MedicalXpress

New candidate genes for schizophrenia identified

October 21 2008

Schizophrenia is a severe psychiatric disease characterized by disorganized behavior, delusions and hallucinations. Sadly, there is no clear understanding of its cause.

Now, in a collaborative study, UCLA and Dutch researchers have identified three new candidate genes for schizophrenia that may contribute to a better understanding of how the disease evolves.

Reporting in the October issue of the *American Journal of Human Genetics*, Roel A. Ophoff, an assistant professor with the Center for Neurobehavioral Genetics at the Semel Institute for Neuroscience and Human Behavior at UCLA, and his colleagues examined the genetic makeup of 54 Dutch patients diagnosed with deficit schizophrenia, a particularly severe form of the disease that is both chronic and debilitating.

Specifically, they looked at a number of large but rare deletions and duplications in the genome of the patients, known as copy number variants, or CNVs. Scientists suspect that such missing or duplicated segments of DNA could be responsible for increased susceptibility to a number of diseases. In this study, the researchers showed that three of these rare CNVs interrupted genes associated with brain function.

"These genes were not implicated in schizophrenia before," said Ophoff, who holds a joint appointment at the University of Utrecht in the Netherlands. "So next, we tested these three genes in a large follow-up

study of more than 750 general-schizophrenia patients and 700 controls. And what surprised us is that roughly 1 percent of schizophrenia patients harbor these genomic deletions."

Changes in these three genes are rare but seem to dramatically increase the risk of developing schizophrenia, Ophoff said. The identification of these new candidate genes will provide a better insight into the underlying biology of schizophrenia and explain why some individuals are at risk to develop the disease.

"Another important step will be to assess the inheritance patterns of such CNVs," Ophoff said. "Since this is an inherited disease affecting approximately 1 percent of the population, this would be valuable toward establishing the clinical relevance of this important class of genomic variations."

Source: University of California - Los Angeles