

Resilience to Alzheimer's disease (Dumitrescu, 2020)

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Brain

Brain Dementia

STUDY SUMMARY

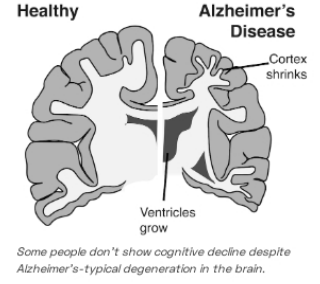
Identification of multiple regions of the genome associated with resilience to Alzheimer's disease.

YOUR RESULT



STUDY DESCRIPTION

Alzheimer's disease is a form of dementia in which brain cells degenerate and die. The condition develops gradually, and over time affects memory, mood, thinking, and behavior. Alzheimer's disease is quite common in seniors, potentially affecting up to half of those older than 85. However, while many people are affected by the degeneration of brain cells, not everyone develops cognitive impairments. These individuals are considered to have "asymptomatic" Alzheimer's disease and little is known about the degree to which genetics influences whether an individual will be asymptomatic or show cognitive decline. This study examined the genomes of over 5,000 individuals to identify variants associated with resilience to developing symptoms of Alzheimer's disease in the presence of degeneration in the brain. Researchers found multiple genomic regions that are potentially linked to resilience to Alzheimer's disease. One region (tagged by the variant rs2571244) that showed a particularly strong association, harbors the gene known as ATP8B1. This gene plays a role in the transport of fat molecules inside cells, a function particularly important for the cells of the brain.



DID YOU KNOW?

Increased education appears to correlate with a decreased risk of developing Alzheimer's disease. Activities such as learning new languages and playing musical instruments can help keep your brain young!

YOUR DETAILED RESULTS

To calculate your genetic predisposition to resilience to Alzheimer's disease we summed up the effects of genetic variants that were linked to resilience to Alzheimer's disease in the [study that this report is based on](#). These variants can be found in the table below. The variants highlighted in green have **positive effect sizes** and increase your genetic predisposition to resilience to Alzheimer's disease. The variants highlighted in blue have **negative effect sizes** and decrease your genetic predisposition to resilience to Alzheimer's disease. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to resilience to Alzheimer's disease. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for resilience to Alzheimer's disease to be -0.16**. To determine whether your score is high or low, we compared it to the scores of 5,000 other Nebula Genomics users. We found that your polygenic score for resilience to Alzheimer's disease is in the **12th percentile**. This means that it is higher than the polygenic scores 12% of people. We consider this to be a **below average genetic predisposition to resilience to Alzheimer's disease**. However, please note that genetic predispositions do not account for important non-genetic factors like lifestyle. Furthermore, the genetics of most traits has not been fully understood yet and many associations between traits and genetic variants remain unknown. For additional explanations, click on the column titles in the table below and visit our [Nebula Library tutorial](#).

VARIANT [Ⓞ]	YOUR GENOTYPE [Ⓞ]	EFFECT SIZE [Ⓞ]	VARIANT FREQUENCY [Ⓞ]	SIGNIFICANCE [Ⓞ]
rs2571244_T NEW	C / C	-0.11 (-)	8%	2.26×10^{-8}
rs12580507_T NEW	C / C	-0.07 (-)	23%	5.64×10^{-7}
rs12127073_G NEW	C / C	0.08 (-)	11%	1.01×10^{-6}
rs1840_T NEW	C / C	0.08 (-)	14%	1.58×10^{-6}
rs7015592_A NEW	A / C	-0.05 (↓)	48%	1.95×10^{-6}
rs12623748_T NEW	NA	0.13 (-)	4%	3.19×10^{-6}
rs982563_C NEW	T / T	-0.06 (-)	23%	6.67×10^{-6}
rs283562_G NEW	T / T	0.05 (-)	44%	6.95×10^{-6}
rs9811609_A NEW	G / G	0.05 (-)	49%	7.56×10^{-6}
rs3846121_C NEW	A / A	0.06 (-)	22%	7.80×10^{-6}
rs1447462_G NEW	A / A	-0.10 (-)	7%	7.85×10^{-6}
rs11074247_T NEW	T / T	-0.05 (↓)	33%	7.88×10^{-6}
rs11605469_T NEW	C / C	-0.10 (-)	6%	9.42×10^{-6}

N/A indicates variants that could not be imputed using the 1000 genomes project datasets and variants that have a frequency of < 5%. Your genome was sequenced at 30x/100x coverage and is not imputed. However, to calculate percentiles, we need to compare your data with other users imputed data. To make the data comparable, we need to exclude some of the variants from your data.