

associated with depression. We now review and update our progress and demonstrate how GWAS data can be leveraged to better understand the phenome-wide effects of depression risk using data from UK Biobank, Generation Scotland and other cohorts. We will discuss the PGC MDD Working Group's medium-long term priorities for depression genetics research.

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### GENETIC RISK FOR DEPRESSION AND TREATMENT RESPONSE IN THE AUSTRALIAN GENETICS OF DEPRESSION STUDY.

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**Abstract:** Genome-wide association studies have become increasingly successful in identifying genetic risk factors for major depression, but further discoveries and dissection of the genetic risk require large cohorts with deep phenotyping. The Australian Genetics of Depression study was established to recruit a large cohort of individuals who have been diagnosed with depression, and to investigate genetic and environmental risk factors for depression and response to commonly prescribed antidepressants. Over a 19-month period in 2017-18, more than 20,000 Australians enrolled in the online study and more than 15,000 have provided a saliva sample and been genotyped. We will present results from the initial wave of genetic analyses with a specific focus on the genetics of antidepressant response and its relationship with polygenic risk to depression.

**Disclosure:** Nothing to disclose.

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### GENETIC ASSOCIATIONS WITH DEPRESSION IN ANCESTRALLY DIVERSE POPULATIONS

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**Abstract:** The majority of previous genome-wide association studies of depression have used samples with European ancestry, raising questions about the genetic factors that shape risk for depression in non-European populations and whether genetic factors are the same across populations. Our goal was to address these gaps by performing a trans-ethnic analysis and constructing the largest mega-analysis of individuals with and without major depressive disorder

(MDD). The rising numbers of biobanks and cohorts with health record linkage - coupled with the high prevalence of MDD in the general population worldwide (8-16%) - provide a unique opportunity to build a resource of diverse ancestry samples.

We used mental health questionnaires and screened electronic health records to identify individuals with depressive symptoms or a clinical diagnosis of MDD. Using data from 241,740 samples (21,300 cases), we carried out joint and ancestry-specific association analyses and meta-analysed the results across studies. We evaluated the evidence for shared causal genetic architecture by estimating trans-ethnic genetic correlations.

Results from this study will fill a critical gap in the field and help to address the underrepresentation of racial/ethnic minorities in psychiatric genetics work.

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### ACHIEVING PRECISION PSYCHIATRY IN AN IMPRECISE WORLD: USING THE EHR SYSTEM TO TEST TRANSLATIONAL PARADIGMS IN PSYCHIATRIC GENETICS

Chair: Lea Davis<sup>1</sup>, Co-chair: Jordan Smoller<sup>2</sup>,  
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**Overall Abstract:** The success of precision psychiatry depends on implementation of translational paradigms in clinical settings. Thus, a major challenge is determining which translational strategies are robust to the imprecision in healthcare delivery systems, in which time with each patient is limited, family histories are often unknown, and complex co-morbidities are the rule rather than the exception. This challenging clinical environment can be re-constructed using the electronic health record (EHR). Moreover, the large-scale collection of genetic material paired with the EHR provides a translational "sandbox" in which to evaluate the potential clinical impact of psychiatric genetic findings in a low-risk research setting. The PsycheMERGE network leverages the resources and existing infrastructure of biobanks paired with EHRs across the country to achieve this goal.

This symposium will provide an overview of the research activities of the PsycheMERGE network and delve deep into early findings and potential translational roadblocks. We will open with a brief overview of the PsycheMERGE network and a collaborative invitation delivered by Dr. Lea Davis (chair) and Dr. Jordan Smoller (co-chair). Dr. Joel Gelenter will begin the session with a presentation on psychiatric genomics research in the Million Veterans Project (MVP), a recent partner in the PsycheMERGE network comprised of a unique patient population. He will describe ongoing efforts across multiple phenotypic domains, discuss preliminary findings, and invite collaborations. Next, Dr. Tian Ge will deliver a presentation on machine learning (ML) in a health care system with a focus on accessibility to ensure knowledge is transmitted effectively. He will explain the goals, mechanics, and pitfalls of ML for risk prediction in