

Genome-wide Associated Schizophrenia Snps Do Not Predict Age-of-onset in Bipolar I Disorder

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Introduction:

Bipolar disorder (BP) and schizophrenia (SCZ) are severe, heritable psychiatric disorders. Genome-wide research suggests that the molecular basis of BP and SCZ overlap (Cross Disorder PGC Group, Lancet, 2013).

The **objective** of our work was to investigate whether polygenic scores based on SCZ-associated SNPs in the PGC sample (www.med.unc.edu/pgc/) might predict the age of onset (AO) in BP-I. We hypothesized that the SCZ associated SNPs might predict the late AO of BP-I due to the common character of the SCZ-associated variants.

Method:

We selected 10,681 non-ambiguous SNPs among the 102,637 SNPs present in the PGC SCZ-sample. Using these SNPs we derived polygenic scores in a Romanian sample of 243 BP-I patients with genome-wide data (604,064 SNPs) to predict the patient AO as dichotomous variable (early onset: AO \leq 24 years; late onset: AO $>$ 24 years). The genotyping of the Romanian patients was performed at the Institute of Human Genetics of Bonn. PLINK 1.07 (Purcell, 2009) was used for computing polygenic scores, means of which were compared by t-test between the early- and the late-AO patient groups.

Results:

2114 out of 10,681 SCZ-SNPs were informative in our sample contributing to polygenic scores in BP-I patients. There was no significant difference in mean polygenic scores between the early- and the late-onset group of BP-I patients ($t=1.14$, $P=0.25$).

Conclusion:

The polygenic scores based on 2114 SCZ-associated common variants did not predict the onset group in our BP-I patients under the AO-cutoff 24 years. Other AO-cutoffs and phenotypic traits (e.g. incongruent psychosis) might be tested.