

GEPHE SUMMARY

Gephebase Gene
WntA

Entry Status
Published

GepheID
GP00001209

Main curator
Martin

PHENOTYPIC CHANGE

Trait Category
Morphology

Trait
Coloration (wing, Mullerian mimicry)

Trait State in Taxon A
Heliconius cydno alithea - polymorphic Ecuadorian population : presence of white hourglass pattern in discal cell

Trait State in Taxon B
Heliconius cydno alithea - polymorphic Ecuadorian population : absence of white hourglass pattern in discal cell

Ancestral State
Unknown

Taxonomic Status
Intraspecific

Taxon A

Latin Name
Heliconius cydno

Common Name
-

Synonyms
Heliconius cydno Doubleday, 1847

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
33424

is Taxon A an Intraspecies?
Yes

Taxon A Description
Heliconius cydno alithea - polymorphic Ecuadorian population : presence of white hourglass pattern in discal cell

Taxon B

Latin Name
Heliconius cydno

Common Name
-

Synonyms
Heliconius cydno Doubleday, 1847

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
33424

is Taxon B an Intraspecies?
Yes

Taxon B Description
Heliconius cydno alithea - polymorphic Ecuadorian population : absence of white hourglass pattern in discal cell

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

GO - Cellular Component
GO:000576 : extracellular region

Presumptive Null
No

Molecular Type
Cis-regulatory

Aberration Type
Indel

Indel Size
1-10 kb

Molecular Details of the Mutation
1.8-kb indel that was perfectly associated with variation in forewing melanin patterning

Experimental Evidence
Linkage Mapping

Main Reference
[Ancient homology underlies adaptive mimetic diversity across butterflies. \(2014\)](#)

Authors
Gallant JR; Imhoff VE; Martin A; Savage WK; Chamberlain NL; Pote BL; Peterson C; Smith GE; Evans B; Reed RD; Kronforst MR; Mullen SP

Abstract
Convergent evolution provides a rare, natural experiment with which to test the predictability of adaptation at the molecular level. Little is known about the molecular basis of convergence over macro-evolutionary timescales. Here we use a combination of positional cloning, population genomic resequencing, association mapping and developmental data to demonstrate that positionally orthologous nucleotide variants in the upstream region of the same gene, *WntA*, are responsible for parallel mimetic variation in two butterfly lineages that diverged >65 million years ago. Furthermore, characterization of spatial patterns of *WntA* expression during development suggests that alternative regulatory mechanisms underlie wing pattern variation in each system. Taken together, our results reveal a strikingly predictable molecular basis for phenotypic convergence over deep evolutionary time.

Additional References
[Diversification of complex butterfly wing patterns by repeated regulatory evolution of a Wnt ligand. \(2012\)](#)

RELATED GEPHE

Related Genes
2 ([aristaless](#), [Optix](#))
Related Haplotypes
1

COMMENTS

Transposon with cis-regulatory effect (Gene Expression Shift) ; Admixture Mapping in Polymorphic Population reinforcing previous Linkage Mapping result.