

GEPHE SUMMARY

Gephebase Gene
opsin - (SWS1)

Entry Status
Published

GepheID
GP00000761

Main curator
Courtier

PHENOTYPIC CHANGE

Trait Category
Physiology

Trait
Color vision (UV-shift)

Trait State in Taxon A
Other birds

Trait State in Taxon B
Rhea americana

Ancestral State
Taxon A

Taxonomic Status
Intergeneric or Higher

	Taxon A	Taxon B
Latin Name	<i>Aves</i>	<i>Rhea americana</i>
Common Name	birds	greater rhea
Synonyms	avian; birds	greater rhea; common rhea
Rank	class	species
Lineage	cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Sauropsida; Sauria; Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda; Coelurosauria	cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Sauropsida; Sauria; Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda; Coelurosauria; Aves; Palaeognathae; Rheiformes; Rheidae; Rhea
Parent	Coelurosauria () - (Rank: no rank)	Rhea () - (Rank: genus)
NCBI Taxonomy ID	8782	8797
is Taxon A an Intraspecies?	No	No

GENOTYPIC CHANGE

Generic Gene Name
OPN1SW

Synonyms
BCP; BOP; CBT

String
9606.ENSP00000249389

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

GO - Molecular Function
GO:0038023 : signaling receptor activity
GO:0008020 : G protein-coupled photoreceptor activity

GO - Biological Process
GO:0007165 : signal transduction
GO:0007186 : G protein-coupled receptor signaling pathway
GO:0001523 : retinoid metabolic process
GO:0018298 : protein-chromophore linkage
GO:0007601 : visual perception
GO:0071482 : cellular response to light stimulus

UniProtKB Homo sapiens
P03999

GenebankID or UniProtKB
AAP23986

GO:0007602 : phototransduction

GO - Cellular Component

GO:0005887 : integral component of plasma membrane

GO:0001750 : photoreceptor outer segment

GO:0097381 : photoreceptor disc membrane

Mutation #1

Presumptive Null

No

Molecular Type

Coding

Aberration Type

SNP

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

S86F and S90C - both have phenotypic effect

Experimental Evidence

Candidate Gene

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Ser	Phe	86

Main Reference

[Complex distribution of avian color vision systems revealed by sequencing the SWS1 opsin from total DNA. \(2003\)](#)

Authors

Odeen A; Hastad O

Abstract

To gain insights into the evolution and ecology of visually acute animals such as birds, biologists often need to understand how these animals perceive colors. This poses a problem, since the human eye is of a different design than that of most other animals. The standard solution is to examine the spectral sensitivity properties of animal retinas through microspectrophotometry—a procedure that is rather complicated and therefore only has allowed examinations of a limited number of species to date. We have developed a faster and simpler molecular method, which can be used to estimate the color sensitivities of a bird by sequencing a part of the gene coding for the ultraviolet or violet absorbing opsin in the avian retina. With our method, there is no need to sacrifice the animal, and it thereby facilitates large screenings, including rare and endangered species beyond the reach of microspectrophotometry. Color vision in birds may be categorized into two classes: one with a short-wavelength sensitivity biased toward violet (VS) and the other biased toward ultraviolet (UVS). Using our method on 45 species from 35 families, we demonstrate that the distribution of avian color vision is more complex than has previously been shown. Our data support VS as the ancestral state in birds and show that UVS has evolved independently at least four times. We found species with the UVS type of color vision in the orders Psittaciformes and Passeriformes, in agreement with previous findings. However, species within the families Corvidae and Tyrannidae did not share this character with other passeriforms. We also found UVS type species within the Laridae and Struthionidae families. Raptors (Accipitridae and Falconidae) are of the violet type, giving them a vision system different from their passeriform prey. Intriguing effects on the evolution of color signals can be expected from interactions between predators and prey. Such interactions may explain the presence of UVS in Laridae and Passeriformes.

Additional References

[The molecular evolution of avian ultraviolet- and violet-sensitive visual pigments. \(2007\)](#)

[Retinal photoreceptors of paleognathous birds: the ostrich \(*Struthio camelus*\) and rhea \(*Rhea americana*\). \(2001\)](#)

Mutation #2

Presumptive Null

No

Molecular Type

Coding

Aberration Type

SNP

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

S86F and S90C - both have phenotypic effect

Experimental Evidence

Candidate Gene

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Ser	Cys	90

Main Reference

[Complex distribution of avian color vision systems revealed by sequencing the SWS1 opsin from total DNA. \(2003\)](#)

Authors

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Abstract

To gain insights into the evolution and ecology of visually acute animals such as birds, biologists often need to understand how these animals perceive colors. This poses a problem, since the human eye is of a different design than that of most other animals. The standard solution is to examine the spectral sensitivity properties of animal retinas through microspectrophotometry—a procedure that is rather complicated and therefore only has allowed examinations of a limited number of species to date. We have developed a faster and simpler molecular method, which can be used to estimate the color sensitivities of a bird by sequencing a part of the gene coding for the ultraviolet or violet absorbing opsin in the avian retina. With our method, there is no need to sacrifice the animal, and it thereby facilitates large screenings, including rare and endangered species beyond the reach of microspectrophotometry. Color vision in birds may be categorized into two classes: one with a short-wavelength sensitivity biased toward violet (VS) and the other biased toward ultraviolet (UVS). Using our method on 45 species from 35 families, we demonstrate that the distribution of avian color vision is more complex than has previously been shown. Our data support VS as the ancestral state in birds and show that UVS has evolved independently at least four times. We found species with the UVS type of color vision in the orders Psittaciformes and Passeriformes, in agreement with previous findings. However, species within the families Corvidae and Tyrannidae did not share this character with other passeriforms. We also found UVS type species within the Laridae and Struthionidae families. Raptors (Accipitridae and Falconidae) are of the violet type, giving them a vision system different from their passeriform prey. Intriguing effects on the evolution of color signals can be expected from interactions between predators and prey. Such interactions may explain the presence of UVS in Laridae and Passeriformes.

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RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

5

EXTERNAL LINKS

COMMENTS

@SeveralMutationsWithEffect