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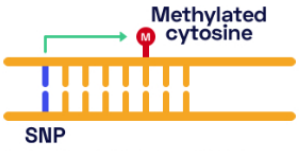
Aging (Gibson, 2019)

Jude Gibson, et al.
PLOS Genetics

Aging



Some genetic variants are linked to aging-associated methylation patterns.

STUDY SUMMARY

Discovery of 10 genetic variants associated with accelerated aging.

YOUR RESULT

16th
PERCENTILE
Below average genetic predisposition to **accelerated aging**

STUDY DESCRIPTION

"Biological age" is a measure of how well a human body is functioning relative to its actual calendar age. Studies have shown that the biological age can be estimated by measuring DNA modifications, known as methylations, across the genome. The presence of these aging-associated modifications is influenced by environmental (e.g. lifestyle) as well as genetic factors. This genome-wide association study examined the genomes of almost 13,500 individuals of European ancestry and discovered 10 genetic variants that are associated with DNA methylation profiles that are linked to accelerated biological aging. Most of the discovered variants are near genes that play a role in the metabolism or the immune system.

DID YOU KNOW?

Biological aging can be slowed down by maintaining a healthy diet, exercising regularly and minimizing stress.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to accelerated aging we summed up the effects of genetic variants that were linked to accelerated aging 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 accelerated aging. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to accelerated aging. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to accelerated aging. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for accelerated aging to be 0.14**. 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 accelerated aging is in the **16th percentile**. This means that it is higher than the polygenic scores 16% of people. We consider this to be a **below average genetic predisposition to accelerated aging**. 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
rs76244256_T	NA	-1.34 (–)	5%	6.23×10^{-26}
rs7744541_A	T / A	0.44 (↑)	42%	1.93×10^{-16}
rs10778517_T NEW	G / G	0.34 (–)	56%	4.46×10^{-10}
rs388649_A NEW	T / T	-0.34 (–)	50%	6.05×10^{-10}
rs2736099_A	A / G	0.37 (↑)	37%	8.58×10^{-10}
rs1011267_A NEW	A / A	-0.33 (↓)	50%	1.58×10^{-9}
rs4712953_A	A / T	0.35 (↑)	73%	3.60×10^{-9}
rs6440667_C NEW	G / G	0.44 (–)	16%	4.28×10^{-9}
rs79070372_A NEW	G / G	0.51 (–)	11%	6.07×10^{-9}
rs62078811_A	G / A	-0.37 (↓)	22%	1.16×10^{-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.