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Common Variant at 16p11.2 Conferring Risk of Psychosis

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Abstract

Epidemiological and genetic data support the notion that schizophrenia and bipolar disorder share genetic risk factors. In our previous genome-wide association (GWA) study, meta-analysis and follow-up (totaling as many as 18,206 cases and 42,536 controls), we identified four loci showing genome-wide significant association with schizophrenia. Here we consider a mixed schizophrenia and bipolar disorder (psychosis) phenotype (addition of 7,469 bipolar disorder cases, 1,535 schizophrenia cases, 333 other psychosis cases, 808 unaffected family members and 46,160 controls). Combined analysis reveals a novel variant at 16p11.2 showing genome-wide significant association (rs4583255[T], OR = 1.08, $P = 6.6 \times 10^{-11}$). The new variant is located within a 593 kb region that substantially increases risk of psychosis when duplicated. In line with the association of the duplication with reduced body mass index (BMI), rs4583255[T] is also associated with lower BMI ($P = 0.0039$ in the public GIANT consortium dataset; $P = 0.00047$ in 22,651 additional Icelanders).

Keywords

schizophrenia; bipolar disorder; association; 16p11.2; cross-disorder

Introduction

Two structural variants, a balanced t(1;11) translocation interrupting the *DISC1* gene and a microdeletion at 22q11.2, were the first genetic polymorphisms to show compelling evidence of association with schizophrenia[1, 2]. More recently, additional microdeletions and microduplications conferring risk of schizophrenia and, in some cases, bipolar disorder have been uncovered[3-10]. These copy number variants (CNVs) confer high to moderate relative risk, however, because they typically change copy number of multiple genes, and may also affect regulation of genes at their margins, they do not generally implicate individual genes.

Common single nucleotide polymorphisms (SNPs) are currently, in addition to structural variants, convincing risk factors for schizophrenia and bipolar disorder, with alleles at more than 20 loci reported to show genome-wide significant association with at least one of the disorders[11-29]. None of these low-risk variants are located inside structural polymorphisms previously shown to be susceptibility factors for schizophrenia or bipolar disorder. Nevertheless, first principles and data from other disorders predict the existence of common variants conferring risk through the same genes as rare structural alleles[30]. The identification of common risk variants within CNV regions may aid in uncovering the causal gene or genes of a CNV, or help to elucidate other aspects of a CNV's association with disease.

Two loci have been reported to harbor common alleles showing genome-wide significant association with both schizophrenia and bipolar disorder[13, 16, 23, 24]. In addition, several common variants initially displaying genome-wide significant association with one of the disorders have been shown, in subsequent studies, to confer risk of the other[31, 32]. Investigations considering schizophrenia and bipolar disorder as a single phenotype also support shared risk alleles[16, 19, 22], and an overlapping polygenetic component has been described by several studies[21, 28]. These genetic data are consistent with current epidemiological investigations, which predict shared genetic risk factors for schizophrenia and bipolar disorder[33].

Previously, we carried out a schizophrenia GWA study, SGENE-plus, followed by meta-analysis of the top 1500 results with data from the International Schizophrenia Consortium (ISC) and the Molecular Genetics of Schizophrenia (MGS) group[15]. Loci having *P* values less than 1×10^{-4} (covered by 39 SNPs located in 33 genomic regions) were followed up in a data set of up to 10,260 schizophrenia cases and 23,500 controls[14]. In this work , we

broaden our phenotype of interest to psychosis (schizophrenia, bipolar disorder and related psychoses), examining the same group of follow-up SNPs in a data set augmented by 7,469 bipolar disorder cases, 1,535 schizophrenia cases, 333 other psychosis cases, 808 unaffected family members and 46,160 controls.

