GEPHE SUMMARY

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

Entry Status
Published

GepheID
GP00001386

Main curator
Martin

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

Latin Name
Bombyx mori (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Bombyx mori^#gephebase-summary-title)

Common Name
domestic silkworm

Synonyms
domestic silkworm; silk moth; silkworm; Bombyx mori 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; Bombycoidea; Bombycidae; Bombycinae; Bombyx

Parent
Bombyx () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7090)

NCBI Taxonomy ID
7091 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7091)

is Taxon A an Infraspecies?
Yes

Taxon A Description
WT Bombyx mori strain (N4; P50) and non-domesticated Bombyx mandarina

Taxon B

Latin Name
Bombyx mori (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Bombyx mori^#gephebase-summary-title)

Common Name
domestic silkworm

Synonyms
domestic silkworm; silk moth; silkworm; Bombyx mori 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; Bombycoidea; Bombycidae; Bombycinae; Bombyx

Parent
Bombyx () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7090)

NCBI Taxonomy ID
7091 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7091)

is Taxon B an Infraspecies?
Yes

Taxon B Description
Bombyx mori strain c05 with pS larval color phenotype or strain p50T with +p phenotype

GENOTYPIC CHANGE

Generic Gene Name
apt

Synonyms
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

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)

UniProtKB Drosophila melanogaster
O61602 (http://www.uniprot.org/uniprot/O61602)

GenebankID or UniProtKB
()

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