cantly and positively correlated with effects on educational attainment, thus identifying long-term potentiation as a plausible molecular mechanism contributing to this multifactorial trait.
Discussion: In ongoing work, we are applying these techniques to neuropsychiatric GWAS data in order to estimate the contribution of AD gene regulation to liability for bipolar disorder, schizophrenia, and other conditions where learning and memory have been shown to be affected. Our sequence-based model of AD regulatory potential shows promise in identifying genetic variation associated with biological capacity to adapt, and may yield biomarkers informative in predicting clinical outcomes of neuromodulation treatment.

Disclosure: Nothing to disclose.

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S29
ACCELERATED CORTICAL THINNING AND VOLUME REDUCTION OVER TIME IN YOUNG PEOPLE AT HIGH GENETIC RISK FOR BIPOLAR DISORDER

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Background: Bipolar disorder (BD) is a familial psychiatric disorder associated with fronto-limbic brain abnormalities. It is unclear whether such abnormalities are present in young relatives without BD, and little is known about structural brain trajectories over time in those at risk.
Methods: BD, and little is known about structural brain trajectories over time in those at risk.

Methods: Magnetic resonance imaging was conducted on 146 subjects at baseline and after a two-year follow-up interval in 90 high-risk individuals with a first degree relative with BD, and 56 participants with no family history of mental illness, with all subjects aged 12-30 years at baseline. Mixed models were used to examine fronto-limbic longitudinal change in gray and white matter volume, cortical thickness, and surface area.
Results: Over time, the HR group, as compared to the control group, showed accelerated cortical thinning and volume reduction in a number of right lateralised frontal regions: inferior frontal gyrus, lateral orbitofrontal cortex, frontal pole, and rostral middle frontal gyrus. Independent of time, the HR group had significantly greater cortical thickness in the left caudal anterior cingulate cortex, and larger volume in the right medial orbitofrontal cortex and right accumbens area compared to controls. Of note, this pattern of divergence from normal brain development did not coincide with new onset of a mood episode during the inter-scan interval.
Discussion: This study provides clear neurobiological evidence of atypical volume and thickness development in HR individuals over a two-year period. This study also demonstrates that neuroanatomical differences in HR individuals may be progressive in some regions and stable in others. This pattern may be indicative of an increased vulnerability for BD.

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S30
THE AUSTRALIAN GENETICS OF BIPOLAR STUDY: WHAT HAPPENS WHEN WE PUBLICALLY ASK FOR VOLUNTEERS?

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Background: We present an overview of our experiences of recruiting participants for a new study seeking to find genetic risk factors influencing Bipolar disorder, and genetic markers that influence response to treatment.
Methods: Recruitment was via a media campaign and prescription based mailouts focusing on recruiting volunteers from the general public who had been treated for bipolar disorder at some stage in their lives. The media campaign involved a physical media launch (held on the 20/11/18) with follow-up via television, radio, print and online interviews and a sequence of social media posts. The prescription based mailout was undertaken during the week starting 1/4/2019. Participation in the study involves reviewing the information and consent documents on the study webpage (https://www.geneticsofbipolar.org.au/), completion of an online questionnaire (based on the CIDI) and providing a saliva sample for DNA extraction (via mail).
Results: Recruitment has been highly successful. Following the media campaign 1,903 participants consented to participate in the study and 1,405 participants had completed the online questionnaire. Following the study invitation mailout 3,206 participants consented to participate in the study and 2,549 participants had completed the online questionnaire. DNA collection is underway and to date over 2,000 samples have been returned.

Participants are predominantly female (63%) with a mean age of 44 (range18-90, sd = 13.5). Importantly, 86% of participants consented to record linkage with Pharmaceutical and Medical Benefits Scheme data which can be used to validate self-reported medication and treatment history. 30% report a diagnosis of Bipolar type I, 41% report Bipolar type II, 24% were unsure. 50% reported a 1st degree relative who has been diagnosed with MDD and 25% with bipolar disorder.
Discussion: Australian residents living with bipolar disorder are highly motivated to participate in research studies if

given the opportunity and provided with avenues to participate.

Disclosure: Nothing to disclose.

