

GEPHE SUMMARY

Gephebase Gene
opsin - rhodopsin1 (RH1)

Entry Status
Published

GepheID
GP00000780

Main curator
Courtier

PHENOTYPIC CHANGE

Trait Category
Physiology

Trait
Color vision (blue shift)

Trait State in Taxon A
littoral cottoid fishes; Lake Baikal

Trait State in Taxon B
abyssal cottoid fishes; Lake Baikal

Ancestral State
Data not curated

Taxonomic Status
Intergeneric or Higher

Taxon A

Latin Name
undetermined Cottoidei 'Lake Baikal'

Common Name
-

Synonyms
Baikalian cottoid fish

Rank
species

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Actinopteri; Neopterygii; Teleostei; Osteoglossocephalai; Clupeocephala; Euteleostomorpha; Neoteleostei; Eurypterygia; Ctenosquamata; Acanthomorpha; Euacanthomorpha; Percormorphaceae; Eupercaria; Perciformes; Cottoidei; unclassified Cottoidei

Parent
unclassified Cottoidei () - (Rank: no rank)

NCBI Taxonomy ID
36479

is Taxon A an Intraspecies?
No

Taxon B

Latin Name
undetermined Cottoidei 'Lake Baikal'

Common Name
-

Synonyms
Baikalian cottoid fish

Rank
species

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Actinopteri; Neopterygii; Teleostei; Osteoglossocephalai; Clupeocephala; Euteleostomorpha; Neoteleostei; Eurypterygia; Ctenosquamata; Acanthomorpha; Euacanthomorpha; Percormorphaceae; Eupercaria; Perciformes; Cottoidei; unclassified Cottoidei

Parent
unclassified Cottoidei () - (Rank: no rank)

NCBI Taxonomy ID
36479

is Taxon B an Intraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
RHO

Synonyms
RP4; OPN2; CSNBAD1

String
9606.ENSP00000296271

Sequence Similarities
Belongs to the G-protein coupled receptor 1 family. Opsin subfamily.

GO - Molecular Function
GO:0046872 : metal ion binding
GO:0004930 : G protein-coupled receptor activity
GO:0008020 : G protein-coupled photoreceptor activity
GO:0005502 : 11-cis retinal binding

GO - Biological Process
GO:0007186 : G protein-coupled receptor signaling pathway
GO:0001523 : retinoid metabolic process
GO:0006468 : protein phosphorylation
GO:0018298 : protein-chromophore linkage

UniProtKB Homo sapiens
P08100

GenebankID or UniProtKB

GO:0007601 : visual perception
 GO:0071482 : cellular response to light stimulus
 GO:0007602 : phototransduction
 GO:0016038 : absorption of visible light
 GO:0045494 : photoreceptor cell maintenance
 GO:0007603 : phototransduction, visible light
 GO:0022400 : regulation of rhodopsin mediated signaling pathway
 GO:0060041 : retina development in camera-type eye
 GO:0016056 : rhodopsin mediated signaling pathway

GO - Cellular Component

GO:0016021 : integral component of membrane
 GO:0005886 : plasma membrane
 GO:0000139 : Golgi membrane
 GO:0005887 : integral component of plasma membrane
 GO:0005794 : Golgi apparatus
 GO:0005911 : cell-cell junction
 GO:0001750 : photoreceptor outer segment
 GO:0097381 : photoreceptor disc membrane
 GO:0060170 : ciliary membrane
 GO:0030660 : Golgi-associated vesicle membrane
 GO:0001917 : photoreceptor inner segment
 GO:0060342 : photoreceptor inner segment membrane
 GO:0042622 : photoreceptor outer segment membrane

Mutation #1

Presumptive Null

No

Molecular Type

Coding

Aberration Type

SNP

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

D83N; A292S

Experimental Evidence

Candidate Gene

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Asp	Asn	83

Main Reference

Spectral tuning and molecular evolution of rod visual pigments in the species flock of cottoid fish in Lake Baikal. (1996)

Authors

Hunt DM; Fitzgibbon J; Slobodyanyuk SJ; Bowmaker JK

Abstract

Lake Baikal in Eastern Siberia is the deepest and one of the largest and most ancient lakes in the world. However, even in the deepest regions, oxygenation levels do not fall below 75-80% of the surface levels. This has enabled a remarkable flock of largely endemic teleost fish of the sub-order Cottoidei to colonize all depth habitats. We have previously shown that species that occupy progressively deeper habitats show a blue shift in the peak wavelength of absorbance (lambda max) of both their rod and cone visual pigments; for the rod pigments, a number of stepwise shifts occur from about 516 nm in littoral species to about 484 nm in abyssal species. By sequencing the rod opsin gene from 11 species of Baikal cottoids that include representatives from all depth habitats, we have been able to identify four amino acid substitutions that would account for these shifts. The effect of each substitution on lambda max is approximately additive and each corresponds to a particular lineage of evolution.

Additional References

Mutation #2

Presumptive Null

No

Molecular Type

Coding

Aberration Type

SNP

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

D83N; A292S

Experimental Evidence

Candidate Gene

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Ala	Ser	292

Main Reference

[Spectral tuning and molecular evolution of rod visual pigments in the species flock of cottoid fish in Lake Baikal. \(1996\)](#)

Authors

Hunt DM; Fitzgibbon J; Slobodyanyuk SJ; Bowmaker JK

Abstract

Lake Baikal in Eastern Siberia is the deepest and one of the largest and most ancient lakes in the world. However, even in the deepest regions, oxygenation levels do not fall below 75-80% of the surface levels. This has enabled a remarkable flock of largely endemic teleost fish of the sub-order Cottoidei to colonize all depth habitats. We have previously shown that species that occupy progressively deeper habitats show a blue shift in the peak wavelength of absorbance (λ_{max}) of both their rod and cone visual pigments; for the rod pigments, a number of stepwise shifts occur from about 516 nm in littoral species to about 484 nm in abyssal species. By sequencing the rod opsin gene from 11 species of Baikal cottoids that include representatives from all depth habitats, we have been able to identify four amino acid substitutions that would account for these shifts. The effect of each substitution on λ_{max} is approximately additive and each corresponds to a particular lineage of evolution.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

COMMENTS

@SeveralMutationsWithEffect