

GEPHE SUMMARY

opsin (<a +opsin+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+opsin+"#gephebase-summary-title)	Gephebase Gene	GP00000755	GepheID
	Entry Status	Martin	Main curator
	Published		

PHENOTYPIC CHANGE

Physiology (<a +physiology+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait+Category=">https://www.gephebase.org/search-criteria?/and+Trait+Category="+Physiology+"#gephebase-summary-title)		Trait Category	
Color vision (blue) (<a +color+vision+(blue)+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait="+Color+vision+(blue)+"#gephebase-summary-title)		Trait	
Loligo forbesi (lambda max 494 nm)		Trait State in Taxon A	
Alloteuthis subulata (lambda max 499 nm)		Trait State in Taxon B	
Data not curated		Ancestral State	
Interspecific (<a +interspecific+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=">https://www.gephebase.org/search-criteria?/and+Taxonomic+Status="+Interspecific+"#gephebase-summary-title)		Taxonomic Status	
Taxon A		Taxon B	
Loligo forbesii (<a +loligo+forbesii+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Loligo+forbesii+"#gephebase-summary-title)		Alloteuthis subulata (<a +alloteuthis+subulata+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Alloteuthis+subulata+"#gephebase-summary-title)	
northern European squid		-	
northern European squid; Loligo forbesii Steenstrup, 1856; Loligo forbesi		Loligo (Alloteuthis) subulata; Loligo subulata; Alloteuthis subulata (Lamarck, 1798)	
species		species	
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Lophotrochozoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea; Decapodiformes; Teuthida; Myopsina; Loliginidae; Loligo		cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Lophotrochozoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea; Decapodiformes; Teuthida; Myopsina; Loliginidae; Alloteuthis	
Loligo () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=6616)		Alloteuthis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=552058)	
6618 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=6618)		54069 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=54069)	
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?	
No		No	

GENOTYPIC CHANGE

opn1sw1		Generic Gene Name	UniProtKB Danio rerio
SWS1; zfvv; uvops; opn1sw2; sws1		Synonyms	GenebankID or UniProtKB
7955.ENSADARP00000067159 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=7955.ENSADARP00000067159)		String	CAA88923 (https://www.ncbi.nlm.nih.gov/nuccore/CAA88923)
Belongs to the G-protein coupled receptor 1 family. Opsin subfamily.		Sequence Similarities	
GO:0008020 : G protein-coupled photoreceptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008020)		GO - Molecular Function	
GO:0009881 : photoreceptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0009881)		GO - Biological Process	
GO:0007186 : G protein-coupled receptor signaling pathway (https://www.ebi.ac.uk/QuickGO/term/GO:0007186)			
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 - Cellular Component

GO:0005887 : integral component of plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005887>)
GO:0001750 : photoreceptor outer segment (<https://www.ebi.ac.uk/QuickGO/term/GO:0001750>)

Presumptive Null

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

Molecular Type

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

Aberration Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

F270S

Experimental Evidence

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

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

Main Reference

The molecular basis of a spectral shift in the rhodopsins of two species of squid from different photic environments. (1993) (<https://pubmed.ncbi.nlm.nih.gov/8108455>)

Authors

Morris A; Bowmaker JK; Hunt DM

Abstract

The molecular basis of spectral tuning of rhodopsin pigments in two squid species is examined. The absorbance spectra of rhodopsin extracts from *Alloteuthis subulata* (lambda max 499 nm) showed a 5 nm red shift compared with *Loligo forbesi* (lambda max 494 nm). The rhodopsin gene sequence of *A. subulata* opsin was determined from polymerase chain reaction (PCR) amplified fragments by using genomic DNA as template. The deduced amino acid sequence was compared with that obtained from the previously published cDNA sequence of *Loligo forbesi*. A total of 22 amino acid differences are present, although only seven can be considered to be non-homologous substitutions. Three of these changes occur in helical transmembrane regions but only one, the substitution of phenylalanine by serine at site 270 in *Alloteuthis subulata*, involves the replacement of an apolar with a hydroxyl-bearing residue at a site located near the centre of helix VI and on the inner face of the retinal-binding pocket. The equivalent site is also used for the spectral tuning of primate cone pigments, an example of convergent evolution. It is proposed that substitution at this site is responsible for the 5 nm red shift. The relation between this spectral shift and the maximum depth distribution of *Alloteuthis subulata* of about 200 m, compared with about 360 m for *Loligo forbesi*, is discussed. An unexpected finding was that the rhodopsin gene of both species appears to lack introns.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS