

GEPHE SUMMARY

opsin - (SWS2) (https://www.gephebase.org/search-criteria/?and+Gene Gephebase=%opsin-(SWS2)%#gephebase-summary-title)	Generic Gene Name	GP00001771	GepheID
	Entry Status	Courtier	Main curator
Published			

PHENOTYPIC CHANGE

Trait Category			
Physiology (https://www.gephebase.org/search-criteria/?and+Trait+Category=%Physiology%#gephebase-summary-title)	Trait		
Color vision (https://www.gephebase.org/search-criteria/?and+Trait=%Color+vision%#gephebase-summary-title)	Trait State in Taxon A		
blue-sensitive cone pigments SWS2 with lambda-max = 430-450 nm	Trait State in Taxon B		
blue-sensitive cone pigments SWS2 with lambda-max = 467 nm	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	Latin Name	Taxon B	Latin Name
Cottidae (https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=%Cottidae%#gephebase-summary-title)		Cottus gobio (https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=%Cottus+gobio%#gephebase-summary-title)	
sculpins	Common Name	bullhead	Common Name
Abyssocottidae; Comephoridae; Cottocomorphidae; sculpins; Baikal oilfishes	Synonyms	bullhead; <i>Cottus gobio</i> Linnaeus, 1758	Synonyms
family	Rank	species	Rank
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Actinopteri; Neopterygii; Teleostei; Osteoglossocephalai; Clupeocephala; Euteleosteomorpha; Neoteleostei; Eurypterygia; Ctenosquamata; Acanthomorpha; Euacanthomorphacea; Percomorphaceae; Eupercaria; Perciformes; Cottioidei; Cottales	Lineage	cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Actinopteri; Neopterygii; Teleostei; Osteoglossocephalai; Clupeocephala; Euteleosteomorpha; Neoteleostei; Eurypterygia; Ctenosquamata; Acanthomorpha; Euacanthomorphacea; Percomorphaceae; Eupercaria; Perciformes; Cottioidei; Cottales; Cottidae; <i>Cottus</i>	Lineage
Cottales () - (Rank: infraorder) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1490021)	Parent	<i>Cottus</i> () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=8098)	Parent
8092 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=8092)	NCBI Taxonomy ID	100952 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=100952)	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

Generic Gene Name			
opn1sw2	Synonyms	Q9W6A8 (http://www.uniprot.org/uniprot/Q9W6A8)	UniProtKB <i>Danio rerio</i>
SWS2; bluops; zfblue; Sl;zK13A21.5; opn1sw1; sws2	String	0	GenebankID or UniProtKB
7955.ENSDARP00000019477 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=7955.ENSDARP00000019477)	Sequence Similarities		
Belongs to the G-protein coupled receptor 1 family. Opsin subfamily.	GO - Molecular Function		
GO:0009882 : blue light photoreceptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0009882)			
GO:0008020 : G protein-coupled photoreceptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008020)			
	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>)

Mutation #1

No (https://www.gephbase.org/search-criteria?/and+Presumptive Null=^No^#gephbase-summary-title)	Presumptive Null
Coding (https://www.gephbase.org/search-criteria?/and+Molecular Type=^Coding^#gephbase-summary-title)	Molecular Type
SNP (https://www.gephbase.org/search-criteria?/and+Aberration Type=^SNP^#gephbase-summary-title)	Aberration Type
Nonsynonymous	SNP Coding Change
Ala118Thr	Molecular Details of the Mutation
Candidate Gene (https://www.gephbase.org/search-criteria?/and+Experimental Evidence=^Candidate Gene^#gephbase-summary-title)	Experimental Evidence

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Ala	Thr	118

Spectral tuning and evolution of short wave-sensitive cone pigments in cottoid fish from Lake Baikal. (2002) (https://pubmed.ncbi.nlm.nih.gov/11993996)	Main Reference
Cowing JA; Poopalasundaram S; Wilkie SE; Bowmaker JK; Hunt DM	Authors

Cowing JA; Poopalasundaram S; Wilkie SE; Bowmaker JK; Hunt DM

The cottoid fishes of Lake Baikal in eastern Siberia provide a unique opportunity to study the evolution of visual pigments in a group of closely related species exposed to different photic environments. Members of this species flock are adapted to different depth habitats down to >1000 m, and both the rod and cone visual pigments display short wave shifts as depth increases. The blue-sensitive cone pigments of the SWS2 class cluster into two species groups with lambda(max) values of 450 and 430 nm, with the pigment in *Cottus gobio*, a cottoid fish native to Britain, forming a third group with a lambda(max) of 467 nm. The sequences of the SWS2 opsin gene from *C. gobio* and from two representatives of the 450 and 430 nm Baikal groups are presented. Approximately 6 nm of the spectral difference between *C. gobio* and the 450 nm Baikal group can be ascribed to the presence of a porphyropsin/rhodopsin mixture in *C. gobio*. Subsequent analysis of amino acid substitutions by site-directed mutagenesis demonstrates that the remainder of the shift from 461 to 450 nm arises from a Thr269Ala substitution and the shift from 450 to 430 nm at least partly from Thr118Ala and Thr118Gly substitutions. The underlying adaptive significance of these substitutions in terms of spectral tuning and signal-to-noise ratio is discussed.

