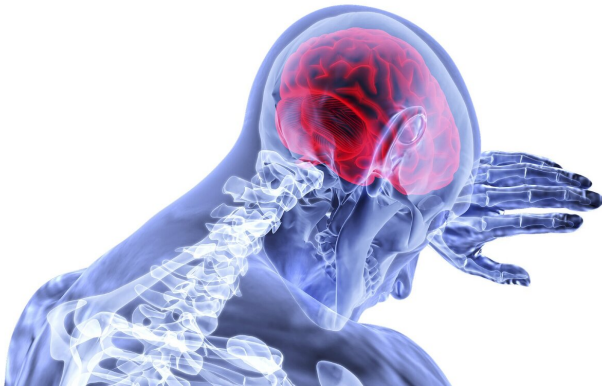


# One-off genetic score can detect stroke risk from birth

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A group of investigators from Australia, Germany, and the UK have shown that genetic data obtained from a single blood draw or saliva sample can be used to identify individuals at a 3-fold increased risk of developing ischaemic stroke, a devastating condition and one of the leading causes of disability and death world-wide. The scientists developed a genetic risk score that is similarly or more predictive than commonly known risk factors for stroke. Their work further suggests that individuals with high genetic risk may require more intensive preventive measures to mitigate stroke risk than is recommended by current guidelines.

Genomic risk prediction, based on an individual's unique DNA sequence, has distinct advantages over established [risk factors](#) as it could be used to infer risk of disease from birth. It may thus allow initiation of preventive strategies before individuals develop conventional risk factors for stroke such as hypertension or hyperlipidemia, said Martin Dichgans, Professor of Neurology and Director at the Institute for Stroke and Dementia Research (ISD), University Hospital, Ludwig-Maximilians-University (LMU) Munich, and one of the leaders of the current study.

The results of this study were published online in the journal, *Nature Communications*. The study utilised large-scale genetic data from research groups worldwide and applied their results to data on 420,000 individuals from the UK Biobank.

The study was led by investigators from the Baker Heart and Diabetes Institute (Australia), University of Cambridge (UK), and Ludwig-Maximilians-University, Munich (Germany).

"The sequencing of the human genome has revealed many insights. For common diseases, such as stroke, it is clear that genetics is not destiny; however, each person does have their own innate risk for any particular disease. The challenge is now how we best incorporate this risk information into [clinical practice](#) so that the public can live healthier and longer." said Dr. Michael Inouye, of the Baker Heart and Diabetes Institute and University of Cambridge, and another leader of the current study.

Stroke is the second most common cause of both death and disability-adjusted life-years worldwide. About 80% of stroke cases are caused by occlusion of a brain supplying artery (so-called 'ischaemic stroke'). The risk of ischaemic stroke is determined by genetic and environmental factors, which act through modifiable risk factors such as hypertension and diabetes.

In the study, the researchers employed a machine learning approach to integrate stroke-related [genetic data](#) from various sources into a single genetic risk score for each individual. They then assessed the performance of this new genetic risk score in the UK Biobank and found that it both outperformed previous genetic scores and had similar predictive performance as other well-known risk factors for stroke, such as smoking status or body mass index.

Importantly, the new genetic risk score was

significantly better than [family history](#) at predicting future ischaemic stroke, to the extent that it could detect the roughly 1 in 400 individuals at 3-fold increased risk.

Individuals at high genetic risk of ischaemic stroke are not without options however, and the researchers further showed that these individuals may still substantially reduce their [stroke risk](#) by minimizing their conventional risk factors. These include lowering blood pressure and body mass index, as well as ceasing smoking.

The study's analyses show that current clinical guidelines may be insufficient for individuals at high genetic risk of stroke, and that these individuals may need more intensive interventions.

With non-invasive, affordable DNA genotyping array technology together with a new genetic risk score for ischaemic [stroke](#), the future looks bright for genomic medicine to enable effective early interventions for those at high risk of strokes and, indeed, other cardiovascular diseases.

**More information:** *Nature Communications* (2019). [DOI: 10.1038/s41467-019-13848-1](https://doi.org/10.1038/s41467-019-13848-1)

Provided by Baker Heart and Diabetes Institute

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