

GEPHE SUMMARY

Gephebase Gene
opsin - rhodopsin (LWRh)

Entry Status
Published

GepheID
GP00000770

Main curator
Martin

PHENOTYPIC CHANGE

Trait Category
Physiology

Trait
Color vision (blue shift)

Trait State in Taxon A
Other butterflies

Trait State in Taxon B
Junonia coenia; Siproeta steneles

Ancestral State
Data not curated

Taxonomic Status
Intergeneric or Higher

	Taxon A	Taxon B
Latin Name	<i>Nymphalidae</i>	<i>Junonia</i>
Common Name	brushfoots	buckeyes
Synonyms	brushfoots; brush-footed butterflies	buckeyes; commodoes; pansies
Rank	family	genus
Lineage	cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Amphimesnoptera; Lepidoptera; Glossata; Neolepidoptera; Heteroneura; Ditrysia; Obtectomera; Papilionoidea	cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Amphimesnoptera; Lepidoptera; Glossata; Neolepidoptera; Heteroneura; Ditrysia; Obtectomera; Papilionoidea; Nymphalinae; Junoniini
Parent	Papilionoidea (butterflies) - (Rank: superfamily)	Junoniini () - (Rank: tribe)
NCBI Taxonomy ID	33415	39707
is Taxon A an Intraspecies?	No	No

GENOTYPIC CHANGE

Generic Gene Name
LWRh

Synonyms
-

String
-

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

GO - Molecular Function
GO:0004930 : G protein-coupled receptor activity
GO:0009881 : photoreceptor activity

GO - Biological Process
GO:0018298 : protein-chromophore linkage
GO:0007601 : visual perception
GO:0007602 : phototransduction

GO - Cellular Component
GO:0016021 : integral component of membrane

UniProtKB Heliconius melpomene
E2DZP1

GenebankID or UniProtKB
AF385332

Mutation #1**Presumptive Null**

No

Molecular Type

Coding

Aberration Type

SNP

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

I17M; S137A=S180A in human LWS/MWS numbering system

Experimental Evidence

Candidate Gene

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Ile	Met	17

Main Reference

Adaptive evolution of color vision as seen through the eyes of butterflies. (2007)

Authors

Frentiu FD; Bernard GD; Cuevas CI; Sison-Mangus MP; Prudic KL; Briscoe AD

Abstract

Butterflies and primates are interesting for comparative color vision studies, because both have evolved middle- (M) and long-wavelength- (L) sensitive photopigments with overlapping absorbance spectrum maxima (λ_{max}) values). Although positive selection is important for the maintenance of spectral variation within the primate pigments, it remains an open question whether it contributes similarly to the diversification of butterfly pigments. To examine this issue, we performed epimicrospectrophotometry on the eyes of five *Limnitis* butterfly species and found a 31-nm range of variation in the λ_{max} values of the L-sensitive photopigments (514-545 nm). We cloned partial *Limnitis* L opsin gene sequences and found a significant excess of replacement substitutions relative to polymorphisms among species. Mapping of these L photopigment λ_{max} values onto a phylogeny revealed two instances within Lepidoptera of convergently evolved L photopigment lineages whose λ_{max} values were blue-shifted. A codon-based maximum-likelihood analysis indicated that, associated with the two blue spectral shifts, four amino acid sites (Ile17Met, Ala64Ser, Asn70Ser, and Ser137Ala) have evolved substitutions in parallel and exhibit significant $d(N)/d(S) > 1$. Homology modeling of the full-length *Limnitis arthemis astyanax* L opsin placed all four substitutions within the chromophore-binding pocket. Strikingly, the Ser137Ala substitution is in the same position as a site that in primates is responsible for a 5- to 7-nm blue spectral shift. Our data show that some of the same amino acid sites are under positive selection in the photopigments of both butterflies and primates, spanning an evolutionary distance >500 million years.

Additional References**Mutation #2****Presumptive Null**

No

Molecular Type

Coding

Aberration Type

SNP

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

I17M; S137A=S180A in human LWS/MWS numbering system

Experimental Evidence

Candidate Gene

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Ser	Ala	137

Main Reference

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Authors

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Abstract

Butterflies and primates are interesting for comparative color vision studies, because both have evolved middle- (M) and long-wavelength- (L) sensitive photopigments with overlapping absorbance spectrum maxima (λ_{max}) values). Although positive selection is important for the maintenance of spectral variation within the primate pigments, it remains an open question whether it contributes similarly to the diversification of butterfly pigments. To examine this issue, we performed epimicrospectrophotometry on the eyes of five *Limnitis* butterfly species and found a 31-nm range of variation in the λ_{max} values of the L-sensitive photopigments (514-545 nm). We cloned partial *Limnitis* L opsin gene sequences and found a significant excess of replacement substitutions relative to polymorphisms among species. Mapping of these L photopigment λ_{max} values onto a phylogeny revealed two instances within Lepidoptera of convergently evolved L photopigment lineages whose λ_{max} values were blue-shifted. A codon-based maximum-likelihood analysis indicated that, associated with the two blue spectral shifts, four amino acid sites (Ile17Met, Ala64Ser, Asn70Ser, and Ser137Ala) have evolved substitutions in parallel and exhibit significant $d(N)/d(S) > 1$. Homology modeling of the full-length *Limnitis arthemis astyanax* L opsin placed all four substitutions within the chromophore-binding pocket. Strikingly, the Ser137Ala substitution is in the same position as a site

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[Additional References](#)

RELATED GEPHE

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1 ([opsin - rhodopsin \(UVRh2\)](#))

[Related Haplotypes](#)

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EXTERNAL LINKS

COMMENTS

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