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Brain expression QTLs and GWAS signals of psychiatric diseases

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Abstract

Genome-wide association studies (GWASs) have identified some common variants associated with psychiatric diseases. While these variants explained some of the disease heritability, their functional effects, largely unknown, may hold clues to disease etiology. Many common SNPs have been found to be associated with gene expression levels in human brain by quantitative trait loci (QTL) mapping. Our and others' studies showed that SNP involved in expression QTL (eQTL) in brains are enriched in multiple psychiatric diseases, including bipolar disorder (BD), autism, obsessive compulsive disorder (OCD), Tourette syndrome (TS) and schizophrenia (SZ). We showed that brain eQTL SNPs (eSNPs) can be used to explain a big proportion of heritability that has been captured by GWAS of several psychiatric diseases. We further analyzed those eSNPs for their overlapping epigenetic marks, and target genes, comparing across diseases, tissue types, and studies. The results suggested novel candidate genes and pathways for psychiatric diseases. Our study concluded that Brain eQTL can be used to discover potential functions of some common SNPs, to assist interpretation of GWAS results of psychiatric diseases. Epigenomic annotation may further clarify functional effects of SNPs. Moreover, BD, autism, SZ, OCD, and TS have different degree of sharing of genetic factors.

Biography

Chunyu Liu has completed his Ph.D at the age of 29 years from the State Key Laboratory of Medical Genetics of China, Hunan Medical University; and had his postdoctoral training at the University of Chicago, Department of Psychiatry. He has published more than 75 papers in reputed journals and six book chapters. He serves as an academic editor of PLoS One and Genetics and Epigenetics, as reviewers for numerous journals and funding agencies, including NIH.