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Coffee consumption (Zhong, 2019)

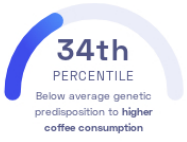
Victor Zhong, et al.
Human Molecular Genetics

Taste

STUDY SUMMARY

Identification of 15 genetic variants correlated to the consumption of coffee.

YOUR RESULT



STUDY DESCRIPTION

There's no denying that coffee helps to power our society! In fact, Americans drink nearly 400 million cups of it daily. While coffee helps us stay productive throughout the day, the opinions about its taste vary. While some need to cover the taste of coffee with milk and sugar to find it palatable, others enjoy the taste of a black cup of joe. Taste perception, such as bitterness and sweetness, and taste preference is known to be heritable. This study attempted to determine genetic factors that correlate with people's consumption of coffee as well as other bitter and sweet drinks. After examining the genomes of nearly 370,000 individuals of European ancestry, the researchers identified 15 genetic variants that are associated with coffee consumption. Of these, 6 variants were newly identified in this study. One of these variants is near a gene that has previously been found to interact with caffeine molecules. Another variant is near a gene that encodes a protein that is involved in smell perception.

DID YOU KNOW?

In addition to the burst of energy it gives, coffee is thought to have many health benefits if consumed in sensible amounts. Type 2 diabetes, Alzheimer's disease, and depression are among the diseases that coffee may help protect against.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to higher coffee consumption we summed up the effects of genetic variants that were linked to higher coffee consumption 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 higher coffee consumption. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to higher coffee consumption. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to higher coffee consumption. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for higher coffee consumption to be 19.69**. 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 higher coffee consumption 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 higher coffee consumption**. 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
rs2472297_T	C / C	2.13 (–)	27%	5.19×10^{-155}
rs4410790_C	T / C	1.98 (↑)	63%	5.59×10^{-141}
rs1057868_T	C / T	1.40 (↑)	29%	5.26×10^{-33}
rs73073176_C	C / C	1.52 (↑)	87%	5.56×10^{-25}
rs1260326_C	T / C	1.17 (↑)	61%	2.62×10^{-19}
rs34060476_G	A / A	1.37 (–)	13%	5.06×10^{-18}
rs66723169_A NEW	C / A	1.21 (↑)	23%	9.88×10^{-17}
rs12699844_C	C / T	1.11 (↑)	47%	1.35×10^{-16}
rs10865548_G NEW	G / G	1.24 (↑)	83%	4.46×10^{-16}
rs2330783_G NEW	G / G	2.13 (↑)	99%	1.57×10^{-12}
rs597045_A NEW	A / T	1.03 (↑)	69%	6.62×10^{-11}
rs117692895_C	NA	2.07 (–)	1%	4.13×10^{-10}
rs574367_T NEW	G / G	1.02 (–)	21%	8.06×10^{-9}
rs1956218_G NEW	A / G	0.91 (↑)	56%	3.62×10^{-8}
rs4719497_T	T / C	1.10 (↑)	87%	4.23×10^{-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.