

GEPHE SUMMARY

<p>zic1/zic4 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=zic1/zic4#gephebase-summary-title)</p> <p>Published</p>	<p>Gephebase Gene</p> <p>Entry Status</p>	<p>GP00002385</p> <p>Santos</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>Fin morphology (skeleton; caudal fin) (https://www.gephebase.org/search-criteria?/and+Trait=Fin+morphology+(skeleton;+caudal+fin)#gephebase-summary-title)</p> <p>wild-type fish</p> <p>double tail mutant</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>Latin Name</p> <p>Betta splendens (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=Betta+splendens#gephebase-summary-title)</p> <p>Common Name</p> <p>Siamese fighting fish</p> <p>Synonyms</p> <p>Siamese fighting fish; Betta splendens Regan, 1910</p> <p>Rank</p> <p>species</p> <p>Lineage</p> <p>cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Actinopteri; Neopterygii; Teleostei; Osteoglossocephalai; Clupecocephala; Euteleostei; Neoteleostei; Eurypterygia; Ctenosquamata; Acanthomorpha; Euacanthomorpha; Percomorphaceae; Anabantaria; Anabantiformes; Anabantoidi; Osphronemidae; Macropodinae; Betta</p> <p>Parent</p> <p>Betta () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=158455)</p> <p>NCBI Taxonomy ID</p> <p>158456 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=158456)</p> <p>is Taxon A an Intraspecies?</p> <p>No</p>	<p>Taxon B</p> <p>Latin Name</p> <p>Betta splendens (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=Betta+splendens#gephebase-summary-title)</p> <p>Common Name</p> <p>Siamese fighting fish</p> <p>Synonyms</p> <p>Siamese fighting fish; Betta splendens Regan, 1910</p> <p>Rank</p> <p>species</p> <p>Lineage</p> <p>cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Actinopteri; Neopterygii; Teleostei; Osteoglossocephalai; Clupecocephala; Euteleostei; Neoteleostei; Eurypterygia; Ctenosquamata; Acanthomorpha; Euacanthomorpha; Percomorphaceae; Anabantaria; Anabantiformes; Anabantoidi; Osphronemidae; Macropodinae; Betta</p> <p>Parent</p> <p>Betta () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=158455)</p> <p>NCBI Taxonomy ID</p> <p>158456 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=158456)</p> <p>is Taxon B an Intraspecies?</p> <p>No</p>
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GENOTYPIC CHANGE

<p>Zic1</p> <p>ZIC; ZNF201; Zic</p> <p>10090.ENSMUSP00000034927 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=10090.ENSMUSP00000034927)</p> <p>Belongs to the GLI C2H2-type zinc-finger protein family.</p> <p>GO - Molecular Function</p> <p>GO:0001228 : DNA-binding transcription activator activity, RNA polymerase II-specific (https://www.ebi.ac.uk/QuickGO/term/GO:0001228)</p> <p>GO:0003700 : DNA-binding transcription factor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003700)</p> <p>GO:0000977 : RNA polymerase II regulatory region sequence-specific DNA binding</p>	<p>Generic Gene Name</p> <p>Synonyms</p> <p>String</p> <p>Sequence Similarities</p>	<p>P46684 (http://www.uniprot.org/uniprot/P46684)</p> <p>0</p>	<p>UniProtKB Mus musculus</p> <p>GenebankID or UniProtKB</p>
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(<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>)

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

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

Deletion Size

100-999 bp

Molecular Details of the Mutation

"We further sequenced the genomes of both homozygous single- and double-tail fish and found in double tail no large sequence variation except for a \sim 180-bp deletion \sim 415-kb downstream of *zic4* (fig. 4C and supplementary fig. S19a, Supplementary Material online). This deletion was located in a cluster of CNEs and coincided with predicted CNE.006008 (supplementary fig. S19b, Supplementary Material online)."

"We observed that the wild-type ST allele significantly enhanced green fluorescent protein (GFP) expression in embryos at 24 hpf, when both *zic1* and *zic4* show differential expression between double-tail and wild-type fish (Moriyama et al. 2012), whereas no visible GFP expression was detected for the st allele (fig. 4E and supplementary table S11, Supplementary Material online). The efficiency of the two alleles as candidate enhancers was further examined using a Dual-Luciferase Reporter Assay, which showed that the ST allele enhanced luciferase expression by \sim 410 \times relative to st allele in Singapore grouper embryonic cell line (fig. 4F)."

"Finally, we deleted this enhancer using the CRISPR-Cas9 system in fighting fish. Considering the efficiency of tested gRNAs and the cluster of CNEs that could have unpredicted functions, we limited the modification to the CNE.006008 region and did not involve the other CNEs (supplementary fig. S20, Supplementary Material online). Genetic analysis revealed that none of these fish had completely deleted CNE.006008, suggesting nonsimultaneous cutting at multiple targeted gRNA positions. These mosaic fish ($n=7$) had significantly more fin rays than the noninjected controls ($P<0.01$; fig. 4G)."

Experimental Evidence

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

Main Reference

Genomic Basis of Striking Fin Shapes and Colors in the Fighting Fish. (2021) (<https://pubmed.ncbi.nlm.nih.gov/33871625>)

Authors

Wang L; Sun F; Wan ZY; Ye B; Wen Y; Liu H; Yang Z; Pang H; Meng Z; Fan B; Alfiko Y; Shen Y; Bai B; Lee MSQ; Piferrer F; Schartl M; Meyer A; Yue GH

Abstract

Resolving the genomic basis underlying phenotypic variations is a question of great importance in evolutionary biology. However, understanding how genotypes determine the phenotypes is still challenging. Centuries of artificial selective breeding for beauty and aggression resulted in a plethora of colors, long-fin varieties, and hyper-aggressive behavior in the air-breathing Siamese fighting fish (*Betta splendens*), supplying an excellent system for studying the genomic basis of phenotypic variations. Combining whole-genome sequencing, quantitative trait loci mapping, genome-wide association studies, and genome editing, we investigated the genomic basis of huge morphological variation in fins and striking differences in coloration in the fighting fish. Results revealed that the double tail, elephant ear, albino, and fin spot mutants each were determined by single major-effect loci. The elephant ear phenotype was likely related to differential expression of a potassium ion channel gene, *kcnh8*. The albinotic phenotype was likely linked to a cis-regulatory element acting on the *mitfa* gene and the double-tail mutant was suggested to be caused by a deletion in a *zic1/zic4* coenhancer. Our data highlight that major loci and cis-regulatory elements play important roles in bringing about phenotypic innovations and establish Bettas as new powerful model to study the genomic basis of evolved changes.

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Additional References

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS