GEPHE SUMMARY

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

GepheID
GP00002419

Entry Status
Published

Main curator
Courtier

PHENOTYPIC CHANGE

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

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

Trait State in Taxon A
clytia color pattern - uniform field of brown pigmented scales with white submarginal crescents and a dark brown body mimicking the toxic common crow, Euploea core

Trait State in Taxon B
dissimilis color pattern - white pigmented and black melanic scales and white and black striped body that mimic the toxic tigers in the genera Tirumala and Parantica

Ancestral State
Unknown

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

Taxon A

Latin Name
Papilio clytia (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Papilio clytia^#gephebase-summary-title)

Common Name
common mime swallowtail

Synonyms
Chilasa clytia; common mime swallowtail; Papilio clytia Linnaeus, 1758

Rank
species

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; Ditrysia; Obtectomera; Papilionoidea; Papilionidae; Papilioninae; Papilionini; Papilio

Parent
Papilio () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7145)

NCBI Taxonomy ID
110796 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 110796)

is Taxon A an Infraspecies?
Yes

Taxon A Description
clytia morph

Taxon B

Latin Name
Papilio clytia (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Papilio clytia^#gephebase-summary-title)

Common Name
common mime swallowtail

Synonyms
Chilasa clytia; common mime swallowtail; Papilio clytia Linnaeus, 1758

Rank
species

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; Ditrysia; Obtectomera; Papilionoidea; Papilionidae; Papilioninae; Papilionini; Papilio

Parent
Papilio () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7145)

NCBI Taxonomy ID
110796 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 110796)

is Taxon B an Infraspecies?
Yes

Taxon B Description
dissimilis morph

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)

UniProtKB Drosophila melanogaster
Q960N3 (http://www.uniprot.org/uniprot/Q960N3)

GenebankID or UniProtKB
()

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

VanKuren NW; Massardo D; Nallu S; Kronforst MR

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 â¼10 My and highlight the puzzling diversity of genes controlling seemingly complex female-limited mimicry polymorphisms.

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Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@Parallelism