

Singapore scientists progresses to map schizophrenia

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Singapore: A group of researchers from Institute of Mental Health (IMH) and A*STAR's Genome Institute of Singapore (GIS) has helped identify over 100 locations in the human genome associated with the risk of developing schizophrenia.

In the genome-wide association study (GWAS), the authors looked at over 80,000 genetic samples from schizophrenia patients and healthy volunteers and found 108 specific locations in the human genome associated with risk for schizophrenia. Eighty-three of those loci had not previously been linked to the disorder.

The study implicates genes expressed in brain tissue, particularly those related to neuronal and synaptic function. These include genes that are active in pathways controlling that are implicated in learning and memory - and pathways involved in signaling between cells in the brain.

Additionally, the researchers found a smaller number of genes associated with schizophrenia that are active in the immune system, a discovery that offers some support for a previously hypothesized link between schizophrenia and immunological processes. The study also found an association between the disorder and the region of the genome that holds DRD2 - the gene that produces the dopamine receptor targeted by all approved medications for schizophrenia - suggesting that other loci uncovered in the study may point to additional therapeutic targets.

"The discovery of these 108 genomic regions has opened the door for further biological and clinical research to discover the genes that are directly linked with schizophrenia development and further understand the molecular mechanisms underneath the association of these genes with schizophrenia. The scientific breakthrough made by this study is a great demonstration

that large-scale genetic association study is a powerful tool for understanding disease genetic susceptibility and revealing novel biological insight into disease mechanism" said Professor Jianjun Liu, Deputy Director, Research Programmes, and Senior Group Leader, Human Genetics, from the Genome Institute of Singapore who is the Co-Principal Investigator of this project and the leader of the genetic study program of the project.

The other co-investigators of the project and co-authors of the paper from IMH's Research Division are Adj Asst Prof Mythily Subramanian, Adj Assoc Prof Sim Kang and Dr Jimmy Lee. "These new findings will also open doors to allow researchers to examine and better clarify the underlying brain connectivity changes associated with these genes and genetic mechanisms. A better understanding of the genetic mechanism and underlying brain changes can potentially allow better detection of illness, monitoring of response with treatment and progression over time," added Adj Assoc Prof Sim Kang.

They were part of the Schizophrenia Working Group of the Psychiatric Genomics Consortium, and the study was part of the five year Translational Clinical Research in Neuroscience which is funded by National Research Foundation.

"The main aim of this 5-year project was to identify the markers that will enable the better and early identification of those who might develop schizophrenia and these include genetic markers," said Professor Chong Siow Ann, vice chairman medical board (Research)-IMH, who is the principal investigator of this project.

Schizophrenia, a debilitating psychiatric disorder that affects approximately 1 out of every 100 people worldwide, is characterized by hallucinations, paranoia, and a breakdown of thought processes, and often emerges in the teens and early 20s. Its lifetime impact on individuals and society is high, both in terms of years of healthy life lost to disability and in terms of financial cost.