GEPHE SUMMARY

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

GepheID
GP00002347

Entry Status
Published

Main curator
Courtier

PHENOTYPIC CHANGE

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

Trait
Fin morphology (skeleton; dorsal fin) (https://www.gephebase.org/search-criteria?/and+Trait=^Fin morphology (skeleton; dorsal fin)^#gephebase-summary-title)

Trait State in Taxon A
presence of dorsal fin
wild goldfish and many strains of domesticated goldfish

Trait State in Taxon B
absence of dorsal fin
8 strains of domesticated goldfish

Ancestral State
Taxon A

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

Taxon A

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

Common Name
goldfish

Synonyms
Carassius carassius auratus; Cyprinus auratus; goldfish; Carassius auratus (Linnaeus, 1758); Cyprinus auratus Linnaeus, 1758; Carassius auratis

Rank
species

Lineage
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

Parent
Carassius () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7956)

NCBI Taxonomy ID
7957 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7957)

is Taxon A an Infraspecies?
No

Taxon B

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

Common Name
goldfish

Synonyms
Carassius carassius auratus; Cyprinus auratus; goldfish; Carassius auratus (Linnaeus, 1758); Cyprinus auratus Linnaeus, 1758; Carassius auratis

Rank
species

Lineage
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

Parent
Carassius () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7956)

NCBI Taxonomy ID
7957 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7957)

is Taxon B an Infraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
Lrp6

Synonyms
Cd; Gw; ska26; skax26; ska<m26Jus>; C030016K15Rik

String
10090.ENSMUSP00000032322 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=10090.ENSMUSP00000032322)

Sequence Similarities
Belongs to the LDLR family.

GO - Molecular Function
GO:0042802 : identical protein binding (https://www.ebi.ac.uk/QuickGO/term/GO:0042802)
GO:0042803 : protein homodimerization activity

UniProtKB Mus musculus
O88572 (http://www.uniprot.org/uniprot/O88572)

GenebankID or UniProtKB
()

(https://www.ebi.ac.uk/QuickGO/term/GO:0042803)
GO:0005102 : signaling receptor binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0005102)
GO:0005109 : frizzled binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005109)
GO:0015026 : coreceptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0015026)
GO:0042813 : Wnt-activated receptor activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0042813)
GO:0017147 : Wnt-protein binding (https://www.ebi.ac.uk/QuickGO/term/GO:0017147)
GO:0005041 : low-density lipoprotein particle receptor activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0005041)
GO:0034185 : apolipoprotein binding (https://www.ebi.ac.uk/QuickGO/term/GO:0034185)
GO:0071936 : coreceptor activity involved in Wnt signaling pathway
(https://www.ebi.ac.uk/QuickGO/term/GO:0071936)
GO:0019210 : kinase inhibitor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0019210)
GO:0019534 : toxin transmembrane transporter activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0019534)

GO - Biological Process

GO:0003401 : axis elongation (https://www.ebi.ac.uk/QuickGO/term/GO:0003401)
GO:0060026 : convergent extension (https://www.ebi.ac.uk/QuickGO/term/GO:0060026)
GO:0007268 : chemical synaptic transmission
(https://www.ebi.ac.uk/QuickGO/term/GO:0007268)
GO:0045944 : positive regulation of transcription by RNA polymerase II
(https://www.ebi.ac.uk/QuickGO/term/GO:0045944)
GO:0006355 : regulation of transcription, DNA-templated
(https://www.ebi.ac.uk/QuickGO/term/GO:0006355)
GO:0009952 : anterior/posterior pattern specification
(https://www.ebi.ac.uk/QuickGO/term/GO:0009952)
GO:0030326 : embryonic limb morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0030326)
GO:0001843 : neural tube closure (https://www.ebi.ac.uk/QuickGO/term/GO:0001843)
GO:0045893 : positive regulation of transcription, DNA-templated
(https://www.ebi.ac.uk/QuickGO/term/GO:0045893)
GO:0060021 : roof of mouth development
(https://www.ebi.ac.uk/QuickGO/term/GO:0060021)
GO:0010976 : positive regulation of neuron projection development
(https://www.ebi.ac.uk/QuickGO/term/GO:0010976)
GO:0050680 : negative regulation of epithelial cell proliferation
(https://www.ebi.ac.uk/QuickGO/term/GO:0050680)
GO:0007204 : positive regulation of cytosolic calcium ion concentration
(https://www.ebi.ac.uk/QuickGO/term/GO:0007204)
GO:0001756 : somitogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0001756)
GO:0001947 : heart looping (https://www.ebi.ac.uk/QuickGO/term/GO:0001947)
GO:0045787 : positive regulation of cell cycle
(https://www.ebi.ac.uk/QuickGO/term/GO:0045787)
GO:0042475 : odontogenesis of dentin-containing tooth
(https://www.ebi.ac.uk/QuickGO/term/GO:0042475)
GO:0098609 : cell-cell adhesion (https://www.ebi.ac.uk/QuickGO/term/GO:0098609)
GO:0009880 : embryonic pattern specification
(https://www.ebi.ac.uk/QuickGO/term/GO:0009880)
GO:0030900 : forebrain development
(https://www.ebi.ac.uk/QuickGO/term/GO:0030900)
GO:0035116 : embryonic hindlimb morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0035116)
GO:0036342 : post-anal tail morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0036342)
GO:0060349 : bone morphogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0060349)
GO:0030901 : midbrain development
(https://www.ebi.ac.uk/QuickGO/term/GO:0030901)
GO:0002053 : positive regulation of mesenchymal cell proliferation
(https://www.ebi.ac.uk/QuickGO/term/GO:0002053)
GO:0048705 : skeletal system morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0048705)
GO:0043065 : positive regulation of apoptotic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0043065)
GO:0021987 : cerebral cortex development
(https://www.ebi.ac.uk/QuickGO/term/GO:0021987)
GO:0042074 : cell migration involved in gastrulation
(https://www.ebi.ac.uk/QuickGO/term/GO:0042074)
GO:0042127 : regulation of cell proliferation
(https://www.ebi.ac.uk/QuickGO/term/GO:0042127)
GO:0034392 : negative regulation of smooth muscle cell apoptotic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0034392)
GO:0051091 : positive regulation of DNA-binding transcription factor activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0051091)
GO:0046849 : bone remodeling (https://www.ebi.ac.uk/QuickGO/term/GO:0046849)
GO:0016055 : Wnt signaling pathway
(https://www.ebi.ac.uk/QuickGO/term/GO:0016055)
GO:0030278 : regulation of ossification

