

## GEPHE SUMMARY

Potassium channel subfamily K ( <a href="https://www.gephebase.org/search-criteria/?and+Gene">https://www.gephebase.org/search-criteria/?and+Gene</a> Gephebase=^Potassium channel subfamily K^#gephebase-summary-title)	Gephebase Gene GP00002348	GephelD Main curator
Published	Entry Status Courtier	

## PHENOTYPIC CHANGE

Trait Category		
Morphology ( <a href="https://www.gephebase.org/search-criteria/?and+Trait">https://www.gephebase.org/search-criteria/?and+Trait</a> Category=^Morphology^#gephebase-summary-title)	Trait	
Fin morphology (skeleton; dorsal fin; caudal fin; tail; paired fin) ( <a href="https://www.gephebase.org/search-criteria/?and+Trait=^Fin+morphology+(skeleton+dorsal+fin+caudal+fin+tail+paired+fin)^#gephebase-summary-title">https://www.gephebase.org/search-criteria/?and+Trait=^Fin+morphology+(skeleton+dorsal+fin+caudal+fin+tail+paired+fin)^#gephebase-summary-title</a> )	Trait State in Taxon A	
median and paired fins of standard size wild goldfish and many strains of domesticated goldfish	Trait State in Taxon B	
elongation of all median and paired fins 14 strains of domesticated goldfish	Ancestral State	
Taxon A		Taxonomic Status
Domesticated ( <a href="https://www.gephebase.org/search-criteria/?and+Taxonomic">https://www.gephebase.org/search-criteria/?and+Taxonomic</a> Status=^Domesticated^#gephebase-summary-title)		
Taxon A	Latin Name	Taxon B
Carassius auratus ( <a href="https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=^Carassius+auratus^#gephebase-summary-title">https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=^Carassius+auratus^#gephebase-summary-title</a> )	Carassius auratus ( <a href="https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=^Carassius+auratus^#gephebase-summary-title">https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=^Carassius+auratus^#gephebase-summary-title</a> )	Latin Name
goldfish	Common Name	Common Name
Carassius carassius auratus; Cyprinus auratus; goldfish; Carassius auratus (Linnaeus, 1758); Cyprinus auratus Linnaeus, 1758; Carassius auratus	Synonyms	Synonyms
species	Rank	Rank
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Actinopteri; Neopterygii; Teleosteii; Osteoglossocephalai; Clupeocephala; Otomorpha; Ostariophysi; Otophysi; Cypriniphysae; Cypriniformes; Cyprinoidei; Cyprinidae; Cyprininae; Carassius	Lineage	Lineage
Carassius () - (Rank: genus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7956">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7956</a> )	Parent	Parent
7957 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7957">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7957</a> )	NCBI Taxonomy ID	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	is Taxon B an Infraspecies?

## GENOTYPIC CHANGE

KCNK5	Generic Gene Name	UniProtKB Homo sapiens
TASK2; K2p5.1; KCNK5b; TASK-2	Synonyms	GenebankID or UniProtKB
9606.ENSP00000352527 ( <a href="http://string-db.org/newstring_cgi/show_network_section.pl?identifier=9606.ENSP00000352527">http://string-db.org/newstring_cgi/show_network_section.pl?identifier=9606.ENSP00000352527</a> )	String	
Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.	Sequence Similarities	
GO:0005249 : voltage-gated potassium channel activity ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0005249">https://www.ebi.ac.uk/QuickGO/term/GO:0005249</a> )	GO - Molecular Function	

GO:0005267 : potassium channel activity  
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005267>)  
GO:0022841 : potassium ion leak channel activity  
(<https://www.ebi.ac.uk/QuickGO/term/GO:0022841>)

#### GO - Biological Process

GO:0006813 : potassium ion transport  
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006813>)  
GO:1990573 : potassium ion import across plasma membrane  
(<https://www.ebi.ac.uk/QuickGO/term/GO:1990573>)  
GO:0071805 : potassium ion transmembrane transport  
(<https://www.ebi.ac.uk/QuickGO/term/GO:0071805>)  
GO:0034765 : regulation of ion transmembrane transport  
(<https://www.ebi.ac.uk/QuickGO/term/GO:0034765>)  
GO:0097623 : potassium ion export across plasma membrane  
(<https://www.ebi.ac.uk/QuickGO/term/GO:0097623>)  
GO:0007588 : excretion (<https://www.ebi.ac.uk/QuickGO/term/GO:0007588>)

GO:0060075 : regulation of resting membrane potential  
(<https://www.ebi.ac.uk/QuickGO/term/GO:0060075>)  
GO:0030322 : stabilization of membrane potential  
(<https://www.ebi.ac.uk/QuickGO/term/GO:0030322>)

#### GO - Cellular Component

GO:0005887 : integral component of plasma membrane  
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005887>)

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

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

Substitution of a hydrophobic amino acid (valine) with a hydrophilic amino acid (glutamic acid) appears to cause a critical alteration of channel gating. In total there are five amino acid substitutions or deletions in kcnk5bS in goldfish with the long-tail phenotype.

Experimental Evidence

Association Mapping (<https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=^Association+Mapping^#gephebase-summary-title>)

	Taxon A	Taxon B	Position
Codon	GTA	GAA	-
Amino-acid	Val	Glu	165

Main Reference

The Genetic Basis of Morphological Diversity in Domesticated Goldfish. (2020) (<https://pubmed.ncbi.nlm.nih.gov/32392470>)

Authors

Kon T; Omori Y; Fukuta K; Wada H; Watanabe M; Chen Z; Iwasaki M; Mishina T; Matsuzaki SS; Yoshihara D; Arakawa J; Kawakami K; Toyoda A; Burgess SM; Noguchi H; Furukawa T  
Abstract

Although domesticated goldfish strains exhibit highly diversified phenotypes in morphology, the genetic basis underlying these phenotypes is poorly understood. Here, based on analysis of transposable elements in the allotetraploid goldfish genome, we found that its two subgenomes have evolved asymmetrically since a whole-genome duplication event in the ancestor of goldfish and common carp. We conducted whole-genome sequencing of 27 domesticated goldfish strains and wild goldfish. We identified more than 60 million genetic variations and established a population genetic structure of major goldfish strains. Genome-wide association studies and analysis of strain-specific variants revealed genetic loci associated with several goldfish phenotypes, including dorsal fin loss, long-tail, telescope-eye, albinism, and heart-shaped tail. Our results suggest that accumulated mutations in the asymmetrically evolved subgenomes led to generation of diverse phenotypes in the goldfish domestication history. This study is a key resource for understanding the genetic basis of phenotypic diversity among goldfish strains.

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Additional References

## RELATED GEPHE

	Related Genes
2 (chordin, Wnt receptor) ( <a href="https://www.gephebase.org/search-criteria?/or+Taxon+ID=^7957^/and+Trait=Fin+morphology/and+groupHaplotypes=true#gephebase-summary-title">https://www.gephebase.org/search-criteria?/or+Taxon+ID=^7957^/and+Trait=Fin+morphology/and+groupHaplotypes=true#gephebase-summary-title</a> )	Related Haplotypes

No matches found.

## EXTERNAL LINKS

## COMMENTS