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S31
ASSOCIATION OF CLOCK GENE VARIANTS AND AMYGDALA VOLUME IN BIPOLAR AFFECTIVE DISORDER AND HEALTHY CONTROLS

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Background: Impaired circadian rhythms have been associated with bipolar affective disorder (BAD) in previous literature. Furthermore, the sleep wake cycle is also important to maintain physiological brain functions such as myelinization processes. In addition, neurodegenerative diseases were associated with genes regulating circadian rhythms (i.e. clock gene) pathways. The amygdala is a brain structure, which is crucial for emotional circuits. Thus, clock genes can potentially influence amygdala structure volumes that are important for mood regulation. Therefore, we analyzed the left and right amygdala volumes in association with core clock genes (ARNTL, NPAS, CLOCK, CRY1-2, PER1-3, REVERBAlpha and GSK3Beta) on multi- and single-SNP level.
Methods: Hypothesis driven genotype extraction of the core clock genes ARNTL, NPAS, CLOCK, CRY1-2, PER1-3, REVERBAlpha and GSK3Beta was conducted for all SNPs available on the Omniexpress 1.2 chip by Illumina. Recoding of genotypes into the additive model with Plink1.7. Linear regression analysis was performed with SPSS 25.0 between the genetic risk score (GRS) summarizing all available SNPs of core clock genes (ARNTL, NPAS, CLOCK, CRY1-2, PER1-3, REVERBAlpha and GSK3Beta), BD and amygdala volume corrected for age and sex. Furthermore, the association between the sum score of each clock gene with amygdala volumes in cases vs. controls was analyzed with linear regression analysis corrected for age and sex. Amygdala volumes were determined by the software FreeSurfer in structural MRI scans (measured by a 3 Tesla Siemens Tim Trio) of 134 study participants with BD ($n = 85$) and healthy controls (HC, $n = 49$). Finally, genotype*group interactions were analyzed with ANCOVAs on single SNP level in more depth.
Results: The GRS of ARNTL was associated with the left amygdala volume ($p = 0.025$, Beta $= 0.161$, corrected $R2 = 0.352$) in our sample. The GRS of NPAS2 SNPs was significantly associated with the left amygdala volume ($p = 0.003$, Beta $= -0.210$, corrected $R2 = 0.389$) and the right amygdala volume ($p = 0.010$, Beta $= -0.189$, corrected $R2 = 0.332$) in all study participants. The right and left amygdala volume did neither differ between BD and HC, nor did the GRS of core clock genes differ between cases and controls. Nevertheless, there are diverse group*genotype interactions on single SNP level, which will be presented based on limited space at the poster session in more detail.
Discussion: Conclusions: We found associations between the NPAS2 and ARNTL with the amygdala volume in all study participants on GRS level. The amygdala is a brain structure, which is crucial for emotional circuits. Thus, clock genes could potentially influence mood via emotional brain circuits. Nevertheless, further research is necessary to analyze the functional effects of structural amygdala changes.

Disclosure: Nothing to disclose.

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S32
CACNA1C, ANK3 AND ZNF804A POLYMORPHISMS ASSOCIATED WITH COGNITIVE SYMPTOMS IN PATIENTS WITH BIPOLAR DISORDER TYPE I

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Background: Genome-wide association studies (GWAS) have allowed for the detection of groups of candidate genes and the formulation of new BD I etiopathogenic theories. However, genetic studies have shown that candidate genes associated with BD may also be associated with other mental disorders, such as schizophrenia, autism, and depression. These findings suggest that candidate genes may be associated with symptomatic dimensions or with phenotypes associated with general mental disorders and not just a single disorder.

Several candidate genes have been described as possibly associated with BD I, among them: the gene that encodes the Calcium Voltage-Gated Channel Subunit Alpha1 C (CACNA1C), and is responsible for the influx of calcium to the cell and its depolarization; the gene that encodes the membrane skeleton protein, ankyrin G (ANK3), and the gene that codes for the Zinc Finger Protein 804A (ZNF804A), whose function is still little-known, but which is highly expressed in the brain, especially in the cortex, hippocampus, and cerebellum.
Methods: Objective: The objective of the present study was to determine the association of four single nucleotide polymorphisms of these genes with clinical symptoms and the cognitive functions in BD I. Methods: The study population consisted of 105 bipolar patients, the participants in this investigation were patients diagnosed with BD I through the Diagnostic Interview for Genetic Studies - DIGS in Psychiatry. Four interest polymorphisms of the genes CACNA1C (rs1006737, rs1024582), ANK3 (rs10994397) and ZNF804A (rs1344706) were genotyped and then statistical association tests were performed with clinical and cognitive variables.
Results: The average age at which the first episode occurred was 27.1 years (SD: 10.14). The length of the illness