

GEPHE SUMMARY

Gephebase Gene

[zic1/zic4](#)

Entry Status

Published

GepheID

GP00002038

Main curator

Courtier

PHENOTYPIC CHANGE

Trait Category

[Morphology](#)

Trait

[Fin morphology \(skeleton; caudal fin\)](#)

Trait State in Taxon A

wild-type - asymmetric caudal fin

Trait State in Taxon B

symmetrical caudal skeleton

Ancestral State

Taxon A

Taxonomic Status

[Intraspecific](#)

Taxon A

Latin Name

Oryzias latipes

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; Clupecocephala; Euteleostomorpha; Neoteleostei; Eurypterygia; Ctenosquamata; Acanthomorphata; Euacanthomorphacea; Percomorphaceae; Ovalentaria; Atherinomorphae; Beloniformes; Adrianichthyoidei; Adrianichthyidae; Oryziinae; *Oryzias*

Parent

Oryzias () - (Rank: genus)

NCBI Taxonomy ID

8090

is Taxon A an Intraspecies?

No

Taxon B

Latin Name

Oryzias latipes

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*

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Parent

Oryzias () - (Rank: genus)

NCBI Taxonomy ID

8090

is Taxon B an Intraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

[Zic1](#)

Synonyms

ZIC; ZNF201; Zic

String

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

GO:0003700 : DNA-binding transcription factor activity

GO:0000977 : RNA polymerase II regulatory region sequence-specific DNA binding

GO:0046872 : metal ion binding

GO:0000981 : DNA-binding transcription factor activity, RNA polymerase II-specific

GO:0000978 : RNA polymerase II proximal promoter sequence-specific DNA binding

GO - Biological Process

UniProtKB *Mus musculus*

[P46684](#)

GenebankID or UniProtKB

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

GO - Cellular Component

GO:0005737 : cytoplasm
GO:0005634 : nucleus

Presumptive Null

No

Molecular Type

Cis-regulatory

Aberration Type

Insertion

Insertion Size

-

Molecular Details of the Mutation

insertion of a large transposon (Albatross) into the enhancer region of the *zic1* and *zic4* genes. Both genes are expressed by a bi-directional promoter. This transposon insertion disrupts the expression of the transcription factors in the dorsal somites and this causes the centralised trunk phenotype. Inoue et al. 2017 show that the transposon "Albatross" is actually way larger and the authors call it "Teratorn". Teratorn is 180-kb long and appears to originate from the fusion of a DNA transposon and a herpesvirus.

Experimental Evidence

Linkage Mapping

Main Reference

The medaka *zic1/zic4* mutant provides molecular insights into teleost caudal fin evolution. (2012)

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)

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

COMMENTS

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

