GEPHE SUMMARY

Gephebase Gene
zic1/zic4 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^zic1/zic4^#gephebase-summary-title)

GepheID
GP00002038

Entry Status
Published

Main curator
Courtier

PHENOTYPIC CHANGE

Trait #1

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

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

Trait State in Taxon A
wild-type â€“ wedge shaped body morphology; small dorsal fin; asymmetric caudal fin

Trait State in Taxon B
Tear-drop shaped body morphology; shape of dorsal fin resembles shape of anal fin; symmetric caudal fin

Trait #2

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

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

Trait State in Taxon A
wild-type - lack of bright pigmentation on the back

Trait State in Taxon B
bright pigmentation on back

Ancestral State
Taxon A

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

Taxon A

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

Common Name
Japanese medaka

Synonyms
Poecilia latipes; Japanese medaka; Japanese rice fish; medaka; Oryzias latipes (Temminck & Schlegel, 1846); Poecilia latipes Temminck & Schlegel, 1846; Orizias latipes

Rank
species

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Actinopteri; Neopterygii; Teleostei; Osteoglossocephalai; Clupeocephala; Euteleosteomorpha; Neoteleostei; Eurypterygia; Ctenosquamata; Acanthomorphata; Euacanthomorphacea; Percomorphaceae; Ovalentaria; Atherinomorphae; Beloniformes; Adrianichthyoidei; Adrianichthyidae; Oryziinae; Oryzias

Parent
Oryzias () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 8089)

NCBI Taxonomy ID
8090 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 8090)

is Taxon A an Infraspecies?
No

Taxon B

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

Common Name
Japanese medaka

Synonyms
Poecilia latipes; Japanese medaka; Japanese rice fish; medaka; Oryzias latipes (Temminck & Schlegel, 1846); Poecilia latipes Temminck & Schlegel, 1846; Orizias latipes

Rank
species

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Actinopteri; Neopterygii; Teleostei; Osteoglossocephalai; Clupeocephala; Euteleosteomorpha; Neoteleostei; Eurypterygia; Ctenosquamata; Acanthomorphata; Euacanthomorphacea; Percomorphaceae; Ovalentaria; Atherinomorphae; Beloniformes; Adrianichthyoidei; Adrianichthyidae; Oryziinae; Oryzias

Parent
Oryzias () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 8089)

NCBI Taxonomy ID
8090 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 8090)

is Taxon B an Infraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name

Zic1

Synonyms

ZIC; ZNF201; Zic

String

10090.ENSMUSP00000034927
(http://string-db.org/newstring_cgi/show_network_section.pl?identifier=
10090.ENSMUSP00000034927)

Sequence Similarities

Belongs to the GLI C2H2-type zinc-finger protein family.

GO - Molecular Function

GO:0001228 : DNA-binding transcription activator activity, RNA polymerase II-specific
(https://www.ebi.ac.uk/QuickGO/term/GO:0001228)
GO:0003700 : DNA-binding transcription factor activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0003700)
GO:0000977 : RNA polymerase II regulatory region sequence-specific DNA binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0000977)
GO:0046872 : metal ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0046872)
GO:0000981 : DNA-binding transcription factor activity, RNA polymerase II-specific
(https://www.ebi.ac.uk/QuickGO/term/GO:0000981)
GO:0000978 : RNA polymerase II proximal promoter sequence-specific DNA binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0000978)

GO - Biological Process

GO:0007417 : central nervous system development
(https://www.ebi.ac.uk/QuickGO/term/GO:0007417)
GO:0045944 : positive regulation of transcription by RNA polymerase II
(https://www.ebi.ac.uk/QuickGO/term/GO:0045944)
GO:0030154 : cell differentiation (https://www.ebi.ac.uk/QuickGO/term/GO:0030154)
GO:0001501 : skeletal system development
(https://www.ebi.ac.uk/QuickGO/term/GO:0001501)
GO:0045893 : positive regulation of transcription, DNA-templated
(https://www.ebi.ac.uk/QuickGO/term/GO:0045893)
GO:0007420 : brain development (https://www.ebi.ac.uk/QuickGO/term/GO:0007420)
GO:0042472 : inner ear morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0042472)
GO:0008589 : regulation of smoothened signaling pathway
(https://www.ebi.ac.uk/QuickGO/term/GO:0008589)
GO:0007389 : pattern specification process
(https://www.ebi.ac.uk/QuickGO/term/GO:0007389)
GO:0042307 : positive regulation of protein import into nucleus
(https://www.ebi.ac.uk/QuickGO/term/GO:0042307)
GO:0021510 : spinal cord development
(https://www.ebi.ac.uk/QuickGO/term/GO:0021510)
GO:0007628 : adult walking behavior
(https://www.ebi.ac.uk/QuickGO/term/GO:0007628)

GO - Cellular Component

GO:0005737 : cytoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005737)
GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)

UniProtKB Mus musculus

P46684 (http://www.uniprot.org/uniprot/P46684)

GenebankID or UniProtKB

()

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

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

Insertion Size

100-1000 kb

Molecular Details of the Mutation

The mutant phenotype is caused by a dramatic decrease of zic1/zic4 expression in the dorsal somites. The insertion of a transposon (â€œAlbatrossâ€) into an enhancer region (downstream of zic4) of the transcription factors zic1 and zic4 causes this phenotype. Both genes are expressed by a bi-directional promoter. The transposon insertion is proposed to interfere with the transcriptional regulation of zic1/zic4; resulting in the disturbance of the expression of the transcription factors in the dorsal somites (the expression of zic1/zic4 in other parts of the body is not affected in this mutant) and ultimately causing a ventralized trunk phenotype. In Inoue et al. (2017) it was shown that the transposon â€œAlbatrossâ€ is actually larger than originally predicted; and is now called â€œTeratornâ€. Teratorn is around 180kb long and appears to originate from the fusion of a DNA transposon and a herpesvirus.

Experimental Evidence

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

Main Reference

The medaka zic1/zic4 mutant provides molecular insights into teleost caudal fin evolution. (2012) (https://pubmed.ncbi.nlm.nih.gov/22386310)

Authors

Moriyama Y; Kawanishi T; Nakamura R; Tsukahara T; Sumiyama K; Suster ML; Kawakami K; Toyoda A; Fujiyama A; Yasuoka Y; Nagao Y; Sawatari E; Shimizu A; Wakamatsu Y; Hibi M; Taira M; Okabe M; Naruse K; Hashimoto H; Shimada A; Takeda H

Abstract

Teleosts have an asymmetrical caudal fin skeleton formed by the upward bending of the caudal-most portion of the body axis, the ural region. This homocercal type of caudal fin ensures powerful and complex locomotion and is regarded as one of the most important innovations for teleosts during adaptive radiation in an aquatic environment. However, the mechanisms that create asymmetric caudal fin remain largely unknown. The spontaneous medaka (teleost fish) mutant, Double anal fin (Da), exhibits a unique symmetrical caudal skeleton that resembles the

diphycercal type seen in Polypterus and Coelacanth. We performed a detailed analysis of the Da mutant to obtain molecular insight into caudal fin morphogenesis. We first demonstrate that a large transposon, inserted into the enhancer region of the zic1 and zic4 genes (zic1/zic4) in Da, is associated with the mesoderm-specific loss of their transcription. We then show that zic1/zic4 are strongly expressed in the dorsal part of the ural mesenchyme and thereby induce asymmetric caudal fin development in wild-type embryos, whereas their expression is lost in Da. Comparative analysis further indicates that the dorsal mesoderm expression of zic1/zic4 is conserved in teleosts, highlighting the crucial role of zic1/zic4 in caudal fin morphogenesis.

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Additional References

Complete fusion of a transposon and herpesvirus created the Teratorn mobile element in medaka fish. (2017) (https://pubmed.ncbi.nlm.nih.gov/28916771)

RELATED GEPHE

Related Genes

1 (tyrosinase (TYR)) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^8090^/and+Trait=Fin morphology/or+Taxon ID=^8090^/and+Trait=Pigmentation/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@TE - The mutant was isolated by chance from a wild population in the 1960s. Validated by Ann Kathrin Heilig.