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Hypothesis-Driven Candidate Genes for Schizophrenia Compared to Genome-Wide Association Results

Ann L. Collins, PhD[1], **Yunjung Kim, PhD**[1], **Pamela Sklar, MD, PhD**[2], **International Schizophrenia Consortium**, **Michael C. O'Donovan, FRCPsych, PhD**[3], and **Patrick F. Sullivan, MD, FRANZCP**[1]

[1]Department of Genetics, University of North Carolina at Chapel Hill, NC, USA

[2]Department of Psychiatry, Mt Sinai School of Medicine, New York, NY, USA

[3]MRC Centre for Neuropsychiatric Genetics and Genomics, School of Medicine, Cardiff University, UK

Abstract

Background—Candidate gene studies have been a key approach to the genetics of schizophrenia. Results of these studies have been confusing and no genes have been unequivocally implicated. The hypothesis-driven candidate gene literature can be appraised via comparison with the results of genome-wide association studies (GWAS).

Methods—We described the characteristics of hypothesis-driven candidate gene studies from SZGene, and used pathway analysis to compare hypothesis-driven candidate genes with GWAS results from the International Schizophrenia Consortium (ISC).

Results—SZGene contained 732 autosomal genes evaluated in 1,374 studies. These genes had poor statistical power to detect genetic effects typical for human diseases, assessed only 3.7% of genes in the genome, and had low marker densities per gene. Most genes were assessed once or twice (76.9%), providing minimal ability to evaluate consensus across studies. The ISC had power of 89% to detect a genetic effect typical for common human diseases and assessed 79% of known autosomal common genetic variation. Pathway analyses did not reveal enrichment of smaller ISC p-values in hypothesis-driven candidate genes nor did a comprehensive evaluation of meta-hypotheses driving candidate gene selection (schizophrenia as a disease of the synapse or neurodevelopment). The most studied hypothesis-driven candidate genes had no notable ISC results (*COMT*, *DRD3*, *DRD2*, *HTR2A*, *NRG1*, *BDNF*, *DTNBP1*, and *SLC6A4*).

Conclusions—We did not find support for the idea that the hypothesis-driven candidate genes studied in the literature were enriched for common variation involved in the etiology of schizophrenia. Larger samples are required definitively to evaluate this conclusion.

Correspond with Drs. Collins or Sullivan: Department of Genetics, CB#7264, 5097 Genomic Medicine, University of North Carolina, Chapel Hill, NC, 27599-7264, USA. Voice: +919-966-3358, FAX: +919-966-3630, pfsulliv@med.unc.edu.

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Keywords

schizophrenia; genetics; candidate gene association; genome-wide association; comparative study; synapse; neuro-developmental

Introduction

Candidate gene studies have been a major focus in schizophrenia research with the SZGene database listing >1400 studies since 1965 (Allen *et al.*, 2008). In contrast, there are ~2200 PubMed citations for "schizophrenia randomized controlled trials". Until five years ago, genetic studies could investigate only an extremely small proportion of the genome due to genotyping and cost limitations. Investigators thus had to focus on small numbers genetic markers, genes, and samples. In hypothesis-driven candidate gene studies, targets were selected based on ideas about pathophysiology or gene location under a linkage peak (Cichon *et al.*, 2009). For most biomedical disorders (including schizophrenia), the results of these studies were inconsistent or confusing (Ioannidis *et al.*, 2001). It is unclear whether this reflects poor choices of candidate genes or inadequate assessment (i.e., small samples or incomplete coverage of common genetic variation).

Genotyping and cost improvements now permit routine assessment of a million or more genetic variants distributed across the genome (Beaudet and Belmont, 2008). GWAS can extract information from most common genetic variants in the genome either through direct assessment of single nucleotide polymorphisms (SNPs) or indirectly via linkage disequilibrium between genotyped SNPs and unmeasured but correlated genetic variants. Despite the advantages of genome-wide genotyping (Hindorff *et al.*, 2009), stringent adjustment for multiple comparisons is required which necessitates the use of large sample collections.

Ten GWAS for schizophrenia have been published (Athanasiu *et al.*, Kirov *et al.*, 2009, Lencz *et al.*, 2007, Need *et al.*, 2009, O'Donovan *et al.*, 2008, Purcell *et al.*, 2009, Shi *et al.*, 2009, Shifman *et al.*, 2008, Stefansson *et al.*, 2009, Sullivan *et al.*, 2008). Given that some GWAS had larger samples and more comprehensive genotyping than typical for the candidate gene literature, GWAS may be better placed to capture true associations than earlier studies. Indeed, GWAS have yielded highly significant and replicated associations for schizophrenia including genetic variation in the MHC region, *TCF4*, and *ZNF804A* (O'Donovan *et al.*, 2008, Purcell *et al.*, 2009, Shi *et al.*, 2009, Stefansson *et al.*, 2009). A lack of congruity has been noted between the hypothesis-driven candidate genes for schizophrenia and the best findings from GWAS. This may be typical for biomedical diseases where results from large GWAS infrequently correspond to *a priori* candidate genes (Hindorff *et al.*, Hindorff *et al.*, 2009).

For schizophrenia, there are multiple reasons for the lack of overlap between GWAS and candidate gene studies. A key possibility is that prior hypotheses about the genetics of schizophrenia are incorrect. However, alternative explanations require exploration before accepting such an important conclusion. First, current GWAS chips provide coverage for most but not all of the genome (International HapMap Consortium, 2005) so particular

regions and non-SNP genetic variation may be covered poorly. Second, power may be insufficient. Although GWAS tend to have large sample sizes by historical standards, the necessity to adjust for around a million statistical tests could result in low power. If that is the explanation, support for the hypotheses underpinning previous candidate genes might be obtained by a more systematic analysis of the GWAS data for evidence for over-representation of smaller p-values than expected by chance (Holmans *et al.*, 2009). Third, individually rare genetic variants of strong effect might also be missed by GWAS studies (although these would also go undetected by most prior candidate gene studies).

The overarching purpose of this paper is to compare hypothesis-driven candidate genes for schizophrenia from SZGene (Allen *et al.*, 2008) with the largest schizophrenia GWAS published to date (International Schizophrenia Consortium, ISC) (Purcell *et al.*, 2009). First, we characterized the hypothesis-driven candidate gene studies. Second, we conducted quantitative comparisons to determine whether the set of hypothesis-driven candidate genes were either enriched for lower p-values in the ISC results or contained markers with predictive power for schizophrenia. Finally, we performed a qualitative comparison of the most studied hypothesis-driven candidate genes with the ISC results.

Method

Hypothesis-driven candidate genes

Candidate genes for schizophrenia were drawn from SZGene (Allen *et al.*, 2008) (courtesy Dr. Lars Bertram on 11/09/2009). SZGene included studies evaluating associations between a genetic variant and schizophrenia and published in a peer-reviewed, English language journal (Allen *et al.*, 2008). Studies were identified via PubMed, bibliographies, and tables of contents. To ensure that the list was not “contaminated” by the results of GWAS, SZGene entries from GWAS were removed as were genes studied only subsequent to identification in a GWAS. As only ISC autosomal results were available, 15 chromosome X genes were dropped. The list of autosomal hypothesis-driven candidate genes for schizophrenia contained 732 genes from 1,374 studies (Table S1).

The goal in creating this list was to enumerate genes thought potentially to be etiological for schizophrenia by researchers in the field. The quality of the individual studies was variable. However, our interest was not in the study results *per se* (which can be strongly impacted by quality) but rather in the choice of a gene.

Samples

The ISC is described elsewhere (International Schizophrenia Consortium, 2008, Purcell *et al.*, 2009). Briefly, we studied 3,322 European cases with DSM-IV or ICD-10 schizophrenia and 3,587 controls from seven sites. All work was approved by institutional review boards. After complete description of the study to the subjects, written informed consent was obtained. Genotyping was performed on DNA extracted from blood using Affymetrix 5.0 or 6.0 arrays. Genotypes were called using Birdsuite (Korn *et al.*, 2008) and imputation conducted using Beagle (Browning and Browning, 2009, Browning and Browning, 2007) against the HapMap3 CEU data resulting in 1,948,385 autosomal SNPs with direct or

imputed genotypes. The primary analysis was logistic regression of disease state on the imputed allele dosages with inclusion of covariates to adjust for population stratification effects. The GAIN study genotyped 1230 SCZ cases and 1136 controls of European ancestry on the Affymetrix 6.0 array (Shi *et al.*, 2009).

Statistical analysis

We first explored the set of hypothesis-driven candidate genes using a variety of descriptive approaches (SAS Institute Inc., 2004, 2005). Quanto was used for power calculations (Gauderman and Morrison, 2006, Gauderman, 2002). We used DAVID (Dennis *et al.*, 2003, Huang da *et al.*, 2009, Sherman *et al.*, 2007) to characterize hypotheses about the pathophysiology of schizophrenia reflected in the hypothesis-driven candidate gene list. DAVID identifies Gene Ontology biological pathways (Harris *et al.*, 2004) with chance-corrected over-representation a given gene list. To account for overlap between pathways, we used the annotation cluster feature in DAVID to focus on higher-level clusters of similar biological processes.

We then compared hypothesis-driven candidate genes for schizophrenia with ISC GWAS results to assess whether the hypothesis-driven candidate gene list had over-representation of smaller ISC p-values than expected by chance. These analyses were conducted using ALIGATOR (Holmans *et al.*, 2009) and InRich (Lee *et al.*, 2011). These programs use different algorithms to assess whether GWAS findings are over-represented for small p-values with reference to a pre-defined set of genes (i.e., a pathway). ALIGATOR uses permutation to account for variable numbers of SNPs per gene, different patterns of linkage disequilibrium between SNPs (within the same gene), and varying gene sizes. We considered SZGene hypothesis-driven candidate genes as a “pathway” and used ALIGATOR to estimate the probability that this list contained an over-representation of smaller ISC GWAS p-values. The ISC GWAS results were input to ALIGATOR which assigned these SNPs to UCSC hg18 RefSeq genes (Pruitt *et al.*, 2005). We determined the significance threshold (generally 0.002–0.004) that designated the top 5% of all genes as “significant” (Holmans *et al.*, 2009). The key statistical comparison is akin to a 2×2 table of whether a gene is in the top 5% by whether a gene is a member of a pathway. Assessing significance is complex due to violation of independence assumptions. ALIGATOR uses a SNP-based permutation algorithm to create a reference distribution for a pathway. InRich controls linkage disequilibrium between genes by comparing a gene set of interest to linkage disequilibrium independent regions. Using the same significance thresholds as in ALIGATOR, we identified linkage disequilibrium independent significant regions from the ISC dataset using the clump function within PLINK (r^2=0.5 over 1Mb). We then used InRich to determine if the candidate gene set showed enrichment for these regions.

Polygenic score analysis was conducted as described in the ISC GWAS paper (Purcell *et al.*, 2009). We used 14,811 SNPs which were genotyped in both the ISC and SCZ GAIN samples and which mapped to candidate genes. We made a polygenic profile based on the risk alleles within these SNPs in the ISC data, and used this profile to create a polygenic score for each individual within the SCZ GAIN sample (an independent target sample). We

used logistic regression between the score of each individual in SCZ GAIN and their case/control status.

Results

Characteristics of hypothesis-driven candidate gene studies of schizophrenia

Table 1 describes hypothesis-driven candidate genes from SZGene (Allen *et al.*, 2008). There were 732 autosomal genes from 1,374 hypothesis-driven candidate gene studies (Table S1). These genes were studied from 1–81 times. Most genes (563, 76.9%) were investigated in one (60.9%) or two studies (16.0%). Although replication is critical in human genetics, there is little capacity to evaluate both false positive and false negative findings. Two-thirds of genes were assessed by ≤3 markers and a median SNP density of 15.4 kb/SNP. The median numbers of cases (191) and controls (214) were modest.

We used pathway analysis to characterize the hypotheses that guided candidate gene selection. The 732 hypothesis-driven candidate genes were entered into DAVID to assess the Gene Ontology biological processes to which these genes belonged. The top four annotation clusters consist of biological processes involved in synaptic transmission, neuronal development and morphogenesis, regulation of synaptic transmission, and response to chemical stimuli (Tables 1 and ***S2***). The full list reflects a diversity of ideas about schizophrenia etiology; as expected, cluster enrichment scores were particularly strong for candidate genes selected under the hypotheses that schizophrenia is a disease of the synapse and/or a neuro-developmental process.

We next evaluated completeness and coverage for the hypothesis-driven candidate genes. First, we estimated statistical power to detect association. Even for relatively large studies (i.e., samples sizes at the 90th percentiles of N_{case}=537 and $N_{control}$=628) and a liberal correction for multiple comparisons (α=0.005, 10 markers), power was 48% to detect genetic effects typical for GWAS of human diseases (median genotypic relative risk=1.28 and median minor allele frequency of 0.29 for disease associations with $p<5\times10^{-8}$) (Hindorff *et al.*, 2009). Second, we assessed genomic coverage. The 732 hypothesis-driven candidate genes represent 3.7% of RefSeq autosomal genes (Pruitt *et al.*, 2005). Marker coverage can be assessed only generally, but included only small proportions of common genetic variation. Finally, of all genes comprising pathways in the top four DAVID annotation clusters, only 6.7% had ever been studied. Although these pathways may be over-inclusive, the main hypotheses guiding selection of hypothesis-driven candidate genes were evaluated incompletely.

Hypothesis-driven candidate gene studies and the ISC GWAS

The ISC GWAS had 3,322 cases, 3,587 controls, and 1,948,385 genotyped and imputed autosomal SNPs. The sample size was 1.36 times greater than the largest hypothesis-driven candidate gene study. Statistical power was 89% to detect a genetic effect corresponding to that typical for SNPs implicated in human disease GWAS (Hindorff *et al.*, 2009) including adjustment for multiple comparisons ($\alpha=5\times10^{-8}$). The ISC reported 1,948,385 associations, which exceeds the total associations in the SZGene database by over 180-fold. The mean

marker density over the genome was 1 SNP/1.6 kb. In comparison to HapMap (r27, phases I +II+III), ISC markers assessed 79.0% of known common variants present in individuals of European ancestry either directly or indirectly with $r^2 \geq 0.8$.

We next investigated coverage and gene size (using strict gene boundaries, ±0 kb). The 732 hypothesis-driven candidate genes were markedly larger than the remaining 18,891 autosomal RefSeq genes (median 33.5 versus 20.5 kb, Wilcoxon $p=4\times10^{-20}$). Importantly, ISC SNP densities were similar in hypothesis-driven candidate genes in comparison to all other autosomal genes (median 1,360 versus 1,379 bases/SNP, Wilcoxon p=0.25). A sizable fraction of autosomal RefSeq genes had no ISC SNPs within their boundaries (18.7%). As expected, genes with no SNPs were markedly smaller (median 4.1 versus 28.2 kb, Wilcoxon $p \approx 0$). As the 732 schizophrenia candidate genes were larger, they were significantly less likely to have no coverage than the remaining RefSeq genes (10.0% versus 19.0%, $p=5\times10^{-11}$). Although this generation of GWAS chips provides partial genomic coverage of common variation, hypothesis-driven candidate genes for schizophrenia had better coverage than other RefSeq genes.

Do the ISC GWAS data support hypothesis-driven candidate genes as significant contributors to schizophrenia risk?

There were no SNPs within the gene boundaries (±0 kb) for 73 hypothesis-driven candidate genes and no SNPs within expanded gene boundaries (±10 kb) for 27 genes (Table S3). Hypothesis-driven candidate genes with no ISC coverage were excluded from enrichment analyses. Of the ~1.9 million ISC SNPs, 56,981 mapped within hypothesis-driven candidate genes (±0 kb) and 65,803 mapped within expanded gene boundaries (±10 kb).

We assessed whether hypothesis-driven candidate genes were over-represented for smaller ISC GWAS p-values using ALIGATOR. The central comparison was whether there was an over-representation of the top 5% of significant genes in the hypothesis-driven candidate gene list in comparison to the remaining annotated genes. In Table 2, there was a nominally significant over-representation of smaller p-values in the ISC data for the full set of hypothesis-driven candidate genes but these values did not survive multiple testing correction. In addition, there was no evidence for over-representation of small ISC p-values in the most studied hypothesis-driven candidate genes (≥3 times, 23.1% of the total).

Pathway analysis can be complex in regions like the MHC that have extensive disequilibrium between genes (Stenzel *et al.*, 2004). When we repeated the ALIGATOR analysis after excluding genes in the MHC region, there was no evidence for over-representation of smaller p-values ($p \sim 0.48$) indicating that the marginal enrichment was due to bias. We repeated the pathway analysis using InRich, which may be more robust than ALIGATOR in regions of high linkage disequilibrium. InRich evaluates regions defined by linkage disequilibrium. We tested the full candidate gene data set, using the same significance thresholds as in ALIGATOR, and found no evidence for enrichment of significant findings in the candidate genes (Table 2). Therefore, the pathway analyses are consistent with the null hypothesis as all p-values were non-significant or marginal and would not survive correction for multiple testing and as removal of the MHC region and

analysis with a program that corrects for linkage disequilibrium indicates the results are a false positive resulting from extensive linkage disequilibrium in the MHC region.

In addition, we evaluated whether the list of historical candidate genes, as a whole, were making a significant contribution to risk of SCZ by evaluating the polygenic score profile. This approach has provided support for an important polygenic contribution to SCZ (Purcell *et al.*, 2009). We created a polygenic score profile for SNPs which mapped to historical candidate genes using the ISC data. We then applied this score to an independent dataset (SCZ GAIN, N=1230 cases and 1136 controls). Independent SCZ cases did not have greater risk scores than controls based on these historical candidate genes (p=0.92). Many hypothesis-driven candidate genes were selected from two over-arching hypotheses, schizophrenia as a synaptic or neurodevelopmental disorder (Table 1). These hypotheses have been incompletely assessed. We used pathway analysis of the ISC data to assess these hypotheses far more completely than has been done previously. The set of 4,808 genes that comprise the synaptic cluster 1 from DAVID did not show over-representation of lower ISC p-values (p-value ~1). This list may be over-inclusive and the candidate genes actually studied might be more refined and appropriate to schizophrenia; however, the subset of 222 cluster 1 genes investigated in a hypothesis-driven candidate gene study did not have over-representation of smaller ISC p-values (p-value ~1). Similarly, genes in DAVID cluster 2 (neuro-development) did not show enrichment for lower ISC p-values for the full set (4,834 genes) or the subset evaluated in a candidate gene study (401 genes, all p-values non-significant).

Qualitative comparisons

Pathway analysis considers sets of genes in aggregate. Negative aggregate results could miss true over-representation of small p-values in a small number of hypothesis-driven candidate genes. Table 3a depicts the ISC findings for the 10 most-studied hypothesis-driven candidate genes. There was inadequate coverage for two small genes (*DRD4* and *APOE*), and the remainder had good SNP densities but weak ISC results with none surviving a liberal gene-wise Bonferroni correction. Figure S2 depicts these genes and highlights regions of conspicuous attention in the literature (*COMT*/val58met, *DRD3*/ser9gly, *DRD2*/Taq1A, *HTR2A*/T102C, *NRG1*/Hap_{ICE}, *BDNF*/val66met, *DTNBP1*, and *SLC6A4*/HTTLPR). The ISC results do not implicate common genetic variation in these genes. Although the region containing *SLC6A4* shows no signal, the widely-studied promoter polymorphism (HTTLPR) was not directly genotyped and neighboring SNPs are in low linkage disequilibrium (Konneker *et al.*, in press).

We also investigated the 35 ISC SNPs with associations $< 5\times10^{-8}$ and all were located from chr6:31.58–32.77 mb in the MHC region (Purcell *et al.*, 2009). These SNPs map to 10 genes (Table 3b), five of which had not previously been the subject of a candidate gene study. Four genes had been studied 1–5 times and one extensively (*NOTCH4*). The strong caveat for Table 3b is the extensive linkage disequilibrium in the MHC region (Figure S1); these genome-wide significant SNPs could reflect one or a few risk variants which may or may not be a candidate gene.

Discussion

The major aim of this study was to evaluate the hypothesis-driven candidate gene literature for schizophrenia with respect to a large GWAS dataset. Hypothesis-driven candidate gene studies have been a major approach to the molecular etiology of schizophrenia. However, we now can perform analyses orders of magnitude more detailed than were possible even five years ago. We wished to determine whether the systematic investigations now allowed by GWAS supported this body of work in aggregate and the degree to which GWAS empirical results support the over-arching concepts that influenced candidate gene selection. We highlight that we did not conduct meta-analyses of the findings of hypothesis-driven candidate gene studies as this has been done elsewhere (Allen *et al.*, 2008).

We acknowledge the advantages of hindsight. The hypothesis-driven candidate gene literature, a body of work to which the present authors have contributed, contains numerous studies that were state-of-the-art when they were done and represent considerable effort by teams of investigators. GWAS will undoubtedly be subject to similar scrutiny as that done here for candidate gene studies. Although the ISC is the largest and most comprehensive schizophrenia GWAS published to date, it still was not ideal. Although statistical power was high by historical standards, we now know that greater power is desirable to detect the small genotypic relative risks characteristic of schizophrenia. In addition, coverage was not necessarily “genome-wide” as some important regions had inadequate genotyping and rare genetic variation was poorly assessed. With these caveats in mind, a number of observations of the historical candidate gene literature emerged from our analyses.

First, hypothesis-driven candidate gene studies had poor statistical power by contemporary standards. Even for a relatively large candidate gene study with power-favorable multiple comparison correction, power would have been poor to detect the genetic effects typical for GWAS of human diseases. As the genetic effects for schizophrenia may be smaller than for other human diseases (Purcell *et al.*, 2009, Shi *et al.*, 2009, Stefansson *et al.*, 2009), nearly all hypothesis-driven candidate gene studies were under-powered. Given what we now know about the genetic architecture of schizophrenia, a typical candidate gene study requires sample sizes ~11,000 cases plus controls for a single marker, 17,500 subjects for 10 markers, and 24,000 subjects for 100 markers (Supplemental Methods). Future association studies of schizophrenia should use similarly realistic power calculations.

Moreover, we demonstrated that hypothesis-driven candidate gene studies generally had poor coverage of common genetic variation. With the resources provided by the HapMap and 1000 Genomes projects coupled with decreases in genotyping costs, researchers can ensure that future genotyping covers the majority of common and rare variation present in their samples.

We were surprised to realize that most genes in the hypothesis-driven candidate gene literature for schizophrenia had been assessed once or twice (76.9%). Given the critical importance of replication in genetic studies of complex traits (Chanock *et al.*, 2007), evaluation of false positives and false negatives is not possible. Positive findings from one

or two studies cannot be viewed as secure (particularly given the distorting potential of publication bias) and, conversely, negative findings may not provide confident exclusion.

If power and coverage are low, we can anticipate false negatives (i.e., true susceptibility loci with non-significant candidate gene findings). For example, GWAS and replication efforts support *TCF4* as a risk locus for schizophrenia (Stefansson *et al.*, 2009). However, a *TCF4* CAG repeat was studied for association with schizophrenia in three studies (Bowen *et al.*, 2000, McInnis *et al.*, 2000, Vincent *et al.*, 1999). All reported negative results which may have lead to the inappropriate exclusion of *TCF4* from consideration.

