

GEPHE SUMMARY

	Gephebase Gene	GephelD
Sox5/6 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase="Sox5/6">#gephebase-summary-title)	GP00002429	Main curator
Published	Entry Status	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 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		Taxon B	
Hypolimnas misippus (#gephebase-summary-title)	Latin Name	Hypolimnas misippus (#gephebase-summary-title)	Latin Name
-	Common Name	-	Common Name
Papilio misippus; Hypolimnas misippus (Linnaeus, 1764); Papilio misippus Linnaeus, 1764; Hypolimnas missipus	Synonyms	Papilio misippus; Hypolimnas misippus (Linnaeus, 1764); Papilio misippus Linnaeus, 1764; Hypolimnas missipus	Synonyms
species	Rank	species	Rank
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	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	Lineage
Hypolimnas (eggflies) - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=76214)	Parent	Hypolimnas (eggflies) - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=76214)	Parent
124412 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=124412)	NCBI Taxonomy ID	124412 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=124412)	NCBI Taxonomy ID
Yes	is Taxon A an Infraspecies?	Yes	is Taxon B an Infraspecies?
Hypolimnas misippus - form misippus	Taxon A Description	Hypolimnas misippus - form immima/inaria	Taxon B Description

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB
-	0	
-	Synonyms	GenebankID or UniProtKB
-	0	
-	String	
	Sequence Similarities	
-	GO - Molecular Function	
-	GO - Biological Process	
-	GO - Cellular Component	

No (https://www.gephebase.org/search-criteria/?and+Presumptive+Null=%No%#gephebase-summary-title)	Presumptive Null
Cis-regulatory (https://www.gephebase.org/search-criteria/?and+Molecular+Type=%Cis-regulatory%#gephebase-summary-title)	Molecular Type
Unknown (https://www.gephebase.org/search-criteria/?and+Aberration+Type=%Unknown%#gephebase-summary-title)	Aberration Type
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.	Molecular Details of the Mutation
Association Mapping (https://www.gephebase.org/search-criteria/?and+Experimental+Evidence=%Association+Mapping%#gephebase-summary-title)	Experimental Evidence
Butterfly Mimicry Polymorphisms Highlight Phylogenetic Limits of Gene Reuse in the Evolution of Diverse Adaptations. (2019) (https://pubmed.ncbi.nlm.nih.gov/31504750)	Main Reference
VanKuren NW; Massardo D; Nallu S; Kronforst MR	Authors
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 Müllerian 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 ~1/410 My and highlight the puzzling diversity of genes controlling seemingly complex female-limited mimicry polymorphisms.	Abstract

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[Additional References](#)

RELATED GEPHE

No matches found.	Related Genes
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS

@Parallelism @SexualTrait