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Psychiatric Genomics: An Update and an Agenda

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Abstract

The Psychiatric Genomics Consortium (PGC) is the largest consortium in the history of psychiatry. In the past decade, this global effort has delivered a rapidly increasing flow of new knowledge about the fundamental basis of common psychiatric disorders, particularly given its dedication to rapid progress and open science. The PGC has recently commenced a program of research designed to deliver “actionable” findings – genomic results that (a) reveal the fundamental biology, (b) inform clinical practice, and (c) deliver new therapeutic targets. This is the central idea of the PGC: to convert the family history risk factor into biologically, clinically, and therapeutically meaningful insights. The emerging findings suggest that we are entering into a phase of accelerated translation of genetic discoveries to impact psychiatric practice within a precision medicine framework.

Introduction

Heredity is intimately related to the history of psychiatry. Clinical observations by early physicians noted the tendency of mental illnesses to run in families. In the 20th century, these anecdotes were systematically evaluated and some were confirmed in rigorous twin, family, and adoption genetic epidemiological studies. This exceptional body of evidence provided a major etiological clue for the field: common psychiatric disorders have a moderate to strong tendency to run in families in large part due to genetic inheritance (1, 2).

We now know that these genetic effects are relatively subtle and non-deterministic: most people with a strong family history are not themselves affected. Moreover, most psychiatric disorders do not “breed true” with increased risks spread across multiple disorders. In fact, the diverse clinical manifestations and variable course observed for many common psychiatric disorders are consistent with complex and relatively subtle genetic effects. For adult-onset common psychiatric disorders in particular, development is often within normal limits, and many experience relapsing/remitting illnesses with preservation of basic neurological function but often with some degree of erosion of higher components of cognition.

In the last decade, it has become technically and economically feasible to interrogate the genome directly with increasing resolution and completeness. Instead of studying the heredity of psychiatric disorders in a general way (e.g., via studies of pedigrees, twins, or adoptees), we can now evaluate the genomes of cases and controls at several levels of precision quickly and inexpensively. Indeed, heritability itself can be assessed directly from genome-wide genetic data (3, 4).

By carefully evaluating the successes and failures of psychiatric genetics in the past three decades, we now have a solid fix on how to dissect the “family history risk factor” into far more precise and mechanistic components. We can identify genetic variants that contribute to risk, and are moving toward understanding the mechanisms by which they act. The field has learned an enormous amount, and is poised to make fundamental advances that could profoundly improve understanding.

In 2009, the Psychiatric Genomics Consortium (PGC) published three foundational papers regarding genome-wide association studies (GWAS) (5-7). GWAS is a genomic study design that focuses on the impact of common genetic variation in almost all genes in the human genome. The initial PGC papers covered the core concepts, history, the rationale, genomic assays, statistical analysis, interpretative framework, and the importance of cross-disorder studies in psychiatry. Full background of the terminology, core concepts, and strategy of GWAS can also be found in these papers. Basic terms are defined in [Table S1](#).

This review provides an update on what we have learned, and puts forth an agenda for the next five years. A key lesson was the need for a global community effort in psychiatric genetics because the

required sample sizes are far beyond the reach of any single group. To enable these studies, in 2007 we formed the PGC (URLs). Our overarching goal is to deliver actionable knowledge, i.e., genetic findings whose biological implications can be used to improve diagnosis, develop rational therapeutics, and craft mechanistic approaches to primary prevention.

Clarity in retrospect

A key unknown was genetic architecture, particularly the sizes of the underlying genetic effects. A decade ago, these were unknown and subject to considerable speculation with hypotheses suggesting that genetic discovery for psychiatric disorders would be anywhere from highly tractable to impossible. If the genetic effects were few, common, and large, relative modest sample sizes would be sufficient. A few early studies hinted that relatively small samples might suffice (e.g., the large effects of APOE on Alzheimer's disease or CFH on age-related macular degeneration) (8, 9), and these may have led to expectations that gene discovery would be straightforward.

The power calculations are not difficult: for a given number of cases and controls (plus assumptions of allele frequency, genetic model, significance threshold, and power), it is easy to compute the minimum detectable genotypic relative risk (GRR). For example, Figure 1a shows the 90% power curve for a GWAS of 1,000 cases and 1,000 controls.

Like most investigators in human complex disease genomics, we had limited data to allow us to narrow bounds on the search space. We quickly learned that optimistic assumptions of large genetic effect sizes for these disorders were incorrect. The initial GWAS for psychiatric disorders had sample sizes ~1,000 cases enabling excellent power to detect $GRR \geq 2.5$. However, these effects were not found for schizophrenia (10), bipolar disorder (11), major depressive disorder (12), or ADHD (13). Figure 1a also shows the 90% power curve for the largest published study of any psychiatric disorder (37,000 cases) (14), and only two of 128 independent loci had $GRR \geq 1.2$. Compellingly, we can now demonstrate that common genetic variants with GRR above ~1.24 for schizophrenia can be excluded with ~100% power.

Genetic effects that are common and large are unusual for human diseases and traits studied using GWAS (Figure 1b). They are occasionally found for less complex and well-measured conditions (e.g., infectious diseases, rare adverse drug reactions, and eye diseases). To our knowledge, the largest common genetic variant associations observed to date in psychiatry are for alcoholism in people of East Asian ancestry ($GRR \sim 6.2$) and clozapine-induced agranulocytosis ($GRR \sim 5.3$) (15, 16).

