P-1328 - GENOME-WIDE ASSOCIATION ANALYSIS WITH BRAIN STRUCTURE MEASURES AS A QUANTITATIVE PHENOTYPE FOR FIRST-EPISODE SCHIZOPHRENIA

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Objective: Schizophrenia (SZ) is a syndrome, which is the most common form with paranoid delusions and auditory hallucinations late in early adulthood or in adolescence, and the changed structure of hippocampus, thalamus, amygdale region. Combined imaging with genetics data, we want to obtain genetic susceptibility loci for SZ.
Method: Imaging and genetics data which were obtained from the Mental Health Centre of the West China Hospital. In our study, we applied a genome-wide study of the change structure of brain regions.
Results: We indentified three genes or chromosomal region through having at least 2 single-nucleotide polymorphisms (SNPs) each significant at $P < 10^{-5}$ for the interaction/main effect model (TBXAS1, PIK3C2G, and IL17A-IL17F).
Conclusion: The genome-wide association study identifies three genes or chromosomal regions, which are related with the volume of hOC3v_V3v_Left hemisphere, Lobule_X_Vermis_Left hemisphere, Lobule_X_Vermis_Right hemisphere and maybe as a risk factor for schizophrenia. This result highlight the usefulness of endophenotype for neuropsychiatric diseases. But these findings are conformed through independent replication studies in future.

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