NEWS

Genetics: New dataset confirms schizophrenia associations

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A new study uses data from more than 10,000 typical individuals to validate candidate regions implicated in schizophrenia. The results were published 5 November in *Schizophrenia Research*[1].

In the past few years, several studies have associated **copy number variations** (CNVs), which are duplications and deletions of chromosomal regions, with **schizophrenia** as well as **autism**. These analyses typically compare the frequency of CNVs in people who have the disorder and control populations.

Each CNV is present in no more than about one percent of individuals with schizophrenia, and is only two to ten times more prevalent in this group than in controls. Because of this, these studies must include large numbers of individuals to find statistically valid associations.

Large datasets that contain genomic information for relatively healthy individuals are scarce, however. As a result, most studies have analyzed a well-established Icelandic dataset, potentially limiting the findings to variants unique to that population.

In the new study, the researchers looked at the prevalence of several schizophrenia-associated CNVs in 10,259 individuals from the **Wellcome Trust Case Control Consortium** **in the U.K., whose genotypes have not been used in previous schizophrenia studies. Individuals in this group have any one of a number of disorders, including heart disease, Crohn's disease, rheumatoid arthritis and diabetes.**

The researchers excluded individuals diagnosed with bipolar disorder because genetic variants in these individuals are known to overlap with those seen in schizophrenia.

They compared the frequency of nine CNVs associated with schizophrenia in the published literature with their prevalence in the control group, and confirmed the association with the disorder for six of these CNVs: deletion of **1q21.1**, **3q29**, **15q11.2**, **15q13.1** and **22q11.2**, and duplication of **16p11.2**.

Deletions of **16p11.2** and **1q21.1** have also been associated with autism.

Associations between schizophrenia and the other three CNVs — duplication of 16p13.1, and deletion of **17p12** or 15q11.2 — do not appear to be statistically valid, according to the new data. In particular, the researchers found that the frequency of the 16p13.1 duplication in the dataset is the same as that previously reported for individuals with schizophrenia.

Looking at the associations between these CNVs and other disorders represented in the U.K. group, they found the highest rate in individuals with diabetes and the lowest in people with rheumatoid arthritis.

Studies have suggested that individuals with rheumatoid arthritis are **less likely than controls** to have children with schizophrenia. This may be because the same genetic variant helps protect against one disorder but increases the risk of developing the other, the researchers say.

References:

1: Grozeva D. *et al. Schizophr. Res.* Epub ahead of print (2011) **PubMed**