

GEPHE SUMMARY

	Gene	Gephebase Gene	GephelD
apontic-like (https://www.gephebase.org/search-criteria?/and+Gene Gephebase^apontic-like^#gephebase-summary-title)		GP00001386	Main curator
	Status	Martin	
Published			

PHENOTYPIC CHANGE

Trait Category			
Morphology (https://www.gephebase.org/search-criteria?/and+Trait Category^Morphology^#gephebase-summary-title)	Trait		
Coloration (larval color pattern) (https://www.gephebase.org/search-criteria?/and+Trait=^Coloration (larval color pattern)^#gephebase-summary-title)	Trait State in Taxon A		
WT Bombyx mori strain (N4; P50) and non-domesticated Bombyx mandarina	Trait State in Taxon B		
Bombyx mori strain c05 with pS larval color phenotype or strain p50T with +p phenotype	Ancestral State		
Taxon A	Taxonomic Status		
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic Status^Domesticated^#gephebase-summary-title)			
Taxon A		Taxon B	
Bombyx mori (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Bombyx+mori^#gephebase-summary-title)	Latin Name	Bombyx mori (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Bombyx+mori^#gephebase-summary-title)	Latin Name
domestic silkworm	Common Name	domestic silkworm	Common Name
domestic silkworm; silk moth; silkworm; Bombyx mori Linnaeus, 1758	Synonyms	domestic silkworm; silk moth; silkworm; Bombyx mori 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; Amphiesmenoptera; Lepidoptera; Glossata; Neolepidoptera; Heteroneura; Ditrysia; Obtectomera; Bombycoidea; Bombycidae; Bombycinae; Bombyx	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; Bombycoidea; Bombycidae; Bombycinae; Bombyx	Lineage
Bombyx () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7090)	Parent	Bombyx () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7090)	Parent
7091 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7091)	NCBI Taxonomy ID	7091 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7091)	NCBI Taxonomy ID
Yes	is Taxon A an Infraspecies?	Yes	is Taxon B an Infraspecies?
WT Bombyx mori strain (N4; P50) and non-domesticated Bombyx mandarina	Taxon A Description	WT Bombyx mori strain c05 with pS larval color phenotype or strain p50T with +p phenotype	Taxon B Description

GENOTYPIC CHANGE

apt	Generic Gene Name	UniProtKB Drosophila melanogaster
	Synonyms	GenebankID or UniProtKB
3041; Apt; CG5393; Dmel\CG5393; l(2)03041; l(2)06369; l(2)09049; l(2)59Ea; l(2)k11531; tdf; TDF; TDF/APT; Tdp; APT; apt-RC; Dmel_CG5393	O61602 (http://www.uniprot.org/uniprot/O61602)	
-	String	
-	Sequence Similarities	
-	GO - Molecular Function	
GO:0003700 : DNA-binding transcription factor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003700)		
GO:0043565 : sequence-specific DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0043565)		
GO:0003729 : mRNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003729)		

GO:0001158 : enhancer sequence-specific DNA binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0001158>)
GO:0003730 : mRNA 3'-UTR binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0003730>)

GO - Biological Process

GO:0007417 : central nervous system development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007417>)
GO:0045944 : positive regulation of transcription by RNA polymerase II
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045944>)
GO:0007507 : heart development (<https://www.ebi.ac.uk/QuickGO/term/GO:0007507>)
GO:0048149 : behavioral response to ethanol
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048149>)
GO:0007274 : neuromuscular synaptic transmission
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007274>)
GO:0010468 : regulation of gene expression
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010468>)
GO:0007298 : border follicle cell migration
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007298>)
GO:0007424 : open tracheal system development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007424>)
GO:0035289 : posterior head segmentation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0035289>)
GO:0007427 : epithelial cell migration, open tracheal system
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007427>)
GO:0046426 : negative regulation of JAK-STAT cascade
(<https://www.ebi.ac.uk/QuickGO/term/GO:0046426>)
GO:0007319 : negative regulation of oskar mRNA translation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007319>)

GO - Cellular Component

GO:0005737 : cytoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005737>)
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

Cis-regulatory (<https://www.gephebase.org/search-criteria/?and+Molecular+Type=%Cis-regulatory%#gephebase-summary-title>)

Aberration Type

Unknown (<https://www.gephebase.org/search-criteria/?and+Aberration+Type=%Unknown%#gephebase-summary-title>)

Molecular Details of the Mutation

233-kb region around apt-like (pS) refined as 33kb interval in apt-like Intron 1 (+p) with uncharacterized haplotype driving apt-like upregulation in derived phenotypes

Experimental Evidence

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

Main Reference

The transcription factor Apontic-like controls diverse colouration pattern in caterpillars. (2014) (<https://pubmed.ncbi.nlm.nih.gov/25233442>)

Authors

Yoda S; Yamaguchi J; Mita K; Yamamoto K; Banno Y; Ando T; Daimon T; Fujiwara H

Abstract

Genetic polymorphisms underlie the convergent and divergent evolution of various phenotypes. Diverse colour patterns on caterpillars, which are ecologically important, are good models for understanding the molecular backgrounds of phenotypic diversity. Here we show that a single evolutionarily conserved gene apontic-like (apt-like) encoding for a putative transcription factor accounts for the silkworm p locus, which causes at least 15 different larval markings involved in branch-like markings and eye-spot formation. The expression of apt-like and melanin synthesis genes are upregulated in association with pigmented areas of marking mutants Striped (p(S)) and normal (+(p)) but not in the non-marking allele plain (p). Functional analyses, ectopic expression, RNAi and TALEN, demonstrate that apt-like causes melanin pigmentation in a cell-autonomous manner. These results suggest that variation in p alleles is caused by the differential expression of the gene apt-like which induces targeted elevation of gene expressions in the melanin synthesis pathway.

Additional References

The evolutionary road from wild moth to domestic silkworm. (2018) (<https://pubmed.ncbi.nlm.nih.gov/29967484>)

Allele-specific knockouts reveal a role for apontic-like in the evolutionary loss of larval melanin pigmentation in the domesticated silkworm, *Bombyx mori*. (2022) (<https://pubmed.ncbi.nlm.nih.gov/35752945>)

RELATED GEPHE

Related Genes

9 (Bm-iAANAT, cardinal, cortex, SCARB1, SCRB15, Wnt1, Carotenoid-binding protein (CBP), Tyrosine hydroxylase, UGT86 (Bm-UGT10286)) (<https://www.gephebase.org/search-criteria/?or+Taxon+ID=%7091%and+Trait=Coloration+and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

Allelic differences between +p and pS were uncharacterized and are included here as a single allelic variant rather than as an allelic series ; TALEN loss-of-function and electroporation experiments validate the role of apt-like in pigment pattern formation