GEPHE SUMMARY

Gephebase Gene

Microphtalmia-associated transcription factor a (MITFA) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Microphtalmia-associated transcription factor a (MITFA)^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00002379

Main curator

Santos

PHENOTYPIC CHANGE

Trait Category

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

Trait

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

Trait State in Taxon A

wild-type pigmented fish

Trait State in Taxon B

lack of black pigments in the fins and body

Ancestral State

Taxon A

Taxonomic Status

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

Taxon A

Latin Name

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

Common Name

Siamese fighting fish

Synonyms

Siamese fighting fish; Betta splendens Regan, 1910

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; Anabantaria; Anabantiformes; Anabantoidei; Osphronemidae; Macropodinae; Betta

Parent

Betta () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 158455)

NCBI Taxonomy ID

158456 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 158456)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

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

Common Name

Siamese fighting fish

Synonyms

Siamese fighting fish; Betta splendens Regan, 1910

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; Anabantaria; Anabantiformes; Anabantoidei; Osphronemidae; Macropodinae; Betta

Parent

Betta () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 158455)

NCBI Taxonomy ID

158456 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 158456)

is Taxon B an Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

-

Synonyms

-

String

-

Sequence Similarities

-

GO - Molecular Function

-

GO - Biological Process

-

GO - Cellular Component

-

UniProtKB

Q6P0E9NULL (http://www.uniprot.org/uniprot/Q6P0E9NULL)

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

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

Deletion Size

100-999 bp

Molecular Details of the Mutation

"Comparison between homozygous albino and wild-type pigmented fish revealed a cluster of indels and SNPs about 25â€‰kb upstream of mitfa, including a 366-bp deletion in the albino mutant. Genotyping this deletion in â^¼1,000 fish revealed that this deletion was strictly correlated with the albino phenotype (supplementary fig. S14 and table S9, Supplementary Material online). These data suggest that the 366-bp deletion is a distant cis-regulatory element and could underlie the albino phenotype."

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.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS