

Largest-ever study into varicose veins shows need for surgery is linked to genetics

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Credit: AI-generated image ([disclaimer](#))

A new international study by Oxford researchers published in *Nature Communications*, establishes for the first time a critical genetic risk score to predict the likelihood of patients suffering with varicose veins to require surgery, as well as pointing the way toward potential new therapies.

Varicose veins are a very common manifestation of chronic venous disease, affecting over 30% of the population in Western countries. In America, chronic venous disease affects over 11 million men and 22 million women aged 40–80 years old. Left untreated it can escalate to multiple [health complications](#) including leg ulcers and ultimately amputations.

In a vast two-stage genome-wide association study of [varicose veins](#) in 401,656 individuals from UK Biobank, and replication in 408,969 individuals from 23andMe, Oxford researchers identified 49 genetic variants that increase the risk of varicose veins. They highlighted pathways including problems with the connective tissues of the body, and the [immune system](#) as key players in varicose vein pathology.

This study was an interdisciplinary collaborative effort across the Medical Sciences Division at the University of Oxford. Researchers from the Nuffield Department of Orthopedics, Rheumatology and Musculoskeletal Sciences (NDORMS), the Nuffield Department of Surgical Sciences (NDS) and the Nuffield Department of Women's & Reproductive Health worked with an American commercial, direct to consumer genotyping company called 23andMe to explore which people were more susceptible to developing varicose veins.

Lead author Dominic Furniss, Professor of Plastic and Reconstructive Surgery at NDORMS commented: "The inclusion of surgeons in the research team was vital as they enabled the identification of patients whose disease was more severe, and they had therefore had surgery. This led to the discovery of 49 genetic variants at 46 areas into the genome that predisposes to varicose veins. This breakthrough greatly improves our team's knowledge of the biology of varicose veins, and it will be the foundation of further research into the biology and potentially new treatment."

Co-author Prof Krina Zondervan Head of Department at the Nuffield Department of Women's & Reproductive Health said: "This large study brings together a great deal of new evidence of the genetics underlying varicose veins, a condition that is highly prevalent in women and in pregnancy. It opens up exciting new avenues for the development of new future treatments."

"Genome-wide association analysis and replication in 810,625 individuals with varicose veins" is published in *Nature Communications*.

More information: Waheed-Ul-Rahman Ahmed et al, Genome-wide association analysis and replication in 810,625 individuals with varicose veins, *Nature Communications* (2022). [DOI: 10.1038/s41467-022-30765-y](https://doi.org/10.1038/s41467-022-30765-y)

Provided by University of Oxford

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