

GEPHE SUMMARY

Gephebase Gene
WntA

Entry Status
Published

GepheID
GP00001210

Main curator
Courtier

PHENOTYPIC CHANGE

Trait Category
Morphology

Trait
Coloration (wing, Mullerian mimicry)

Trait State in Taxon A
Heliconius cydno galanthus - "Ac" melanic patch absent = white hourglass pattern present

Trait State in Taxon B
Heliconius pacheus "Ac" melanic patch present = yellow hourglass pattern absent

Ancestral State
Unknown

Taxonomic Status
Intraspecific

	Taxon A	Taxon B
Latin Name	<i>Heliconius cydno</i>	<i>Heliconius pacheus</i>
Common Name	-	-
Synonyms	Heliconius cydno Doubleday, 1847	Heliconius cydno pacheus; Heliconius pacheus Salvin, 1871
Rank	species	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	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)	Heliconius () - (Rank: genus)
NCBI Taxonomy ID	33424	33428
is Taxon A an Intraspecies?	Yes	Yes
Taxon A Description	Heliconius cydno galanthus - "Ac" melanic patch absent = white hourglass pattern present	Heliconius pacheus "Ac" melanic patch present = yellow hourglass pattern absent

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

UniProtKB Vanessa cardui
A0A077DF90

GenebankID or UniProtKB
JN944585

GO - Cellular Component
GO:0005576 : extracellular region

Presumptive Null
No

Molecular Type
Cis-regulatory

Aberration Type
Unknown

Molecular Details of the Mutation

Complex cis-regulatory haplotype : 170 fixed differences were detected among comparisons of allopatric *H. c. galanthus* and *H. pachinus*

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

Ancient homology underlies adaptive mimetic diversity across butterflies. (2014)

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