

GEPHE SUMMARY

<p>Low-density lipoprotein receptor-related protein 2 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^Low-density+lipoprotein+receptor-related+protein+2^#gephebase-summary-title)</p> <p>Published</p>	<p>Gephebase Gene</p> <p>GP00002349</p> <p>Courtier</p> <p>Entry Status</p>	<p>GepheID</p> <p>Main curator</p>
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PHENOTYPIC CHANGE

<p>Morphology (https://www.gephebase.org/search-criteria?/and+Trait+Category=^Morphology^#gephebase-summary-title)</p> <p>Organ size (eye; enlarged) (https://www.gephebase.org/search-criteria?/and+Trait=^Organ+size+(eye;+enlarged)^#gephebase-summary-title)</p> <p>eyes of standard size wild goldfish and many strains of domesticated goldfish</p> <p>enlarged eyes 4 four Telescope-eye strains of domesticated goldfish</p> <p>Taxon A</p> <p>Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Domesticated^#gephebase-summary-title)</p>	<p>Trait Category</p> <p>Trait</p> <p>Trait State in Taxon A</p> <p>Trait State in Taxon B</p> <p>Ancestral State</p> <p>Taxonomic Status</p>	<p>Taxon A</p> <p>Carassius auratus (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Carassius+auratus^#gephebase-summary-title)</p> <p>goldfish</p> <p>Carassius carassius auratus; Cyprinus auratus; goldfish; Carassius auratus (Linnaeus, 1758); Cyprinus auratus Linnaeus, 1758; Carassius auratus</p> <p>species</p> <p>cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Actinopteri; Neopterygii; Teleostei; Osteoglossocephalai; Clupeocephala; Otomorpha; Ostariophysi; Otophysi; Cypriniphysae; Cypriniformes; Cyprinoidei; Cyprinidae; Cyprininae; Carassius</p> <p>Carassius () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7956)</p> <p>7957 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7957)</p> <p>No</p>	<p>Latin Name</p> <p>Common Name</p> <p>Synonyms</p> <p>Rank</p> <p>Lineage</p> <p>Parent</p> <p>NCBI Taxonomy ID</p> <p>is Taxon A an Intraspecies?</p>	<p>Taxon B</p> <p>Carassius auratus (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Carassius+auratus^#gephebase-summary-title)</p> <p>goldfish</p> <p>Carassius carassius auratus; Cyprinus auratus; goldfish; Carassius auratus (Linnaeus, 1758); Cyprinus auratus Linnaeus, 1758; Carassius auratus</p> <p>species</p> <p>cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Actinopteri; Neopterygii; Teleostei; Osteoglossocephalai; Clupeocephala; Otomorpha; Ostariophysi; Otophysi; Cypriniphysae; Cypriniformes; Cyprinoidei; Cyprinidae; Cyprininae; Carassius</p> <p>Carassius () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7956)</p> <p>7957 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7957)</p> <p>No</p>	<p>Latin Name</p> <p>Common Name</p> <p>Synonyms</p> <p>Rank</p> <p>Lineage</p> <p>Parent</p> <p>NCBI Taxonomy ID</p> <p>is Taxon B an Intraspecies?</p>
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GENOTYPIC CHANGE

<p>LRP2</p> <p>DBS; GP330; LRP-2</p> <p>9606.ENSP00000263816 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=9606.ENSP00000263816)</p> <p>Belongs to the LDLR family.</p> <p>GO:0005509 : calcium ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005509) GO:0017124 : SH3 domain binding (https://www.ebi.ac.uk/QuickGO/term/GO:0017124)</p>	<p>Generic Gene Name</p> <p>Synonyms</p> <p>String</p> <p>Sequence Similarities</p> <p>GO - Molecular Function</p>	<p>UniProtKB Homo sapiens</p> <p>P98164 (http://www.uniprot.org/uniprot/P98164)</p> <p>GenebankID or UniProtKB</p> <p>()</p>
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GO:0031994 : insulin-like growth factor I binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0031994>)
GO:0051087 : chaperone binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0051087>)
GO:0042562 : hormone binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0042562>)
GO:0005041 : low-density lipoprotein particle receptor activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005041>)
GO:0038024 : cargo receptor activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0038024>)
GO:0140318 : protein transporter activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0140318>)

