# Autism Genes May be In All of US Researchers Say

**by Shaun Heasley, *Disability Scoop***
Genetic variants responsible for autism exist in varying degrees throughout the population – both in those on the spectrum and among typically-developing individuals – a new study suggests.

Both inherited and spontaneously-occurring genetic differences associated with autism may underlie a wide range of behavioral and developmental traits, with those who have the developmental disorder exhibiting the most severe presentations.

That's the result of a study published recently in the journal Nature Genetics. "There has been a lot of strong but indirect evidence that has suggested these findings," said Mark Daly of the Broad Institute of MIT and Harvard and a senior author of the study. "Once we had measurable genetic signals in hand – both polygenic risk and specific de novo mutations known to contribute to ASD – we were able to make an incontrovertible case that the genetic risk contributing to autism is genetic risk that exists in all of us, and influences our behavior and social communication."
For the study, researchers looked at data collected on more than 5,600 kids at age 8 through the Avon Longitudinal Study of Parents and Children, which has followed thousands of children born in 1991 and 1992 since pregnancy and their families. This information was compared to data collected through a handful of other studies that included over 13,000 children with autism and more than 16,000 controls.

"These data strongly suggest that genetic influences on ASD risk — both inherited and de novo — influence typical variation in the population," the researchers wrote in their findings.

The study may explain why some family members of those with autism share traits with those on the spectrum even if they don't carry a diagnosis. And, the researchers said their findings point to a new way to look at the genetic risk for neuropsychiatric disorders.

"Many traits that related to disease risk – like blood pressure or cholesterol levels – demonstrate a similar continuum of risk, with contributions from common and rare genetic variants, plus environmental and chance events. The present study demonstrates how this continuum applies to a condition generally thought of as either existing or not," said George Davey Smith of the University of Bristol in England, who is a coauthor of the study.