GEPHE SUMMARY

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

Entry Status
Published

GepheID
GP00002660

Main curator
Courtier

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 - absence of yellow band

Trait State in Taxon B
Heliconius - presence of yellow band

Ancestral State
Taxon A

Taxonomic Status
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intraspecific^#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

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

Insertion Size

1-10 kb

Molecular Details of the Mutation

Insertion of two transposable elements (BovB-like and Helitron-like)

Experimental Evidence

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

Main Reference

Cortex cis-regulatory switches establish scale colour identity and pattern diversity in Heliconius. (2021) (https://pubmed.ncbi.nlm.nih.gov/34280087)

Authors

Livraghi L; Hanly JJ; Van Bellghem SM; Montejo-Kovacevich G; van der Heijden ES; Loh LS; Ren A; Warren IA; Lewis JJ; Concha C; Hebberecht L; Wright CJ; Walker JM; Foley J; Goldberg ZH; Arenas-Castro H; Salazar C; Perry MW; Papa R; Martin A; McMillan WO; Jiggins CD

Abstract

In Heliconius butterflies, wing colour pattern diversity and scale types are controlled by a few genes of large effect that regulate colour pattern switches between morphs and species across a large mimetic radiation. One of these genes, cortex, has been repeatedly associated with colour pattern evolution in butterflies. Here we carried out CRISPR knockouts in multiple Heliconius species and show that cortex is a major determinant of scale cell identity. Chromatin accessibility profiling and introgression scans identified cis-regulatory regions associated with discrete phenotypic switches. CRISPR perturbation of these regions in black hindwing genotypes recreated a yellow bar, revealing their spatially limited activity. In the H. melpomene/timareta lineage, the candidate CRE from yellow-barred phenotype morphs is interrupted by a transposable element, suggesting that cis-regulatory structural variation underlies these mimetic adaptations. Our work shows that cortex functionally controls scale colour fate and that its cis-regulatory regions control a phenotypic switch in a modular and pattern-specific fashion.

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 @TE