

New Alzheimer risk gene discovered

November 21 2019



Credit: CC0 Public Domain

A new paper in the *Journal of Neuropathology & Experimental Neurology* finds a gene that may help explain a large part of the genetic risk for developing Alzheimer disease.

Late-onset Alzheimer disease, the most common form of the illness, is a devastating neurological condition with aspects of heritable risk that are

incompletely understood. Unfortunately, the complexity of the human genome and shortcomings of earlier research are limiting factors, so that some genetic phenomena were not surveyed completely in prior studies. For example, there are many incompletely mapped genomic regions, and areas with repetitive sequences, that could not be studied previously.

Although Alzheimer's is known to be largely heritable, a substantial proportion of the actual genetic risk for the disease has remained unexplained, despite extensive studies. This knowledge gap is known to researchers as the "missing (or hidden) heritability" problem. For example, while heritability explained 79% of late-onset Alzheimer disease risk in a Swedish twin study, common risk variants identified by previous genetic studies explained only 20% to 50% of late-onset Alzheimer disease. In other words, a relatively large amount of genetic influence on late-onset Alzheimer disease risk was not explained by prior genetic studies.

Recent advances in sequencing technologies have enabled more comprehensive studies. Such developments allow for more precise and accurate identification of genetic material than was available in earlier gene variant studies.

In the present study, researchers analyzed Alzheimer's Disease Sequencing Project data derived from over 10,000 people (research volunteers who agreed to have their [genetic data](#) evaluated in combination with their disease status), with the goal of identifying genetic variation associated with late-onset Alzheimer disease.

Preliminary results found evidence of late-onset Alzheimer disease -linked genetic variation within a segment of a gene called Mucin 6. Although the underlying mechanisms are mostly still unknown, researchers here believe that it's possible to draw credible and testable hypotheses based on these results. For example, the genetic variant that

was associated with Alzheimer's disease risk may implicate a biochemical pathway in the brain that then represents a potential therapeutic target, a topic for future studies.

Corresponding authors were Yuriko Katsumata and Peter Nelson, both from the University of Kentucky. Dr. Nelson said of this study, "Our findings were made in a group of patients that is relatively small for a genetics study—some recent studies included hundreds of thousands of research subjects! That [small sample size](#) means two things: first, we should exercise caution and we need to make sure the phenomenon can be replicated in other groups; and second, it implies that there is a very large effect size—the [genetic variation](#) is strongly associated with the disease."

More information: Yuriko Katsumata et al, Alzheimer Disease Pathology-Associated Polymorphism in a Complex Variable Number of Tandem Repeat Region Within the MUC6 Gene, Near the AP2A2 Gene, *Journal of Neuropathology & Experimental Neurology* (2019). [DOI: 10.1093/jnen/nlz116](#)

Provided by Oxford University Press

Citation: New Alzheimer risk gene discovered (2019, November 21) retrieved 25 April 2024 from <https://medicalxpress.com/news/2019-11-alzheimer-gene.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.