

GEPHE SUMMARY

opsin - rhodopsin1 (RH1) (https://www.gephebase.org/search-criteria?/and+Gene)		Gephebase Gene		GepheID
Gephebase="opsin - rhodopsin1 (RH1)"#gephebase-summary-title)			GP00000787	
		Entry Status	Courtier	Main curator
Published				

PHENOTYPIC CHANGE

Physiology (https://www.gephebase.org/search-criteria?/and+Trait)		Trait Category	
Category="Physiology"#gephebase-summary-title)			
Color vision (blue-shift) (<a color"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait="Color)		Trait	
vision (blue-shift)"#gephebase-summary-title)			
Mammal ancestor		Trait State in Taxon A	
Tursiops truncatus; other cetaceans		Trait State in Taxon B	
Data not curated		Ancestral State	
Intergeneric or Higher (https://www.gephebase.org/search-criteria?/and+Taxonomic)		Taxonomic Status	
Status="Intergeneric or Higher"#gephebase-summary-title)			
Taxon A		Taxon B	
Mammalia		Tursiops truncatus	
(https://www.gephebase.org/search-criteria?/and+Taxon and		(https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Tursiops	
Synonyms="Mammalia"#gephebase-summary-title)		truncatus"#gephebase-summary-title)	
mammals		bottlenose dolphin	
mammals		bottlenose dolphin; Atlantic bottle-nosed dolphin; bottle-nosed dolphin; Tursiops truncatus	
class		Gervais, 1855	
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia;		species	
Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii;		cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia;	
Dipnotetrapodomorpha; Tetrapoda; Amniota		Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii;	
Amniota (amniotes) - (Rank: no rank)		Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria;	
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32524)		Laurasiatheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae; Tursiops	
40674		Tursiops () - (Rank: genus)	
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 40674)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9738)	
is Taxon A an Intraspecies?		9739	
No		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9739)	
		is Taxon B an Intraspecies?	
		No	

GENOTYPIC CHANGE

RHO		Generic Gene Name		UniProtKB Homo sapiens
RP4; OPN2; CSNBAD1		Synonyms		P08100 (http://www.uniprot.org/uniprot/P08100)
9606.ENSPP00000296271		String		GenebankID or UniProtKB
(http://string-db.org/newstring.cgi/show_network_section.pl?identifier=				NP_001267588 (https://www.ncbi.nlm.nih.gov/nuccore/NP_001267588)
9606.ENSPP00000296271)				
Belongs to the G-protein coupled receptor 1 family. Opsin subfamily.		Sequence Similarities		
GO:0046872 : metal ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0046872)		GO - Molecular Function		
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>)

Mutation #1

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

D83N; A292S; A299S

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	Asp	Asn	83

Main Reference

Mechanism of spectral tuning in the dolphin visual pigments. (1998) (<https://pubmed.ncbi.nlm.nih.gov/9471225>)

Authors

Fasick JL; Robinson PR

Abstract

The absorption maxima of both rod and cone visual pigments of the bottlenose dolphin (*Tursiops truncatus*) are blue-shifted relative to those of terrestrial mammals. A comparison of the sequence of the dolphin rod photopigment gene with that of the bovine rod suggests that, fo the 28 nonidentical amino acids, three amino acid substitutions at positions 83, 292, and 299 in the dolphin rod pigment are responsible for the 10 nm blue shift in absorption maxima. A similar comparison of the dolphin long-wavelength sensitive (LWS) cone photopigment gene with those of the human LWS cones suggests that a single substitution at position 292 (using the convention of rhodopsin numbering) in the dolphin LWS cone

pigment results in a blue shift in absorption maxima. A mutagenesis study reveals that the combination of the three dolphin specific substitutions in the bovine rod pigment (83D to 83N, 292A to 292S, and 299A to 299S) causes a blue shift from the wild-type lambdamax of 499 nm to 389 nm. The single substitution in the dolphin LWS cone pigment (292S to 292A) causes a red shift from the wild-type lambdamax of 524 nm to 552 nm. The interactions of the three amino acids identified in the rod pigment with the chromophore may be a general mechanism for blue shifting in rod visual pigments. Furthermore, the single substitution in the dolphin LWS opsin gene is a novel mechanism of wavelength modulation in mammalian LWS pigments.

Additional References

Vertebrate rhodopsin adaptation to dim light via rapid meta-II intermediate formation. (2010) (<https://pubmed.ncbi.nlm.nih.gov/19858068>)
Elucidation of phenotypic adaptations: Molecular analyses of dim-light vision proteins in vertebrates. (2008) (<https://pubmed.ncbi.nlm.nih.gov/18768804>)

Mutation #2

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; A292S; A299S

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	Ala	Ser	292

Main Reference

Mechanism of spectral tuning in the dolphin visual pigments. (1998) (<https://pubmed.ncbi.nlm.nih.gov/9471225>)

Authors

Fasick JI; Robsinson PR

Abstract

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Mutation #3

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; A292S; A299S

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	Ala	Ser	299

Main Reference

Mechanism of spectral tuning in the dolphin visual pigments. (1998) (<https://pubmed.ncbi.nlm.nih.gov/9471225>)

Authors

Fasick JI; Robsinson PR

The absorption maxima of both rod and cone visual pigments of the bottlenose dolphin (*Tursiops truncatus*) are blue-shifted relative to those of terrestrial mammals. A comparison of the sequence of the dolphin rod photopigment gene with that of the bovine rod suggests that, for the 28 nonidentical amino acids, three amino acid substitutions at positions 83, 292, and 299 in the dolphin rod pigment are responsible for the 10 nm blue shift in absorption maxima. A similar comparison of the dolphin long-wavelength sensitive (LWS) cone photopigment gene with those of the human LWS cones suggests that a single substitution at position 292 (using the convention of rhodopsin numbering) in the dolphin LWS cone pigment results in a blue shift in absorption maxima. A mutagenesis study reveals that the combination of the three dolphin specific substitutions in the bovine rod pigment (83D to 83N, 292A to 292S, and 299A to 299S) causes a blue shift from the wild-type λ_{max} of 499 nm to 389 nm. The single substitution in the dolphin LWS cone pigment (292S to 292A) causes a red shift from the wild-type λ_{max} of 524 nm to 552 nm. The interactions of the three amino acids identified in the rod pigment with the chromophore may be a general mechanism for blue shifting in rod visual pigments. Furthermore, the single substitution in the dolphin LWS opsin gene is a novel mechanism of wavelength modulation in mammalian LWS pigments.

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RELATED GEPHE

Related Genes

3 (opsin - (SWS1), opsin - rhodopsin (LWS), opsin - rhodopsin (MWS=duplicate of LWS)) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=~40674~/and+Trait=Color vision/or+Taxon ID=~9739~/and+Trait=Color vision/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

6 ([https://www.gephebase.org/search-criteria?/or+Gene Gephebase=~opsin - rhodopsin1 \(RH1\)~/and+Taxon ID=~40674~/or+Gene Gephebase=~opsin - rhodopsin1 \(RH1\)~/and+Taxon ID=~9739~/#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene Gephebase=~opsin - rhodopsin1 (RH1)~/and+Taxon ID=~40674~/or+Gene Gephebase=~opsin - rhodopsin1 (RH1)~/and+Taxon ID=~9739~/#gephebase-summary-title))

EXTERNAL LINKS

COMMENTS

@SeveralMutationsWithEffect