

GEPHE SUMMARY

cortex (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=~cortex^#gephebase-summary-title)	Gephebase Gene	GP00002419	GepheID
Published	Entry Status	Courtier	Main curator

PHENOTYPIC CHANGE

Morphology (https://www.gephebase.org/search-criteria?/and+Trait+Category=~Morphology^#gephebase-summary-title)	Trait Category		
Coloration (wing; mimicry) (https://www.gephebase.org/search-criteria?/and+Trait=~Coloration+(wing;+mimicry)^#gephebase-summary-title)	Trait		
clytia color pattern - uniform field of brown pigmented scales with white submarginal crescents and a dark brown body mimicking the toxic common crow, <i>Euploea core</i>	Trait State in Taxon A		
dissimilis color pattern - white pigmented and black melanic scales and white and black striped body that mimic the toxic tigers in the genera <i>Tirumala</i> and <i>Parantica</i>	Trait State in Taxon B		
Unknown	Ancestral State		
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Intraspecific^#gephebase-summary-title)	Taxonomic Status		
	Taxon A	Taxon B	
	Latin Name	Latin Name	
Papilio clytia (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Papilio+clytia^#gephebase-summary-title)	Papilio clytia (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Papilio+clytia^#gephebase-summary-title)	Papilio clytia (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Papilio+clytia^#gephebase-summary-title)	
common mime swallowtail	Common Name	common mime swallowtail	Common Name
Chilasa clytia; common mime swallowtail; <i>Papilio clytia</i> Linnaeus, 1758	Synonyms	Chilasa clytia; common mime swallowtail; <i>Papilio clytia</i> 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; Endopterygota; Amphiesmenoptera; Lepidoptera; Glossata; Neolepidoptera; Heteroneura; Dityrsia; Obtectomera; Papilionoidea; Papilionidae; Papilioninae; Papilionini; Papilio	Lineage	cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Endopterygota; Amphiesmenoptera; Lepidoptera; Glossata; Neolepidoptera; Heteroneura; Dityrsia; Obtectomera; Papilionoidea; Papilionidae; Papilioninae; Papilionini; Papilio	Lineage
Papilio () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7145)	Parent	Papilio () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7145)	Parent
110796 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=110796)	NCBI Taxonomy ID	110796 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=110796)	NCBI Taxonomy ID
Yes	is Taxon A an Intraspecies?	Yes	is Taxon B an Intraspecies?
clytia morph	Taxon A Description	dissimilis morph	Taxon B Description

GENOTYPIC CHANGE

cort	Generic Gene Name	Q960N3 (http://www.uniprot.org/uniprot/Q960N3)	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		
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 (<https://www.gephebase.org/search-criteria?and+Presumptive+Null=~No~#gephebase-summary-title>)

Molecular Type

Unknown (<https://www.gephebase.org/search-criteria?and+Molecular+Type=~Unknown~#gephebase-summary-title>)

Aberration Type

Unknown (<https://www.gephebase.org/search-criteria?and+Aberration+Type=~Unknown~#gephebase-summary-title>)

Molecular Details of the Mutation

Mapping to a 500-kb region that contains the cortex gene

Experimental Evidence

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

Main Reference

Butterfly Mimicry Polymorphisms Highlight Phylogenetic Limits of Gene Reuse in the Evolution of Diverse Adaptations. (2019) (<https://pubmed.ncbi.nlm.nih.gov/31504750>)

Authors

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Abstract

Some genes have repeatedly been found to control diverse adaptations in a wide variety of organisms. Such gene reuse reveals not only the diversity of phenotypes these unique genes control but also the composition of developmental gene networks and the genetic routes available to and taken by organisms during adaptation. However, the causes of gene reuse remain unclear. A small number of large-effect Mendelian loci control a huge diversity of mimetic butterfly wing color patterns, but reasons for their reuse are difficult to identify because the genetic basis of mimicry has primarily been studied in two systems with correlated factors: female-limited Batesian mimicry in *Papilio swallowtails* (Papilionidae) and non-sex-limited MÃ¼llerian mimicry in *Heliconius longwings* (Nymphalidae). Here, we break the correlation between phylogenetic relationship and sex-limited mimicry by identifying loci controlling female-limited mimicry polymorphism *Hypolimnas misippus* (Nymphalidae) and non-sex-limited mimicry polymorphism in *Papilio clytia* (Papilionidae). The *Papilio clytia* polymorphism is controlled by the genome region containing the gene cortex, the classic P supergene in *Heliconius numata*, and loci controlling color pattern variation across Lepidoptera. In contrast, female-limited mimicry polymorphism in *Hypolimnas misippus* is associated with a locus not previously implicated in color patterning. Thus, although many species repeatedly converged on cortex and its neighboring genes over 120 My of evolution of diverse color patterns, female-limited mimicry polymorphisms each evolved using a different gene. Our results support conclusions that gene reuse occurs mainly within ~10 My and highlight the puzzling diversity of genes controlling seemingly complex female-limited mimicry polymorphisms.

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Additional References

RELATED GEPHE

No matches found.

Related Genes

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS

@Parallelism

