Researchers identify autism genes using new approach

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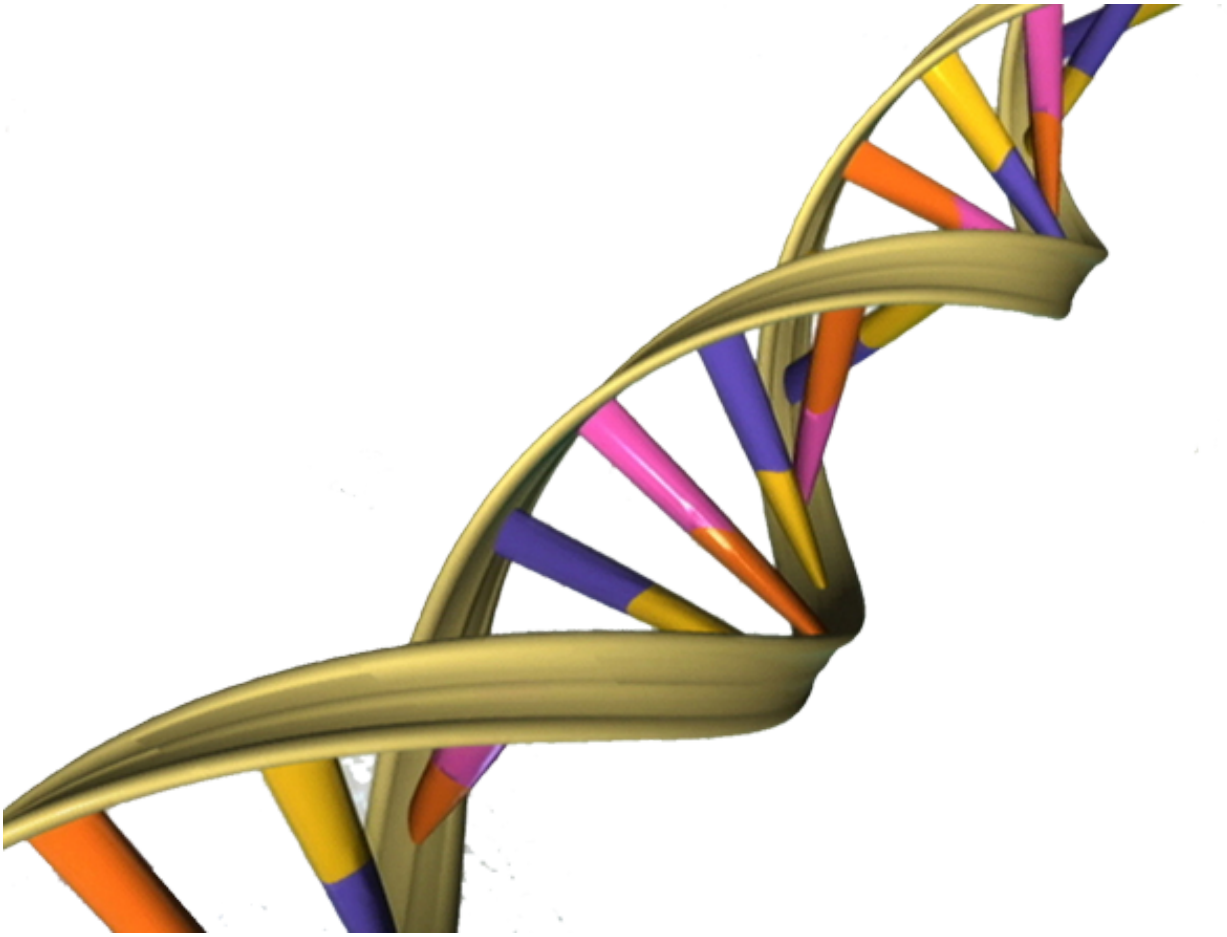

A depiction of the double helical structure of DNA. Its four coding units (A, T, C, G) are color-coded in pink, orange, purple and yellow. Credit: NHGRI

Princeton University and Simons Foundation researchers have developed a machine-learning approach that for the first time analyzes the entire human genome to predict which genes may cause autism spectrum disorder, raising the number of genes that could be linked to the disorder from 65 to 2,500.

The findings will appear in the journal *Nature Neuroscience*.

ASD is a complex neurodevelopment disorder with a strong genetic basis , but only about 65 autism genes out of an estimated 400 to 1,000 have been found through sequencing studies. Because of the how complex autism is, sequencing/genetics studies alone are severely underpowered to uncover the genetic basis of autism.

So, the Princeton-led team developed a complementary machine-learning approach using a functional map of the brain to provide a genome-wide prediction of autism risk genes, including hundreds of candidates for which there is minimal or no prior genetic evidence. The new approach was validated in a large independent case-control sequencing study. The researchers also built a user-friendly, interactive web portal (asd.princeton.edu), where any biomedical researcher or clinician can access and investigate the study's results.

"Our work is significant because geneticists can use our predictions to direct future sequencing studies, enabling much faster and cheaper discovery of autism genes," says lead author Arjun Krishnan, an associate research scholar at Princeton. "Researchers can use our predictions to prioritize and interpret results of whole-genome sequencing studies of ASD. Biomedical researchers can use these predictions and our analysis to put any gene in specific autism-associated functional, developmental and anatomical contexts. We provide a systematic prioritization of potential 'causal' genes within eight of the most frequent autism-linked large copy number variant intervals. We

find that perturbations caused by these intervals converge on specific pathways linking them to autism."

Senior author Olga Troyanskaya, a professor of computer science and genomics at Princeton, adds: "Our paper describes the first prediction of genes associated with autism spectrum disorder across the whole human genome. The method we developed can, for the first time, identify ASD-associated genes even if they have not been previously linked to autism. We achieve this by using a functional map of the brain (brain-specific gene network) generated by integrating thousands of genomic datasets."

More information: Genome-wide prediction and functional characterization of the genetic basis of autism spectrum disorder, DOI: 10.1038/nn.4353

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