GEPHE SUMMARY

Gephebase Gene

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

GepheID

GP00001966

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 ; 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 Pachliopta swallowtails

Ancestral State

Unknown

Taxonomic Status

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

Taxon A

Latin Name

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

Common Name

common Mormon

Synonyms

common Mormon; Papilio polytes 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

76194 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 76194)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

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

Common Name

common Mormon

Synonyms

common Mormon; Papilio polytes 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

76194 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 76194)

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)
GO:0001077 : proximal promoter DNA-binding transcription activator activity, RNA

UniProtKB Drosophila melanogaster

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

GenebankID or UniProtKB

()

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

More than 1000 nucleotide substitutions differentiate mimetic and non-mimetic dsx alleles. The non-mimetic Cyrus Dsx protein folds much like other insects (such as Bombyx mori) whereas the mimetic polytes protein structure is highly divergent. Knockdown experiments show that female-specific dsx isoforms expressed from the inverted H allele (dsx(H)) induce mimetic coloration patterns and simultaneously repress non-mimetic patterns.

Experimental Evidence

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

Main Reference

doublesex is a mimicry supergene. (2014) (https://pubmed.ncbi.nlm.nih.gov/24598547)

Authors

Kunte K; Zhang W; Tenger-Trolander A; Palmer DH; Martin A; Reed RD; Mullen SP; Kronforst MR

Abstract

One of the most striking examples of sexual dimorphism is sex-limited mimicry in butterflies, a phenomenon in which one sex--usually the female--mimics a toxic model species, whereas the other sex displays a different wing pattern. Sex-limited mimicry is phylogenetically widespread in the swallowtail butterfly genus Papilio, in which it is often associated with female mimetic polymorphism. In multiple polymorphic species, the entire wing pattern phenotype is controlled by a single Mendelian 'supergene'. Although theoretical work has explored the evolutionary dynamics of supergene mimicry, there are almost no empirical data that address the critical issue of what a mimicry supergene actually is at a functional level. Using an integrative approach combining genetic and association mapping, transcriptome and genome sequencing, and gene expression analyses, we show that a single gene, doublesex, controls supergene mimicry in Papilio polytes. This is in contrast to the long-held view that supergenes are likely to be controlled by a tightly linked cluster of loci. Analysis of gene expression and DNA sequence variation indicates that isoform expression differences contribute to the functional differences between dsx mimicry alleles, and protein sequence evolution may also have a role. Our results combine elements from different hypotheses for the identity of supergenes, showing that a single gene can switch the entire wing pattern among mimicry phenotypes but may require multiple, tightly linked mutations to do so.

Additional References

A genetic mechanism for female-limited Batesian mimicry in Papilio butterfly. (2015) (https://pubmed.ncbi.nlm.nih.gov/25751626)
Tracing the origin and evolution of supergene mimicry in butterflies. (2017) (https://pubmed.ncbi.nlm.nih.gov/29116078)

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 a single gene. An inversion whose breakpoints flank dsx prevents recombination between the divergent alleles of dox. The divergent alleles are about 130 kb. @Inversion