NEWS

Genetics: Rare mutations slightly more common in autism

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Duplications and deletions of genetic regions linked to autism are rare in individuals referred for genetic testing, but occur at a higher rate then in the general population, according to a study published in the September issue of *Genetics in Medicine*[1].

Over the past decade, researchers have identified several large **copy number variations** (CNVs) — deletions or duplications of genetic regions — that increase the likelihood of **developing autism** or other neurological disorders. Each CNV is present in only a fraction of individuals with the disorder, however, and not every individual who carries one of these CNVs develops autism.

For example, studies estimate that a deletion of the **16p11.2** region is present in **one percent of individuals with autism** and **leads to autism-like symptoms** in 30 percent of the carriers.

In the new study, researchers looked at the DNA of 15,749 individuals referred for genetic testing for developmental disability, intellectual disability, autism or other disorders. This very large data set allowed them to better hone in on the rate at which rare CNVs lead to disease.

Overall, the researchers found that 2,321 individuals, or 15 percent, have CNVs that are likely to have negative effects. A CNV is considered potentially harmful if it disrupts known genes and is inherited from affected family members.

This result is strikingly similar to a study of 15,767 children with developmental disabilities, which found that CNVs account for **14 percent of the disease burden** in the children.

The researchers also found that, of 1,412 CNVs for which they had genetic information from the parents, 566 are *de novo*, meaning they are not present in either parent. Of these, 513 are likely to be harmful, the researchers say.

The study also looked in detail at 14 recurrent CNVs, including the 16p11.2 and 22q11.2 autism-associated regions, and compared the data with those from 10,118 controls culled from recent publications.

Each of these 14 CNVs is rare in individuals with a diagnosis, but significantly more common in those individuals than in controls, the study found. For example, the 22q11.2 deletion is present in 93 cases and no controls, and the 16p11.2 deletion is present in 67 cases and 5 controls.

None of the CNVs are present in more than one percent of individuals with a diagnosis, confirming that CNVs, although important in autism, are generally rare.

References:

1: Kaminsky E.B. *et al. Genet. Med.* **13**, 777-784 (2011) **PubMed**