Materials and methods

Samples

The genome-wide typed ("SGENE-plus"; 2,663 cases and 13,498 controls) and meta-analysis ("SGENE-plus+ISC+MGS") samples (in total, 7,946 cases and 19,036 controls) used here were identical to those used in our previous schizophrenia GWA study and meta-analysis[15] . The primary psychosis follow-up samples employed consisted of follow-up samples from our previous GWA follow-up study (9,246 schizophrenia cases and 22,356 controls)[14], plus an additional 9,337 psychosis cases (1,535 schizophrenia, 7,469 bipolar disorder, 333 related psychoses) and 46,968 controls/unaffected family members. The primary follow-up samples were genotyped or imputed for all follow-up markers. The secondary follow-up samples consisted of 1,014 cases and 1,144 controls from the Göttingen Research Association for Schizophrenia (GRAS)[34, 35] study. These samples, which also had been used for secondary follow-up in our previous GWA follow-up study[14], were genotyped for SNPs that were genome-wide significant in the combined meta-analysis and primary follow-up samples. Table 1 summarizes the schizophrenia and psychosis datasets used in previous and current work, and Supplementary Table 1 includes details on the individual study groups. The autism samples (3,672 cases, 16,103 controls, 4,206 family members) derived from AGP, AGRE and nine European study groups (Supplementary Table 2). Further information on ascertainment and diagnosis for the psychosis and autism samples is provided in the Supplementary Material.

Genotyping and association analysis

Genotyping was carried out using Illumina and Affymetrix genome-wide arrays,Centaurus assays (Nanogen), Taqman assays, the Sequenom MassArray iPLEX genotyping system and the Roche LightCycler480 system (Supplementary Tables 1 and 2). Quality control and imputation were performed, by study group, as described in the Supplementary Methods. Case-control or family-based association analyses were carried out for each study group. For the case-control analyses, population stratification was controlled for using genomic control or principal components. Summary statistics from the various study groups were combined as described previously[15]. BMI measurements were adjusted for age and sex, and inverse standard normal transformed. Analysis was carried out by regressing the adjusted, transformed data on rs4583255[T] count.

Expression Analysis

For the three brain data sets[36-38], expression levels were inverse normal transformed and regressed on the number of rs4583255-T alleles with gender, age at death, post-mortem interval, brain source, expression experiment batch, pH (Colantuoni *et al*[36] only), sample expression level based on the total number of transcripts detected (Webster *et al*[38] only) and Alzheimer's disease patient status (Webster *et al*[38] only) as covariates. To incorporate data from different brain regions (Gibbs *et al*[37]) or different probes (*KCTD13* in Colantuoni *et al*[36]) derived from the same individual, a mixed-effects model with individual as a random effect was used. Results from the three data sets were combined using inverse-variance weighted meta-analysis. The Dutch whole blood data set included control samples from two studies[39, 40]. Analysis was performed using linear regression in Plink[41] taking age and gender as covariates. The Icelandic blood data set has been described previously[42], and analysis was carried out as detailed in that work[42].

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Results

We assembled a psychosis (schizophrenia, bipolar disorder and related psychoses) primary follow-up dataset made up of 36 study groups containing a total of 18,583 cases, 68,516 controls and 808 unaffected family members (Supplementary Table 1). In each study group, allelic association analysis was carried out for 39 SNPs from 33 genomic regions (these SNPs covered *P* values less than 1×10^{-4} in the SGENE-plus+ISC+MGS meta-analysis at $r^2 = 0.3$). Results from the various study groups were combined using inverse-variance weighted meta-analysis.

At 31 of the 33 loci, ORs in the psychosis follow-up group were in the same direction as in the discovery data set (SGENE-plus+ISC+MGS) (Supplementary Table 3). A similar pattern had been observed in the schizophrenia follow-up set—ORs were in the same direction at 30 of the 33 loci[14]. These results indicate that the set of variants chosen for follow-up was enriched for risk alleles ($P = 7.0 \times 10^{-7}$ for schizophrenia, and $P = 6.5 \times 10^{-8}$ for psychosis).

