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Alzheimer's disease (Wightman, 2021)

Douglas Wightman, et al.
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Brain | Aging | Dementia

An individual's risk of developing Alzheimer's increases with age.

STUDY SUMMARY

This report is based on a study that discovered 7 novel genetic variants associated with predisposition to Alzheimer's disease.

YOUR RESULT

STUDY DESCRIPTION

The brain is made up of billions of nerve cells that work to connect and communicate to one another. In Alzheimer's disease, these connections are progressively lost and can seriously affect a person's ability to carry out daily activities. Alzheimer's disease usually begins after the age of 60, and the risk of developing the condition goes up as an individual gets older. Though age is associated with Alzheimer's disease, genetics also contribute to an individual's predisposition to the condition. In order to better understand the likelihood of developing Alzheimer's disease related to the genome, scientists studied the genomes of over 1.1 million individuals of European ancestry. This study identified 7 genetic variants associated with Alzheimer's disease that have not previously been connected to the condition. These variants are found near genes such as TNIP1 and HAVCR2, which are both involved in inflammation, which contributes to the destruction of brain tissue in Alzheimer's disease.

DID YOU KNOW?

As the population of the United States ages, Alzheimer's is becoming a more common cause of death. Although deaths from many other major causes have decreased significantly, official records indicate that deaths from Alzheimer's disease have risen.

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 0.44**. 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 **62nd percentile**. This means that it is higher than the polygenic scores 62% of people. We consider this to be an **above average 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	GENE	EFFECT SIZE	VARIANT FREQUENCY	SIGNIFICANCE
rs429358_T	T / T	APOE	-0.32 (↓)	84%	1.00×10^{-300}
rs4663105_C	A / A	BIN1	-0.14 (–)	41%	3.92×10^{-68}
rs1582763_G	A / A	MS4A4A	-0.13 (–)	62%	3.40×10^{-33}
rs561655_G	G / A	PICALM	0.10 (↑)	35%	1.24×10^{-26}
rs187370608_G	G / G	TREM2	0.93 (↑)	> 99%	1.26×10^{-25}
rs679515_C	C / C	CR1	-0.15 (↓)	82%	2.42×10^{-26}
rs1532278_T	T / T	CLU	0.09 (↑)	39%	1.57×10^{-22}
rs9369716_T	A / T	CD2AP	-0.14 (↓)	27%	1.70×10^{-17}
rs12590654_G	G / G	RIN3	-0.07 (↓)	67%	6.63×10^{-17}
rs6069737_T	C / C	CASS4	-0.14 (–)	8%	6.73×10^{-16}
rs7384878_T	C / T	ZCWPW1/NYAP1	-0.09 (↓)	69%	9.41×10^{-16}
rs12151021_G	A / G	ABCA7	0.09 (↑)	68%	2.81×10^{-15}
rs602602_T	T / A	ADAM10	-0.11 (↓)	70%	6.22×10^{-15}
rs7912495_G	A / A	USP6NL/ECHDC3	-0.10 (–)	46%	7.68×10^{-15}
rs1846190_A	G / G	HLA-DRB1	-0.11 (–)	30%	2.66×10^{-14}
rs11218343_T	T / T	SORL1	-0.19 (↓)	96%	1.33×10^{-13}
rs4504245_G	G / G	CLNK	0.05 (↑)	79%	5.23×10^{-12}
rs117618017_T	C / C	APH1B	0.11 (–)	13%	7.00×10^{-12}
rs3935067_G	G / C	EPHA1-AS1	0.05 (↑)	62%	4.69×10^{-11}
rs7146179_G	G / G	FERMT2	0.11 (↑)	89%	6.99×10^{-11}
rs1354106_G	G / G	CD33	-0.06 (↓)	37%	2.21×10^{-10}
rs28394864_G	G / G	ABI3	0.04 (↑)	54%	4.90×10^{-10}
rs2632516_G	G / G	TSPOAP1-AS1	-0.10 (↓)	54%	7.46×10^{-10}
rs2154482_T	T / T	APP	-0.08 (↓)	44%	7.66×10^{-10}
rs6891966_G NEW	A / G	HAVCR2	-0.10 (↓)	77%	7.91×10^{-10}
rs6504163_T	T / T	ACE	-0.06 (↓)	61%	1.23×10^{-9}
rs871269_T NEW	T / T	TNIP1	-0.07 (↓)	32%	1.37×10^{-9}
rs1761461_C NEW	C / A	LILRB2	-0.11 (↓)	49%	1.56×10^{-9}
rs708382_T NEW	T / T	GRN	0.08 (↑)	61%	1.98×10^{-9}
rs5011436_C NEW	A / C	TMEM106B	0.06 (↑)	41%	2.70×10^{-9}
rs61732533_G	G / G	SHARPIN	0.18 (↑)	95%	3.14×10^{-9}
rs7597763_C	A / C	INPPD5	-0.06 (↓)	45%	4.65×10^{-9}
rs3740688_T	G / T	MADD/SPI1	-0.02 (↓)	54%	8.78×10^{-9}
rs2452170_G NEW	A / A	NTN5	0.08 (–)	47%	1.72×10^{-8}
rs7209200_T	T / T	SCIMP/RABEP1	0.04 (↑)	33%	3.18×10^{-8}
rs7902657_T	T / T	CCDC6	-0.04 (↓)	54%	3.68×10^{-8}