

Shared Genetic Risk Factors between Schizophrenia and Subjective Sleep Quality and Duration in a Population-based Cohort of Australian Twins

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Disruption of circadian rhythms and perceived changes in sleep quality are common features of psychiatric disorders. Insomnia or hypersomnia are commonly reported in major depressive disorder (MDD) and bipolar disorder.

The observation of circadian disruption in psychiatric disorder patients, and the high heritability of schizophrenia and bipolar disorder ($h^2 \sim 0.8$) has led to the hypothesis that polymorphisms in genes encoding components of the circadian clock may influence susceptibility to psychiatric disorders. A large number of candidate gene studies have been conducted to test this hypothesis, with no consistently replicated findings.

Hypothesis-free genome-wide association studies from the Psychiatric Genomics Consortium (PGC) have begun to identify genetic variants that confer risk to psychiatric disorders. Specifically, 108 individual loci have been identified for schizophrenia, the largest of any psychiatric study to date. None of the identified associations were found in genes encoding core components of the molecular clock. However, genes associated with schizophrenia may still be associated with sleep and circadian phenotypes.

In this study, the results from the PGC schizophrenia study were used to build a predictor to test whether those who carry more schizophrenia risk alleles have poorer self-reported sleep quality. 2,887 twins from the Australian Twin Registry who had also been genotyped using a GWAS chip were asked to report on the quality of their sleep on a 5-point scale. After correcting for age, sex and BMI, those carrying more schizophrenia alleles had significantly poorer sleep quality ($p = 0.001$). These results indicate that there are shared genetic risk factors for schizophrenia and subjective sleep quality in the population. Furthermore, investigation of correlation between results from the PGC schizophrenia analysis and those from a large consortium-based GWAS of sleep duration, also found significant evidence of genetic overlap.