Next, we performed a joint analysis of the discovery and psychosis follow-up sets. To account for testing two phenotypes (schizophrenia and psychosis), the genome-wide significance threshold was set at $P < (5 \times 10^{-8})/2$, or 2.5×10^{-8}. Five SNPS, residing at three loci, exceeded this threshold (Supplementary Table 3). Two of the loci—the MHC region and 11q21.2 near *NRGN*—had been genome-wide significant in the previous schizophrenia analysis; a third locus, in *TAOK2* at 16p11.2, was novel (Supplementary Table 3). Following the addition of data from a further 1,014 schizophrenia cases and 1,144 controls, the variant at the novel locus, rs4583255[T], was associated with psychosis with increased significance (OR = 1.08, $P = 6.6 \times 10^{-11}$, Table 1). rs4583255[T]'s association with psychosis fit the multiplicative model ($P = 0.42$), and there was no evidence of OR heterogeneity ($P = 0.71$, $I^2 = 0$, Supplementary Table 4).

In examination of the follow-up samples by diagnosis, the novel variant, rs4583255[T], showed significant association with both schizophrenia and bipolar disorder ($P = 0.0011$ and 0.00026), with OR of 1.06 and 1.08, respectively (independent controls were used for the two analyses; see Supplementary Table 5). We also investigated association with bipolar disorder for variants that had shown genome-wide significant association with schizophrenia in our previous study[14]. Following correction for eight tests, rs12807809[T], near *NRGN*, was significantly associated with bipolar disorder ($P = 0.0023$) with an OR identical to that of the schizophrenia follow-up samples (OR = 1.09). The remaining schizophrenia susceptibility variants did not show nominally-significant association with bipolar disorder —yet OR confidence intervals for the two disorders overlapped for at least some variants at all loci (Supplementary Table 5).

Intriguingly, the newly-identified SNP is located in a nearly 600 kb region that confers risk of schizophrenia and bipolar disorder when duplicated[5, 6, 28]. Copy number gain of the region also is associated with autism[6, 43-45], reduced head circumference[46, 47], and low BMI[47]. We obtained large data sets to examine association of rs4583255[T] with both autism and BMI. Based on 3,672 cases, 16,103 controls and 4,206 unaffected family members from the Autism Genetic Resource Exchange (AGRE), the Autism Genome Project (AGP) and nine European study groups (Supplementary Table 2), we found no evidence of association with autism spectrum disorder (ASD), strict autism or multiplex ASD (ASD, OR = 1.00, $P = 0.98$; strict autism, OR = 1.02, $P = 0.66$; multiplex ASD, OR = 1.07, $P = 0.22$; Supplementary Table 6), although power to detect association at the OR found in the follow-up psychosis samples was modest (at a 0.05 significance level, power was about 57% for ASD, 42% for strict autism, and 23% for multiplex ASD). In contrast,

we found significant association of rs4583255[T] with low BMI in the published GIANT consortium GWAS dataset of 123,865 individuals[48] (P = 0.0039) and in 22,651 Icelanders who were not included in the GIANT study (P = 0.00047).

Recently, a study examining the effect of altered expression of 16p11.2 CNV region genes on zebrafish head size identified *KCTD13* as the major driver of head size change, with *MAPK3* and *MVP* named as possible modifiers[49]. These results motivated us to examine association of rs4583255[T] with expression of *KCTD13*, *MAPK3*, and *MVP* in human brain. Using data from three publicly-available data sets with at least 50 European-ancestry adult brains each (total N = 565)[36-38], we found that rs4583255[T] was significantly associated with expression of *MAPK3* (effect = 0.12 s.d., P = 0.011), but not significantly associated with expression of *KCTD13* or *MVP* (Supplementary Table 7). We also investigated association of rs4583255[T] with gene expression in blood using data sets from Iceland (N=972)[42] and the Netherlands (N = 437)[39, 40]. Consistent with the brain results, rs4583255[T] was significantly associated with higher expression of *MAPK3* (for Iceland , $P = 9.4 \times 10^{-15}$; for the Netherlands, P = 0.014 for probe 3870601,and P = 0.042 for probe 234040), but not significantly associated with expression of *KCTD13* or *MVP*.

Discussion

In this study, we uncovered a novel variant at 16p11.2, rs4583255[T], showing genome-wide significant association with psychosis (OR = 1.08, $P = 6.6 \times 10^{-11}$). In follow-up samples, ORs were similar for schizophrenia and bipolar disorder (OR = 1.06 and 1.08, respectively), and association was significant for both (P = 0.0011 and P = 0.00026, respectively). Thus, rs4583255[T] is a compelling example of a genetic variant that confers risk across traditional diagnostic boundaries.

