

GEPHE SUMMARY

Optix (https://www.gephebase.org/search-criteria?/and+Gene Gephebase="Optix" #gephebase-summary-title)	Gephebase Gene	GP00000796	GepheID
Published	Entry Status	Martin	Main curator

PHENOTYPIC CHANGE

Morphology (https://www.gephebase.org/search-criteria?/and+Trait Category="Morphology" #gephebase-summary-title)	Trait Category		
Coloration (wing, Mullerian mimicry) (<a coloration"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait="Coloration (wing, Mullerian mimicry) #gephebase-summary-title)	Trait		
Heliconius erato	Trait State in Taxon A		
Heliconius himera	Trait State in Taxon B		
Data not curated	Ancestral State		
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status="Intraspecific" #gephebase-summary-title)	Taxonomic Status		

Taxon A		Taxon B	
	Latin Name		Latin Name
Heliconius erato (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Heliconius erato" #gephebase-summary-title)	Heliconius erato	Heliconius himera (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Heliconius himera" #gephebase-summary-title)	Heliconius himera
crimson-patched longwing	Common Name	-	Common Name
crimson-patched longwing; Heliconius erato (Linnaeus, 1764)	Synonyms	-	Synonyms
species	Rank	species	Rank
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; Nymphalidae; Heliconiinae; Heliconiini; Heliconius	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; Nymphalidae; Heliconiinae; Heliconiini; Heliconius	Lineage
Heliconius () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=33431)	Parent	Heliconius () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=33416)	Parent
33431 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=33431)	NCBI Taxonomy ID	33442 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=33442)	NCBI Taxonomy ID
No	is Taxon A an Intraspecies?	No	is Taxon B an Intraspecies?

GENOTYPIC CHANGE

Optix	Generic Gene Name	Q95RW8 (http://www.uniprot.org/uniprot/Q95RW8)	UniProtKB Drosophila melanogaster
anon-WO0153538.79; CG18455; D-Six3; Dmel\CG18455; Dsix3; opt; optix; OPTIX; opx; six3; Six3	Synonyms	AEO13434 (https://www.ncbi.nlm.nih.gov/nuccore/AEO13434)	GenebankID or UniProtKB
7227.FBpp0302920 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=7227.FBpp0302920)	String		
Belongs to the SIX/Sine oculis homeobox family.	Sequence Similarities		
GO:0043565 : sequence-specific DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0043565)	GO - Molecular Function		
GO:0001205 : distal enhancer DNA-binding transcription activator activity, RNA 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/or+Taxon ID=^33442^/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=^33442^#gephebase-summary-title>)

EXTERNAL LINKS

COMMENTS