Ethnic diversity helps identify more genomic regions linked to diabetes-related traits

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By including multi-ethnic participants, a largescale genetic study has identified more regions of the genome linked to type 2 diabetes-related traits than if the research had been conducted in Europeans alone.

The international MAGIC collaboration, made up of more than 400 global academics, conducted a genome-wide association meta-analysis led by the University of Exeter. Now published in *Nature Genetics*, their findings demonstrate that expanding research into different ancestries yields more and better results, as well as ultimately benefitting global patient care.

Up to now, nearly 87 percent of genomic research of this type has been conducted in Europeans. This means that the way these findings are implemented may not optimally benefit people from non-European ancestries.

The team analysed data across a wide range of cohorts, encompassing more than 280,000 people without diabetes. Researchers looked at glycaemic traits, which are used to diagnose diabetes and monitor sugar and insulin levels in the blood.

The researchers incorporated 30 percent of the overall cohort with individuals of East Asian, Hispanic, African-American, South Asian and sub-Saharan African origin. By doing so, they discovered 24 more loci—or regions of the genome -linked to glycaemic traits than if they had conducted the research in Europeans alone.

Professor Inês Barroso, of the University of Exeter, who led the research, said: "Type 2 diabetes is an increasingly huge global health challenge- with most of the biggest increases occurring outside of Europe. While there are a lot of shared genetic factors between different countries and cultures, our research tells us that they do differ, in ways that we need to understand. It's critical to ensuring we can deliver a precision diabetes medicine approach that optimises treatment and care for everyone."

First author Dr. Ji Chen, of the University of Exeter, said: "We discovered 24 additional regions of the genome by including cohorts which were more ethnically diverse than we would have done if we'd restricted our work to Europeans. Beyond the moral arguments for ensuring research is reflective of global populations, our work demonstrates that this approach generates better results."

The team found that though some loci were not detected in all ancestries, they were still useful to capture information about the glycaemic trait in that ancestry. Co-author Cassandra Spracklen, Assistant Professor at the University of Massachusetts-Amherst, said: "Our findings matter because we're moving towards using genetic scores to weigh up a person's risk of diabetes. We

know that scores developed exclusively in individuals of one ancestry don't work well in people of a different ancestry. This is important as increasingly healthcare is moving towards a more precise approach. Failing to account for genetic variation according to ancestry will impact our ability to accurately diagnose diabetes."

The study is entitled "The Trans-Ancestral Genomic Architecture of Glycemic Traits," and is published in *Nature Genetics*.

More information: The trans-ancestral genomic architecture of glycemic traits, *Nature Genetics* (2021). DOI: 10.1038/s41588-021-00852-9 , www.nature.com/articles/s41588-021-00852-9

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