Among the variants that showed genome-wide significant association with schizophrenia in our previous study[14],only rs12807809[T] showed significant association with bipolar disorder in the current work. Nevertheless, OR confidence intervals for schizophrenia and bipolar disorder overlapped for most risk alleles. Very large data sets will be necessary to establish conclusively where these variants fall on the spectrum of conferring risk of one disorder, exclusively, to conferring equal risk of either.

To our knowledge, this is the first case in which a common risk allele showing genome-wide significant association with psychosis has turned out to be located within a CNV that had been previously associated with psychosis. Both copy number gain and loss of the 16p11.2 region are associated with multiple phenotypes. Duplication is associated with psychosis[5, 6, 28], both copy number gain and loss are associated with autism and developmental delay[6, 43-45], and duplication and deletion lead to reduction and enlargement, respectively, of head circumference and BMI[46, 47].

In this work, we found that rs4583255[T] also confers risk of reduced BMI (P = 0.0039 in GIANT, P = 0.00047 in additional Icelanders). This result supports the suggestion, made previously[47], that the duplication's effects on psychosis and BMI have a single origin, presumably in the brain. We did not find evidence of association of rs4583255[T] with autism, although we were somewhat underpowered to detect an effect of the same size as in psychosis, especially for sub-phenotypes.

We found that rs4583255[T] was associated with increased expression in adult brain and blood of *MAPK3*, one of the 16p11.2 genes identified as involved in causing head circumference changes in zebrafish[49]. Caution is required in interpretation of this result, however, as the significance in brain is marginal, and, furthermore, gene expression in the

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pre-adult brain may be most relevant for the development of psychosis. Data from only extremely small numbers of European-ancestry brains at pre-adult stages were available; thus, investigation of the association of rs4583255[T] with gene expression at these stages was precluded.

In conclusion, in this work, we broadened our phenotype of interest to psychosis, identifying a new common risk allele, rs4583255[T], with similar ORs for schizophrenia and bipolar disorder. The novel variant is located within a duplication previously associated with psychosis, and, in line with the duplication's effects, also confers risk of low BMI. In the future, knowledge of this common variant association may prove useful to studies aimed at further understanding the mechanism through which the duplication exerts its effects on neurodevelopmental and anthropomorphic phenotypes.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Appendix

Genetic Risk and Outcome in Psychosis (GROUP)

