

GEPHE SUMMARY

Gephebase Gene		GepheID
opsin - rhodopsin1 (RH1) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase="opsin - rhodopsin1 (RH1)"#gephebase-summary-title)		GP00000785
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 (blue-shift) (<a color"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait="Color vision (blue-shift)"#gephebase-summary-title)		Trait State in Taxon A	
Bos bovis		Trait State in Taxon B	
Orcinus orca		Ancestral State	
Taxon A		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	
Bos taurus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Bos taurus"#gephebase-summary-title)		Orcinus orca (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Orcinus orca"#gephebase-summary-title)	
Common Name		Common Name	
cattle		killer whale	
Synonyms		Synonyms	
Bos bovis; Bos primigenius taurus; cattle; bovine; cow; dairy cow; domestic cattle; domestic cow; Bos taurus Linnaeus, 1758; Bos Taurus		killer whale; Orca; Orcinus orca (Linnaeus, 1758)	
Rank		Rank	
species		species	
Lineage		Lineage	
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Laurasiatheria; Artiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos		cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Laurasiatheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae; Orcinus	
Parent		Parent	
Bos (oxen, cattle) - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9903)		Orcinus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9732)	
NCBI Taxonomy ID		NCBI Taxonomy ID	
9913 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9913)		9733 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9733)	
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		AAO16237 (https://www.ncbi.nlm.nih.gov/nuccore/AAO16237)
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>)

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 both have phenotypic effect

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

Spectral Tuning of Killer Whale (Orcinus orca) Rhodopsin: Evidence for Positive Selection and Functional Adaptation in a Cetacean Visual Pigment. (2016)
(<https://pubmed.ncbi.nlm.nih.gov/26486871>)

Authors

Dungan SZ; Kosyakov A; Chang BS

Abstract

Cetaceans have undergone a remarkable evolutionary transition that was accompanied by many sensory adaptations, including modification of the visual system for underwater environments. Recent sequencing of cetacean genomes has made it possible to begin exploring the molecular basis of these adaptations. In this study we use in vitro expression methods to experimentally characterize the first step of the visual transduction cascade, the light activation of rhodopsin, for the killer whale. To investigate the spectral effects of amino

acid substitutions thought to correspond with absorbance shifts relative to terrestrial mammals, we used the orca gene as a background for the first site-directed mutagenesis experiments in a cetacean rhodopsin. The S292A mutation had the largest effect, and was responsible for the majority of the spectral difference between killer whale and bovine (terrestrial) rhodopsin. Using codon-based likelihood models, we also found significant evidence for positive selection in cetacean rhodopsin sequences, including on spectral tuning sites we experimentally mutated. We then investigated patterns of ecological divergence that may be correlated with rhodopsin functional variation by using a series of clade models that partitioned the data set according to phylogeny, habitat, and foraging depth zone. Only the model partitioning according to depth was significant. This suggests that foraging dives might be a selective regime influencing cetacean rhodopsin divergence, and our experimental results indicate that spectral tuning may be playing an adaptive role in this process. Our study demonstrates that combining computational and experimental methods is crucial for gaining insight into the selection pressures underlying molecular evolution.

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Additional References

Rod monochromacy and the coevolution of cetacean retinal opsins. (2013) (<https://pubmed.ncbi.nlm.nih.gov/23637615>)

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 both have phenotypic effect

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	83

Main Reference

Spectral Tuning of Killer Whale (*Orcinus orca*) Rhodopsin: Evidence for Positive Selection and Functional Adaptation in a Cetacean Visual Pigment. (2016) (<https://pubmed.ncbi.nlm.nih.gov/26486871>)

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RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@SeveralMutationsWithEffect