Genetic architecture and models of disease

Elucidation of the genetic architecture underlying these disorders is the major goal of the PGC. How many susceptibility or protective variants are there? What are their frequencies and effect sizes? How do they exert their effects? Do these variants interact with one another or with environmental risk factors? Crucially for biological understanding, which genes are affected by these variants?

It is heuristically useful to consider the bookends. The extreme models are that psychiatric disorders are caused by (a) the cumulative impact of hundreds or thousands of common genetic variants each of subtle effect (common-disease/common-variant model) or (b) many different gene-disrupting variants of strong effect (multiple rare variant model). In the latter model, every person with a serious psychiatric disorder would have a strong effect variant and these would cluster in a set of genes important to brain development and function.

These models were passionately debated. Some authors expressed profound hope that the multiple rare variant model was broadly explanatory (17-19). Others favored a common disease/common variant model, arguing that psychiatric phenotypes are comparatively subtle. Most investigators were agnostic. The PGC wished to design studies that would be informative whatever the underlying model (5).

The initial strategy of the PGC

A consistent lesson from the history of psychiatric genomics was that these are very hard problems: any search is going to be far more difficult than anticipated. Although we were hopeful that the initial

GWAS might deliver insights, we created the PGC in order to hedge our bets: we needed a framework to aggregate data across studies with exceptional care and rigor if we were to progress. A critical step was to convince all groups that sharing individual data was essential – this is a foundational principle of the PGC and allows optimal quality control and analysis.

Moreover, to ensure progress, an “open-science” perspective was required. Genome-wide summary statistics of all PGC analyses are available for widespread use (URLs), and the vast majority of PGC genotype data that can be deposited are available to qualified researchers in a controlled-access repository. We recently have made available a list of the top loci from PGC analyses (both published and in preparation).

These early strategic decisions proved important: results from the first wave of psychiatric GWAS, circa 2008, were unimpressive. Although we were careful not to hype GWAS (5, 6), some prominent commentators voiced strong doubts about its value – even though careful review of the early results showed unequivocal indications of genetic effects. The first wave studies were simply underpowered, and combining studies to increase power was logical. Nevertheless, we persisted, and a 2012 letter signed by 96 psychiatric genetics investigators (“Don’t give up on GWAS”) anticipated the utility of GWAS should sample sizes increase (20).

To date, the PGC has published 24 main papers and 51 secondary analysis papers (Table S2). At least 141 additional papers have made use of PGC results. Many PGC papers are highly cited, but chief among them is the schizophrenia Nature (14) report which ranks among the most highly cited papers in 2014. The PGC is among the leading genomic consortia worldwide for open science and data sharing. These successes are a testimony to the fact-based strategy and persistence of the PGC.

An update

What have we learned? We now have a sizable body of empirical results relevant to the common “versus” rare variant debate. All common psychiatric disorders with sufficiently large samples have a predominant common-disease/common variant contribution (21-23). Indeed, this is widely seen across human complex diseases like type 2 diabetes mellitus (24), and anthropometric traits like height (25) and body mass (26). Demonstrating a major role of common genetic variation on risk for human complex traits (including psychiatric disorders) is so widely and consistently documented that it is no longer particularly newsworthy.

There is a variable contribution of rare variation of strong effect. This tends to be larger for early onset, severe disorders and lesser for disorders with normal-range developmental trajectories and adult onset (Figure 2a). However, even for psychiatric disorders with many proven examples of rare variants of strong effect (e.g., intellectual disability or early-onset Alzheimer’s disease), there is always a contribution of common variation. Rare variant studies have proven more difficult than anticipated: to confidently identify rare variants of strong effect in typical clinical samples requires very large sample sizes, perhaps as many as ~100K cases (27). The protein-coding parts of the genome are replete with inconsequential variation, and current ways to predict functional consequences are imprecise (28). There is a lot of noise, and the signal is sparser and weaker than anticipated.

Table 1b shows current sample sizes and notable findings for the nine PGC working groups. Schizophrenia has accumulated the most data for both common and rare variation. Figure 2b shows significant results from GWAS, copy number variation (CNV), and exome sequencing studies (14, 29,

30). Most findings are for common variation. Multiple rare CNVs have been implicated; most are multi-genic and all increase risk for several psychiatric disorders and neurological diseases (29). SETD1A is the only gene implicated to date by whole exome sequencing studies (30), but other such studies have only found hints of biological pathways by focusing on extremely rare variation (31, 32). It was widely anticipated that exon variation in the 0.005 to 0.01 allele frequency range would be readily found but this has not been observed (33), and a recent study of height required over 700,000 subjects to identify loci in this range (34). In a direct comparison, common variation had 14- 28 times more impact on risk for schizophrenia than rare CNVs or rare exonic variation (35).

Another major finding has been the repeated empirical documentation of important genetic overlap (particularly common variation) between most or all adult- and childhood-onset psychiatric disorders (21, 22). It is clear that psychiatric nosology has not “carved nature at the joints”. Moreover, the common variant genetic architecture of many disorders blends into normal phenomena. For example, there are sizable genetic correlations of MDD with personality traits like neuroticism and easily-assessed depressive symptom measures. Other findings suggest re- conceptualizations may be needed. For example, anorexia nervosa had a significant positive genetic correlation with schizophrenia, significant negative genetic correlations with body mass index and unfavorable metabolic measures, and significant positive genetic correlations with favorable metabolic factors. This pattern of findings suggests that the roots of anorexia may be not only psychiatric, but also metabolic in origin.

This is an evolving area with regular increases in confident knowledge. To encourage rapid dissemination of results, the PGC regularly compiles and shares a list of the strongest findings for the disorders it studies (URLs).

PGC, an agenda

Attempts to understand the genetic basis of psychiatric disorders – to untangle and concretize the family history risk factor – have never been easy. However, by incorporating empirical results, a data-driven and logical way forward has emerged, and it is likely that these efforts will continue to yield important new knowledge. Many groups are active in this area, but the PGC has emerged as the key umbrella organization for a large portion of this work. A basic description of the PGC and its core principles is given in [Table 1a](#). Key technical aspects include its dedication to rigorous methodologies and its stance as a “mega-analysis” consortium with PGC members sharing individual-level genotype and phenotype data.

With continued support from the NIMH (and new support from NIDA), the PGC recently initiated a program of research designed to deliver “actionable” findings, genomic results that (a) reveal the fundamental biology, (b) inform clinical practice, and (c) deliver new therapeutic targets. This is the central idea of the PGC: to convert the family history risk factor into biologically, clinically, and therapeutically meaningful insights. This program of research has six aims, three focused on common variation and three on rare variation ([Table 1c](#)).

[Aim 1](#) (common variation) is the core business of the PGC: to conduct progressively larger GWAS mega-analyses and systematic cross-disorder analyses (36). [Figure 3a](#) depicts the progression of sample sizes with time. Our goal is for each of the nine disorder working groups to obtain GWAS data on 100,000 cases. More information on case definitions can be found in [Table S3](#).

[Figure 3b](#) encapsulates experience with sample size and numbers of significant associations. Some disorders have a fortuitous architecture; e.g., inflammatory bowel disease obtained a considerable number of findings with relatively small samples. For most other complex traits, the path is slower but, with sufficient samples, discovery becomes linear. [Figure 3c](#) shows an idealized cartoon of the sigmoid-like discovery process from “dead zone” to asymptote. We suggest that the goal is to get to a “good enough” point where most genes are identified at least once and the majority of genes in salient biological processes are highlighted. This can provide an etiologic scaffold for studies that use

other methods to identify interacting partners in gene networks and pathways that underlie pathogenesis. There may be on the order of 1,000 genes involved in schizophrenia (37) (for comparison, ~13,000 genes are expressed in brain and ~2,000 at the synapse). Most PGC groups have at least one

association, several are accumulating moderate numbers of loci, and schizophrenia and MDD appear to be in the linear phase (Table 1b).

The PGC has extended its initial efforts in three ways. First, we added four new and highly motivated groups (eating disorders, obsessive-compulsive disorder/Tourette syndrome, post-traumatic stress disorder, and substance use disorders). Provisional groups for anxiety disorders and Alzheimer's disease have been formed. Second, we hope to markedly increase inclusion of non-European samples (Figure S1). For example, the PGC is now completing a paper based on over 12,000 schizophrenia cases from East Asia. The post-traumatic stress disorder and substance use disorders groups are studying increasingly larger samples of African-Americans. The Stanley Center of the Broad Institute has launched major sample collection efforts for multiple severe psychiatric disorders in Africa, South America, and Asia.

This work is crucial for generalizability, and it is likely that most (but not all) associations will be observed across the world. Finally, the PGC has engaged academic and industry experts to understand the therapeutic salience of the findings (38). Indeed, the empirical targets of antipsychotic medications are markedly enriched for the results of schizophrenia GWAS and this enrichment became clearer with increasing sample sizes, as has the potential pharmacological relevance of calcium channels for psychiatry (39). The design of rational therapeutics has been an elusive goal for psychiatric indications, and improved genomic knowledge is a pre-competitive activity that can make novel drug discovery more efficient (40).

Aim 2 (common variation) concerns the analysis of genetic risk scores (GRS). For a complex disease or trait, GRS is a single, normally distributed variable that captures the cumulative effect of risk alleles inherited by an individual (e.g., for schizophrenia, bipolar disorder, or body mass index). Computing a GRS requires a training set (i.e., GWAS results) and genome-wide genotypes on independent test subjects (e.g., a population cohort or participants in a clinical trial). The PGC has made training sets publicly available for multiple disorders (URLs). This allows researchers to compute GRS for whatever use they deem appropriate. GRS are not yet sufficiently discriminating to be useful clinically (14) but are among the first demonstrably valid biomarkers for psychiatric disorders. GRS derived from PGC results have been widely used in psychiatric research for generating patient strata, exploring diagnostic boundaries, identifying cognitive and behavioral correlates of genetic risk that predate clinical disorders, and evaluating the validity of putative cognitive or imaging phenotypes (41). Even social scientists have embraced the approach, seeing opportunities to study how genetic factors interact with the social environment to influence health and broader outcomes (42).

The PGC will systematically evaluate GRS in three contexts: (a) Development: use data from large longitudinal cohorts to evaluate the developmental effects of GRS; (b) Clinical symptoms: analyze relationship between clinical descriptors and GRS to understand clinical relevance; and (c) analyze GRS by environment interactions in epidemiological samples.

Aim 3 (common variation) will use GWAS results to estimate pairwise genetic correlations among all PGC disorders with all obtainable CNS-relevant diseases and quantitative traits (e.g., epilepsy, neuroimaging, personality, IQ). We will develop a comprehensive portrait of genetic influences across a broad set of brain phenotypes with the intention of improving nosology.

For example, the pairwise genetic correlations (URLs) among anorexia nervosa, ADHD, ASD, bipolar disorder, MDD, and schizophrenia are almost all significant and positive (the exceptions are all correlations of ASD and anorexia nervosa-ADHD, certainly influenced by small sample sizes) (43). This suggests that the common variant genetic architectures – the fundamental liability to these disorders – overlap importantly. After evaluating the disorder-level genetic correlations (22), we will systematically expand our queries to encompass within disorder genetic correlations (e.g., male vs female, early vs later onset) as well as genetic correlations with putative components (e.g., cognition, personality, body mass).

Aim 4 (rare variation) will continue the PGC's CNV efforts (29). The PGC CNV group has created a

pipeline to call CNVs from the initial intensity files using multiple algorithms followed by careful quality control and analysis. The initial schizophrenia paper has been published, and this group is now working on bipolar disorder, ADHD, and PTSD, and will include more groups with time.

Aim 5 (rare variation) is a “cheap-seq” aim. We will conduct inexpensive (~\$50/subject) schizophrenia-focused sequencing of 200 genes in 20,000 subjects. Genes will be selected based on all available sequencing results. For 200 genes, we will increase power far more cost-effectively than whole exome (10x cheaper) or whole genome sequencing (25x cheaper) in the same time frame. We propose an efficient and affordable way to markedly increase sample sizes for the most promising loci in a new sample of 20,000 subjects.

Aim 6 (rare variation) will systematically evaluate ~100 large pedigrees to search for genetic variants of large effect. We have engaged the large network of PGC clinicians in this task. Most experienced clinicians have encountered unusual pedigrees with high concentrations of severe psychiatric disorders. For example, one pedigree has >100 individuals with a severe psychiatric disorder and eight pedigrees have ≥20 affected individuals. Other pedigrees are from genetic isolates where inter-pedigree marriage is common. Still other pedigrees have extensive comorbidity with intellectual disability and epilepsy. No one has systematically and comprehensively evaluated a large collection of densely affected pedigrees using comprehensive genomic assays (karyotyping, identity-by-descent, CNVs, whole genome sequencing, and GRS) combined with a rigorous statistical framework.

Actionability. For the common variant aims, Aim 1 is of biological, clinical, and therapeutic relevance. Aim 2 and Aim 3 are important clinically and for nosology. Of the rare variant aims, all are important biologically and therapeutically (given their potential to identify single genes whose mutational disruption carries high risk).

Issues in the process of being solved

Empirical results from psychiatric genomics have begun to answer many questions. However, we point to two major unresolved issues. First, many GWAS signals are complex. Exactly how these connect to specific genes to enable precise experimentation is solvable but requires functional genomic or functional cellular data. [Figure 4a](#) shows the CACNA1C intronic association for schizophrenia; a subsequent study suggested that these SNPs interact with a regulatory element for CACNA1C (44). [Figure 4b](#) depicts the region surrounding DRD2 (which encodes the protein targeted by most antipsychotics). This association has been functionally connected to the gene via DNA-DNA interactions (45). [Figure 4c](#) shows a multigenic region – the association region covers many genes (most of which are expressed in brain) that have been associated with multiple human traits. Finally, [Figure 4d](#) depicts an intergenic region that is associated with schizophrenia but not near a known protein-coding gene.

These are typical for GWAS results, identifying relatively broad loci with multiple genome-wide significant markers. Although localization is imprecise, the associated genomic regions are clearly informative as they implicate salient biological pathways (46) and increasingly specific genomic features (47). Full elucidation requires functional genomic data generated from relevant cell types including gene expression (48), DNA-DNA looping (45), and epigenomics (49). To facilitate this work, the NIMH has funded the psychENCODE consortium (49) to conduct an array of functional genomic assays on brain tissue from people with severe psychiatric disorders and controls (URLs).

Second, the extant cross-disorder studies of psychiatric disorders show non-trivial genetic overlap between most or all disorders. The results clearly show that our diagnostic categories do not define pathophysiological entities. It is plausible that a focus on components would be valuable (e.g.,

cognition, mood stability, or innate anxiety-fearfulness). The resolution of these issues will address major unanswered questions: from a genetic perspective, what are these disorders? How are they similar and how are they different?

Common complaints

Briefly, there are three common complaints about the work of the PGC. First, “the results don’t matter” – the readouts are broad with small effect sizes, and the effect sizes of individual associated

loci are small. In fact, the results are delivering increasingly useful and targeted knowledge (discussed under Aim 1 above) (38, 39, 46). The small effect sizes do not constrain the potential utility of targeting the identified genes or pathways – drugs targeting those pathways can have major effects. Unlike 10 years ago, pharmaceutical companies are following this area closely as genomic data are increasingly crucial to drug development (40).

Second, “what about unaccounted heritability (h^2)?” Heritability estimated from genome-wide SNP data (SNP- h^2) depends on technical issues and sample size. The comparator is estimated from twin or family data (twin- h^2 or pedigree- h^2), but these are assumption-laden and imprecise. “Unaccounted h^2 ” is the difference between these, and attempts to reconcile two fundamentally different entities. Still, when the genomic study is sufficiently large as with schizophrenia, SNP- h^2 is around half of the pedigree- h^2 . A point often missed, however, is that explaining h^2 is a minor goal. The main goals of the PGC are to gain biological, clinical, and therapeutic insights, which can arise regardless of the magnitude of heritability accounted for.

Third, because most PGC analyses are based on categorical, case vs control analyses, “PGC cases lack clinical depth”. This was by intention: over 10 years ago (37), some of us reasoned that fast phenotype characterization that led to affordably large sample sizes was the logical first step (as opposed to large numbers of phenotypes on small numbers of subjects). This was always the first step. The success of this strategy is seen, not only in the genome-wide significant loci that we have discovered, but also in the many phenotypes that have been associated with PGC GRS in both clinical and population samples. The second step, ongoing now, is detailed characterization of genetically informative subsets of cases (e.g., Aim 2). In addition, some PGC working groups (e.g., Substance Use Disorders) are currently analyzing quantitative phenotypes.

Conclusion

The PGC is the largest and most systematic genomics effort in the history of psychiatry. In the next five years, we propose to markedly up-scale our work. By tackling nature as it is and not as we might want it to be, we hope to provide considerable new knowledge about the fundamental basis of psychiatric disorders. Our long-standing commitment to global collaboration, open science, and rapid progress means that we will make our results and tools available in a timely manner. Prediction of the future is always hazardous but, given that we finally have a minimally adequate toolkit for genomics, it is possible that we are entering a golden age of research into the fundamental basis of severe mental illness.

Conflicts of Interest

PFS is a scientific advisor for Pfizer, Inc. and received an honorarium from F. Hoffmann-La Roche AG. CMB is a consultant for and grant recipient from Shire. Cardiff University received an honorarium from F. Hoffmann-La Roche AG for a presentation by MOD in 2015. OAA received a speaker’s honorarium from Lundbeck in 2016. Multiple drug companies work with the PGC in a manner equivalent to academic investigators.

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URLs

European Bioinformatics Institute, <https://www.ebi.ac.uk/gwas>

LD-Hub, <http://ldsc.broadinstitute.org>

psychENCODE, <https://psychencode.org>

Psychiatric Genomics Consortium, general information, <https://pgc.unc.edu>

Psychiatric Genomics Consortium, results, <http://www.med.unc.edu/pgc/results-and-downloads>

Psychiatric Genomics Consortium, monthly talks, <http://www.med.unc.edu/pgc/worldwide>

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PGC background data

- In continuous existence from 2007 to the present
- International, over 800 scientists from 40 countries
- The nine PGC working groups study: attention-deficit hyperactivity disorder, autism, bipolar disorder, eating disorders, major depressive disorder, obsessive-compulsive disorder/Tourette syndrome, post-traumatic stress disorder, schizophrenia, and substance use disorders. Provisional groups for anxiety disorders and Alzheimer's disease were added in 2016
- Current goals are to obtain genome-wide association data on 100,000 cases for each disorder
- Includes groups focused on cross-disorders analysis, copy number variation, statistical analysis, pathway analysis
- The PGC has published 24 main papers and 51 secondary analysis papers (Table S1). At least 141 papers have made use of PGC results. PGC core

principles

- Given the human, medical, and societal impact of psychiatric disorders, the PGC is passionate about rapid progress, and is a world leader in data and results sharing
- Open, inclusive, participatory, and democratic science
- Core PGC activities are commercially "pre-competitive": identifying the genomic results is a public good, and part of the fundamental characterization of these psychiatric disorders
- Rigorous methodology, commitment to producing robust, replicable, and secure findings. Strong empirical focus, healthily questioning of prior knowledge and assumptions

"Mega-analysis" framework: PGC members share raw genotype data so that all samples can be processed using a uniform quality control, imputation, and analysis pipeline

PGC group	N _{case}	Hits	Twin ² -h	SNP ² -h	Strongest genetic correlation
Schizophrenia	60,995	155	81%	45%	Bipolar disorder
MDD	130,664	20+	30-40%	14%	Neuroticism
Bipolar disorder	20,352	19	80%	21%	
ADHD	20,183	12	70-80%	22%	Educational attainment
Autism spectrum disorder	18,381	3	75%	12%	Subjective well-being
Anorexia nervosa	3,495	1	56%	~20%	Metabolic traits
Substance use disorders	3,772	1	50%	~10%	Smoking
Tourette syndrome	4,232	1	60-80%	58%	OCD
OCD	2,688	0	45-65%	37%	Tourette syndrome
PTSD	3,749	0	30-40%	5-35%	Schizophrenia

Common genetic variation: continue & expand ongoing work of the PGC to increase knowledge.

SNPs. (a) The core business of the PGC: progressively larger GWAS mega-analyses for all disorders studied by the PGC. (b) Systematic cross-disorder analyses. (c) Pathway analyses to clarify biological implications. Critically, we have engaged academic and industry experts in psychopharmacology to maximize therapeutic implications of the findings.

Genetic risk scores (GRS). (a) Development: use data from large longitudinal cohorts to evaluate the developmental effects of GRS. (b) Clinical symptoms: analyze relationship between clinical descriptors and GRS to understand clinical relevance. (c) GxE: analyze GRS x environment interactions.

Brainstorm initiative. Apply novel statistical methods to GWAS results to estimate pairwise genetic correlations among all PGC disorders and with all obtainable CNS-relevant diseases/quantitative traits (e.g., epilepsy, neuroimaging, personality, IQ) to develop a comprehensive portrait of genetic influences across a broad set of brain phenotypes.

Rare variation: enhance discovery of alleles with larger effects on risk.

CNVs. Analyze rare CNVs in all PGC disorders via high-quality mega-analyses, and perform cross-disorder analyses to reveal pleiotropic genetic effects.

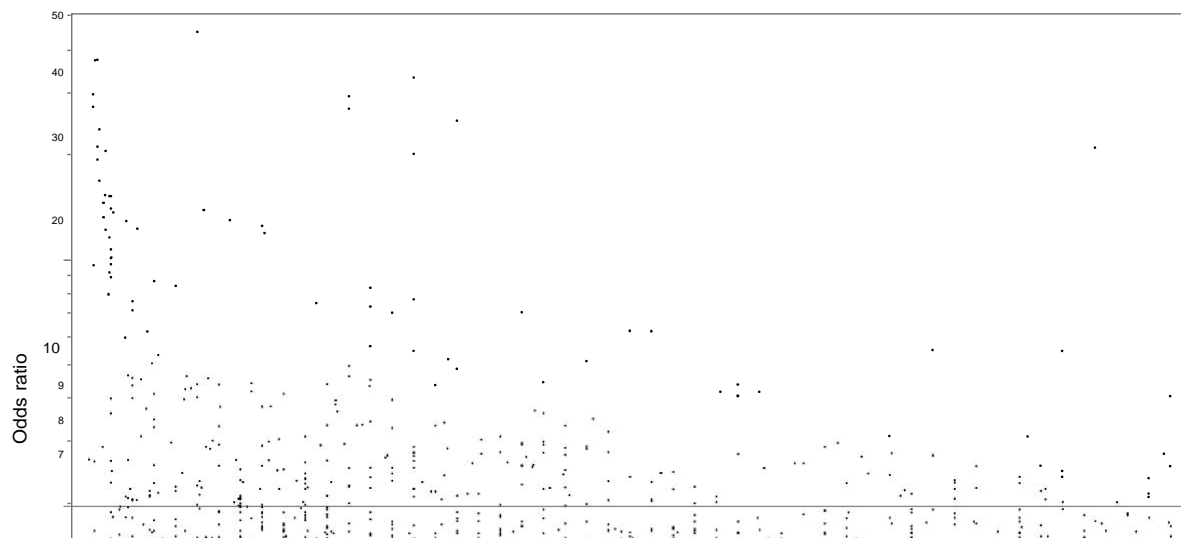
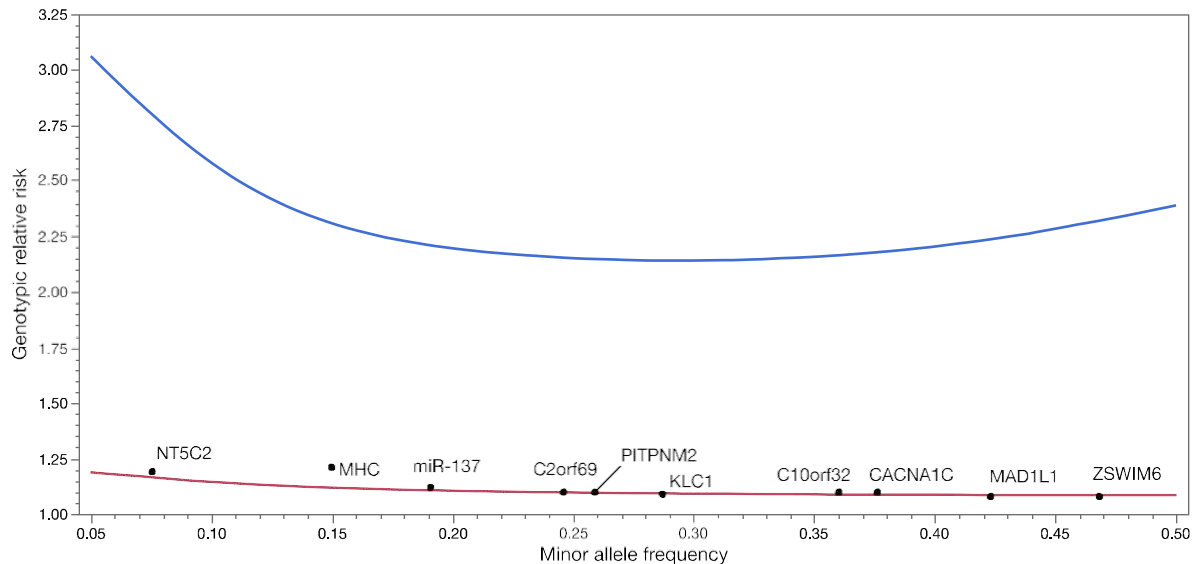
Sequencing. Characterize the full spectrum of genetic variation for SCZ (especially rare variants of strong effect) in regions implicated in Aim 1. Inexpensively sequence coding and regulatory regions of ~200 candidate genes in 20,000 independent subjects.

Pedigree sequencing. The large network of PGC clinicians has identified unusual pedigrees densely affected with psychiatric disorders. Systematically evaluate ~100 pedigrees for CNVs, high levels of GRS, and whole genome sequencing to enable searches for rare variants of strong effect.

Table 1a. PGC background information and core principles (URLs).

Table 1b. Update, current findings for each PGC working group. Ncase=number of cases. Hits=independent associations reaching genome-wide significance. Twin-h =heritability estimated from twin studies. SNP-h =heritability estimated from GWAS results.

Table 1c. Current projects for the PGC.



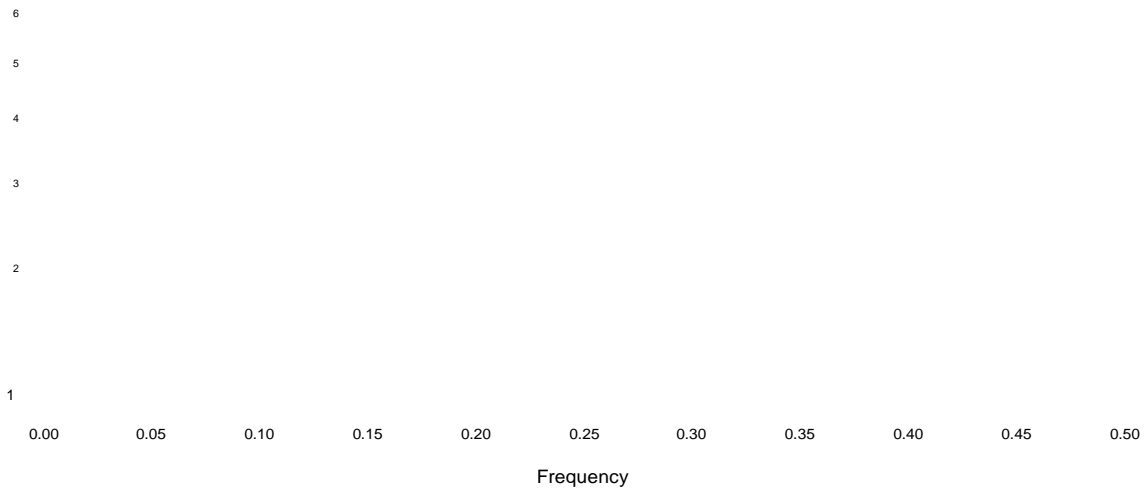


Figure 1a. Statistical power. Upper curve (blue) shows minimum detectable genotypic relative risks for common variants for 1,000 cases and 1,000 controls (90% power, additive model, lifetime risk 0.01, $\alpha=5e-8$). Lower curve (red) shows 90% power for the PGC 2014 schizophrenia paper (37,000 cases and 113,000 controls, additive model, lifetime morbid risk 0.01, $\alpha=5e-8$). Black dots show the top 10 loci in the PGC schizophrenia report. These loci are highly significant with P-values ranging from $1.7e-13$ to $3.8e-32$.

Figure 1b. Odds ratios (OR, \log_{10}) and allele frequencies from published GWAS. From EBI-NHGRI GWAS catalog (URLs, accessed 1/27/2017), contains 2,308 GWAS published 3/2005-7/2016. There are 9,485 SNP-trait associations ($P \leq 1e-8$) including 7,487 SNPs and 870 traits. Dots show frequency and OR (OR transformed to be >1 and allele frequencies to 0-0.50). Contours show densest areas of the plot. Horizontal lines show 50th (1.22) and 90th (1.95) percentiles for ORs: most associations are subtle. Of 62 associations with $OR > 5$, most are for infectious disease (31; e.g., influenza susceptibility), pharmacogenomic (13; e.g., rare adverse drug reactions like flucloxacillin-induced liver injury), eye disease (4; e.g., glaucoma), or pigmentation (2; e.g., blue vs. brown eyes). Only a few diseases have atypically large ORs (e.g., celiac disease, melanoma, membranous nephropathy, myasthenia gravis, ovarian cancer, Parkinson's disease, progressive supranuclear palsy, thyrotoxic hypokalemic periodic paralysis, and type 1 diabetes). The only psychiatric finding was alcohol consumption and ALDH2 in individuals of East Asian ancestry.

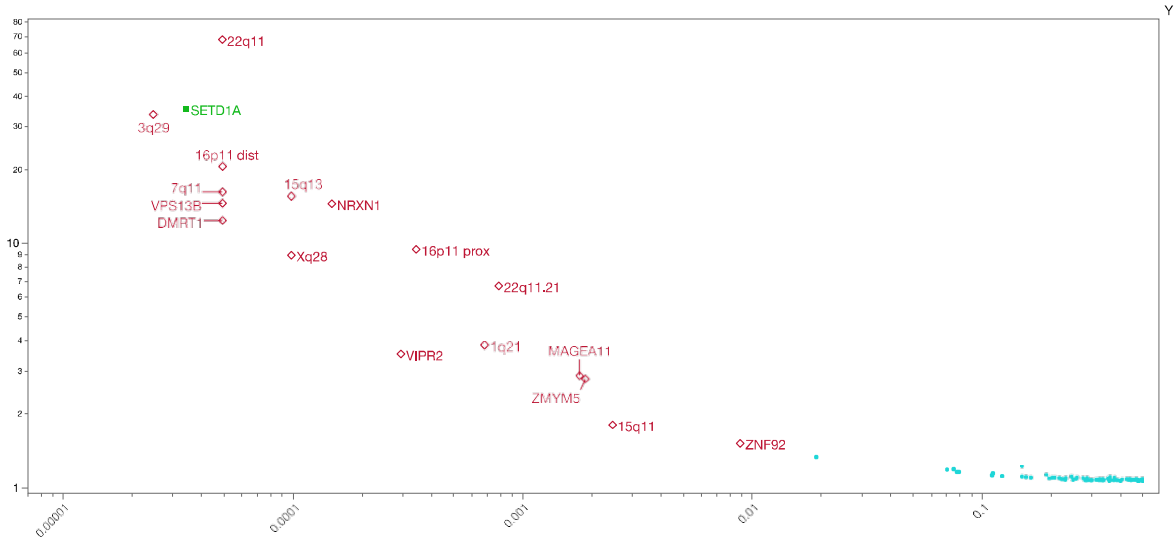
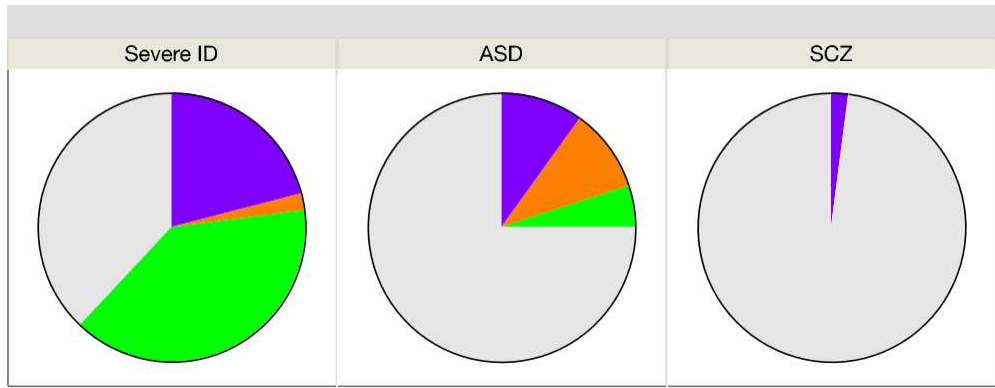


