

Genetic breakthrough another step to understanding schizophrenia

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(Medical Xpress)—A consortium of scientists from 20 countries, including researchers from The University of Western Australia, has made a major breakthrough in understanding the genetic basis of the debilitating disorder, schizophrenia.

More than 175 scientists from 99 institutions across Europe, the United States of America and Australia contributed to a genome-wide association analysis which identified 13 new risk loci for schizophrenia.

In an article published in the journal, *Nature Genetics*, the study authors write that the results provide deeper insight into the genetic architecture of schizophrenia than ever before achieved, and provide a pathway to further research.

"For the first time, there is a clear path to increased knowledge of the etiology of schizophrenia through the application of standard, off-the-shelf genomic technologies for elucidating the effects of common variation," the authors wrote.

Schizophrenia is a complex [mental disorder](#) which affects about one per cent of people over their lifetime, leading to prolonged or recurrent episodes that impair severely social functioning and quality of life.

In terms of the 'global burden of disease and disability' index, developed by the World Health Organization, it ranks among the top 10 disorders, along with cancer, heart disease, diabetes and other non-communicable diseases.

Winthrop Professor Assen Jablensky, director of UWA's Centre for Clinical Research in Neuropsychiatry (CCRN) at Graylands Hospital, and Professor Luba Kalaydjieva, of the UWA-affiliated Western Australian Institute for Medical Research (WAIMR), led the UWA research team which took part in the study.

Professor Jablensky said that while a strong [genetic component](#) in the causation of schizophrenia had been well established, the role of specific genes and the mechanisms of their regulation remained largely unknown.

"Until recently, results of [genetic linkage](#) and association studies could explain only a small fraction of the estimated heritability of the disorder and of its '[genetic architecture](#)'," Professor Jablensky said.

However recent technological advances, enabling efficient coverage of the entire human genome with millions of single nucleotide polymorphisms (SNPs) as genetic markers, had given rise to a new generation of genome-wide association studies (GWAS), which trace the DNA differences between people affected with the disease and healthy control individuals.

"Since the effects of individual SNPs are quite tiny, their reliable measurement requires very large samples of adequately diagnosed patients and controls," Professor Jablensky said.

"This recent study reports on a major breakthrough in the understanding of the [genetic basis](#) of schizophrenia, achieved through meta-analysis of GWAS datasets contributed by a large international Psychiatric Genomics Consortium (PGC) - which includes the UWA research team."

A WA case-control sample consisting of 893 schizophrenia patients and healthy controls was part of a collection of 21,246 schizophrenia cases and 38,072 controls from 19 research centres and consortia across Europe, Australia and the USA.

The study found that a total of 8300 SNPs contribute to the risk for schizophrenia and account for at least 32 per cent of the variance in liability.

"A particularly important result of this study is that

many of these SNPs are located on a molecular pathway involved in neuronal calcium signalling, which suggests a novel pathogenetic link in the causation of schizophrenia and possibly other psychotic disorders," Professor Jablensky said.

He said ongoing and future studies by the UWA research team would aim to further refine the genetic analyses of the WA schizophrenia study (which at present includes 1259 persons), and to test neurobiological hypotheses about the treatment responses of genetically defined subsets of patients.

The article, "Genome-wide association analysis identifies 13 new risk loci for [schizophrenia](#)," was published in the August 25 online edition of *Nature Genetics*.

Provided by University of Western Australia

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