

GEPHE SUMMARY

Doublesex (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=~Doublesex^#gephebase-summary-title)	Gephebase Gene	GP00001967	GepheID
Published	Entry Status	Courtier	Main curator

PHENOTYPIC CHANGE

Morphology (https://www.gephebase.org/search-criteria?/and+Trait+Category=~Morphology^#gephebase-summary-title)	Trait Category		
Coloration (wing ; Batesian mimicry) (https://www.gephebase.org/search-criteria?/and+Trait=~Coloration+wing+;+Batesian+mimicry^#gephebase-summary-title)	Trait		
non-mimetic female	Trait State in Taxon A		
female mimetic to distantly related and toxic swallowtails in the genera <i>Pachliopta</i> and <i>Atrophaneura</i>	Trait State in Taxon B		
Unknown	Ancestral State		
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Intraspecific^#gephebase-summary-title)	Taxonomic Status		
	Taxon A		Taxon B
Papilio memnon (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Papilio+memnon^#gephebase-summary-title)	Latin Name	Papilio memnon (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Papilio+memnon^#gephebase-summary-title)	Latin Name
-	Common Name	-	Common Name
Papilio memnon Linnaeus, 1758	Synonyms	Papilio memnon Linnaeus, 1758	Synonyms
species	Rank	species	Rank
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Amphimesnoptera; Lepidoptera; Glossata; Neolepidoptera; Heteroneura; Dityrsia; Obtectomera; Papilionoidea; Papilionidae; Papilioninae; Papilionini; Papilio	Lineage	cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Amphimesnoptera; Lepidoptera; Glossata; Neolepidoptera; Heteroneura; Dityrsia; Obtectomera; Papilionoidea; Papilionidae; Papilioninae; Papilionini; Papilio	Lineage
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
76198 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=76198)	NCBI Taxonomy ID	76198 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=76198)	NCBI Taxonomy ID
No	is Taxon A an Intraspecies?	No	is Taxon B an Intraspecies?

GENOTYPIC CHANGE

dsx	Generic Gene Name	P23023 (http://www.uniprot.org/uniprot/P23023)	UniProtKB <i>Drosophila melanogaster</i>
CG11094; Dmdsx; DmellCG11094; Dsx; DSX; dsxF; dsxM; Hr; ix-62c	Synonyms	0	GenebankID or UniProtKB
7227.FBpp0303107 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=7227.FBpp0303107)	String		
-	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>)

No ([https://www.gephebase.org/search-criteria?/and+Presumptive Null=~No^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive+Null=~No^#gephebase-summary-title)) Presumptive Null

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

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

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. Molecular Details of the Mutation

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

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

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

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. Abstract

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

No matches found.

Related Genes

No matches found.

Related Haplotypes

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