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Team uncovers possible risk gene for schizophrenia

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An international team of researchers has identified a risk gene for schizophrenia, including a potentially causative mutation, using genome-wide association data-mining techniques and independent replications.

The results of the research, led by Xiangning Chen, Ph.D., associate professor of psychiatry and human and molecular genetics in Virginia Commonwealth University's School of Medicine and the Virginia Institute for Psychiatric and Behavioral Genetics, and Kenneth S. Kendler, M.D., professor of psychiatry and human and molecular genetics in VCU's School of Medicine and the Virginia Institute for Psychiatric and Behavioral Genetics, are reported in the September issue of the journal *Molecular Psychiatry*.

In recent years, scientists have used genome-wide association studies to identify possible candidate genes responsible for diseases that include type 2 diabetes, lung cancer, Parkinson's disease, rheumatoid arthritis and systemic lupus erythematosus. However, the same approach was not as successful for the study of schizophrenia.

According to Chen, one of the many possible reasons is that many genes are involved in schizophrenia and the effect of each individual gene is relatively small. For this reason, he said, results obtained from individual samples tend to fluctuate.

Chen said that to obtain consistent results researchers need to consider the results from many independent samples. The team used that

approach in this study by first screening two genome-wide association datasets with statistic, genomic, informatic and genetic data and then ranking the top candidate. Chen said that the selected candidates were verified by more than 20 independent samples.

According to Chen, the work is one of the largest genetic studies of schizophrenia and included more than 33,000 participants that identify cardiomyopathy associated 5, or CMYA5, as a risk gene for schizophrenia. Its function is unknown at this time.

"While its implication for patient care is not clear at this moment, it is fair to say that our paper provides a new target for future research and a practical method to identify other potential risk genes. The findings are one of the most consistent findings in recent literature," said Chen.

Provided by Virginia Commonwealth University