

GEPHE SUMMARY

	Gephebase Gene	GepheID
opsin - rhodopsin1 (RH1) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase="opsin - rhodopsin1 (RH1)"#gephebase-summary-title)	GP00000792	
	Entry Status	Main curator
Published	Courtier	

PHENOTYPIC CHANGE

	Trait Category		
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category="Physiology"#gephebase-summary-title)		Trait	
Color vision (red-shift) (https://www.gephebase.org/search-criteria?/and+Trait ="Color vision (red-shift)"#gephebase-summary-title)			
	Trait State in Taxon A		
Other deep-water fishes		Trait State in Taxon B	
Aristostomias scintillans - can detect its own far-red bioluminescence			
	Ancestral State		
Data not curated		Taxonomic Status	
Intergeneric or Higher (https://www.gephebase.org/search-criteria?/and+Taxonomic Status="Intergeneric or Higher"#gephebase-summary-title)			
	Taxon A		Taxon B
	Latin Name		Latin Name
Stomiidae (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Stomiidae"#gephebase-summary-title)		Aristostomias scintillans (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Aristostomias scintillans"#gephebase-summary-title)	
	Common Name		Common Name
barbeled dragonfishes		shiny loosejaw	
	Synonyms		Synonyms
barbeled dragonfishes		shiny loosejaw; Aristostomias scintillans (Gilbert, 1915)	
	Rank		Rank
family		species	
	Lineage		Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Actinopteri; Neopterygii; Teleostei; Osteoglossocephalai; Clupeocephala; Euteleosteomorpha; Stomiatii; Stomiiformes		cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Actinopteri; Neopterygii; Teleostei; Osteoglossocephalai; Clupeocephala; Euteleosteomorpha; Stomiatii; Stomiiformes; Stomiidae; Malacosteinae; Aristostomias	
	Parent		Parent
Stomiiformes () - (Rank: order) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=48438)		Aristostomias () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=319439)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
123351 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=123351)		319440 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=319440)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Homo sapiens
RHO		P08100 (http://www.uniprot.org/uniprot/P08100)
	Synonyms	GenebankID or UniProtKB
RP4; OPN2; CSNBAD1		AGI55881 (https://www.ncbi.nlm.nih.gov/nuccore/AGI55881)
	String	
9606.ENSPP00000296271 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=9606.ENSPP00000296271)		
	Sequence Similarities	
Belongs to the G-protein coupled receptor 1 family. Opsin subfamily.		
	GO - Molecular Function	
GO:0046872 : metal ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0046872)		
GO:0004930 : G protein-coupled receptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004930)		
GO:0008020 : G protein-coupled photoreceptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008020)		
GO:0005502 : 11-cis retinal binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005502)		
	GO - Biological Process	

GO:0007186 : G protein-coupled receptor signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007186>)
GO:0001523 : retinoid metabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0001523>)
GO:0006468 : protein phosphorylation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006468>)
GO:0018298 : protein-chromophore linkage
(<https://www.ebi.ac.uk/QuickGO/term/GO:0018298>)
GO:0007601 : visual perception (<https://www.ebi.ac.uk/QuickGO/term/GO:0007601>)
GO:0071482 : cellular response to light stimulus
(<https://www.ebi.ac.uk/QuickGO/term/GO:0071482>)
GO:0007602 : phototransduction (<https://www.ebi.ac.uk/QuickGO/term/GO:0007602>)
GO:0016038 : absorption of visible light
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016038>)
GO:0045494 : photoreceptor cell maintenance
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045494>)
GO:0007603 : phototransduction, visible light
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007603>)
GO:0022400 : regulation of rhodopsin mediated signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0022400>)
GO:0060041 : retina development in camera-type eye
(<https://www.ebi.ac.uk/QuickGO/term/GO:0060041>)
GO:0016056 : rhodopsin mediated signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016056>)

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:0000139 : Golgi membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0000139>)
GO:0005887 : integral component of plasma membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005887>)
GO:0005794 : Golgi apparatus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005794>)
GO:0005911 : cell-cell junction (<https://www.ebi.ac.uk/QuickGO/term/GO:0005911>)
GO:0001750 : photoreceptor outer segment
(<https://www.ebi.ac.uk/QuickGO/term/GO:0001750>)
GO:0097381 : photoreceptor disc membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0097381>)
GO:0060170 : ciliary membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0060170>)
GO:0030660 : Golgi-associated vesicle membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0030660>)
GO:0001917 : photoreceptor inner segment
(<https://www.ebi.ac.uk/QuickGO/term/GO:0001917>)
GO:0060342 : photoreceptor inner segment membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0060342>)
GO:0042622 : photoreceptor outer segment membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042622>)

Presumptive Null

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

Molecular Type

Coding ([https://www.gephebase.org/search-criteria?/and+Molecular Type="+Coding^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular Type=))

Aberration Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

D83N; M183F; M253L; F261Y; T289G; S292L; M317I - all together shift to red (see table S4 of Yokoyama PNAS) - individual changes not tested

Experimental Evidence

Candidate Gene ([https://www.gephebase.org/search-criteria?/and+Experimental Evidence="+Candidate Gene^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental Evidence=))

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

Main Reference

Elucidation of phenotypic adaptations: Molecular analyses of dim-light vision proteins in vertebrates. (2008) (<https://pubmed.ncbi.nlm.nih.gov/18768804>)

Authors

Yokoyama S; Tada T; Zhang H; Britt L

Abstract

Vertebrate ancestors appeared in a uniform, shallow water environment, but modern species flourish in highly variable niches. A striking array of phenotypes exhibited by contemporary animals is assumed to have evolved by accumulating a series of selectively advantageous mutations. However, the experimental test of such adaptive events at the molecular level is remarkably difficult. One testable phenotype, dim-light vision, is mediated by rhodopsins. Here, we engineered 11 ancestral rhodopsins and show that those in early ancestors absorbed light maximally (lambda(max)) at 500 nm, from which contemporary rhodopsins with variable lambda(max)s of 480-525 nm evolved on at least 18 separate occasions. These highly environment-specific adaptations seem to have occurred largely by amino acid replacements at 12 sites, and most of those at the remaining 191 (approximately 94%) sites have undergone neutral evolution. The comparison between these results and those inferred by commonly-used parsimony and Bayesian methods demonstrates that statistical tests of positive selection can be misleading without experimental support and that the molecular basis of spectral tuning in rhodopsins should be elucidated by mutagenesis analyses using ancestral pigments.

RELATED GEPHE

No matches found.

Related Genes

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS