

GEPHE SUMMARY

csf1 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=^csf1^#gephebase-summary-title)	Gephebase Gene	GP00002366	GepheID
	Entry Status	Santos	Main curator
	Published		

PHENOTYPIC CHANGE

Morphology (https://www.gephebase.org/search-criteria?/and+TraitCategory=^Morphology^#gephebase-summary-title)		Trait Category	
Coloration (https://www.gephebase.org/search-criteria?/and+Trait=^Coloration^#gephebase-summary-title)		Trait	
no red coloration in the pectoral fins		Trait State in Taxon A	
red coloration in the pectoral fins		Trait State in Taxon B	
Taxon A		Ancestral State	
Interspecific (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=^Interspecific^#gephebase-summary-title)		Taxonomic Status	
Taxon A		Taxon B	
Oryzias celebensis (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Oryziascelebensis^#gephebase-summary-title)		Oryzias woworae (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Oryziaswoworae^#gephebase-summary-title)	
Celebes medaka		-	
Haplochilus celebensis; Celebes medaka; Haplochilus celebensis Weber, 1894; Oryzias celebensis (Weber, 1894)		Oryzias woworae Parenti & Hadiaty, 2010	
species		species	
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Actinopteri; Neopterygii; Teleostei; Osteoglossocephalai; Clupecocephala; Euteleosteomorpha; Neoteleostei; Eurypterygia; Ctenosquamata; Acanthomorpha; Euacanthomorphacea; Percomorphaceae; Ovalentaria; Atherinomorphae; Beloniformes; Adrianichthyoidei; Adrianichthyidae; Oryziinae; Oryzias		cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Actinopteri; Neopterygii; Teleostei; Osteoglossocephalai; Clupecocephala; Euteleosteomorpha; Neoteleostei; Eurypterygia; Ctenosquamata; Acanthomorpha; Euacanthomorphacea; Percomorphaceae; Ovalentaria; Atherinomorphae; Beloniformes; Adrianichthyoidei; Adrianichthyidae; Oryziinae; Oryzias	
Oryzias () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 8089)		Oryzias () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 8089)	
126373 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 126373)		1221322 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 1221322)	
No		No	

GENOTYPIC CHANGE

CSF1		Generic Gene Name		UniProtKB Homo sapiens
MCSF; CSF-1		Synonyms		GenebankID or UniProtKB
9606.ENSPO0000327513 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=9606.ENSPO0000327513)		String		
-		Sequence Similarities		
GO:0042802 : identical protein binding (https://www.ebi.ac.uk/QuickGO/term/GO:0042802)		GO - Molecular Function		
GO:0042803 : protein homodimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0042803)				

GO:0005125 : cytokine activity (<https://www.ebi.ac.uk/QuickGO/term/GO:0005125>)
GO:0008083 : growth factor activity (<https://www.ebi.ac.uk/QuickGO/term/GO:0008083>)
GO:0005157 : macrophage colony-stimulating factor receptor binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005157>)

GO - Biological Process

GO:0045087 : innate immune response
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045087>)
GO:1901215 : negative regulation of neuron death
(<https://www.ebi.ac.uk/QuickGO/term/GO:1901215>)
GO:0008284 : positive regulation of cell proliferation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0008284>)
GO:0046579 : positive regulation of Ras protein signal transduction
(<https://www.ebi.ac.uk/QuickGO/term/GO:0046579>)
GO:0010628 : positive regulation of gene expression
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010628>)
GO:0001503 : ossification (<https://www.ebi.ac.uk/QuickGO/term/GO:0001503>)
GO:0006954 : inflammatory response
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006954>)
GO:0007265 : Ras protein signal transduction
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007265>)
GO:0042476 : odontogenesis (<https://www.ebi.ac.uk/QuickGO/term/GO:0042476>)
GO:0040018 : positive regulation of multicellular organism growth
(<https://www.ebi.ac.uk/QuickGO/term/GO:0040018>)
GO:0030316 : osteoclast differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0030316>)
GO:0030335 : positive regulation of cell migration
(<https://www.ebi.ac.uk/QuickGO/term/GO:0030335>)
GO:0030224 : monocyte differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0030224>)
GO:0010759 : positive regulation of macrophage chemotaxis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010759>)
GO:0030278 : regulation of ossification
(<https://www.ebi.ac.uk/QuickGO/term/GO:0030278>)
GO:0060444 : branching involved in mammary gland duct morphogenesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0060444>)
GO:0030225 : macrophage differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0030225>)
GO:0048873 : homeostasis of number of cells within a tissue
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048873>)
GO:0007169 : transmembrane receptor protein tyrosine kinase signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007169>)
GO:0003006 : developmental process involved in reproduction
(<https://www.ebi.ac.uk/QuickGO/term/GO:0003006>)
GO:0038145 : macrophage colony-stimulating factor signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0038145>)
GO:0061519 : macrophage homeostasis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0061519>)
GO:0060763 : mammary duct terminal end bud growth
(<https://www.ebi.ac.uk/QuickGO/term/GO:0060763>)
GO:0060611 : mammary gland fat development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0060611>)
GO:0061518 : microglial cell proliferation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0061518>)
GO:0042117 : monocyte activation (<https://www.ebi.ac.uk/QuickGO/term/GO:0042117>)
GO:0035702 : monocyte homeostasis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0035702>)
GO:0097529 : myeloid leukocyte migration
(<https://www.ebi.ac.uk/QuickGO/term/GO:0097529>)
GO:0001780 : neutrophil homeostasis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0001780>)
GO:0002158 : osteoclast proliferation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0002158>)
GO:0001954 : positive regulation of cell-matrix adhesion
(<https://www.ebi.ac.uk/QuickGO/term/GO:0001954>)
GO:1902228 : positive regulation of macrophage colony-stimulating factor signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:1902228>)
GO:0010744 : positive regulation of macrophage derived foam cell differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010744>)
GO:0045651 : positive regulation of macrophage differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045651>)
GO:1905523 : positive regulation of macrophage migration
(<https://www.ebi.ac.uk/QuickGO/term/GO:1905523>)
GO:1904141 : positive regulation of microglial cell migration
(<https://www.ebi.ac.uk/QuickGO/term/GO:1904141>)
GO:0045657 : positive regulation of monocyte differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045657>)
GO:0032946 : positive regulation of mononuclear cell proliferation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0032946>)

