

GEPHE SUMMARY

pax7a (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~pax7a~#gephebase-summary-title)	Gephebase Gene	GP00001423	GepheID
	Entry Status	Prigent	Main curator
	Published		

PHENOTYPIC CHANGE

		Trait Category	
Morphology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~Morphology~#gephebase-summary-title)		Trait	
Coloration (scales) (https://www.gephebase.org/search-criteria?/and+Trait=~Coloration(scales)~#gephebase-summary-title)		Trait State in Taxon A	
Labeotropheus trewavasae & Metriaclima zebra large blotched morph		Trait State in Taxon B	
Labeotropheus trewavasae & Metriaclima zebra light blotched morph		Ancestral State	
Unknown		Taxonomic Status	
Intraspecific (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~Intraspecific~#gephebase-summary-title)			
Taxon A		Taxon B	
Labeotropheus trewavasae		Labeotropheus trewavasae	
(https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=~Labeotropheus trewavasae~#gephebase-summary-title)		(https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=~Labeotropheus trewavasae~#gephebase-summary-title)	
Common Name		Common Name	
-		-	
Synonyms		Synonyms	
scrapermouth mbuna; Labeotropheus trewavasae Fryer, 1956; Labeotropheus trewavassae		scrapermouth mbuna; Labeotropheus trewavasae Fryer, 1956; Labeotropheus trewavassae	
Rank		Rank	
species		species	
Lineage		Lineage	
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; Cichlomorphae; Cichliformes; Cichlidae; African cichlids; Pseudocrenilabrinae; Haplochromini; Labeotropheus		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; Cichlomorphae; Cichliformes; Cichlidae; African cichlids; Pseudocrenilabrinae; Haplochromini; Labeotropheus	
Parent		Parent	
Labeotropheus () - (Rank: genus)		Labeotropheus () - (Rank: genus)	
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 57306)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 57306)	
NCBI Taxonomy ID		NCBI Taxonomy ID	
120210		120210	
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 120210)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 120210)	
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?	
No		No	

GENOTYPIC CHANGE

		Generic Gene Name	
Pax7		P47239 (http://www.uniprot.org/uniprot/P47239)	UniProtKB Mus musculus
		Synonyms	GenebankID or UniProtKB
Pax-7		XM_004548579 (https://www.ncbi.nlm.nih.gov/nucore/XM_004548579)	
		String	
10090.ENSMUSP00000030508			
(http://string-db.org/newstring.cgi/show_network_section.pl?identifier=10090.ENSMUSP00000030508)			
		Sequence Similarities	
Belongs to the paired homeobox family.			
		GO - Molecular Function	
GO:0003700 : DNA-binding transcription factor activity			
(https://www.ebi.ac.uk/QuickGO/term/GO:0003700)			
GO:0043565 : sequence-specific DNA binding			
(https://www.ebi.ac.uk/QuickGO/term/GO:0043565)			
GO:0000983 : transcription factor activity, RNA polymerase II core promoter sequence-			

specific DNA binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0000983>)
GO - Biological Process

- GO:0045944 : positive regulation of transcription by RNA polymerase II
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045944>)
GO:0006355 : regulation of transcription, DNA-templated
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006355>)
GO:0009887 : animal organ morphogenesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009887>)
GO:0051216 : cartilage development (<https://www.ebi.ac.uk/QuickGO/term/GO:0051216>)
GO:0006338 : chromatin remodeling (<https://www.ebi.ac.uk/QuickGO/term/GO:0006338>)
GO:0010468 : regulation of gene expression
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010468>)
GO:0010453 : regulation of cell fate commitment
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010453>)
GO:0007519 : skeletal muscle tissue development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007519>)
GO:2000288 : positive regulation of myoblast proliferation
(<https://www.ebi.ac.uk/QuickGO/term/GO:2000288>)
GO:0021904 : dorsal/ventral neural tube patterning
(<https://www.ebi.ac.uk/QuickGO/term/GO:0021904>)
GO:0048706 : embryonic skeletal system development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048706>)
GO:0060415 : muscle tissue morphogenesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0060415>)
GO:0048663 : neuron fate commitment
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048663>)
GO:0031062 : positive regulation of histone methylation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0031062>)
GO:0043393 : regulation of protein binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043393>)
GO:0014813 : skeletal muscle satellite cell commitment
(<https://www.ebi.ac.uk/QuickGO/term/GO:0014813>)
GO:0043403 : skeletal muscle tissue regeneration
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043403>)
GO:0021527 : spinal cord association neuron differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0021527>)

GO - Cellular Component

- GO:0005634 : nucleus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005634>)
GO:0005667 : transcription factor complex
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005667>)

No (https://www.gephebase.org/search-criteria?/and+Presumptive Null="No"#gephebase-summary-title)	Presumptive Null
Cis-regulatory (<a cis-regulatory"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Molecular Type=">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
unknown	Molecular Details of the Mutation
Candidate Gene (https://www.gephebase.org/search-criteria?/and+Experimental Evidence="Candidate Gene"#gephebase-summary-title)	Experimental Evidence
An allelic series at pax7a is associated with colour polymorphism diversity in Lake Malawi cichlid fish. (2017) (https://pubmed.ncbi.nlm.nih.gov/28027432)	Main Reference
Roberts RB; Moore EC; Kocher TD	Authors
	Abstract

Despite long-standing interest in the evolution and maintenance of discrete phenotypic polymorphisms, the molecular genetic basis of such polymorphism in the wild is largely unknown. Female sex-associated blotched colour polymorphisms found in cichlids of Lake Malawi, East Africa, represent a highly successful polymorphic phenotype, found and maintained in four genera across the geographic expanse of the lake. Previously, we identified an association with an allelic variant of the paired-box transcription factor gene pax7a and blotched colour morphs in Lake Malawi cichlid fishes. Although a diverse range of blotched phenotypes are present in Lake Malawi cichlid species, they all appeared to result from an allele of pax7a that produces increased levels of transcript. Here, we examine the developmental and genetic basis of variation among blotched morphs. First, we confirm that pax7a-associated blotch morphs result primarily from modulation of melanophore development and survival. From laboratory crosses and natural population studies, we identify at least three alleles of pax7a associated with discrete subtypes of blotched morphs, in addition to the ancestral pax7a allele. Genotypes at pax7a support initial evolution of a novel pax7a allele to produce the blotched class of morphs, followed by subsequent evolution of that pax7a blotched allele to produce additional alleles associated with discrete colour morphs. Variant alleles of pax7a produce different levels of pax7a transcript, correlating with pigmentation phenotype at the cellular level. This naturally selected allelic series should serve as a case study for understanding the molecular genetic control of pax7a expression and the evolution of sex-associated alleles.

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Additional References

RELATED GEPHE

	Related Genes
No matches found.	
	Related Haplotypes
2 (<a #gephebase-summary-title"="" and+taxon="" gephebase="pax7a" href="https://www.gephebase.org/search-criteria?/or+Gene Gephebase=" id="120210" or+gene="" pax7a"="">https://www.gephebase.org/search-criteria?/or+Gene Gephebase="pax7a"/and+Taxon ID="120210"/or+Gene Gephebase="pax7a"/and+Taxon ID="120210"#gephebase-summary-title)	

EXTERNAL LINKS

COMMENTS

@SexualTrait