OCD GWAS Results, August 2017 Release

Introduction

This is the GWAS result file from the meta-analysis of OCD by International Obsessive Compulsive Disorder Foundation Genetics Collaborative (IOCDF-GC) and OCD Collaborative Genetics Association Studies (OCGAS). The GWAS result was released in August 2017.

Citation

International Obsessive Compulsive Disorder Foundation Genetics Collaborative (IOCDF-GC) and OCD Collaborative Genetics Association Studies (OCGAS). Revealing the complex genetic architecture of obsessive compulsive disorder using meta-analysis. *Mol Psychiatry*. 2017 Aug. doi:10.1038/mp.2017.154

Stewart SE, Yu D, Scharf JM, Neale BM, Fagerness JA, Mathews CA, International Obsessive Compulsive Disorder Foundation Genetics Collaborative (IOCDF-GC) et al. Genome wide association study of obsessive-compulsive disorder. *Mol Psychiatry*. 2013; 18:788–798.

Mattheisen M, Samuels JF, Wang Y, Greenberg BD, Fyer AJ, McCracken JT et al. Genome-wide association study in obsessive-compulsive disorder: results from the OCGAS. *Mol Psychiatry* 2015; 20: 337–344.

Disclaimer

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Methods

The samples in this study contains the individuals from two previously published OCD GWAS projects, the first OCD GWAS performed by IOCDF-GC and a family based OCD GWAS performed by OCGAS. Only individuals of European ancestry from these original GWAS samples were included in this study, yielding 1429 cases, 5089 controls and 285 trios from IOCDF-GC and 344 cases and 630 trios from OCGAS. Additional 1033 screened controls from the Genomic Psychiatry Cohort were included as ancestry matching controls for OCGAS cases. All cases met DSM-IV (Diagnostic and Statistical Manual of Mental Disorders, 4th edition) criteria for OCD. Controls from the IOCDF-GC GWAS were unscreened. Additional information on the IOCDF-GC and OCGAS samples and methods has been previously published. This work was approved by the relevant institutional review boards at all participating sites, and all participants provided written informed consent.

We imputed genotype-level data from the IOCDF-GC (except the Dutch samples that were imputed separately, see below), OCGAS and Genomic Psychiatry Cohort samples using IMPUTE2 and reference haplotypes from the 1000 Genomes Project (Phase I integrated variant set release); NCBI build 37 (hg19) was constructed with SHAPEIT2. We assessed genetic relatedness between samples through identity-by descent estimation between all sample pairs using PLINK and retained only one member of each pair of samples with pi_hat > 0.2. Samples were excluded if they had a call rate of < 0.98, an absolute value of F_HET > 0.20, ambiguous genotypic sex, or discrepant status between genotypic sex and phenotypic sex. SNPs were excluded from pre-imputation data set if the call rate was < 0.98, MAF < 0.01, case–control differential missingness was > 0.02, or the P-value of Hardy–Weinberg equilibrium was < 1.0×10^{-6} for controls and < 1.0×10^{-10} for cases. After imputation, SNPs were excluded if IMPUTE2 info was < 0.6, IMPUTE2 certainty was < 0.9, or MAF was < 0.01. We assessed population structure using multidimensional scaling and, as previously observed, samples of Ashkenazi Jewish or Afrikaans (South African) ethnicity clustered as separate groups. We conducted separate association analyses for each case–control subpopulation (IOCDF-GC European (IOEU), IOCDF-GC Ashkenazi Jewish (IOAJ), IOCDF-GC South African (IOSA), OCGAS case–control (OCCC)) and trio sample (IOCDF-GC trios (IOTR) and OCGAS trios (OCTR); as probands versus pseudo-controls). We defined 'pseudo-controls' as the nontransmitted haplotype pairs from parents to affected offspring in the trio samples.

Because of more stringent data sharing restrictions for Dutch cases, imputation and summary statistics for the Dutch cases and ancestry matched controls (IODU) were calculated separately by the site investigators following the same imputation and quality control (QC) procedures. We then performed meta-analysis using the summary statistics of all case–control subpopulations (including IODU) and trio samples using METAL with the inverse variance method on SNPs that passed QC in at least 500 cases and 500 controls.

File Description

ocd_aug2017.gz: Full OCD GWAS meta-analysis (2,688 cases, 7,037 controls)

CHR	Chromosome (hg19)
SNP	Marker name
BP	Base pair location (hg19)
A1	Reference allele for OR (may or may not be minor allele)
A2	Alternative allele
INFO	Imputation information score
OR	Odds ratio for the effect of the A1 allele
SE	Standard error of the log(OR)
P	P-value for association test in the meta-analysis

Data Use Agreement

The PGC has made the full results from all published PGC studies available for download. If you download these data, you and your immediate collaborators ("investigators") acknowledge and agree to all of the following conditions:

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6. Investigators will never attempt to identify any participant.

Experience has taught us that the appropriate use of these data requires considerable attention to detail, prior experience, and technical skill. Errors are easy to make. If investigators use these data, any and all consequences are entirely their responsibility.