

GEPHE SUMMARY

	Gephebase Gene	GephelD
Microphthalmia-associated transcription factor a (MITFA) (https://www.gephebase.org/search-criteria/?and+Gene Gephebase=^Microphthalmia-associated transcription factor a (MITFA)^#gephebase-summary-title)	GP00002379	Main curator
	Entry Status	
Published	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	Taxon B
Betta splendens (https://www.gephebase.org/search-criteria/?and+Taxon and Synonyms=^Betta splendens^#gephebase-summary-title)	Latin Name	Latin Name
Siamese fighting fish	Common Name	Common Name
Siamese fighting fish; Betta splendens Regan, 1910	Synonyms	Synonyms
species	Rank	Rank
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Actinopteri; Neopterygii; Teleostei; Osteoglossocephalai; Clupeocephala; Euteleosteomorpha; Neoteleostei; Eurypterygia; Ctenosquamata; Acanthomorpha; Euacanthomorphacea; Percomorphaceae; Anabantaria; Anabantiformes; Anabantoidei; Osphronemidae; Macropodinae; Betta	Lineage	Lineage
Betta () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 158455)	Parent	Parent
158456 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 158456)	NCBI Taxonomy ID	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB
-		
-	Synonyms	GenebankID or UniProtKB
-	0	
-	String	
-	Sequence Similarities	
-	GO - Molecular Function	
-	GO - Biological Process	
-	GO - Cellular Component	
-		Presumptive Null

No ([#gephebase-summary-title\)](https://www.gephebase.org/search-criteria?/and+Presumptive+Null=%No)

Molecular Type

Cis-regulatory ([#gephebase-summary-title\)](https://www.gephebase.org/search-criteria?/and+Molecular+Type=%Cis-regulatory)

Aberration Type

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

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 25kb upstream of mitfa, including a 366-bp deletion in the albino mutant. Genotyping this deletion in ~41,000 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 ([#gephebase-summary-title\)](https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=%Linkage+Mapping)

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

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS