Reaching new heights in largest ever genome study

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Children's growth will be easier to assess following a University of Queensland-led study analyzing the genetic variants that influence height.

Dr. Loic Yengo and Professor Peter Visscher from UQ's Institute for Molecular Bioscience have worked with 600 researchers in the largest-ever genome-wide association study (GWAS).

The study analyzed data from 5.4 million people and uncovered 12,000 genetic variants influencing height.

"Eighty percent of height differences between people are determined by genetic factors," Dr. Yengo said.

"The 12,000 variants that we found explain 40 percent of height differences, meaning we've opened the door for DNA to be used to predict height more accurately than ever before.

"Currently, a child's height is best predicted using the average height of their two biological parents, but using this genomic data, pediatricians will be able to get a better estimate.

"It will put parents' minds at ease if children are growing as their genes predict, or it will trigger further medical investigation and help pick up potential issues sooner."

The findings could also be used in police investigations to predict height from a suspect's DNA sample at a crime scene.

"In smaller studies, findings appeared scattered in the genome but the huge sample size in this study means that, for the first time, we have seen height-associated variants cluster, particularly near genes involved in skeletal growth disorders," Dr. Yengo said.

Dr. Yengo said the study included more than one million people of non-European descent which was higher than usual for a GWAS study.

"While this is an achievement, the data is still skewed to people of European ancestry, a known problem in genetic studies," he said.

"There is a growing number of worldwide initiatives to collect more diverse genetic data because it is critical to widen the benefit of genetic studies to all populations."

The team now plans to dive deeper to identify the remaining genetic factors for height.

"These other factors will be harder to find as they each have a lesser effect and we may need at least 20 million samples to complete that herculean task," Dr. Yengo said.

The height study also paves the way for research into other traits and diseases controlled by genes.

The study was carried out in collaboration with Professor Joel Hirschhorn from Boston Children's Hospital and Harvard Medical School; Dr. Andrew Wood from University of Exeter; Professor Yukinori Okada from Osaka University Graduate School of Medicine and other researchers in the GIANT consortium.

This study is published in *Nature*.

  More information: Loïc Yengo, A saturated map of common genetic variants associated with human height, *Nature* (2022). DOI: 10.1038/s41586-022-05275-y.
www.nature.com/articles/s41586-022-05275-y

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