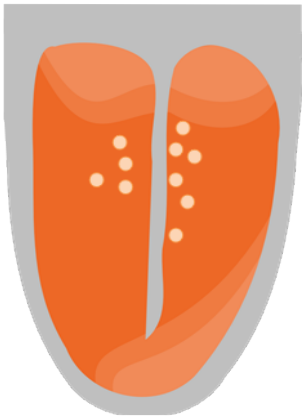
Updated 05/01/2024

TASTE 2 RECEPTOR MEMBER 38 (TAS2R38)

The Bitter Truth About Taste

Biology Background

- The Taste 2 Receptor Member 38 (TAS2R38) gene produces the TAS2R38 protein, which functions as a receptor to perceive a wide range of bitter compounds.
- Bitter taste receptors, including TAS2R38, are proteins found on the taste cells of the tongue.

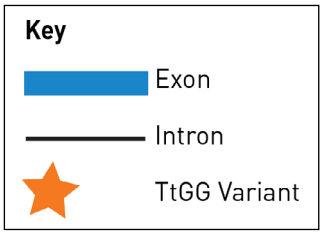


Tongue

Genomic Locus

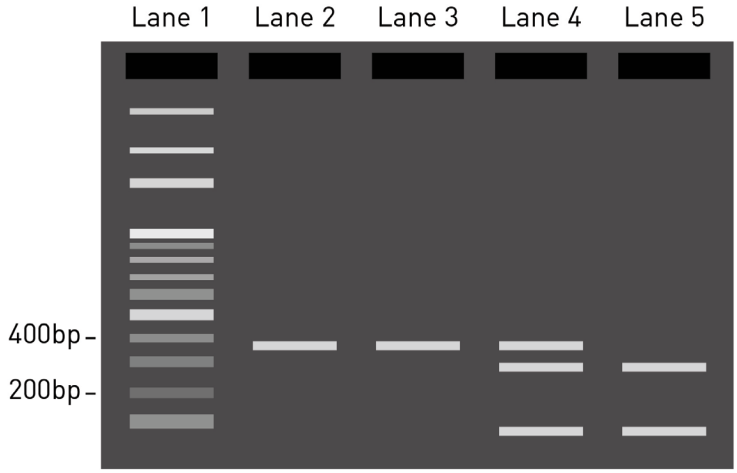
The TAS2R38 gene is located on chromosome 7. The TAS2R38 gene is 1,143 base pairs in length and consists of a single exon and no introns, encoding a 333 amino acid protein.

The TtGG Variants



- In this assay, you are studying three single nucleotide polymorphisms (SNPs) in the TAS2R38 gene (see stars). Each of these variants affects the amino acid sequence of the TAS2R38 protein.
- The SNPs are located at base pairs 145, 785, and 886 (corresponding to amino acids 49, 262, and 296). There are eight possible combinations of these three SNPs, producing eight possible alleles.
- The alleles are written as three letters representing the three SNPs. For example, one possible allele is GTA. The G is the variant at the 145, the T is the variant at 785, and the A is the variant at 886.
- The eight alleles each produce a different version of the TAS2R38 protein, which each have different levels of sensitivity for detecting bitter compounds.
- The variant at 785 (C or T) contains a site for the restriction enzyme Fnu4H1 to cut the DNA when a C is present. Cut versus uncut DNA segments can be detected on a gel.

TAS2R38 Gel



Lane 1: DNA ladder

Lane 2: Undigested sample, 365 bp

Lane 3: Homozygous T genotype, 365 bp

Lane 4: Heterozygous TC genotype, 75 bp, 290 bp, 365 bp

Lane 5: Homozygous C genotype, 75 bp, 290 bp

Please note that only the second variant (C or T) can be detected by size.

Population Genetics

- Current data suggest that the vast majority of the current human population have the CCG allele and/or the GTA allele. This includes individuals with a homozygous CCG genotype (which corresponds to the super taster phenotype), a homozygous GTA genotype (which corresponds to the non-taster phenotype), and a heterozygous CCG/GTA genotype (which corresponds to the taster phenotype).
- Other combinations of the eight possible alleles produce additional genotypes that correspond to intermediate-taster phenotypes.

Influence on Human Health

- TAS2R38 is one of the most well studied taste receptors.
- It has been shown to be accountable for perception of bitter-tasting compounds, such as phenylthiocarbamide (PTC).
- TAS2R38 variants play a role in how we perceive the taste of common bitter foods such as brussels sprouts, cabbage, and broccoli.

Sources

» Online Mendelian Inheritance in Man (OMIM) https://www.omim.org/entry/607751
» National Center for Biotechnology Information (NCBI) Gene https://www.ncbi.nlm.nih.gov/gene/5726
» NCBI Reference SNP (rs) reports
  » https://www.ncbi.nlm.nih.gov/snp/rs713598
  » https://www.ncbi.nlm.nih.gov/snp/rs1726866
  » https://www.ncbi.nlm.nih.gov/snp/rs10246939
» Review on TAS2R38 and its impacts on PTC receptivity see: Risso et al. Global diversity in the TAS2R38 bitter taste receptor: revisiting a classic evolutionary PROPosal. Nature Scientific Reports (2015)
» The Human Protein Atlas
» UCSC Genome Browser