Second, it is possible that the major hypotheses that drove the selection of many candidate genes are incorrect. SZGene candidate genes were selected for many different reasons and some resulted from genome-wide linkage screens (most notably *NRG1* and *DTNBP1*) (Stefansson *et al.*, 2002, Straub *et al.*, 2002). However, the ISC GWAS results did not lend support for common variation contributing to schizophrenia - either for candidate genes from the literature as a whole, or for the specific pathways from which candidate genes were frequently selected. For the full set of hypothesis-driven candidate genes, there was nominally significant support for an over-representation of small ISC p-values. However, the effect was marginal, and the results were not significant when corrected for potential bias caused by linkage disequilibrium between genes. We found no support for an aggregate effect of hypothesis-driven candidate genes contributing to SCZ risk using a risk profile generated from the SNPs within these genes. This pattern of results is not consistent with robust or notable collective contribution of common variation within the hypothesis-driven candidate genes to schizophrenia based on the ISC data. However, it is possible that subsets of the heterogeneous list of historical candidate genes are enriched for smaller ISC p-values. We thus tested the two over-arching, “meta-hypotheses” which have been highly influential – notions of schizophrenia as a disease of the synapse and as a neuro-developmental disease. To our knowledge, these two larger-scale ideas have not been tested for empirical support in aggregate. We found no evidence to support a genetic basis for these two hypotheses in perhaps the most comprehensive analysis yet conducted. In addition, we specifically evaluated eight of the ten most studied historical candidate genes and the ISC GWAS results provide no support for common genetic variation associated with schizophrenia. We note that the strongest ISC GWAS findings were in the MHC region. Genes from the expanded MHC region do appear in the hypothesis-driven candidate gene literature. Most notably, *NOTCH4* had genome wide significant SNPs in the ISC data and was highly studied (24 times; both positive and negative studies) in the candidate gene literature. However, given the high LD in the region (Table S1), we cannot localize the MHC signal more specifically. We cannot therefore either directly validate or exclude *NOTCH4* as involved in schizophrenia susceptibility.

Finally, more generally, there are now numerous guidelines for candidate gene studies (Chanock *et al.*, 2007, Pearson and Manolio, 2008). If these guidelines are followed at all stages of the scientific process (from study design through review), the published literature will better reflect the genetic architecture of schizophrenia.

No single study can disprove a meta-hypothesis in psychiatry, and our conclusions are bounded by the statistical power of the ISC sample. However, it is notable that the ISC GWAS results do not support enrichment of schizophrenia susceptibility loci within the candidate genes. These results suggest – but do not prove – that many traditional ideas about the genetic basis of schizophrenia may be incorrect. Indeed, the singular advantage of genomic surveys is that they are unbiased by prior knowledge and can yield novel and unexpected findings. Given current knowledge of the genetic architecture of schizophrenia and the capacity to assess common and rare variation across the genome, it is possible that the next few years will lead to marked changes in major hypotheses about the genetic basis of schizophrenia.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Table 1

Characteristics of hypothesis-driven candidate gene studies and the ISC GWAS.

Characteristic	Candidate gene studies	ISC
Studies	1,375	-
Genes (autosomal)	732	-
Markers (autosomal)		
Total	6,934	1,948,385
Markers per gene, median (IQR)	2 (1–5)	9 (1–34)
Genes with 1, 2, or 3 markers	65.9%	n/a
Marker density per gene as kb/SNP, median (IQR)	15.4 (4.69–46.2)	1.38 (0.69–2.47)
Sample size	Median (range) [a]	Actual
Total subjects	412 (27–5,623)	6,909
Number of cases	191 (5–2,434)	3,322
Number of controls	214 (12–4,899)	3,587
Major annotation clusters from pathway analysis	Enrichment score	
Synaptic transmission	52.2	n/a
Neuronal development and morphogenesis	32.4	
Regulation of synaptic transmission	22.6	
Response to chemical stimuli	22.2	
Statistical power [b]	0.48	0.89
Proportion of autosomal RefSeq genes studied [c]	0.037	0.902
Proportion of genes in top 4 DAVID annotation clusters studied	0.067	n/a

[a] Biased due to subject overlap across publications.

[b] See text for assumptions.

[c] For ISC, assuming gene boundaries expanded by ±10 kb and SNP density < 20 kb/SNP.

IQR=inter-quartile range. FDR=false discovery rate. GRR=genotypic relative risk. MAF=minor allele frequency.

Table 2

Testing for over-representation of smaller ISC GWAS p-values in hypothesis-driven candidate genes for schizophrenia and genes corresponding to major hypotheses.

Gene list	Boundary ± 0 kb	Boundary ± 10 kb
SZGene hypothesis-driven candidate genes		
Full set of genes	0.05	0.02
Full set, excluding MHC region	0.48	0.49
Full set, LD correction (InRich)	0.63	0.19
Genes studied ≥3 times	0.19	0.45
Genes studied ≥3 times, excluding MHC region	0.65	0.52
Genes in DAVID cluster 1 (synaptic transmission)		
Full set of 4808 genes	1	1
Subset of 222 hypothesis-driven candidate genes	0.99	1
Genes in DAVID cluster 2 (neuronal development and morphogenesis)		
Full set of 4834 genes	1	1
Subset of 401 hypothesis-driven candidate genes	0.73	0.95

Empirical p-values (from ALIGATOR unless otherwise noted) testing for over-representation of smaller ISC GWAS p-values in a given gene list in comparison to that expected by chance (10,000 permutations). SNPs were mapped to strict (±0 kb) or expanded (±10 kb) gene boundaries. SNP thresholds to select the top 5% of genes varied from 0.002 – 0.004.

Table 3a

ISC results for the ten most studied genes from SZGene.

SZGene studies	Gene	Product	Gene location (hg18)	ISC SNPs (±10kb)	Density kb/SNP	Minimum P-value	Bonferroni correction
81	*COMT*	catechol-O-methyltransferase	chr22:18309262-18337496	43	1.1	0.042	1
71	*DRD3*	dopamine receptor D3	chr3:115330246-115380589	54	1.3	0.082	1
67	*DRD2*	dopamine receptor D2	chr11:112785526-112851211	90	1	0.14	1
57	*HTR2A*	serotonin receptor 2A	chr13:46305513-46368176	118	0.7	0.017	1
45	*DRD4*	dopamine receptor D4	chr11:627304-630703	1	n/a	n/a	n/a
41	*NRG1*	neuregulin 1	chr8:31616809-32742100	1211	0.9	0.019	1
40	*BDNF*	brain-derived neurotrophic factor	chr11:27633017-27700181	39	2.2	0.0039	0.15
32	*APOE*	apolipoprotein E	chr19:50100878-50104490	1	n/a	n/a	n/a
32	*DTNBP1*	dystrobrevin binding protein 1	chr6:15631017-15771250	140	1.1	0.026	1
32	*SLC6A4*	serotonin transporter	chr17:25547505-25587080	27	2.2	0.097	1

Table 3b

Genes with genome-wide significant ISC results and studies from SZGene.

SNP	ISC p-value	SNP location (hg18)	*Gene*	Product	SZGene studies
rs1150752	3.3e-9	chr6:32172704	*TNXB*	tenascin XB	4
rs3132956	3.7e-9	chr6:32287416	*NOTCH4*	Notch homolog 4 (Drosophila)	24
rs389884	9.9e-9	chr6:32048876	*STK19*	serine/threonine kinase 19	0
rs9268208	1.2e-8	chr6:32388569	*C6orf10*	chromosome 6 open reading frame 10	0
rs1270942	1.2e-8	chr6:32026839	*CFB*	complement factor B	5
rs3130614	2.5e-8	chr6:31584437	*MICB*	MHC class I polypeptide-related sequence B	2
rs2734583	2.9e-8	chr6:31613459	*BAT1*	HLA-B associated transcript 1	1
rs3117577	3.0e-8	chr6:31835453	*MSH5*	mutS homolog 5	0
rs2187668	3.5e-8	chr6:32713862	*HLA-DQA1*	major histocompatibility complex, class II, DQ alpha 1	0
rs3135394	4.1e-8	chr6:32516475	*HLA-DRA*	major histocompatibility complex, class II, DR alpha	0