

## GEPHE SUMMARY

**Gephebase Gene**  
WntA

**Entry Status**  
Published

**GepheID**  
GP00001212

**Main curator**  
Martin

## PHENOTYPIC CHANGE

**Trait Category**  
Morphology

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

**Trait State in Taxon A**  
Heliconius himera - central color patch

**Trait State in Taxon B**  
Heliconius erato etylus - distal color patch

**Ancestral State**  
Data not curated

**Taxonomic Status**  
Intraspecific

### Taxon A

**Latin Name**  
*Heliconius himera*

**Common Name**  
-

**Synonyms**  
-

**Rank**  
species

**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

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

**NCBI Taxonomy ID**  
33442

**is Taxon A an Intraspecies?**  
No

### 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; Amphimesnoptera; 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 etylus - distal color patch

## GENOTYPIC CHANGE

**Generic Gene Name**  
WntA

**Synonyms**  
-

**String**  
-

**Sequence Similarities**  
Belongs to the Wnt family.

**GO - Molecular Function**  
GO:0005102 : signaling receptor binding

**GO - Biological Process**  
GO:0007275 : multicellular organism development  
GO:0016055 : Wnt signaling pathway

**GO - Cellular Component**  
GO:0005576 : extracellular region

**UniProtKB** *Vanessa cardui*  
A0A077DF90

**GenebankID or UniProtKB**  
JN944589

**Presumptive Null**

No

**Molecular Type**

Cis-regulatory

**Aberration Type**

Unknown

**Molecular Details of the Mutation**

Not identified

**Experimental Evidence**

Linkage Mapping

**Main Reference**

Diversification of complex butterfly wing patterns by repeated regulatory evolution of a Wnt ligand. (2012)

**Authors**

Martin A; Papa R; Nadeau NJ; Hill RI; Counterman BA; Halder G; Jiggins CD; Kronforst MR; Long AD; McMillan WO; Reed RD

**Abstract**

Although animals display a rich variety of shapes and patterns, the genetic changes that explain how complex forms arise are still unclear. Here we take advantage of the extensive diversity of Heliconius butterflies to identify a gene that causes adaptive variation of black wing patterns within and between species. Linkage mapping in two species groups, gene-expression analysis in seven species, and pharmacological treatments all indicate that cis-regulatory evolution of the WntA ligand underpins discrete changes in color pattern features across the Heliconius genus. These results illustrate how the direct modulation of morphogen sources can generate a wide array of unique morphologies, thus providing a link between natural genetic variation, pattern formation, and adaptation.

**Additional References****RELATED GEPHE****Related Genes**

1 (Optix)

**Related Haplotypes**

2

**COMMENTS**

See follow-up paper : Van Belleghem et al. for high-resolution Association Mapping of the H. erato etylus allele