

Scientists ID more than 1,200 genes linked to educational attainment

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An international research team including CU Boulder scientists has identified more than 1,200 genetic variants associated with how much schooling an individual completes and developed a "polygenic score" predictive of more than 11 percent of the variation in educational attainment between individuals.

With more than 1.1 million participants from 15 countries, the study, published today in the journal *Nature Genetics*, is among the largest human genetics studies to date.

The authors say the findings shed new light on the role genetics play in influencing complex human behaviors.

"It moves us in a clearer direction in understanding the genetic architecture of complex behavior traits like [educational attainment](#)," said co-first author Robbee Wedow, a graduate student in CU Boulder's Department of Sociology and researcher with the Institute for Behavioral Genetics.

For the quantitative meta-analysis, led by the Social Science Genetic Association Consortium, Wedow worked with dozens of researchers over two years to analyze genetic information and questionnaires assessing number of school years completed from participants age 30 and older of European descent.

The information was derived from 71 datasets, including very large datasets from the UK Biobank and the personal genomics company 23andMe.

A smaller, previous study had found that 74 gene variants, including many involved in brain development, were moderately predictive of educational attainment. By using a far larger sample size for the current study, researchers were able to identify 1,271 associated gene variants, including those involved with neuron-to-neuron communication and neurotransmitter secretion.

The researchers stressed that individual gene variants have little predictive value.

"It would be completely misleading to characterize our results as identifying [genes](#) for education," said corresponding author Daniel Benjamin, an associate professor at the Center for Economic and Social Research at University of Southern California.

Combined, the 1,271 variants explain about 4 percent of the variation in educational attainment across individuals.

But when scientists included the effects of all of the variants they measured across the genome to develop a new polygenic score, they found that the score was predictive of 11-13 percent of variation in years of completed schooling. That makes the score's predictive power for educational attainment equivalent to that of demographic factors, like household income or maternal education.

"That is a large effect for a polygenic score, especially for a behavioral outcome," said Wedow.

Wedow stresses that, while useful for research, the polygenic score is by no means deterministic.

"Having a low polygenic score absolutely does not mean that someone won't achieve a high level of education," he said, noting that ambition, family situation, socioeconomic status and other factors play a bigger role than genes. "As with many other outcomes, it is a complex interplay between environment and genetics that matters."

He notes that the meta-analysis looked only at participants of European descent. More research that includes individuals of diverse backgrounds is needed, and additional gene variants associated with academic achievement will inevitably be discovered, he said.

But the findings are useful for social and medical scientists who can now

use them to explore how the effects of genetic variants vary across different environmental conditions and to paint a clearer picture of the interplay between genetics and the environment in shaping educational attainment and related outcomes.

"The most exciting part of this study is the polygenic score. Its level of predictive power for a behavioral outcome is truly remarkable," said Wedow.

More information: Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals, *Nature Genetics* (2018). [DOI: 10.1038/s41588-018-0147-3](https://doi.org/10.1038/s41588-018-0147-3)

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