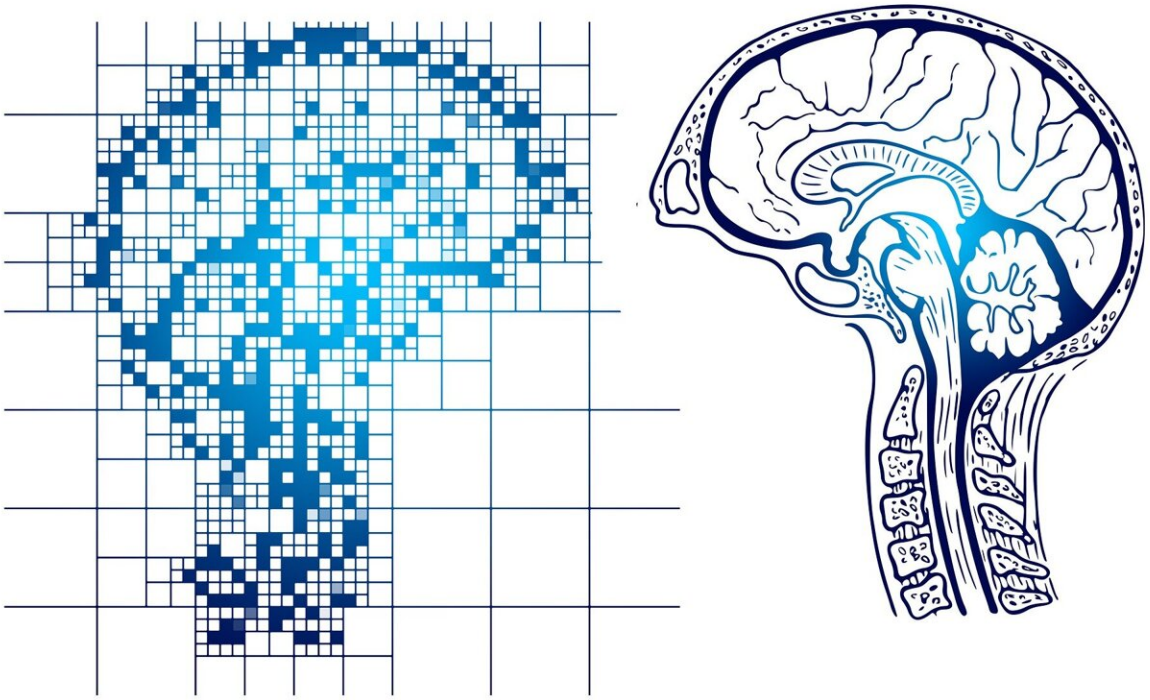
Researchers develop algorithm to help predict Alzheimer's risk in various ethnic populations

July 20 2023



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Using data from diverse populations around the world, researchers from Children's Hospital of Philadelphia (CHOP) have developed an

algorithm to help predict the risk of developing Alzheimer's disease based on genetic information in patients with a wide variety of ethnic backgrounds.

While additional ethnicities should be included in future studies, this work aims to eliminate disparities in diagnosis of the disease. The findings were published online in the journal *Alzheimer's & Dementia*.

Alzheimer's disease affects approximately one in 10 patients aged 65 or older, according to the U.S. Centers for Disease Control. An early diagnosis may enable early intervention to minimize the damage to the central nervous system. Multiple gene variants have been associated with the disease, and some of these variants appear in patients of different ancestry.

Researchers had previously developed genomic informed risk assessment (GIRA) algorithms using known genomic information about Alzheimer's disease. However, studies using GIRA to identify genetic variants associated with the disease have largely been carried out in white patients of European ancestry. Using an international cohort of patient data, researchers wanted to develop a GIRA algorithm that was representative of a wide variety of ancestries to eliminate potential discrepancies and biases in how the tool is used to help patients.

"Using data from the International HundredK+ Cohorts Consortium (IHCC), we were able to examine the effectiveness of our GIRA algorithm in under-represented populations," said study author Hui-Qi Qu, Ph.D., a bioinformatics scientist in the Center for Applied Genomics (CAG) at CHOP. "We were able to demonstrate the feasibility of developing a GIRA algorithm for Alzheimer's disease that predicts disease predisposition across diverse populations around the globe."

The researchers developed their GIRA algorithm to assess Alzheimer's risk based on variants of the apolipoprotein E (APOE) gene—which has been implicated in Alzheimer's risk—as well as polygenic risk scores by other genomic markers and other variables including age, sex and ethnicity.

Using this GIRA algorithm, which was tested in different ethnic populations, the researchers were able to identify certain proteins related to female infertility and autoimmune thyroiditis as contributors to the risk of developing Alzheimer's disease. The GIRA model performed better than polygenic risk scores alone in East Asian populations from Japan and Korea and in South Asian populations of Pakistani and Bangladeshi origin.

The study lacked a well-phenotyped Alzheimer's disease cohort of African origin, but the current polygenic risk score system was additionally validated in people from different regions of Africa. The authors also worked with the Davos Alzheimer Collaborative (DAC) and hope to recruit more people of African ancestry to the cohort to further study their Alzheimer's risk.

"The IHCC cohorts represent an incredibly rich resource for collaborative research with a trans-ethnic focus that will help alleviate largely neglected populations and their unique health needs," said senior study author Hakon Hakonarson, MD, Ph.D., director of the CAG center at CHOP and co-leader of the scientific and cohort enhancement strategy for IHCC.

"We believe with more validation and efforts from additional diversity cohorts, this model could be applied to a range of diseases to improve health care services for patients who may have been underrepresented in clinical research."

More information: Patrick M. Sleiman et al, Trans-ethnic genomic informed risk assessment for Alzheimer's disease: An International Hundred K+ Cohorts Consortium study, *Alzheimer's & Dementia* (2023). DOI: 10.1002/alz.13378