

# Researchers identify over 2,000 genetic signals linked to blood pressure in study of over 1 million people

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Credit: Pavel Danilyuk from Pexels

Researchers led by Queen Mary University of London have discovered over a hundred new regions of the human genome, also known as

genomic loci, that appear to influence a person's blood pressure. In total, over 2,000 independent genetic signals for blood pressure are now reported, demonstrating that blood pressure is a highly complex trait influenced by thousands of different genetic variants.

The study, published in *Nature Genetics*, is one of the largest such genomic studies of blood pressure to date, including data from over 1 million individuals and laying the groundwork for researchers to better understand how blood pressure is regulated.

To understand the genetics of blood pressure, the researchers combined four [large datasets](#) from [genome-wide association studies](#) (GWAS) of blood pressure and hypertension. After analyzing the data, they found over 2,000 genomic loci linked to blood pressure, including 113 new regions.

The analyses also implicated hundreds of previously unreported genes that affect blood pressure. Such insights could point to potential new drug targets, and help to advance precision medicine in the early detection and prevention of hypertension ([high blood pressure](#)).

From these analyses, the researchers were able to calculate polygenic risk scores, which combine the effects of all genetic variants together to predict blood pressure and risk for hypertension. For example, these risk scores show that individuals with highest genetic risk have mean systolic blood pressure levels which are ~17 mmHg higher than those with lowest genetic risk, and a 7-fold increased risk of hypertension. Therefore, these polygenic risk scores can discriminate between patients according to their hypertension risk, and reveal clinically meaningful differences in blood pressure.

"We have now revealed a much larger proportion of the genetic contribution of blood pressure than was previously known," says Helen

Warren, Senior Lecturer in Statistical Genetics at Queen Mary University of London and senior last author of the study.

"We are making our polygenic risk scores data publicly available. There are many different potential applications of genetic risk scores, so it will be exciting to see how our blood pressure scores can be used to address more clinically relevant questions in the future."

"This large study builds on over 18 years of blood pressure GWAS research. Our results provide new resources for understanding biological mechanisms and importantly new polygenic risk scores for early identification and stratification of people at risk for cardiovascular diseases," says Patricia Munroe, Professor of Molecular Medicine at Queen Mary University of London, also a senior author of the paper.

Polygenic risk scores have potential to serve as a useful tool in precision medicine, but more diverse genomic data is needed for them to be applicable broadly in routine health care. While the collected data was mostly from people of European ancestry (due to limited availability of diverse datasets when the study was started), the researchers found that the polygenic risk scores were also applicable to people of African ancestry, who have previously been underrepresented in genetic studies.

This African ancestry result was confirmed through analyzing data from the National Institute of Health's (NIH) "All of Us" Research Program in the U.S., which aims to build one of the largest biomedical data resources and accelerate research to improve human health.

An estimated 30% of adults in the UK have high blood pressure, known as hypertension. High blood pressure often runs in families, meaning that there is a [genetic component](#) to developing the condition in addition to environmental contributions such as a high-salt diet, lack of exercise, smoking and stress.

When blood pressure is consistently too high, it can damage the heart and blood vessels throughout the body, increasing a person's risk for heart disease, kidney disease, stroke and other conditions.

The study combined previously published genetic data from the UK Biobank, a large-scale biomedical database and research resource containing genetic and health information from half a million UK participants (N~450,000 individuals); the International Consortium for Blood Pressure (N~300,000 individuals combined from 77 different cohort studies); and the U.S. Department of Veterans Affairs' Million Veteran Program (N~220,000 individuals), with new data from Vanderbilt University Medical Center's biorepository, BioVU (N~50,000 individuals).

**More information:** Genome-wide analysis in over 1 million individuals of European ancestry yields improved polygenic risk scores for blood pressure traits, *Nature Genetics* (2024). [DOI: 10.1038/s41588-024-01714-w](https://doi.org/10.1038/s41588-024-01714-w)

Provided by Queen Mary, University of London

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