# GEPHE SUMMARY

Gephebase Gene

cortex (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^cortex^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00001805

Main curator

Martin

# PHENOTYPIC CHANGE

Trait Category

Morphology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Morphology^#gephebase-summary-title)

Trait

Coloration (wing) (https://www.gephebase.org/search-criteria?/and+Trait=^Coloration (wing)^#gephebase-summary-title)

Trait State in Taxon A

Heliconius - wirld-type pattern

Trait State in Taxon B

Heliconius - ivory mutant - white wing

Ancestral State

Taxon A

Taxonomic Status

Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Domesticated^#gephebase-summary-title)

## Taxon A

Latin Name

Heliconius melpomene (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Heliconius melpomene^#gephebase-summary-title)

Common Name

postman butterfly

Synonyms

postman butterfly; common postman; Heliconius melpomene (Linnaeus, 1758)

Rank

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

Parent

Heliconius () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 33416 )

NCBI Taxonomy ID

34740 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 34740 )

is Taxon A an Infraspecies?

No

## Taxon B

Latin Name

Heliconius melpomene (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Heliconius melpomene^#gephebase-summary-title)

Common Name

postman butterfly

Synonyms

postman butterfly; common postman; Heliconius melpomene (Linnaeus, 1758)

Rank

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

Parent

Heliconius () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 33416 )

NCBI Taxonomy ID

34740 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 34740 )

is Taxon B an Infraspecies?

No

# GENOTYPIC CHANGE

Generic Gene Name

cort

Synonyms

CG11330; cor; Cort; Dmel\CG11330

String

7227.FBpp0078949 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0078949 )

Sequence Similarities

Belongs to the WD repeat CORT family.

GO - Molecular Function

GO:0010997 : anaphase-promoting complex binding (https://www.ebi.ac.uk/QuickGO/term/GO:0010997)
GO:0097027 : ubiquitin-protein transferase activator activity (https://www.ebi.ac.uk/QuickGO/term/GO:0097027)

GO - Biological Process

GO:0048477 : oogenesis (https://www.ebi.ac.uk/QuickGO/term/GO:0048477)

UniProtKB Drosophila melanogaster

Q960N3 (http://www.uniprot.org/uniprot/Q960N3)

GenebankID or UniProtKB

()

GO:0045143 : homologous chromosome segregation
(https://www.ebi.ac.uk/QuickGO/term/GO:0045143)
GO:0031145 : anaphase-promoting complex-dependent catabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0031145)
GO:0007349 : cellularization (https://www.ebi.ac.uk/QuickGO/term/GO:0007349)
GO:0007343 : egg activation (https://www.ebi.ac.uk/QuickGO/term/GO:0007343)
GO:0007144 : female meiosis I (https://www.ebi.ac.uk/QuickGO/term/GO:0007144)
GO:0007147 : female meiosis II (https://www.ebi.ac.uk/QuickGO/term/GO:0007147)
GO:0007143 : female meiotic nuclear division
(https://www.ebi.ac.uk/QuickGO/term/GO:0007143)
GO:0007279 : pole cell formation (https://www.ebi.ac.uk/QuickGO/term/GO:0007279)
GO:1905786 : positive regulation of anaphase-promoting complex-dependent catabolic process (https://www.ebi.ac.uk/QuickGO/term/GO:1905786)
GO:1904668 : positive regulation of ubiquitin protein ligase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:1904668)

GO - Cellular Component

GO:0005737 : cytoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005737)

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

Deletion (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Deletion^#gephebase-summary-title)

Deletion Size

10-100 kb

Molecular Details of the Mutation

78-kb deletion in the 5â€² region of the cortex gene that includes a facultative 5â€²UTR exon detected in larval wing disk transcriptomes. Phenotypic effect confirmed by CRISPR mutagenesis of this exon. The ivory deletion causes the loss of 1 of 2 promoters.

Experimental Evidence

Association Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Association Mapping^#gephebase-summary-title)

Main Reference

A large deletion at the cortex locus eliminates butterfly wing patterning. (2022) (https://pubmed.ncbi.nlm.nih.gov/35099556)

Authors

Hanly JJ; Livraghi L; Heryanto C; McMillan WO; Jiggins CD; Gilbert LE; Martin A

Abstract

As the genetic basis of natural and domesticated variation has been described in recent years, a number of hotspot genes have been repeatedly identified as the targets of selection, Heliconius butterflies display a spectacular diversity of pattern variants in the wild and the genetic basis of these patterns has been well-described. Here, we sought to identify the mechanism behind an unusual pattern variant that is instead found in captivity, the ivory mutant, in which all scales on both the wings and body become white or yellow. Using a combination of autozygosity mapping and coverage analysis from 37 captive individuals, we identify a 78-kb deletion at the cortex wing patterning locus, a gene which has been associated with wing pattern evolution in H. melpomene and 10 divergent lepidopteran species. This deletion is undetected among 458 wild Heliconius genomes samples, and its dosage explains both homozygous and heterozygous ivory phenotypes found in captivity. The deletion spans a large 5′ region of the cortex gene that includes a facultative 5′UTR exon detected in larval wing disk transcriptomes. CRISPR mutagenesis of this exon replicates the wing phenotypes from coding knock-outs of cortex, consistent with a functional role of ivory-deleted elements in establishing scale color fate. Population demographics reveal that the stock giving rise to the ivory mutant has a mixed origin from across the wild range of H. melpomene, and supports a scenario where the ivory mutation occurred after the introduction of cortex haplotypes from Ecuador. Homozygotes for the ivory deletion are inviable while heterozygotes are the targets of artificial selection, joining 40 other examples of allelic variants that provide heterozygous advantage in animal populations under artificial selection by fanciers and breeders. Finally, our results highlight the promise of autozygosity and association mapping for identifying the genetic basis of aberrant mutations in captive insect populations.

Additional References

## RELATED GEPHE

Related Genes

2 (Optix, WntA) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^34740^/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

1 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^cortex^/and+Taxon ID=^34740^/or+Gene Gephebase=^cortex^/and+Taxon ID=^34740^#gephebase-summary-title)

## EXTERNAL LINKS

## COMMENTS

@Parallelism