

TOOLBOX

Postmortem brains hold sequencing potential

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Researchers have extracted and sequenced **DNA from 52 postmortem brains** from the **Autism Tissue Program**, providing a resource to study mutations and gene expression differences in the brains of people with the disorder. The methods and initial results are outlined in the January issue of *Autism Research*.

Although most genetic information can be obtained from blood cells, gene expression changes specific to neurons can only be seen in brain tissue. The Autism Tissue Program is a repository of postmortem brains of individuals with autism and related disorders, as well as of controls.

Several studies have used postmortem brains to identify structural differences in the brains of people with autism, such as **the thickness of neurons** or **the presence of inflammation**. However, genetic information taken directly from neurons is another informative use of such a valuable and rare resource.

Copy number variations, or CNVs — duplications or deletions of DNA regions — are believed to be one of the **most common genetic causes of autism**. Postmortem tissue yields DNA that is of high enough quality to detect CNVs, according to the new study. This is only possible with frozen brains, however, and not those that are chemically preserved.

Researchers sequenced DNA from Brodmann area 19 — a brain region involved in visual processing — from 52 brains, including 27 from people who had autism. The autism brains contain 155 CNVs not present in controls according to one sequencing apparatus, and 166 according to another. The researchers also identified 31 unique large CNVs, of which 21 overlap with known autism-associated genes, including **NRXN1**.

The researchers used the Brodmann area for the trial study because it is not believed to be central to autism, preserving tissue from other brain regions for future work.

