

## GEPHE SUMMARY

**Gephebase Gene**  
Optix

**Entry Status**  
Published

**GepheID**  
GP00000797

**Main curator**  
Martin

## PHENOTYPIC CHANGE

**Trait Category**  
Morphology

**Trait**  
Coloration (wing, Mullerian mimicry)

**Trait State in Taxon A**  
Heliconius erato- Postman

**Trait State in Taxon B**  
Heliconius erato - rayed

**Ancestral State**  
Data not curated

**Taxonomic Status**  
Intraspecific

### Taxon A

**Latin Name**  
*Heliconius erato*

**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; Amphimesmenoptera; Lepidoptera; Glossata; Neolepidoptera; Heteroneura; Ditrysia; Obtectomera; Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius

**Parent**  
Heliconius () - (Rank: genus)

**NCBI Taxonomy ID**  
33431

**is Taxon A an Intraspecies?**  
Yes

**Taxon A Description**  
Heliconius erato- Postman

### Taxon B

**Latin Name**  
*Heliconius erato*

**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; Amphimesmenoptera; Lepidoptera; Glossata; Neolepidoptera; Heteroneura; Ditrysia; Obtectomera; Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius

**Parent**  
Heliconius () - (Rank: genus)

**NCBI Taxonomy ID**  
33431

**is Taxon B an Intraspecies?**  
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

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

**GO - Molecular Function**  
GO:0043565 : sequence-specific DNA binding  
GO:0001205 : distal enhancer DNA-binding transcription activator activity, RNA polymerase II-specific  
GO:0000976 : transcription regulatory region sequence-specific DNA binding

**GO - Biological Process**  
GO:0045892 : negative regulation of transcription, DNA-templated

**UniProtKB Drosophila melanogaster**  
Q95RW8

**GenebankID or UniProtKB**  
AEO13434

GO:0048749 : compound eye development  
GO:0001751 : compound eye photoreceptor cell differentiation  
GO:0048856 : anatomical structure development  
GO:0001745 : compound eye morphogenesis  
GO:0048813 : dendrite morphogenesis  
GO:0007458 : progression of morphogenetic furrow involved in compound eye morphogenesis

**GO - Cellular Component**

GO:0005634 : nucleus  
GO:0005667 : transcription factor complex

**Presumptive Null**  
Unknown

**Molecular Type**  
Cis-regulatory

**Aberration Type**  
Unknown

**Molecular Details of the Mutation**  
Not identified

**Experimental Evidence**  
Linkage Mapping

**Main Reference**  
optix drives the repeated convergent evolution of butterfly wing pattern mimicry. (2011)

**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)

## RELATED GEPHE

**Related Genes**  
1 (WntA)  
**Related Haplotypes**  
1

## EXTERNAL LINKS

## COMMENTS