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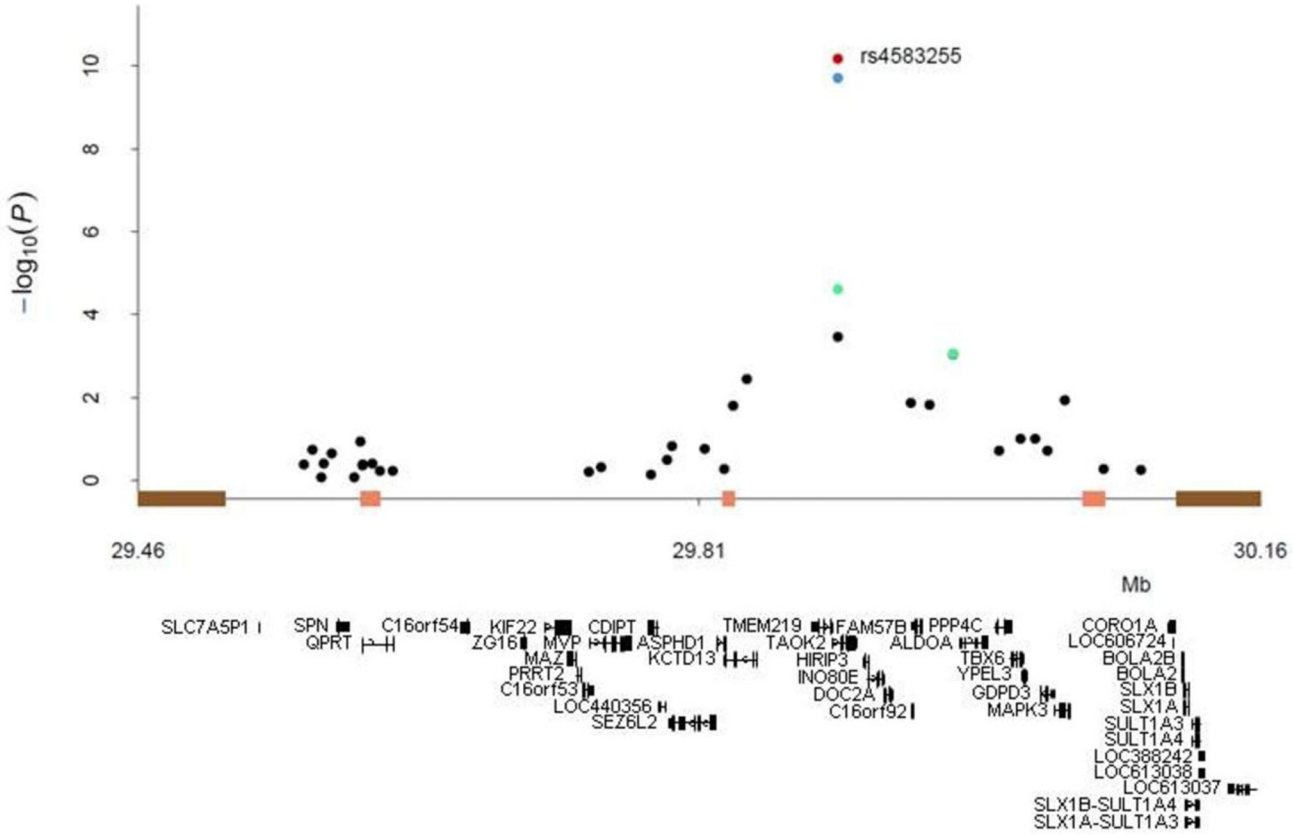

Figure 1.

Association results and structure of the 16p11.2 region. Bars on the x-axis indicate segmental duplications (brown) and recombination hotspots (pink). Association results are illustrated for SGENE-plus (black), SGENE-plus+MGS+ISC (green), SGENE-plus+MGS +ISC plus the primary psychosis follow-up (blue), and SGENE-plus+MGS+ISC plus the primary psychosis and secondary schizophrenia follow-up (red). RefSeq genes in the region are shown below the plot.

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Table 1

Relevant datasets

Dataset	case phenotype	markers examined	N		initial use	overlap with other sets
			cases	controls + family members		
SGENE-plus GWAS	SZ	314,868	2,663	13,498	Stefansson[15]	no
SGENE-plus+ISC+MGS	SZ	1,500	7,946	19,036	Stefansson[15]	includes SGENE-plus GWAS
primary schizoprenia follow-up	SZ	39	9,246	22,356	Steinberg[14]	no
primary psychosis follow-up	SZ, BP, rel	39	18,583	69,324	this work	includes primary schizophrenia follow-up
secondary follow-up	SZ	8; 1[1]	1,014	1,144	Steinberg[14]	no

SZ, schizophrenia; BP, bipolar disorder; rel, related psychoses [1]eight markers were examined in this set in the previous work[14], an additional marker is genotyped in the current work

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Table 2
Genome-wide association of rs4583255[T] with psychosis

	N				
study group	**cases**	**controls**	**family members**	**OR (95% CI)**	***P* value**
SGENE-plus+ISC+MGS (SZ)	7,946	19,036	0	1.10 (1.05, 1.15)	2.5×10^{-5}
primary psychosis follow-up (SZ,BP,rel)	18,583	68,516	808	1.07 (1.04, 1.10)	9.2×10^{-7}
secondary follow-up (SZ)	1,014	1,144	0	1.10 (0.97, 1.24)	0.14
combined	27,543	88,696	808	1.08 (1.05, 1.10)	6.6×10^{-11}

SZ, schizophrenia; BP, bipolar disorder; rel, related psychoses; OR, odds ratio; CI, confidence interval