GEPHE SUMMARY

Gephebase Gene

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

Entry Status

Published

GepheID

GP00001967

Main curator

Courtier

PHENOTYPIC CHANGE

Trait Category

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

Trait

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

Trait State in Taxon A

non-mimetic female

Trait State in Taxon B

female mimetic to distantly related and toxic swallowtails in the genera Pachliopta and Atrophaneura

Ancestral State

Unknown

Taxonomic Status

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

Taxon A

Latin Name

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

Common Name

-

Synonyms

Papilio memnon 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; Papilionidae; Papilioninae; Papilionini; Papilio

Parent

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

NCBI Taxonomy ID

76198 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 76198)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

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

Common Name

-

Synonyms

Papilio memnon 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; Papilionidae; Papilioninae; Papilionini; Papilio

Parent

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

NCBI Taxonomy ID

76198 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 76198)

is Taxon B an Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

dsx

Synonyms

CG11094; Dmdsx; Dmel\CG11094; Dsx; DSX; dsxF; dsxM; Hr; ix-62c

String

7227.FBpp0303107 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0303107)

Sequence Similarities

-

GO - Molecular Function

GO:0042803 : protein homodimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0042803)
GO:0000977 : RNA polymerase II regulatory region sequence-specific DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0000977)
GO:0008270 : zinc ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0008270)

UniProtKB Drosophila melanogaster

P23023 (http://www.uniprot.org/uniprot/P23023)

GenebankID or UniProtKB

()

GO:0001077 : proximal promoter DNA-binding transcription activator activity, RNA polymerase II-specific (https://www.ebi.ac.uk/QuickGO/term/GO:0001077)
GO:0001078 : proximal promoter DNA-binding transcription repressor activity, RNA polymerase II-specific (https://www.ebi.ac.uk/QuickGO/term/GO:0001078)

GO - Biological Process

GO:0045944 : positive regulation of transcription by RNA polymerase II (https://www.ebi.ac.uk/QuickGO/term/GO:0045944)
GO:0006357 : regulation of transcription by RNA polymerase II (https://www.ebi.ac.uk/QuickGO/term/GO:0006357)
GO:0007530 : sex determination (https://www.ebi.ac.uk/QuickGO/term/GO:0007530)
GO:0045892 : negative regulation of transcription, DNA-templated (https://www.ebi.ac.uk/QuickGO/term/GO:0045892)
GO:0045893 : positive regulation of transcription, DNA-templated (https://www.ebi.ac.uk/QuickGO/term/GO:0045893)
GO:0046660 : female sex differentiation (https://www.ebi.ac.uk/QuickGO/term/GO:0046660)
GO:0048086 : negative regulation of developmental pigmentation (https://www.ebi.ac.uk/QuickGO/term/GO:0048086)
GO:0048071 : sex-specific pigmentation (https://www.ebi.ac.uk/QuickGO/term/GO:0048071)
GO:0035215 : genital disc development (https://www.ebi.ac.uk/QuickGO/term/GO:0035215)
GO:0007485 : imaginal disc-derived male genitalia development (https://www.ebi.ac.uk/QuickGO/term/GO:0007485)
GO:0016199 : axon midline choice point recognition (https://www.ebi.ac.uk/QuickGO/term/GO:0016199)
GO:0007619 : courtship behavior (https://www.ebi.ac.uk/QuickGO/term/GO:0007619)
GO:0045497 : female analia development (https://www.ebi.ac.uk/QuickGO/term/GO:0045497)
GO:0019101 : female somatic sex determination (https://www.ebi.ac.uk/QuickGO/term/GO:0019101)
GO:0007486 : imaginal disc-derived female genitalia development (https://www.ebi.ac.uk/QuickGO/term/GO:0007486)
GO:0045496 : male analia development (https://www.ebi.ac.uk/QuickGO/term/GO:0045496)
GO:0008049 : male courtship behavior (https://www.ebi.ac.uk/QuickGO/term/GO:0008049)
GO:0045433 : male courtship behavior, veined wing generated song production (https://www.ebi.ac.uk/QuickGO/term/GO:0045433)
GO:0046661 : male sex differentiation (https://www.ebi.ac.uk/QuickGO/term/GO:0046661)
GO:0045498 : sex comb development (https://www.ebi.ac.uk/QuickGO/term/GO:0045498)
GO:0018993 : somatic sex determination (https://www.ebi.ac.uk/QuickGO/term/GO:0018993)

GO - Cellular Component

GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)

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

A locus containing three genes (dsx; Nach-like and UXT) displays dimorphic sequences strictly associated with the mimetic/nonmimetic phenotypes. Expression of dox; UXT but not Nach-like showed differences correlated with phenotype in female hind wings.

Experimental Evidence

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

Main Reference

Parallel evolution of Batesian mimicry supergene in two Papilio butterflies, P. polytes and P. memnon. (2018) (https://pubmed.ncbi.nlm.nih.gov/29675466)

Authors

Iijima T; Kajitani R; Komata S; Lin CP; Sota T; Itoh T; Fujiwara H

Abstract

Batesian mimicry protects animals from predators when mimics resemble distasteful models. The female-limited Batesian mimicry in Papilio butterflies is controlled by a supergene locus switching mimetic and nonmimetic forms. In Papilio polytes, recent studies revealed that a highly diversified region (HDR) containing doublesex (dsx-HDR) constitutes the supergene with dimorphic alleles and is likely maintained by a chromosomal inversion. In the closely related Papilio memnon, which exhibits a similar mimicry polymorphism, we performed whole-genome sequence analyses in 11 butterflies, which revealed a nearly identical dsx-HDR containing three genes (dsx, Nach-like, and UXT) with dimorphic sequences strictly associated with the mimetic/nonmimetic phenotypes. In addition, expression of these genes, except that of Nach-like in female hind wings, showed differences correlated with phenotype. The dimorphic dsx-HDR in P. memnon is maintained without a chromosomal inversion, suggesting that a separate mechanism causes and maintains allelic divergence in these genes. More abundant accumulation of transposable elements and repetitive sequences in the dsx-HDR than in other genomic regions may contribute to the suppression of chromosomal recombination. Gene trees for Dsx, Nach-like, and UXT indicated that mimetic alleles evolved independently in the two Papilio species. These results suggest that the genomic region involving the above three genes has repeatedly diverged so that two allelic sequences of this region function as developmental switches for mimicry polymorphism in the two Papilio species. The supergene structures revealed here suggest that independent evolutionary processes with different genetic mechanisms have led to parallel evolution of similar female-limited polymorphisms underlying Batesian mimicry in Papilio butterflies.

Additional References

Identification of doublesex alleles associated with the female-limited Batesian mimicry polymorphism in Papilio memnon. (2016) (https://pubmed.ncbi.nlm.nih.gov/27708422)

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

Locus previously thought to be a @Supergene - is actually narrowed down to three genes. An inversion prevents recombination between the divergent alleles. @TE repeats @Parallelism Gene trees for Dsx; Nach-like and UXT indicate that mimetic alleles evolved independently in the two Papilio species. @Inversion