GEPHE SUMMARY

Gephebase Gene
Optix (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Optix^#gephebase-summary-title)

GepheID
GP00000797

Entry Status
Published

Main curator
Martin

PHENOTYPIC CHANGE

Trait Category
Morphology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Morphology^#gephebase-summary-title)

Trait
Coloration (wing, Mullerian mimicry) (https://www.gephebase.org/search-criteria?/and+Trait=^Coloration (wing, Mullerian mimicry)^#gephebase-summary-title)

Trait State in Taxon A
Heliconius erato- Postman

Trait State in Taxon B
Heliconius erato - rayed

Ancestral State
Data not curated

Taxonomic Status
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intraspecific^#gephebase-summary-title)

Taxon A

Latin Name
Heliconius erato (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Heliconius erato^#gephebase-summary-title)

Common Name
crimson-patched longwing

Synonyms
crimson-patched longwing; Heliconius erato (Linnaeus, 1764)

Rank
species

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Amphiesmenoptera; Lepidoptera; Glossata; Neolepidoptera; Heteroneura; Ditrysia; Obtectomera; Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius

Parent
Heliconius () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 33416)

NCBI Taxonomy ID
33431 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 33431)

is Taxon A an Infraspecies?
Yes

Taxon A Description
Heliconius erato- Postman

Taxon B

Latin Name
Heliconius erato (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Heliconius erato^#gephebase-summary-title)

Common Name
crimson-patched longwing

Synonyms
crimson-patched longwing; Heliconius erato (Linnaeus, 1764)

Rank
species

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Amphiesmenoptera; Lepidoptera; Glossata; Neolepidoptera; Heteroneura; Ditrysia; Obtectomera; Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius

Parent
Heliconius () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 33416)

NCBI Taxonomy ID
33431 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 33431)

is Taxon B an Infraspecies?
Yes

Taxon B Description
Heliconius erato - rayed

GENOTYPIC CHANGE

Generic Gene Name
Optix

Synonyms
anon-WO0153538.79; CG18455; D-Six3; Dmel\CG18455; Dsix3; opt; optix; OPTIX; opx; six3; Six3

String
7227.FBpp0302920 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0302920)

Sequence Similarities
Belongs to the SIX/Sine oculis homeobox family.

GO - Molecular Function
GO:0043565 : sequence-specific DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0043565)
GO:0001205 : distal enhancer DNA-binding transcription activator activity, RNA

UniProtKB Drosophila melanogaster
Q95RW8 (http://www.uniprot.org/uniprot/Q95RW8)

GenebankID or UniProtKB
AEO13434 (https://www.ncbi.nlm.nih.gov/nuccore/AEO13434)

polymerase II-specific (https://www.ebi.ac.uk/QuickGO/term/GO:0001205)
GO:0000976 : transcription regulatory region sequence-specific DNA binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0000976)

GO - Biological Process

GO:0045892 : negative regulation of transcription, DNA-templated
(https://www.ebi.ac.uk/QuickGO/term/GO:0045892)
GO:0048749 : compound eye development
(https://www.ebi.ac.uk/QuickGO/term/GO:0048749)
GO:0001751 : compound eye photoreceptor cell differentiation
(https://www.ebi.ac.uk/QuickGO/term/GO:0001751)
GO:0048856 : anatomical structure development
(https://www.ebi.ac.uk/QuickGO/term/GO:0048856)
GO:0001745 : compound eye morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0001745)
GO:0048813 : dendrite morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0048813)
GO:0007458 : progression of morphogenetic furrow involved in compound eye
morphogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0007458)

GO - Cellular Component

GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)
GO:0005667 : transcription factor complex
(https://www.ebi.ac.uk/QuickGO/term/GO:0005667)

Presumptive Null

Unknown (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Unknown^#gephebase-summary-title)

Molecular Type

Cis-regulatory (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Cis-regulatory^#gephebase-summary-title)

Aberration Type

Unknown (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Unknown^#gephebase-summary-title)

Molecular Details of the Mutation

Not identified

Experimental Evidence

Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Linkage Mapping^#gephebase-summary-title)

Main Reference

optix drives the repeated convergent evolution of butterfly wing pattern mimicry. (2011) (https://pubmed.ncbi.nlm.nih.gov/21778360)

Authors

Reed RD; Papa R; Martin A; Hines HM; Counterman BA; Pardo-Diaz C; Jiggins CD; Chamberlain NL; Kronforst MR; Chen R; Halder G; Nijhout HF; McMillan WO

Abstract

Mimicry--whereby warning signals in different species evolve to look similar--has long served as a paradigm of convergent evolution. Little is known, however, about the genes that underlie the evolution of mimetic phenotypes or to what extent the same or different genes drive such convergence. Here, we characterize one of the major genes responsible for mimetic wing pattern evolution in Heliconius butterflies. Mapping, gene expression, and population genetic work all identify a single gene, optix, that controls extreme red wing pattern variation across multiple species of Heliconius. Our results show that the cis-regulatory evolution of a single transcription factor can repeatedly drive the convergent evolution of complex color patterns in distantly related species, thus blurring the distinction between convergence and homology.

Additional References

Wing patterning gene redefines the mimetic history of Heliconius butterflies. (2011) (https://pubmed.ncbi.nlm.nih.gov/22084094)

RELATED GEPHE

Related Genes

1 (WntA) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^33431^/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

1 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^Optix^/and+Taxon ID=^33431^/or+Gene Gephebase=^Optix^/and+Taxon ID=^33431^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS