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Dental caries (Shungin, 2019)

Dmitry Shungin, et al.
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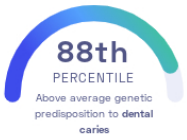
Mouth | Teeth

Tooth cavities start small but if left untreated will destroy an entire tooth.

STUDY SUMMARY

This report is based on a study that discovered 47 genetic variants associated with tooth decay and cavities.

YOUR RESULT



STUDY DESCRIPTION

The enamel is the outermost covering of the teeth that acts as a tough shell. However, bacteria, excess sugar, and acid can degrade the enamel over time. This breakdown leads to the formation of cavities and the destruction of the inner parts of the tooth, a condition known as caries. While caries is usually caused by poor oral hygiene and dietary choices, research suggests that some individuals may have a genetic predisposition to cavity formation. This genome-wide association study of over 475,000 individuals and identified 47 genetic variants associated with caries. One of the variants is located near a gene known as CA12 that is known to play a role in controlling pH (acid) levels in the body. Other genes linked to cavities include 11 genes that have been previously associated with body fat traits and 9 genes that have been connected to height.

DID YOU KNOW?

Many diseases are linked to your oral health, including heart disease, osteoporosis, and diabetes.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to dental caries we summed up the effects of genetic variants that were linked to dental caries 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 dental caries. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to dental caries. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to dental caries. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for dental caries to be 0.13**. 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 dental caries is in the **88th percentile**. This means that it is higher than the polygenic scores 88% of people. We consider this to be an **above average genetic predisposition to dental caries**. 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
rs1122171_T NEW	T / T	C5orf66	0.04 (↑)	59%	2.84×10^{-62}
rs9366651_T NEW	G / T	HLA	-0.03 (↓)	51%	2.66×10^{-28}
rs72748936_T NEW	T / C	CA12	-0.03 (↓)	46%	1.31×10^{-26}
rs121908120_A NEW	NA	WNT10A	-0.08 (–)	3%	2.03×10^{-22}
rs4971099_A NEW	G / G	KRTCAP2	-0.02 (–)	55%	7.47×10^{-16}
rs11672900_A NEW	G / G	MAMSTR	-0.02 (–)	47%	4.67×10^{-14}
rs10048146_A NEW	G / G	FOXL1	-0.03 (–)	81%	5.20×10^{-14}
rs10987008_A NEW	T / T	PBX3	0.02 (–)	64%	7.47×10^{-14}
rs1482698_C NEW	G / G	FGF10	0.02 (–)	38%	1.47×10^{-13}
rs28822480_A NEW	G / A	MC4R	0.02 (↑)	29%	7.08×10^{-13}
rs62106258_T NEW	T / T	FAM150B	0.04 (↑)	95%	8.60×10^{-12}
rs1569414_T NEW	T / T	FAM118A	-0.02 (↓)	73%	1.19×10^{-11}
rs10811723_A NEW	A / G	DMRTA1	-0.02 (↓)	30%	3.41×10^{-11}
rs7852129_A NEW	A / A	PRUNE2	-0.03 (↓)	89%	7.91×10^{-11}
rs72694438_A NEW	G / G	AMY1C	0.02 (–)	21%	2.25×10^{-10}
rs6495046_C NEW	C / G	NEO1	-0.02 (↓)	36%	3.47×10^{-10}
rs9831002_T NEW	T / G	KCNH8	-0.02 (↓)	49%	8.79×10^{-10}
rs10851907_A NEW	G / A	CHRNA3	0.02 (↑)	41%	1.03×10^{-9}
rs7429279_A NEW	A / C	RARB	0.02 (↑)	41%	1.28×10^{-9}
rs7217268_A NEW	A / G	LOC100499467	0.02 (↑)	38%	1.48×10^{-9}
rs185566659_A NEW	NA	OPA1	0.04 (–)	3%	1.54×10^{-9}
rs80270335_T NEW	C / C	ALK	0.03 (–)	9%	2.10×10^{-9}
rs8054556_A NEW	G / G	TMEM219	0.02 (–)	46%	2.23×10^{-9}
rs2652452_A NEW	C / C	KCNJ3	-0.02 (–)	45%	3.27×10^{-9}
rs9905793_A NEW	G / G	HOXB-AS2	0.03 (–)	9%	6.51×10^{-9}
rs263771_A NEW	C / A	ZNF804A	0.02 (↑)	23%	6.53×10^{-9}
rs57067187_T NEW	C / C	BAHCC1	0.01 (–)	63%	6.90×10^{-9}
rs4816017_A NEW	G / A	HAO1	-0.02 (↓)	29%	7.08×10^{-9}
rs61790808_A NEW	A / G	STAG1	-0.02 (↓)	64%	9.10×10^{-9}
rs11676272_A NEW	G / G	ADCY3	-0.01 (–)	52%	1.07×10^{-8}
rs34559440_T NEW	T / T	KCNJ2	-0.02 (↓)	68%	1.14×10^{-8}
rs1108343_T NEW	T / T	SALL1	0.02 (↑)	36%	1.32×10^{-8}
rs3865314_A NEW	A / C	NPEPPS	0.01 (↑)	51%	1.48×10^{-8}
rs898797_T NEW	C / T	LOC157273	0.01 (↑)	59%	1.52×10^{-8}
rs5922945_T NEW	C / C	HDX	-0.02 (–)	34%	1.55×10^{-8}
rs2046850_T NEW	C / C	SYT14	-0.02 (–)	19%	1.77×10^{-8}
rs3820640_T NEW	T / T	ITPKB	0.02 (↑)	84%	2.65×10^{-8}
rs55769264_A NEW	G / A	CDH9	0.01 (↑)	45%	2.84×10^{-8}

rs10772314_A NEW	A / A	KLRAP1	-0.01 (↓)	40%	3.16×10^{-8}
rs149467613_A NEW	G / G	P2RY2	-0.03 (–)	5%	3.21×10^{-8}
rs7918807_T NEW	T / T	STFA1P	0.01 (↑)	52%	3.58×10^{-8}
rs1352724_A NEW	C / C	EFNA5	-0.02 (–)	22%	3.64×10^{-8}
rs2238651_T NEW	C / C	CRLF1	0.02 (–)	24%	4.39×10^{-8}
rs2072693_T NEW	T / G	RHCG	0.01 (↑)	48%	4.92×10^{-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.