

GEPHE SUMMARY

cortex (#gephebase-summary-title)	Gephebase Gene	GP00002660	GephelD
Published	Entry Status	Courtier	Main curator

PHENOTYPIC CHANGE

Trait Category			
Morphology (#gephebase-summary-title)	Trait		
Coloration (wing) (<a ?and+taxonomicstatus='%Intraspecific"' href="https://www.gephebase.org/search-criteria/?and+Trait=%Coloration(wing)#gephebase-summary-title)</td><td>Trait State in Taxon A</td><td></td><td></td></tr> <tr> <td>Heliconius - absence of yellow band</td><td>Trait State in Taxon B</td><td></td><td></td></tr> <tr> <td>Heliconius - presence of yellow band</td><td>Ancestral State</td><td></td><td></td></tr> <tr> <td>Taxon A</td><td>Taxonomic Status</td><td></td><td></td></tr> <tr> <td>Intraspecific (#gephebase-summary-title)			
Taxon A		Taxon B	
Heliconius melpomene (#gephebase-summary-title))	Latin Name	Heliconius melpomene (#gephebase-summary-title))	Latin Name
postman butterfly	Common Name	postman butterfly	Common Name
postman butterfly; common postman; Heliconius melpomene (Linnaeus, 1758)	Synonyms	postman butterfly; common postman; Heliconius melpomene (Linnaeus, 1758)	Synonyms
species	Rank	species	Rank
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	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	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
34740 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=34740)	NCBI Taxonomy ID	34740 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=34740)	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

cort	Generic Gene Name	UniProtKB Drosophila melanogaster
CG11330; cor; Cort; Dmel\CG11330	Synonyms	GenebankID or UniProtKB
7227.FBpp0078949 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=7227.FBpp0078949)	String	0
Belongs to the WD repeat CORT family.	Sequence Similarities	
GO:0010997 : anaphase-promoting complex binding (https://www.ebi.ac.uk/QuickGO/term/GO:0010997)	GO - Molecular Function	
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)		

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 ([#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive+Null=^No))

Molecular Type

Cis-regulatory ([#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular+Type=^Cis-regulatory))

Aberration Type

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

Insertion Size

1-10 kb

Molecular Details of the Mutation

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

Experimental Evidence

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

Main Reference

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

Authors

Livragli 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.

Â© 2021, Livraghi et al.

Additional References

RELATED GEPHE

2 (Optix, WntA) (https://www.gephebase.org/search-criteria?/or+Taxon+ID=^34740#/gephebase-summary-title)	Related Genes
1 (https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=^cortex#/gephebase-summary-title)	Related Haplotypes

EXTERNAL LINKS

COMMENTS

@Parallelism @TE