GO:0042488 : positive regulation of odontogenesis of dentin-containing tooth
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042488>)
GO:0045672 : positive regulation of osteoclast differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045672>)
GO:0045860 : positive regulation of protein kinase activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045860>)
GO:0051247 : positive regulation of protein metabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0051247>)
GO:0010743 : regulation of macrophage derived foam cell differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010743>)
GO:0002931 : response to ischemia (<https://www.ebi.ac.uk/QuickGO/term/GO:0002931>)
GO - Cellular Component

GO:0016021 : integral component of membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)
GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)
GO:0016020 : membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0016020>)
GO:0005576 : extracellular region (<https://www.ebi.ac.uk/QuickGO/term/GO:0005576>)
GO:0016604 : nuclear body (<https://www.ebi.ac.uk/QuickGO/term/GO:0016604>)
GO:0005615 : extracellular space (<https://www.ebi.ac.uk/QuickGO/term/GO:0005615>)
GO:0005788 : endoplasmic reticulum lumen
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005788>)
GO:0048471 : perinuclear region of cytoplasm
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048471>)
GO:1990682 : CSF1-CSF1R complex (<https://www.ebi.ac.uk/QuickGO/term/GO:1990682>)

No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=~No~#gephebase-summary-title)	Presumptive Null
Cis-regulatory (https://www.gephebase.org/search-criteria?/and+Molecular Type=~Cis-regulatory~#gephebase-summary-title)	Molecular Type
Unknown (https://www.gephebase.org/search-criteria?/and+Aberration Type=~Unknown~#gephebase-summary-title)	Aberration Type
-	Molecular Details of the Mutation
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Linkage Mapping~#gephebase-summary-title)	Experimental Evidence
Genome editing reveals fitness effects of a gene for sexual dichromatism in Sulawesian fishes. (2021) (https://pubmed.ncbi.nlm.nih.gov/33649298)	Main Reference
Ansai S; Mochida K; Fujimoto S; Mokodongan DF; Sumarto BKA; Masengi KWA; Hadiaty RK; Nagano AJ; Toyoda A; Naruse K; Yamahira K; Kitano J	Authors

Sexual selection drives rapid phenotypic diversification of mating traits. However, we know little about the causative genes underlying divergence in sexually selected traits. Here, we investigate the genetic basis of male mating trait diversification in the medaka fishes (genus <i>Oryzias</i>) from Sulawesi, Indonesia. Using linkage mapping, transcriptome analysis, and genome editing, we identify <i>csf1</i> as a causative gene for red pectoral fins that are unique to male <i>Oryzias woworae</i> . A cis-regulatory mutation enables androgen-induced expression of <i>csf1</i> in male fins. <i>csf1</i> -knockout males have reduced red coloration and require longer for mating, suggesting that coloration can contribute to male reproductive success. Contrary to expectations, non-red males are more attractive to a predatory fish than are red males. Our results demonstrate that integrating genomics with genome editing enables us to identify causative genes underlying sexually selected traits and provides a new avenue for testing theories of sexual selection.	Abstract
	Additional References

RELATED GEPHE

No matches found.	Related Genes
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS