We report on the first GWAS meta-analyses for PPD (EUR ancestry and trans-ancestry). This represents the largest and most comprehensive genetic study of PPD to date. While no loci reach genome-wide significance, our analyses provide valuable insights into the genetic basis of PPD. First, we find many significant genetic correlations between PPD and other psychiatric disorders, medical diseases, and biomedical traits. In addition, cell type enrichment analyses implicate GABAergic neurons in the pathogenesis of PPD.

Of particular note, results for PPD implicate inhibitory neurons in the thalamus, and cholinergic neurons of the septal nucleus in the hypothalamus. This pattern of results may be unique to PPD, as they were not observed in large GWAS of MDD (**Figure 3**) (23). These findings are salient because the two neuronal populations can be characterized by the neurotransmitter GABA (26), the primary inhibitory neurotransmitter in the central nervous system. These findings converge with evidence from transgenic rodent models (27) and human imaging studies (28) that suggest alterations in hypothalamic/thalamic regions to be associated with PPD. This is particularly intriguing in light of our results implicating GABAergic neurons, which is the target system of brexanolone, the only FDA approved medication specifically indicated for PPD (14, 15). Brexanolone is a synthetic formulation of allopregnanolone and a positive allosteric modulator of GABA_A receptors (29). Given the broad distribution of GABA_A receptors throughout the central nervous system, our results may help clarify the mechanism of action of this PPD therapeutic.

In order to achieve genome-wide significant results for PPD increased sample sizes are needed. Locus discovery for PPD can be expected to follow a trajectory similar to that seen for MDD, where robust SNP discovery required samples in excess of 100,000 cases (23). Equally important, however, will be ensuring that increases in sample size are accompanied by diversity of ancestry representation. As of 2019, a disproportionate majority (>78%) of participants in published GWAS are of European ancestry (30). Increasing representation of more diverse populations not only results in enhanced power of genomic studies and experimental methods (e.g. locus discovery, fine-mapping, genetic scores), but more importantly, it addresses the widespread health disparities that exist across research and medicine (31, 32). We estimated

the h^2_{SNP} to be 0.14, which supports PPD as a complex disorder with genetic and environmental risk factors. As future studies work to increase participants of non-European ancestry, they should also take the opportunity to collect data on environmental contributors that have been shown to increase PPD risk, but disproportionately affect women of color, such as adverse life events and discrimination (33-36).

With this work, we take some of the first steps to increasing diversity in psychiatric genomics. PPD indiscriminately affects women from every part of the world. Therefore, we made every effort to include genetic data from all women who chose to participate in research. These early efforts to diversify our analyses already shows promise. Our trans-ancestry analysis increased statistical associations of two loci compared to the EUR-ancestry alone, with one falling just below genome-wide levels of significance (rs10879002, $p = 7.26 \times 10^{-8}$).

In analyses of the genetic relationships of PPD with other psychiatric disorders, diseases, and biomedical traits, we found the largest and most significant genetic correlation with MDD. However, this could be due, in part, to selection bias of our cases. Many of our PPD cases were identified as part of larger MDD collections, most notably UK Biobank (where PPD was identified using MDD algorithms) and the Australian Genetics of Depression Study, which combined make up 45% of all our PPD cases. Further, the genetic correlations reflect the diverse clinical presentations of PPD despite its diagnostic categorization as a subtype of MDD (37-39). Previous history of MDD or anxiety disorders are known risk factors for PPD, which is consistent with the high genetic correlations we observe. Additionally, the significant genetic correlation with insomnia suggests a potential role for this phenotype in PPD pathology, given the postpartum period is often associated with disrupted sleep (40-45). Finally, genetic correlations with traits such as age of menarche and PCOS, support a model for PPD pathology related to fluctuations in reproductive hormones (46, 47). These associations are supported by previous work identifying enrichment of ovarian tissue genes among PPD associated variants (10). Notably, the r_g with PCOS has not been reported with MDD, supporting potentially distinct biologically underpinnings between PPD and MDD.

This study also has limitations that should be kept in mind when interpreting the results. First, our study follows the conventional GWAS examining PPD control-status. All cases reported depression in the postpartum period and a majority of controls screened had no reported depression and a pregnancy. This approach, however, does not account for the heterogeneity in PPD risk factors (e.g. previous psychiatric diagnoses) or presentation (e.g. symptom combinations, onset, duration, severity). These features are critical in defining PPD, but not always collected. Within the cohorts used here, there was a range of psychiatric histories (e.g. MDD, bipolar disorder, unknown), a broadly defined postpartum period (up to 12 months in some cases), and multiple ascertainment methods. Increased phenotyping should take place alongside efforts to increase sample sizes, which would also power appropriate conditional analyses. Further, it should be noted that sex is a confounder in our r_g and cell type enrichment analyses. The summary statistics used in these analyses, specifically MDD, all include males. This leads to the possibility that the observed patterns of correlation and enrichment reflect etiological differences in depression between men and women generally, rather than something specific to PPD. However, in GWAS that have stratified by sex, there is high r_g between sexes (48, 49). Further, secondary analyses were limited to European ancestry summary statistics. This highlights the lack of trans-ancestry analyses available. As more diverse GWAS are run, post-GWAS analyses need to be developed that utilize trans-ancestry results to identify causes and inform therapeutics development for PPD and other complex disorders.

PPD is a more homogeneous presentation compared to MDD, though there is still substantial phenotypic heterogeneity in the presentation of PPD. Symptom onset, duration, and severity are all important aspects of the disorder to consider when examining etiological factors. However, PPD is not an often collected phenotype, making it difficult to include specific symptom dimensions in work like GWAS. We recommend future data collection efforts utilize screening tools, such as the lifetime version of the EPDS (50), to ascertain a more complete symptom profile in addition to case status. Biological sample collection and maternal psychiatric screening, including psychiatric history, can be incorporated as a part of perinatal or early pediatric clinic visits. These visits present the opportunity to collect a large amount of data

as part of routine care for new mothers, which can increase sample sizes for future GWAS and address PPD heterogeneity.

In summary, we report the first genome-wide association meta-analyses for PPD. While no genome-wide significant loci were identified, this report contributes valuable new data about the genetic contributions to PPD. A direct comparison between PPD and MDD suggests a common genetic contribution between the two disorders. However, heritability estimates, cell type enrichments, and other genetic correlations suggest genetic components that may distinguish PPD from MDD. Notably, top GWAS loci implicate GABAergic neurons, which converges with imaging studies and the only current medication specifically indicated for PPD. Future studies, incorporating larger and more diverse sample sizes are needed to further clarify the genetic architecture of PPD.

METHODS

Study Participants

In total, we included 18,770 women with a history of PPD and 58,461 controls across 20 cohorts collected internationally. **Table S1** summarizes the source and genetic data for cases and controls for each sample. Full details for each cohort are given in the Supplementary Material. Overall, case definition required a lifetime diagnosis of PPD within one year of childbirth and were identified via: 1) review of electronic medical records (3/20 cohorts), 2) Edinburgh Postnatal Depression Scale (EPDS; 11/20 cohorts), 3) structured clinical interview (3/20 cohorts), or 4) other self-report (3/20 cohorts). Individuals identified using structured methodological review of medical records and population registries required diagnoses to meet international consensus criteria (DSM-IV, ICD-9, ICD-10). In addition, the EPDS a common and widely use PPD screening instrument (51-54), was used to screen participants. The EPDS is a 10-item self-report assessment, focusing on current symptoms, and minimizes confounding of somatic symptoms of PPD with the demands inherent to parenting an infant (e.g., insomnia) (51). We also screen using the modified version of the EPDS capable of screening for a lifetime history of PPD (50). For both the standard and lifetime versions of the EPDS, PPD symptoms are rated on a scale of 0 – 30 with higher scores indicating greater symptom severity. When using the EPDS, cases were defined having scores ≥ 13 , consistent with PPD (55). In a majority of cases (19/20 cohorts), controls were screened for the absence of lifetime MDD and were required to have a least one live, term birth (≥ 36 weeks' gestation).

All sites had documented permission from local ethical committees, all participants provided informed consent for studies done in settings and countries where this was required.

Genotyping and Quality Control

Genotyping procedures can be found in the primary reports for each cohort (**Supplementary Methods** and summarized in **Table S1**). Individual genotype data for each cohort were processed by the collaborating research teams using comparable procedures. SNPs were imputed using the Haplotype Reference Consortium (56) reference panel for samples of

European Ancestry, the TOPMED (57) reference panel for samples of African ancestry, and 1000 Genomes Asian (ASN) (58) reference panel for samples of East Asian ancestry. More detailed information on sample quality control and association testing for each cohort is provided in the **Supplementary Material**.

GWAS Meta-Analyses

Two meta-analyses for PPD case-control status were performed for EUR ancestry and trans-ancestry. A fixed effects meta-analysis was conducted on EUR cohorts using the inverse-variance method in METAL (59). A conventional random effects meta-analysis was conducted on all cohorts (EUR, AFR, and EAS) using the inverse-variance method in METASOFT (60). For both meta-analyses heterogeneity was assessed with Cochran's I^2 statistic. Test statistic inflation (λ) was calculated for each individual GWAS (Figures S2 and S12) and for the overall meta-analyses (**Figures 1b and 1d**) using all SNPs with minor allele frequency (MAF) > 0.01 to identify residual population stratification or systematic technical artifact. EUR GWAS summary statistics were subjected to linkage disequilibrium (LD) score regression (LDSC) analyses on high-quality common SNPs (INFO score > 0.9 and MAF > 0.01) to examine the LDSC intercept as a more specific measure of inflation of the GWAS test statistic (24) due to residual artifact or stratification (Table S2). The genome-wide significance threshold was set at a p-value of 5.0×10^{-8} .

Heritability Estimation and Genetic Correlations

LDSC was used to estimate h_{SNP}^2 from EUR and EAS genome-wide association summary statistics. Estimates of h_{SNP}^2 on the liability scale depend on the assumed lifetime prevalence of PPD in the population (K), and we assumed a conservative K = 0.10 but also evaluated a range of estimates of K to explore sensitivity, including 95% confidence intervals for the EUR meta-analysis (**Figure S3**). For EUR and EAS heritability estimates, precomputed LD score references provided by LDSC were used.

To estimate h_{SNP}^2 from AFR samples, we used GCTA (61, 62). The direct estimation of heritability from genome-wide common variant data was possible given access to genotype level data included in AFR mega-analysis.

We used LDSC to estimate r_g between PPD and a range of other disorders, diseases, and human traits. The intent of these comparisons was to evaluate the extent of shared common variant genetic architectures to suggest hypotheses about the fundamental genetic basis of PPD. The full list of summary statistics used can be found in Table S4. All summary statistics were standardized to human genome build hg19 (using liftOver) with all RSIDs annotated to GRCh37, Release 92 (63). Summary statistics were processed using LDSC using default parameters and precomputed LD score references provided by LDSC.

Tissue and Cell-Type Enrichment Analysis

We performed tissue and cell-type enrichment analysis aiming to identify relevant tissues and cell types underlying PPD. First, we analyzed GTEx gene expression data (v8) (25) in 27 human tissues after excluding: 1) tissues with less than 100 donors, 2) non-natural tissues (such as cell lines), and 3) testis tissues (64). Second, for the cell-type specific analysis, we used single-cell RNA sequencing data with over 160K high-quality cells sampled from 19 regions in the entire mouse central nervous system and peripheral nervous system (26). We analyzed these data at the cell-type level, including 39 broad cell types (referred to as “level 4” for cell type clustering in the paper) and 251 refined cell types (“level 5” in the paper, after filtering five cell types with fewer than 20 cells). We considered only protein-coding genes with 1:1 orthology between human and mouse for the calculation of expression specificity. For both expression datasets, we calculated a metric of gene expression specificity as previously described (64); it measures, for each gene, its expression in a specific tissue or cell-type relative to its total expression across all tissues or cell types. As in previous studies (64, 65), we utilized the genes with the top 10% specificity values in each tissue or cell-type for the enrichment analyses.

We used partitioned LD score regression (pLDSC) (66) to test the enrichment of tissues and cell types in the EUR PPD GWAS results. Our analyses using pLDSC evaluated if the SNPs within

100kb regions of the top 10% specifically expressed genes were enriched for SNP-based heritability. For each tissue or cell-type, we computed the LD scores for this cell-type-specific annotation and added it to the baseline model of 53 functional annotations. We assessed the enrichment of tissue or cell-types using the coefficient z-scores and computed one-sided p-values. We have used the European samples in the phase 3 of 1000 Genome Project as the reference panel. Results were corrected for multiple testing using false discovery rate within each dataset.

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CONFLICTS OF INTEREST

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FIGURE 1. Results of genome-wide association meta-analyses for PPD. (A) Manhattan plot for association tests from fixed effects meta-analysis of EUR-ancestry (17,339 PPD cases and 53,426 screened controls). Genomic position (chromosomes 1-22 and X-chromosome) is shown on the x-axis and statistical significance as $-\log(P)$ is shown on the y-axis. The solid red horizontal line indicates the genome-wide significance threshold of 5×10^{-8} , and the dashed red horizontal line indicates the suggestive threshold of 1×10^{-6} . **(B)** Association test quantile-quantile plot of observed versus expected $-\log_{10}(P)$ values from the EUR meta-analysis. The 95% confidence interval of expected values is shown in grey. Test-statistic inflation value, λ , is 1.04. **(C)** Manhattan plot for association tests from trans-ancestry random effects meta-analysis (18,770 PPD cases and 58,461 screened controls). **(D)** Association test quantile-quantile plot of observed versus expected $-\log_{10}(P)$ values from the trans-ancestry meta-analysis. Test-statistic inflation value, λ , is 0.94.

FIGURE 2. Genetic correlations (r_g) between PPD and psychiatric disorders, medical diseases, and biomedical traits. Significant r_g values with false discovery rate < 0.05 are shown. Error bars indicate standard error. Dashed vertical line indicates $r_g = 1$.

FIGURE 3. Cell type enrichment analyses performed using Partitioned LD Score Regression. Nominally significant values with $p < 0.05$ are shown. Labels indicate the enriched tissue or cell-type. Solid red line indicates findings with $p < 0.01$.

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