GEPHE SUMMARY

Gephebase Gene

TAS1R2 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^TAS1R2^#gephebase-summary-title)

GepheID

GP00001109

Entry Status

Published

Main curator

Martin

PHENOTYPIC CHANGE

Trait Category

Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)

Trait

Taste sensitivity (sugar) (https://www.gephebase.org/search-criteria?/and+Trait=^Taste sensitivity (sugar)^#gephebase-summary-title)

Trait State in Taxon A

Other mammals

Trait State in Taxon B

Felidae: cats; tiger; cheetah

Ancestral State

Taxon A

Taxonomic Status

Intergeneric or Higher (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intergeneric or Higher^#gephebase-summary-title)

Taxon A

Latin Name

Mammalia (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Mammalia^#gephebase-summary-title)

Common Name

mammals

Synonyms

mammals

Rank

class

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota

Parent

Amniota (amniotes) - (Rank: no rank) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32524)

NCBI Taxonomy ID

40674 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 40674)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

Felidae (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Felidae^#gephebase-summary-title)

Common Name

cat family

Synonyms

cat family

Rank

family

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Laurasiatheria; Carnivora; Feliformia

Parent

Feliformia () - (Rank: suborder) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 379583)

NCBI Taxonomy ID

9681 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9681)

is Taxon B an Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

TAS1R2

Synonyms

TR2; T1R2; GPR71

String

9606.ENSP00000364520 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=9606.ENSP00000364520)

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

UniProtKB Homo sapiens

Q8TE23 (http://www.uniprot.org/uniprot/Q8TE23)

GenebankID or UniProtKB

XM_015538133 (https://www.ncbi.nlm.nih.gov/nuccore/XM_015538133)

(https://www.ebi.ac.uk/QuickGO/term/GO:0007186)
GO:0032467 : positive regulation of cytokinesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0032467)
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 - 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:0043235 : receptor complex (https://www.ebi.ac.uk/QuickGO/term/GO:0043235)
GO:1903767 : sweet taste receptor complex
(https://www.ebi.ac.uk/QuickGO/term/GO:1903767)

Presumptive Null

Yes (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Yes^#gephebase-summary-title)

Molecular Type

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

Aberration Type

Deletion (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Deletion^#gephebase-summary-title)

Deletion Size

100-999 bp

Molecular Details of the Mutation

247bp deletion in exon 3 and stop codons in exons 4 and 6.

Experimental Evidence

Candidate Gene (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Candidate Gene^#gephebase-summary-title)

Main Reference

Pseudogenization of a sweet-receptor gene accounts for cats' indifference toward sugar. (2005) (https://pubmed.ncbi.nlm.nih.gov/16103917)

Authors

Li X; Li W; Wang H; Cao J; Maehashi K; Huang L; Bachmanov AA; Reed DR; Legrand-Defretin V; Beauchamp GK; Brand JG

Abstract

Although domestic cats (Felis silvestris catus) possess an otherwise functional sense of taste, they, unlike most mammals, do not prefer and may be unable to detect the sweetness of sugars. One possible explanation for this behavior is that cats lack the sensory system to taste sugars and therefore are indifferent to them. Drawing on work in mice, demonstrating that alleles of sweet-receptor genes predict low sugar intake, we examined the possibility that genes involved in the initial transduction of sweet perception might account for the indifference to sweet-tasting foods by cats. We characterized the sweet-receptor genes of domestic cats as well as those of other members of the Felidae family of obligate carnivores, tiger and cheetah. Because the mammalian sweet-taste receptor is formed by the dimerization of two proteins (T1R2 and T1R3; gene symbols Tas1r2 and Tas1r3), we identified and sequenced both genes in the cat by screening a feline genomic BAC library and by performing PCR with degenerate primers on cat genomic DNA. Gene expression was assessed by RT-PCR of taste tissue, in situ hybridization, and immunohistochemistry. The cat Tas1r3 gene shows high sequence similarity with functional Tas1r3 genes of other species. Message from Tas1r3 was detected by RT-PCR of taste tissue. In situ hybridization and immunohistochemical studies demonstrate that Tas1r3 is expressed, as expected, in taste buds. However, the cat Tas1r2 gene shows a 247-base pair microdeletion in exon 3 and stop codons in exons 4 and 6. There was no evidence of detectable mRNA from cat Tas1r2 by RT-PCR or in situ hybridization, and no evidence of protein expression by immunohistochemistry. Tas1r2 in tiger and cheetah and in six healthy adult domestic cats all show the similar deletion and stop codons. We conclude that cat Tas1r3 is an apparently functional and expressed receptor but that cat Tas1r2 is an unexpressed pseudogene. A functional sweet-taste receptor heteromer cannot form, and thus the cat lacks the receptor likely necessary for detection of sweet stimuli. This molecular change was very likely an important event in the evolution of the cat's carnivorous behavior.

Additional References

Cats lack a sweet taste receptor. (2006) (https://pubmed.ncbi.nlm.nih.gov/16772462)

RELATED GEPHE

Related Genes

4 (TAS1R1, TAS1R3, TAS2R16, TAS2R38) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^40674^/and+Trait=Taste sensitivity/or+Taxon ID=^9681^/and+Trait=Taste sensitivity/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

https://omia.org/OMIA001617/9685/