Figure 2a. Genetic causes of severe intellectual disability (ID) (50), autism spectrum disorder (51, 52), and schizophrenia (53), including copy number variation (CNV), inherited known recessives, and single nucleotide variants (SNV). For severe ID, most SNV and CNV are de novo. The unknown grouping includes common variation, undiscovered rare genetic causes, phenocopies, and causation due to non-genetic effects.

Figure 2b. Significant genetic associations for schizophrenia. Y-axis is \log_{10} of odds ratio. X-axis is \log_{10} of allele frequency in controls. Odds ratios transformed to be >1 and frequencies to be ≤ 0.5 . The dots on the lower right (cyan) shows common-variant associations for schizophrenia ($P < 1e-8$) (14). Open diamonds (red) show copy number variation associated with schizophrenia (29). Filled square (green) shows the lone variant identified using whole exome sequencing (30).

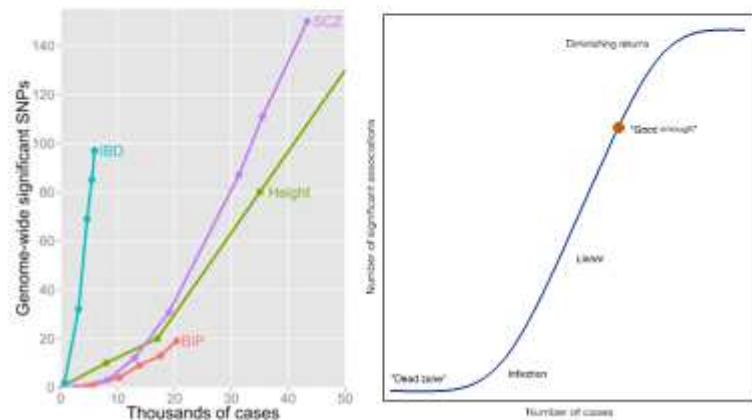
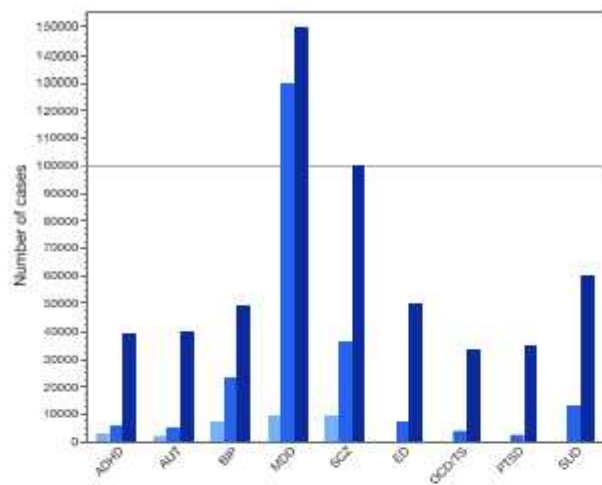


Figure 3a. Numbers of cases for PGC GWAS analyses. For the original five PGC disorders (ADHD, SCZ), there are three bars for the numbers of cases in the initial "PGC1" reports, the next round of papers ("PGC2"), and projected numbers by 2019. For the four disorders added in 2013 (ED, SUD), the PGC2 and projected PGC3 numbers are shown. Abbreviations: ADHD=attention-deficit hyperactivity disorder, AUT=autism, BIP=bipolar disorder,

MDD=major depressive disorder, SCZ=schizophrenia, ED=eating disorders, OCD/TS=obsessive-compulsive disorder/Tourette syndrome, PTSD=post-traumatic stress disorder, and SUD=substance use disorders.

Figure 3b. Relation between numbers of cases and genome-wide significant SNPs in GWAS. Lines show discovery paths for inflammatory bowel disease (IBD), schizophrenia (SCZ), height, and bipolar disorder (BIP). IBD has an exceptional genetic architecture and excellent clinical diagnostic specificity that enabled considerable discovery with relatively smaller numbers of cases. SCZ, height, and BIP follow more typical and approximately similar discover paths

Figure 3c. Hypothetical cartoon of the relation between number of cases and genome-wide significant associations for a human complex disease or trait. Complexities arising from the true nature of the initially unknown genetic architecture could change the form of this curve importantly. There is an initial dead zone whose length depends how many cases are accrued and the largest effect size. This is followed by an inflection point where the significant associations begin to accumulate and then a linear phase.

