

NEWS

Postmortem brain analysis points to autism candidate genes

BY EMILY SINGER

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An in-depth analysis of tissue from a large number of autism brains eases some of the qualms about their use in research, according to a poster presented Monday at the **2012 Society for Neuroscience annual meeting** in New Orleans.

Andrew West and his collaborators have analyzed postmortem brain tissue from 35 people with autism and 27 controls. They ultimately plan to analyze 200 samples, an order of magnitude larger than most postmortem autism studies, says West, assistant professor of neurology at the University of Alabama, Birmingham.

The researchers have also done extensive analysis of the quality of the brain tissue. They found that several of the factors that people worried would throw off gene expression data — such as the time elapsed between death and tissue collection or the method of collection — can be corrected for using novel statistical approaches.

They have so far identified up to 30 genes, as well as several sets of genes, whose expression patterns are significantly altered in autism brain tissue.

West declined to name his top candidates for autism risk because the data are unpublished. But he said that two genes the researchers plan to pursue code for proteins involved in a rate-limiting step of the production of certain chemical messengers in the brain. He cautions that the results are preliminary, however. "It's almost too good to be true," he says.

Postmortem brain tissue is both a highly valuable and potentially troublesome resource for studying autism. When and how the tissue is collected is thought to affect the quality of the samples and hence the outcome of the analysis.

The number of samples available for research is severely limited, on the order of 100 worldwide. West's analysis includes samples that were later lost in a high-profile **freezer malfunction** at Harvard University in May.

They found that even when the autism tissue is of poor quality, it shows typical gene expression patterns, as measured by a factor called expression quantitative trait loci or eQTLs. These are genetic variations that predict the expression of a certain gene.

The data that West and his colleagues have analyzed so far come from samples of the visual cortex, chosen primarily because there are many of these samples available. They also plan to analyze samples from the medial prefrontal cortex and the frontal cortex.

In addition to gene expression data, the researchers have measured methylation patterns, chemical markers that influence gene expression. Differences in both expression and methylation patterns for a particular gene would provide additional evidence that the gene is important in autism.

The researchers haven't yet analyzed the methylation data, however. Each gene in each sample involves 20 million reads and takes a day to analyze, says West. "We've had a supercomputer tied up for the last year."

This article has been modified from the original. An earlier version reported that the pilot study is an order of magnitude larger than most postmortem autism studies, but this will not be the case until the full study is completed.

Correction: For more reports from the 2012 Society for Neuroscience annual meeting, please [click here](#).