GEPHE SUMMARY

Gephebase Gene

Fgfr1a1 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Fgfr1a1^#gephebase-summary-title)

GepheID

GP00000313

Entry Status

Published

Main curator

Martin

PHENOTYPIC CHANGE

Trait Category

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

Trait

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

Trait State in Taxon A

Cyprinus carpio - scaled

Trait State in Taxon B

Cyprinus carpio - "Mirror phenotype"

Ancestral State

Taxon A

Taxonomic Status

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

Taxon A

Latin Name

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

Common Name

common carp

Synonyms

common carp; carp; fancy carp; koi; mirror carp; Cyprinus carpio Linnaeus, 1758; Cyprinus cyprio; Cyrpinus carpio

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; Cyprinoidea; Cyprinidae; Cyprinus

Parent

Cyprinus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7961)

NCBI Taxonomy ID

7962 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7962)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

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

Common Name

common carp

Synonyms

common carp; carp; fancy carp; koi; mirror carp; Cyprinus carpio Linnaeus, 1758; Cyprinus cyprio; Cyrpinus carpio

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; Cyprinoidea; Cyprinidae; Cyprinus

Parent

Cyprinus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7961)

NCBI Taxonomy ID

7962 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7962)

is Taxon B an Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

fgfr1a

Synonyms

cb231; fgfr1; FGFR-1-A; sb:cb231; bFGF-R-1-A; si:ch211-198o12.1

String

7955.ENSDARP00000069260 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=7955.ENSDARP00000069260)

Sequence Similarities

Belongs to the protein kinase superfamily. Tyr protein kinase family. Fibroblast growth factor receptor subfamily.

GO - Molecular Function

GO:0004888 : transmembrane signaling receptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004888)
GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)
GO:0008201 : heparin binding (https://www.ebi.ac.uk/QuickGO/term/GO:0008201)
GO:0004714 : transmembrane receptor protein tyrosine kinase activity

UniProtKB Danio rerio

Q90Z00 (http://www.uniprot.org/uniprot/Q90Z00)

GenebankID or UniProtKB

ACJ66723 (https://www.ncbi.nlm.nih.gov/nuccore/ACJ66723)

(https://www.ebi.ac.uk/QuickGO/term/GO:0004714)
GO:0017134 : fibroblast growth factor binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0017134)
GO:0005007 : fibroblast growth factor-activated receptor activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0005007)

GO - Biological Process

GO:0043066 : negative regulation of apoptotic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0043066)
GO:0030154 : cell differentiation (https://www.ebi.ac.uk/QuickGO/term/GO:0030154)
GO:0070374 : positive regulation of ERK1 and ERK2 cascade
(https://www.ebi.ac.uk/QuickGO/term/GO:0070374)
GO:0008284 : positive regulation of cell proliferation
(https://www.ebi.ac.uk/QuickGO/term/GO:0008284)
GO:0043406 : positive regulation of MAP kinase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0043406)
GO:0009953 : dorsal/ventral pattern formation
(https://www.ebi.ac.uk/QuickGO/term/GO:0009953)
GO:0042664 : negative regulation of endodermal cell fate specification
(https://www.ebi.ac.uk/QuickGO/term/GO:0042664)
GO:0009968 : negative regulation of signal transduction
(https://www.ebi.ac.uk/QuickGO/term/GO:0009968)
GO:0018108 : peptidyl-tyrosine phosphorylation
(https://www.ebi.ac.uk/QuickGO/term/GO:0018108)
GO:0008543 : fibroblast growth factor receptor signaling pathway
(https://www.ebi.ac.uk/QuickGO/term/GO:0008543)
GO:0060249 : anatomical structure homeostasis
(https://www.ebi.ac.uk/QuickGO/term/GO:0060249)
GO:0048738 : cardiac muscle tissue development
(https://www.ebi.ac.uk/QuickGO/term/GO:0048738)
GO:0031101 : fin regeneration (https://www.ebi.ac.uk/QuickGO/term/GO:0031101)
GO:0001889 : liver development (https://www.ebi.ac.uk/QuickGO/term/GO:0001889)
GO:0021628 : olfactory nerve formation
(https://www.ebi.ac.uk/QuickGO/term/GO:0021628)
GO:0071699 : olfactory placode morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0071699)
GO:0010863 : positive regulation of phospholipase C activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0010863)
GO:0036342 : post-anal tail morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0036342)
GO:0048916 : posterior lateral line development
(https://www.ebi.ac.uk/QuickGO/term/GO:0048916)
GO:0045471 : response to ethanol (https://www.ebi.ac.uk/QuickGO/term/GO:0045471)
GO:0043589 : skin morphogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0043589)

GO - Cellular Component

GO:0005886 : plasma membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005886)
GO:0005737 : cytoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005737)
GO:0005829 : cytosol (https://www.ebi.ac.uk/QuickGO/term/GO:0005829)
GO:0005887 : integral component of plasma membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0005887)
GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)
GO:0043235 : receptor complex (https://www.ebi.ac.uk/QuickGO/term/GO:0043235)
GO:0031410 : cytoplasmic vesicle (https://www.ebi.ac.uk/QuickGO/term/GO:0031410)

Presumptive Null

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

Glu664Lys

Experimental Evidence

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

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

Main Reference

Duplication of fgfr1 permits Fgf signaling to serve as a target for selection during domestication. (2009) (https://pubmed.ncbi.nlm.nih.gov/19733072)

Authors

Rohner N; BercsÃ©nyi M; OrbÃ¡n L; Kolanczyk ME; Linke D; Brand M; NÃ¼sslein-Volhard C; Harris MP

Abstract

The genetic basis of morphological variation both within and between species has been a lasting question in evolutionary biology and one of considerable recent debate. It is thought that

changes in postembryonic development leading to variations in adult form often serve as a basis for selection . Thus, we investigated the genetic basis of the development of adult structures in the zebrafish via a forward genetic approach and asked whether the genes and mechanisms found could be predictive of changes in other species. Here we describe the spiegeldanio (spd) zebrafish mutation, which leads to reduced scale formation in the adult. The affected gene is fibroblast growth factor receptor 1 (fgfr1), which is known to have an essential embryonic function in vertebrate development. We find that the zebrafish has two paralogs encoding Fgfr1 and show that they function redundantly during embryogenesis. However, only one paralog is required for formation of scales during juvenile development. Furthermore, we identify loss-of-function alleles changing the coding sequence of Fgfr1a1 that have been independently selected twice during the domestication of the carp (Cyprinus carpio). These findings provide evidence for the role for gene duplication in providing the raw material for generation of morphological diversity.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

1 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^Fgfr1a1^/and+Taxon ID=^7962^/or+Gene Gephebase=^Fgfr1a1^/and+Taxon ID=^7962^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS