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Alzheimer's disease (Kunkle, 2019)

Brian Kunkle, et al.
Nature Genetics

Brain Dementia

STUDY SUMMARY

Identification of 5 novel genetic loci correlated to a person's risk of developing late-onset Alzheimer's disease.

YOUR RESULT

STUDY DESCRIPTION

Alzheimer's disease is a common cause of dementia, characterized by the degeneration of brain cells. Late-onset Alzheimer's is the most typical form of Alzheimer's disease and typically results in the progressive impairment of cognitive abilities. Heredity is known to have a component in determining a person's risk of developing Alzheimer's disease. By examining the genetic information of nearly 95,000 participants of European descent, this study identified 5 new variants that appear to correlate with an individual's risk of developing late-onset Alzheimer's disease. Some of these variants are located near genes that may affect the accumulation of proteins that disrupt brain function. Other variants are in proximity of genes that are thought to be involved in the functioning of the immune system. Collectively, these variants explain an estimated 7% of the heritability for late-onset Alzheimer's disease.

DID YOU KNOW?

Chronic stress can harm areas of the brain related to memory, and increase a person's risk of Alzheimer's disease. Relaxing activities such as breathing exercises, mediation, and yoga can help manage stress.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to Alzheimer's disease we summed up the effects of genetic variants that were linked 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 Alzheimer's disease. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to Alzheimer's disease. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to Alzheimer's disease. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for Alzheimer's disease to be -0.53**. 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 Alzheimer's disease is in the **6th percentile**. This means that it is higher than the polygenic scores 6% of people. We consider this to be a **low genetic predisposition 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
rs429358_C	T / T	1.20 (-)	22%	1.20×10^{-881}
rs6733839_T	C / C	0.18 (-)	41%	2.10×10^{-44}
rs3851179_T	T / C	-0.13 (↓)	36%	6.00×10^{-25}
rs4844610_A	C / C	0.16 (-)	19%	3.60×10^{-24}
rs9331896_C	C / C	-0.13 (↓)	39%	4.60×10^{-24}
rs7933202_C	C / C	-0.12 (↓)	39%	1.90×10^{-19}
rs3752246_G	G / C	0.14 (↑)	18%	3.10×10^{-16}
rs75932628_T	NA	0.73 (-)	1%	2.70×10^{-15}
rs73223431_T	C / C	0.10 (-)	37%	6.30×10^{-14}
rs3740688_G	G / T	-0.08 (↓)	45%	5.40×10^{-13}
rs11218343_C	NA	-0.22 (-)	4%	2.90×10^{-12}
rs9271058_A	A / T	0.10 (↑)	27%	1.40×10^{-11}
rs7920721_G NEW	A / A	0.08 (-)	39%	1.80×10^{-11}
rs9473117_C	A / C	0.09 (↑)	28%	1.20×10^{-10}
rs10808026_A	C / C	-0.11 (-)	20%	1.30×10^{-10}
rs12539172_T	T / C	-0.08 (↓)	30%	9.30×10^{-10}
rs17125924_G	A / A	0.13 (-)	9%	1.40×10^{-9}
rs10933431_G	C / C	-0.09 (-)	22%	3.40×10^{-9}
rs138190086_A NEW	NA	0.26 (-)	2%	5.30×10^{-9}
rs593742_G NEW	A / G	-0.07 (↓)	30%	6.80×10^{-9}
rs12881735_C	T / T	-0.08 (-)	22%	7.40×10^{-9}
rs7185636_C NEW	T / T	-0.08 (-)	18%	2.40×10^{-8}
rs2830500_A NEW	C / C	-0.07 (-)	31%	2.60×10^{-8}
rs6024870_A	G / G	-0.13 (-)	9%	3.50×10^{-8}

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.