(https://www.ebi.ac.uk/QuickGO/term/GO:0030278)
GO:0071542 : dopaminergic neuron differentiation
(https://www.ebi.ac.uk/QuickGO/term/GO:0071542)
GO:0035115 : embryonic forelimb morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0035115)
GO:0060535 : trachea cartilage morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0060535)
GO:0060070 : canonical Wnt signaling pathway
(https://www.ebi.ac.uk/QuickGO/term/GO:0060070)
GO:0071397 : cellular response to cholesterol
(https://www.ebi.ac.uk/QuickGO/term/GO:0071397)
GO:0035108 : limb morphogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0035108)
GO:0060603 : mammary gland duct morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0060603)
GO:0072659 : protein localization to plasma membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0072659)
GO:0014029 : neural crest formation (https://www.ebi.ac.uk/QuickGO/term/GO:0014029)
GO:0060444 : branching involved in mammary gland duct morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0060444)
GO:0042733 : embryonic digit morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0042733)
GO:0060596 : mammary placode formation
(https://www.ebi.ac.uk/QuickGO/term/GO:0060596)
GO:0021795 : cerebral cortex cell migration
(https://www.ebi.ac.uk/QuickGO/term/GO:0021795)
GO:0045780 : positive regulation of bone resorption
(https://www.ebi.ac.uk/QuickGO/term/GO:0045780)
GO:0035261 : external genitalia morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0035261)
GO:0045599 : negative regulation of fat cell differentiation
(https://www.ebi.ac.uk/QuickGO/term/GO:0045599)
GO:0006469 : negative regulation of protein kinase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0006469)
GO:0060325 : face morphogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0060325)
GO:0110135 : Norrin signaling pathway
(https://www.ebi.ac.uk/QuickGO/term/GO:0110135)
GO:0090245 : axis elongation involved in somitogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0090245)
GO:0061310 : canonical Wnt signaling pathway involved in cardiac neural crest cell
differentiation involved in heart development
(https://www.ebi.ac.uk/QuickGO/term/GO:0061310)
GO:0061324 : canonical Wnt signaling pathway involved in positive regulation of cardiac
outflow tract cell proliferation (https://www.ebi.ac.uk/QuickGO/term/GO:0061324)
GO:0021587 : cerebellum morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0021587)
GO:0009950 : dorsal/ventral axis specification
(https://www.ebi.ac.uk/QuickGO/term/GO:0009950)
GO:0048596 : embryonic camera-type eye morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0048596)
GO:0060059 : embryonic retina morphogenesis in camera-type eye
(https://www.ebi.ac.uk/QuickGO/term/GO:0060059)
GO:0021872 : forebrain generation of neurons
(https://www.ebi.ac.uk/QuickGO/term/GO:0021872)
GO:0021861 : forebrain radial glial cell differentiation
(https://www.ebi.ac.uk/QuickGO/term/GO:0021861)
GO:0021943 : formation of radial glial scaffolds
(https://www.ebi.ac.uk/QuickGO/term/GO:0021943)
GO:0001702 : gastrulation with mouth forming second
(https://www.ebi.ac.uk/QuickGO/term/GO:0001702)
GO:0048699 : generation of neurons
(https://www.ebi.ac.uk/QuickGO/term/GO:0048699)
GO:0030917 : midbrain-hindbrain boundary development
(https://www.ebi.ac.uk/QuickGO/term/GO:0030917)
GO:2000051 : negative regulation of non-canonical Wnt signaling pathway
(https://www.ebi.ac.uk/QuickGO/term/GO:2000051)
GO:2000151 : negative regulation of planar cell polarity pathway involved in cardiac muscle
tissue morphogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:2000151)
GO:2000162 : negative regulation of planar cell polarity pathway involved in cardiac right
atrium morphogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:2000162)
GO:2000168 : negative regulation of planar cell polarity pathway involved in neural tube
closure (https://www.ebi.ac.uk/QuickGO/term/GO:2000168)
GO:2000164 : negative regulation of planar cell polarity pathway involved in outflow tract
morphogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:2000164)
GO:2000166 : negative regulation of planar cell polarity pathway involved in pericardium
morphogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:2000166)
GO:2000149 : negative regulation of planar cell polarity pathway involved in ventricular
septum morphogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:2000149)
GO:0001933 : negative regulation of protein phosphorylation

