AN ANALYSIS OF GENETIC RISK FACTORS FOR LONG-TERM FUNCTIONAL OUTCOME IN BIPOLAR DISORDER AND SCHIZOPHRENIA

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BACKGROUND
So far, psychiatric genetics mainly focused on cross-sectional disease phenotypes. The longitudinal course of mental illness, however, is of utmost clinical importance due to its impact on the individual and the societal burden of disease. Hence, there is a definite need to study the genetics of longitudinal measures, or variables that are indicators for the course of the illness. Two ways of looking at the GAF score: the phenotype level of functioning, as measured by GAF scores, and the overlap of genetic risk factors between schizophrenia (SZ) and BD.

METHODS
The phenotype level of functioning was assessed by GAF score. The GAF score - described in DSM-IV-TR - is a numeric scale (0-100) that is used for rating the psychological, social, and occupational functioning of adults.

RESULTS
We observed no statistically significant differences for contrast between GAF extremes in BD and SZ. The genome wide association analysis comprised 410,827 SNPs which fulfilled the following conditions: the estimated minor allele effect (risk or protective) was consistent across the 3 independent samples (GAIN BD, BOMA BD, BOMA SZ). Further, the SNP had either a consistently high statistical evidence (meta-analysis p ~ 10-8) or the SNP was a top SNP (meta-analysis p~10-6) for one of the two phenotypes.

DISCUSSION
Although no statistical significance was reached, we identified consistent regions where the obtained evidence came close to the multiplex testing adjusted significance threshold for 410,827 SNPs in the meta-analysis. It is of interest to note that the phenotype differs to some extent between BOMA and GAIN samples.

OUTLOOK
Collaborating with the Psychiatric Genomics Consortium (PGC), we will be able to leverage even larger sample sizes to increase the power of our analyses. These analyses are currently underway. These P-value wide association analyses, adjusting for sex and duration of illness.

Table 2 Meta-analysis across 2 samples (GAIN BD, BOMA BD)

Table 3 Meta-analysis across 3 samples (GAIN BD, BOMA BD, BOMA SZ)

Table 1 Samples studied

Statistical analyses focused on the overlap of genetic data between the three samples (487,774 SNPs).

Figure 1

Figure 2 Manhattan plot

Genome wide association analysis for contrast between GAF extremes in BD and SZ.

Statistical analyses focused on the overlap of genetic data between the three samples (487,774 SNPs).

DISCUSSION
The authors declare no conflict of interest.