

GEPHE SUMMARY

	Gephebase Gene	GephelD
Doublesex (https://www.gephebase.org/search-criteria?/and+GeneGephebase=^Doublesex^#gephebase-summary-title)	GP00001966	Main curator
Published	Entry Status	Courtier

PHENOTYPIC CHANGE

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

Taxon A		Taxon B	
	Latin Name		Latin Name
Papilio polytes (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Papilio+polytes^#gephebase-summary-title)		Papilio polytes (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Papilio+polytes^#gephebase-summary-title)	
common Mormon	Common Name	common Mormon	Common Name
common Mormon; Papilio polytes Linnaeus, 1758	Synonyms	common Mormon; Papilio polytes Linnaeus, 1758	Synonyms
species	Rank	species	Rank
	Lineage		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		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	
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
76194 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 76194)	NCBI Taxonomy ID	76194 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 76194)	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Drosophila melanogaster
dsx	Synonyms	P23023 (http://www.uniprot.org/uniprot/P23023)	GenebankID or UniProtKB
CG11094; Dmdsx; Dmel\CG11094; Dsx; DSX; dsxF; dsxM; Hr; ix-62c	String	0	
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			

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.gephbase.org/search-criteria?/and+Presumptive+Null=^No^#gephbase-summary-title>)

Molecular Type

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

Aberration Type

Unknown (<https://www.gephbase.org/search-criteria?/and+Aberration+Type=^Unknown^#gephbase-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.gephbase.org/search-criteria?/and+Experimental+Evidence=^Linkage+Mapping^#gephbase-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