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Lewy body dementia (Chia, 2021)

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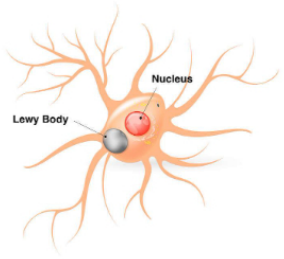
Dementia | Brain



Lewy bodies are clumps of proteins that form inside nerve cells and damage them.

STUDY SUMMARY

This report is based on a study that discovered 5 genetic variants associated with Lewy body dementia.

YOUR RESULT

34th
PERCENTILE
Below average genetic predisposition to **Lewy body dementia**

STUDY DESCRIPTION

Dementia is a term used to describe a collection of symptoms related to cognitive decline. These symptoms typically impair thinking, memory, and communication. Lewy body dementia (LBD) is the third most common cause of dementia, following Alzheimer's disease and vascular dementia. LBD is characterized by the formation of clumps of proteins known as Lewy bodies in the brain. While scientists aren't sure what leads to the formation of Lewy bodies, genetics may confer an increased risk. This study analyzed genomic data from over 6,500 individuals of European ancestry and discovered 5 regions of the genome associated with Lewy body dementia, two of which were newly discovered in this study. These two regions harbor the BIN1 and TMEM175 genes. BIN1 encodes a protein that helps other proteins interact. It was previously associated with Alzheimer's disease. TMEM175 encodes a channel protein that regulates the flow of potassium within cells and was previously connected to Parkinson's disease.

DID YOU KNOW?

Up to two-thirds of individuals with Lewy body dementia have sleep related symptoms including sleep talking and violent arm and leg movements.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to Lewy body dementia we summed up the effects of genetic variants that were linked to Lewy body dementia 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 Lewy body dementia. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to Lewy body dementia. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to Lewy body dementia. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for Lewy body dementia to be 0.00**. 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 Lewy body dementia is in the **34th percentile**. This means that it is higher than the polygenic scores 34% of people. We consider this to be a **below average genetic predisposition to Lewy body dementia**. 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
rs769449_A	G / G	0.90 (–)	10%	2.57×10^{-101}
rs7680557_C	A / A	-0.24 (–)	50%	3.28×10^{-17}
rs2230288_T	NA	1.06 (–)	1%	4.63×10^{-16}
rs6733839_T NEW	C / C	0.22 (–)	36%	1.04×10^{-10}
rs6599388_T NEW	C / C	0.22 (–)	31%	2.61×10^{-9}

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.