(https://www.ebi.ac.uk/QuickGO/term/GO:0001933)
GO:0071901 : negative regulation of protein serine/threonine kinase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0071901)
GO:0014033 : neural crest cell differentiation
(https://www.ebi.ac.uk/QuickGO/term/GO:0014033)
GO:0021915 : neural tube development
(https://www.ebi.ac.uk/QuickGO/term/GO:0021915)
GO:0003344 : pericardium morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0003344)
GO:0045778 : positive regulation of ossification
(https://www.ebi.ac.uk/QuickGO/term/GO:0045778)
GO:0090009 : primitive streak formation
(https://www.ebi.ac.uk/QuickGO/term/GO:0090009)
GO:0090118 : receptor-mediated endocytosis involved in cholesterol transport
(https://www.ebi.ac.uk/QuickGO/term/GO:0090118)
GO:0060284 : regulation of cell development
(https://www.ebi.ac.uk/QuickGO/term/GO:0060284)
GO:0051593 : response to folic acid (https://www.ebi.ac.uk/QuickGO/term/GO:0051593)
GO:0060042 : retina morphogenesis in camera-type eye
(https://www.ebi.ac.uk/QuickGO/term/GO:0060042)
GO:0021794 : thalamus development (https://www.ebi.ac.uk/QuickGO/term/GO:0021794)
GO:0021874 : Wnt signaling pathway involved in forebrain neuroblast division
(https://www.ebi.ac.uk/QuickGO/term/GO:0021874)
GO:0090244 : Wnt signaling pathway involved in somitogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0090244)

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:0016020 : membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0016020)
GO:0045121 : membrane raft (https://www.ebi.ac.uk/QuickGO/term/GO:0045121)
GO:0005623 : cell (https://www.ebi.ac.uk/QuickGO/term/GO:0005623)
GO:0005769 : early endosome (https://www.ebi.ac.uk/QuickGO/term/GO:0005769)
GO:0005783 : endoplasmic reticulum
(https://www.ebi.ac.uk/QuickGO/term/GO:0005783)
GO:0043025 : neuronal cell body (https://www.ebi.ac.uk/QuickGO/term/GO:0043025)
GO:0031410 : cytoplasmic vesicle (https://www.ebi.ac.uk/QuickGO/term/GO:0031410)
GO:0045202 : synapse (https://www.ebi.ac.uk/QuickGO/term/GO:0045202)
GO:0009986 : cell surface (https://www.ebi.ac.uk/QuickGO/term/GO:0009986)
GO:1990851 : Wnt-Frizzled-LRP5/6 complex
(https://www.ebi.ac.uk/QuickGO/term/GO:1990851)
GO:1990909 : Wnt signalosome (https://www.ebi.ac.uk/QuickGO/term/GO:1990909)

Presumptive Null

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

Molecular Type

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

Aberration Type

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

Molecular Details of the Mutation

Lrp6 gene expression is reduced in goldfish with the dorsal fin loss phenotype. Only four amino acid substitutions in the coding region and all of them are conserved or semi-conserved in zebrafish or medaka lrp6 orthologs. There is a 313-bp deletion in intron 21 of lrp6S in goldfish with the dorsal fin loss phenotype. This intronic deletion may affect induction and proper production of lrp6S mRNA at embryonic stages.

Experimental Evidence

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

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, Potassium channel subfamily K) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^7957^/and+Trait=Fin morphology/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

Loss of Lrp6 activity in zebrafish gives rise to a similar fin phenotype.