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Study characterizes epigenetic signatures of autism in brain tissue

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Neurons in the prefrontal cortex of individuals with autism show changes at numerous sites across the genome, according to a study being published Online First by the *Archives of General Psychiatry*.

Autism spectrum disorders are a group of complex illnesses with different causes and origins. Neuronal dysfunction in the cerebral cortex and other regions of the brain could contribute to the cognitive and behavioral defects in autism, according to background information in the article. Neurons are nerve cells that send and receive electrical signals within the body.

Hennady P. Shulha, Ph.D., of the University of Massachusetts Medical School, Worcester, Mass., and colleagues examined the postmortem brain tissue of 16 individuals diagnosed with autism spectrum disorder (average age 17.4 years; range 2 to 60 years) and 16 controls without autism (ranging in age from less than one year to 70 years). The tissue was obtained through the Autism Tissue Program.

The study searched, on a genome-wide scale, for genes that show an abnormal epigenetic signature – specifically histone methylation. Histones are small proteins attached to the DNA that control gene expression and activity. While genetic information is encoded by the (genome's) DNA sequence, methylation and other types of histone modifications regulate genome organization and gene expression.

The study found hundreds of loci (the places genes occupy on

chromosomes) across the genome affected by altered histone methylation in the brains of autistic individuals. However, only a small percentage – less than 10 percent – of the affected genes were affected by DNA mutations. It remains to be determined whether or not genetic changes elsewhere in the genome contributed to the observed epigenetic changes, or whether non-genetic factors were responsible for the disease process in some of the affected individuals.

"Prefrontal cortex neurons from subjects with autism show changes in chromatin (the substance of chromosomes) structures at hundreds of loci genome-wide, revealing considerable overlap between genetic and epigenetic risk maps of developmental brain disorders," the authors conclude.

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