

## GEPHE SUMMARY

aristales (https://www.gephebase.org/search-criteria?/and+Gene Gephebase= <sup>^</sup> aristales <sup>^</sup> #gephebase-summary-title)	Gephebase Gene	GP00002059	GepheID
Published	Entry Status	Courtier	Main curator

## PHENOTYPIC CHANGE

Morphology (https://www.gephebase.org/search-criteria?/and+Trait Category= <sup>^</sup> Morphology <sup>^</sup> #gephebase-summary-title)	Trait Category		
Coloration (wing, Mullerian mimicry) (https://www.gephebase.org/search-criteria?/and+Trait= <sup>^</sup> Coloration (wing, Mullerian mimicry) <sup>^</sup> #gephebase-summary-title)	Trait		
Heliconius cydno - yellow morph (recessive allele) - yellow is due to a yellow pigment; the ommochrome precursor 3-hydroxy-L-kynurenine (3-OHK)	Trait State in Taxon A		
Heliconius cydno - white morph (dominant allele) - white is a structural color	Trait State in Taxon B		
	Ancestral State		
	Taxon A		
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status= <sup>^</sup> Intraspecific <sup>^</sup> #gephebase-summary-title)	Taxonomic Status		
	Taxon A		Taxon B
Heliconius cydno (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms= <sup>^</sup> Heliconius cydno <sup>^</sup> #gephebase-summary-title)	Latin Name	Heliconius cydno (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms= <sup>^</sup> Heliconius cydno <sup>^</sup> #gephebase-summary-title)	Latin Name
-	Common Name	-	Common Name
Heliconius cydno Doubleday, 1847	Synonyms	Heliconius cydno Doubleday, 1847	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; Dityrsia; 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; Dityrsia; Obtectomera; Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius	Lineage
Heliconius () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 33416 )	Parent	Heliconius () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 33416 )	Parent
33424 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 33424 )	NCBI Taxonomy ID	33424 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 33424 )	NCBI Taxonomy ID
No	is Taxon A an Intraspecies?	No	is Taxon B an Intraspecies?

## GENOTYPIC CHANGE

al	Generic Gene Name	Q06453 (http://www.uniprot.org/uniprot/Q06453)	UniProtKB Drosophila melanogaster
A1; Al; AL; CG3935; Dmel\CG3935; L13-4; lambda13-4	Synonyms	()	GenebankID or UniProtKB
7227.FBpp0077713 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0077713 )	String		
Belongs to the paired homeobox family.	Sequence Similarities		
GO:000977 : RNA polymerase II regulatory region sequence-specific DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:000977)	GO - Molecular Function		
GO:000981 : DNA-binding transcription factor activity, RNA polymerase II-specific (https://www.ebi.ac.uk/QuickGO/term/GO:000981)	GO - Biological Process		

GO:0022416 : chaeta development (<https://www.ebi.ac.uk/QuickGO/term/GO:0022416>)

GO:0045892 : negative regulation of transcription, DNA-templated

(<https://www.ebi.ac.uk/QuickGO/term/GO:0045892>)

GO:0048800 : antennal morphogenesis

(<https://www.ebi.ac.uk/QuickGO/term/GO:0048800>)

GO:0007480 : imaginal disc-derived leg morphogenesis

(<https://www.ebi.ac.uk/QuickGO/term/GO:0007480>)

GO:0035015 : elongation of arista core

(<https://www.ebi.ac.uk/QuickGO/term/GO:0035015>)

GO:0035218 : leg disc development (<https://www.ebi.ac.uk/QuickGO/term/GO:0035218>)

GO - Cellular Component

GO:0005634 : nucleus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005634>)

GO:0032991 : protein-containing complex

(<https://www.ebi.ac.uk/QuickGO/term/GO:0032991>)

Presumptive Null

No (<https://www.gephebase.org/search-criteria?/and+Presumptive+Null=~No~#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

gain of expression - exact mutation unknown

Experimental Evidence

Linkage Mapping (<https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=~Linkage+Mapping~#gephebase-summary-title>)

Main Reference

Aristaless Controls Butterfly Wing Color Variation Used in Mimicry and Mate Choice. (2018) (<https://pubmed.ncbi.nlm.nih.gov/30415702>)

Authors

Westerman EL; VanKuren NW; Massardo D; Tenger-Trolander A; Zhang W; Hill RI; Perry M; Bayala E; Barr K; Chamberlain N; Douglas TE; Buerkle N; Palmer SE; Kronforst MR

Abstract

Neotropical *Heliconius* butterflies display a diversity of warningly colored wing patterns, which serve roles in both MÃ¼llerian mimicry and mate choice behavior. Wing pattern diversity in *Heliconius* is controlled by a small number of unlinked, Mendelian "switch" loci [1]. One of these, termed the K locus, switches between yellow and white color patterns, important mimicry signals as well as mating cues [2-4]. Furthermore, mate preference behavior is tightly linked to this locus [4]. K controls the distribution of white versus yellow scales on the wing, with a dominant white allele and a recessive yellow allele. Here, we combine fine-scale genetic mapping, genome-wide association studies, gene expression analyses, population and comparative genomics, and genome editing with CRISPR/Cas9 to characterize the molecular basis of the K locus in *Heliconius* and to infer its evolutionary history. We show that white versus yellow color variation in *Heliconius cydno* is due to alternate haplotypes at a putative cis-regulatory element (CRE) downstream of a tandem duplication of the homeodomain transcription factor *aristaless*. *Aristaless1* (*al1*) and *aristaless2* (*al2*) are differentially regulated between white and yellow wings throughout development with elevated expression of *al1* in developing white wings, suggesting a role in repressing pigmentation. Consistent with this, knockout of *al1* causes white wings to become yellow. The evolution of wing color in this group has been marked by retention of the ancestral yellow color in many lineages, a single origin of white coloration in *H. cydno*, and subsequent introgression of white color from *H. cydno* into *H. melpomene*.

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Additional References

## RELATED GEPHE

Related Genes

2 (*WntA*, *Optix*) (<https://www.gephebase.org/search-criteria?/or+Taxon+ID=~33424~/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

## EXTERNAL LINKS

## COMMENTS

Knockout of *al1* causes white wings to become yellow. The evolution of wing color in this group has been marked by retention of the ancestral yellow color in many lineages; a single origin of white coloration in *H. cydno*, and subsequent introgression of white color from *H. cydno* into *H. melpomene*. @Introgression