GEPHE SUMMARY

Gephebase Gene

Sox5/6 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Sox5/6^#gephebase-summary-title)

GepheID

GP00002429

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

Hypolimnas misippus - form misippus

Trait State in Taxon B

Hypolimnas misippus - form immima/inaria

Ancestral State

Unknown

Taxonomic Status

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

Taxon A

Latin Name

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

Common Name

-

Synonyms

Papilio misippus; Hypolimnas misippus (Linnaeus, 1764); Papilio misippus Linnaeus, 1764; Hypolimnas missipus

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; Nymphalidae; Nymphalinae; Junoniini; Hypolimnas

Parent

Hypolimnas (eggflies) - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 76214)

NCBI Taxonomy ID

124412 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 124412)

is Taxon A an Infraspecies?

Yes

Taxon A Description

Hypolimnas misippus - form misippus

Taxon B

Latin Name

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

Common Name

-

Synonyms

Papilio misippus; Hypolimnas misippus (Linnaeus, 1764); Papilio misippus Linnaeus, 1764; Hypolimnas missipus

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; Nymphalidae; Nymphalinae; Junoniini; Hypolimnas

Parent

Hypolimnas (eggflies) - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 76214)

NCBI Taxonomy ID

124412 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 124412)

is Taxon B an Infraspecies?

Yes

Taxon B Description

Hypolimnas misippus - form immima/inaria

GENOTYPIC CHANGE

Generic Gene Name

-

Synonyms

-

String

-

Sequence Similarities

-

GO - Molecular Function

-

GO - Biological Process

-

GO - Cellular Component

-

UniProtKB

()

GenebankID or UniProtKB

()

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

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

Molecular Details of the Mutation

A 10 kb intergenic region located 48kb upstream of the Sox5/6 gene is strongly associated with the wing phenotype. This cis-regulatory change may also affect another neighboring gene, such as pink.

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 â¼410 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 @SexualTrait