Additional References

Mutation #2	Presumptive Null
No (https://www.gephbase.org/search-criteria?/and+Presumptive Null=^No^#gephbase-summary-title)	Molecular Type
Coding (https://www.gephbase.org/search-criteria?/and+Molecular Type=^Coding^#gephbase-summary-title)	Aberration Type
SNP (https://www.gephbase.org/search-criteria?/and+Aberration Type=^SNP^#gephbase-summary-title)	SNP Coding Change
Nonsynonymous	Molecular Details of the Mutation
Gly215Pro	Experimental Evidence
Candidate Gene (https://www.gephbase.org/search-criteria?/and+Experimental Evidence=^Candidate Gene^#gephbase-summary-title)	

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Gly	Pro	215

Spectral tuning and evolution of short wave-sensitive cone pigments in cottoid fish from Lake Baikal. (2002) (https://pubmed.ncbi.nlm.nih.gov/11993996)	Main Reference
Cowing JA; Poopalasundaram S; Wilkie SE; Bowmaker JK; Hunt DM	Authors

The cottoid fishes of Lake Baikal in eastern Siberia provide a unique opportunity to study the evolution of visual pigments in a group of closely related species exposed to different photic environments. Members of this species flock are adapted to different depth habitats down to >1000 m, and both the rod and cone visual pigments display short wave shifts as depth increases. The blue-sensitive cone pigments of the SWS2 class cluster into two species groups with lambda(max) values of 450 and 430 nm, with the pigment in *Cottus gobio*, a cottoid fish native to Britain, forming a third group with a lambda(max) of 467 nm. The sequences of the SWS2 opsin gene from *C. gobio* and from two representatives of the 450 and 430 nm Baikal groups are presented. Approximately 6 nm of the spectral difference between *C. gobio* and the 450 nm Baikal group can be ascribed to the presence of a porphyropsin/rhodopsin mixture in *C. gobio*. Subsequent analysis of amino acid substitutions by site-directed mutagenesis demonstrates that the remainder of the shift from 461 to 450 nm arises from a Thr269Ala substitution and the shift from 450 to 430 nm at least partly from Thr118Ala and Thr118Gly substitutions. The underlying adaptive significance of these substitutions in terms of spectral tuning and signal-to-noise ratio is discussed.

Additional References

Mutation #3

No (https://www.gepheebase.org/search-criteria/?and+Presumptive+Null=%No%#gepheebase-summary-title)	Presumptive Null
Coding (https://www.gepheebase.org/search-criteria/?and+Molecular+Type=%Coding%#gepheebase-summary-title)	Molecular Type
SNP (https://www.gepheebase.org/search-criteria/?and+Aberration+Type=%SNP%#gepheebase-summary-title)	Aberration Type
Nonsynonymous	SNP Coding Change
Ala269Pro	Molecular Details of the Mutation
Candidate Gene (https://www.gepheebase.org/search-criteria/?and+Experimental+Evidence=%Candidate+Gene%#gepheebase-summary-title)	Experimental Evidence

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Ala	Thr	269

Spectral tuning and evolution of short wave-sensitive cone pigments in cottoid fish from Lake Baikal. (2002) (https://pubmed.ncbi.nlm.nih.gov/11993996)	Main Reference
Cowing JA; Poopalasundaram S; Wilkie SE; Bowmaker JK; Hunt DM	Authors
The cottoid fishes of Lake Baikal in eastern Siberia provide a unique opportunity to study the evolution of visual pigments in a group of closely related species exposed to different photic environments. Members of this species flock are adapted to different depth habitats down to >1000 m, and both the rod and cone visual pigments display short wave shifts as depth increases. The blue-sensitive cone pigments of the SWS2 class cluster into two species groups with lambda(max) values of 450 and 430 nm, with the pigment in <i>Cottus gobio</i> , a cottoid fish native to Britain, forming a third group with a lambda(max) of 467 nm. The sequences of the SWS2 opsin gene from <i>C. gobio</i> and from two representatives of the 450 and 430 nm Baikal groups are presented. Approximately 6 nm of the spectral difference between <i>C. gobio</i> and the 450 nm Baikal group can be ascribed to the presence of a porphyropsin/rhodopsin mixture in <i>C. gobio</i> . Subsequent analysis of amino acid substitutions by site-directed mutagenesis demonstrates that the remainder of the shift from 461 to 450 nm arises from a Thr269Ala substitution and the shift from 450 to 430 nm at least partly from Thr118Ala and Thr118Gly substitutions. The underlying adaptive significance of these substitutions in terms of spectral tuning and signal-to-noise ratio is discussed.	Abstract

Additional References

RELATED GEPHE

No matches found.	Related Genes
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS

@SeveralMutationsWithEffect

