

TAS1R3 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=TAS1R3 #gephebase-summary-title)	Gephebase Gene	GP00001110	GepheID
Published	Entry Status	Martin	Main curator

Trait Category		Taxon A		Taxon B	
Physiology (#https://www.gephebase.org/search-criteria?/and+Trait+Category=~Physiology)	Trait				
Taste sensitivity (sugar) (#https://www.gephebase.org/search-criteria?/and+Trait=~Taste+sensitivity)	Trait				
Mus musculus - taster	Trait State in Taxon A				
Mus musculus - non taster	Trait State in Taxon B				
Data not curated	Ancestral State				
Intraspecific (#https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Intraspecific)	Taxonomic Status				
		Taxon A		Taxon B	
Mus musculus	Latin Name	Mus musculus	Latin Name		
(#https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Mus+musculus)		(#https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Mus+musculus)			
house mouse	Common Name	house mouse	Common Name		
house mouse; mouse; Mus musculus Linnaeus, 1758; mice	Synonyms	house mouse; mouse; Mus musculus Linnaeus, 1758; mice	Synonyms		
C57BL/6xCBA/CaJ hybrid	Rank	C57BL/6xCBA/CaJ hybrid	Rank		
species	Lineage	species	Lineage		
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus	Parent	cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus	Parent		
Mus () - (Rank: subgenus)	NCBI Taxonomy ID	Mus () - (Rank: subgenus)	NCBI Taxonomy ID		
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=862507)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=862507)			
10090		10090			
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=10090)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=10090)			
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?			
No		No			

TAS1R3	Generic Gene Name	Q7RTX0 (http://www.uniprot.org/uniprot/Q7RTX0)	UniProtKB Homo sapiens
T1R3; TR3	Synonyms	EDL15046 (https://www.ncbi.nlm.nih.gov/nuccore/EDL15046)	GenebankID or UniProtKB
9606.ENSPP00000344411 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=9606.ENSPP00000344411)	String		
	Sequence Similarities		
Belongs to the G-protein coupled receptor 3 family. TAS1R subfamily.			
	GO - Molecular Function		
GO:0046982 : protein heterodimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0046982)			
GO:0004930 : G protein-coupled receptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004930)			
GO:0008527 : taste receptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008527)			
	GO - Biological Process		
GO:0007186 : G protein-coupled receptor signaling pathway			

(<https://www.ebi.ac.uk/QuickGO/term/GO:0007186>)
GO:0001582 : detection of chemical stimulus involved in sensory perception of sweet taste
(<https://www.ebi.ac.uk/QuickGO/term/GO:0001582>)
GO:0050916 : sensory perception of sweet taste
(<https://www.ebi.ac.uk/QuickGO/term/GO:0050916>)
GO:0050917 : sensory perception of umami taste
(<https://www.ebi.ac.uk/QuickGO/term/GO:0050917>)

GO - Cellular Component

GO:0016021 : integral component of membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)
GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)
GO:0005887 : integral component of plasma membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005887>)
GO:1903767 : sweet taste receptor complex
(<https://www.ebi.ac.uk/QuickGO/term/GO:1903767>)

Presumptive Null

No ([https://www.gephebase.org/search-criteria?/and+Presumptive Null="+No`#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive Null=))

Molecular Type

Coding ([https://www.gephebase.org/search-criteria?/and+Molecular Type="+Coding`#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular Type=))

Aberration Type

SNP ([https://www.gephebase.org/search-criteria?/and+Aberration Type="+SNP`#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Aberration Type=))

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

I60T; is predicted to introduce a novel N-linked glycosylation site which might interfere with receptor dimerization

Experimental Evidence

Linkage Mapping ([https://www.gephebase.org/search-criteria?/and+Experimental Evidence="+Linkage Mapping`#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental Evidence=))

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

Main Reference

Tas1r3, encoding a new candidate taste receptor, is allelic to the sweet responsiveness locus Sac. (2001) (<https://pubmed.ncbi.nlm.nih.gov/11326277>)

Authors

Max M; Shanker YG; Huang L; Rong M; Liu Z; Campagne F; Weinstein H; Damak S; Margolskee RF

Abstract

The ability to taste the sweetness of carbohydrate-rich foodstuffs has a critical role in the nutritional status of humans. Although several components of bitter transduction pathways have been identified, the receptors and other sweet transduction elements remain unknown. The Sac locus in mouse, mapped to the distal end of chromosome 4 (refs. 7-9), is the major determinant of differences between sweet-sensitive and -insensitive strains of mice in their responsiveness to saccharin, sucrose and other sweeteners. To identify the human Sac locus, we searched for candidate genes within a region of approximately one million base pairs of the sequenced human genome syntenous to the region of Sac in mouse. From this search, we identified a likely candidate: T1R3, a previously unknown G protein-coupled receptor (GPCR) and the only GPCR in this region. Mouse Tas1r3 (encoding T1r3) maps to within 20,000 bp of the marker closest to Sac (ref. 9) and, like human TAS1R3, is expressed selectively in taste receptor cells. By comparing the sequence of Tas1r3 from several independently derived strains of mice, we identified a specific polymorphism that assorts between taster and non-taster strains. According to models of its structure, T1r3 from non-tasters is predicted to have an extra amino-terminal glycosylation site that, if used, would interfere with dimerization.

Additional References

A candidate taste receptor gene near a sweet taste locus. (2001) (<https://pubmed.ncbi.nlm.nih.gov/11319557>)

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