GO - Biological Process

GO:0043066 : negative regulation of apoptotic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043066>)
GO:0001843 : neural tube closure (<https://www.ebi.ac.uk/QuickGO/term/GO:0001843>)
GO:0006898 : receptor-mediated endocytosis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006898>)
GO:0001523 : retinoid metabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0001523>)
GO:0008283 : cell proliferation (<https://www.ebi.ac.uk/QuickGO/term/GO:0008283>)
GO:0008584 : male gonad development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0008584>)
GO:0051897 : positive regulation of protein kinase B signaling
(<https://www.ebi.ac.uk/QuickGO/term/GO:0051897>)
GO:0001822 : kidney development (<https://www.ebi.ac.uk/QuickGO/term/GO:0001822>)
GO:0006897 : endocytosis (<https://www.ebi.ac.uk/QuickGO/term/GO:0006897>)
GO:0006629 : lipid metabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006629>)
GO:0030900 : forebrain development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0030900>)
GO:0003148 : outflow tract septum morphogenesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0003148>)
GO:0030001 : metal ion transport (<https://www.ebi.ac.uk/QuickGO/term/GO:0030001>)
GO:0097242 : amyloid-beta clearance
(<https://www.ebi.ac.uk/QuickGO/term/GO:0097242>)
GO:0007605 : sensory perception of sound
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007605>)
GO:0015031 : protein transport (<https://www.ebi.ac.uk/QuickGO/term/GO:0015031>)
GO:0003281 : ventricular septum development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0003281>)
GO:0050769 : positive regulation of neurogenesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0050769>)
GO:0060068 : vagina development (<https://www.ebi.ac.uk/QuickGO/term/GO:0060068>)
GO:0030514 : negative regulation of BMP signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0030514>)
GO:0071363 : cellular response to growth factor stimulus
(<https://www.ebi.ac.uk/QuickGO/term/GO:0071363>)
GO:0035904 : aorta development (<https://www.ebi.ac.uk/QuickGO/term/GO:0035904>)
GO:0060982 : coronary artery morphogenesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0060982>)
GO:1904447 : folate import across plasma membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:1904447>)
GO:0140058 : neuron projection arborization
(<https://www.ebi.ac.uk/QuickGO/term/GO:0140058>)
GO:1905167 : positive regulation of lysosomal protein catabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:1905167>)
GO:0070447 : positive regulation of oligodendrocyte progenitor proliferation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0070447>)
GO:0061156 : pulmonary artery morphogenesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0061156>)
GO:0044321 : response to leptin (<https://www.ebi.ac.uk/QuickGO/term/GO:0044321>)
GO:0003139 : secondary heart field specification
(<https://www.ebi.ac.uk/QuickGO/term/GO:0003139>)
GO:0045056 : transcytosis (<https://www.ebi.ac.uk/QuickGO/term/GO:0045056>)
GO:0150104 : transport across blood-brain barrier
(<https://www.ebi.ac.uk/QuickGO/term/GO:0150104>)
GO:0003223 : ventricular compact myocardium morphogenesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0003223>)
GO:0042359 : vitamin D metabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042359>)

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:0016324 : apical plasma membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016324>)
GO:0070062 : extracellular exosome (<https://www.ebi.ac.uk/QuickGO/term/GO:0070062>)
GO:0043235 : receptor complex (<https://www.ebi.ac.uk/QuickGO/term/GO:0043235>)
GO:0005794 : Golgi apparatus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005794>)

GO:0030669 : clathrin-coated endocytic vesicle membrane
 (https://www.ebi.ac.uk/QuickGO/term/GO:0030669)
 GO:0030425 : dendrite (https://www.ebi.ac.uk/QuickGO/term/GO:0030425)
 GO:0005783 : endoplasmic reticulum
 (https://www.ebi.ac.uk/QuickGO/term/GO:0005783)
 GO:0030424 : axon (https://www.ebi.ac.uk/QuickGO/term/GO:0030424)
 GO:0005764 : lysosome (https://www.ebi.ac.uk/QuickGO/term/GO:0005764)
 GO:0009897 : external side of plasma membrane
 (https://www.ebi.ac.uk/QuickGO/term/GO:0009897)
 GO:0005765 : lysosomal membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005765)
 GO:0031904 : endosome lumen (https://www.ebi.ac.uk/QuickGO/term/GO:0031904)
 GO:0031526 : brush border membrane
 (https://www.ebi.ac.uk/QuickGO/term/GO:0031526)
 GO:0005905 : clathrin-coated pit (https://www.ebi.ac.uk/QuickGO/term/GO:0005905)

Mutation #1

Yes (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Yes^#gephebase-summary-title) Presumptive Null
 Coding (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Coding^#gephebase-summary-title) Molecular Type
 SNP (https://www.gephebase.org/search-criteria?/and+Aberration Type=^SNP^#gephebase-summary-title) Aberration Type
 Nonsense SNP Coding Change
 - Molecular Details of the Mutation
 Association Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Association Mapping^#gephebase-summary-title) Experimental Evidence

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Tyr	STP	3425

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

Mutation #2

Yes (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Yes^#gephebase-summary-title) Presumptive Null
 Coding (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Coding^#gephebase-summary-title) Molecular Type
 SNP (https://www.gephebase.org/search-criteria?/and+Aberration Type=^SNP^#gephebase-summary-title) Aberration Type
 Nonsense SNP Coding Change
 - Molecular Details of the Mutation
 Association Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Association Mapping^#gephebase-summary-title) Experimental Evidence

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Gly	STP	4480

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

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Additional References

Mutation #3

Presumptive Null

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

Molecular Type

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

Aberration Type

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

Insertion Size

10-100 kb

Molecular Details of the Mutation

13-kbp retrotransposon insertion of a foamy-like endogenous retrovirus in intron 45 in the Black T Telescope-eye strain. Almost no normal lrp2aL mRNA was expressed in the Black Telescope-eye strain.

Experimental Evidence

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

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

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Additional References

RELATED GEPHE

No matches found.

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EXTERNAL LINKS

COMMENTS

©TE In mouse LRP2 plays the role of sonic hedgehog (shh) clearance receptor and regulates shh-induced cell proliferation at the retinal margin, resulting in a large eye phenotype.

