GEPHE SUMMARY

Gephebase Gene

Wnt1 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Wnt1^#gephebase-summary-title)

GepheID

GP00001385

Entry Status

Published

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 strains (p50 and N4) and non-domesticated Bombyx mandarina

Trait State in Taxon B

Bombyx mori - multi lunar (L) phenotype with periodic patterns

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 strains (p50 and N4) 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 - multi lunar (L) phenotype with periodic patterns

GENOTYPIC CHANGE

Generic Gene Name

wg

Synonyms

l; beta-catenin; Br; CG4889; Dint-1; Dm Wg; Dm-1; Dmel\CG4889; DWint-1; dWnt; DWnt-1; fg; Gla; int-1; l(2)02657; l(2)rO727; l(2)SH1281; l(2)SH2 1281; l(2)wg; Sp; spd; Wg; WG; wgl; wnt; Wnt; WNT; Wnt-1; Wnt/Wg; wnt1; Wnt1

String

7227.FBpp0079060 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0079060)

Sequence Similarities

Belongs to the Wnt family.

GO - Molecular Function

GO:0048018 : receptor ligand activity (https://www.ebi.ac.uk/QuickGO/term/GO:0048018)

UniProtKB Drosophila melanogaster

P09615 (http://www.uniprot.org/uniprot/P09615)

GenebankID or UniProtKB

()

GO:0005109 : frizzled binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005109)
GO:0016015 : morphogen activity (https://www.ebi.ac.uk/QuickGO/term/GO:0016015)
GO:0050840 : extracellular matrix binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0050840)
GO:0005539 : glycosaminoglycan binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0005539)
GO:0043395 : heparan sulfate proteoglycan binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0043395)

GO - Biological Process

GO:0061382 : Malpighian tubule tip cell differentiation
(https://www.ebi.ac.uk/QuickGO/term/GO:0061382)
GO:0007616 : long-term memory (https://www.ebi.ac.uk/QuickGO/term/GO:0007616)
GO:0008284 : positive regulation of cell proliferation
(https://www.ebi.ac.uk/QuickGO/term/GO:0008284)
GO:0007398 : ectoderm development
(https://www.ebi.ac.uk/QuickGO/term/GO:0007398)
GO:0007476 : imaginal disc-derived wing morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0007476)
GO:0007498 : mesoderm development
(https://www.ebi.ac.uk/QuickGO/term/GO:0007498)
GO:0030707 : ovarian follicle cell development
(https://www.ebi.ac.uk/QuickGO/term/GO:0030707)
GO:0008587 : imaginal disc-derived wing margin morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0008587)
GO:0048728 : proboscis development
(https://www.ebi.ac.uk/QuickGO/term/GO:0048728)
GO:0035220 : wing disc development
(https://www.ebi.ac.uk/QuickGO/term/GO:0035220)
GO:0008544 : epidermis development
(https://www.ebi.ac.uk/QuickGO/term/GO:0008544)
GO:0035225 : determination of genital disc primordium
(https://www.ebi.ac.uk/QuickGO/term/GO:0035225)
GO:0007391 : dorsal closure (https://www.ebi.ac.uk/QuickGO/term/GO:0007391)
GO:0061331 : epithelial cell proliferation involved in Malpighian tubule morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0061331)
GO:0007444 : imaginal disc development
(https://www.ebi.ac.uk/QuickGO/term/GO:0007444)
GO:0045572 : positive regulation of imaginal disc growth
(https://www.ebi.ac.uk/QuickGO/term/GO:0045572)
GO:0007367 : segment polarity determination
(https://www.ebi.ac.uk/QuickGO/term/GO:0007367)
GO:0035277 : spiracle morphogenesis, open tracheal system
(https://www.ebi.ac.uk/QuickGO/term/GO:0035277)
GO:0010002 : cardioblast differentiation
(https://www.ebi.ac.uk/QuickGO/term/GO:0010002)
GO:2000648 : positive regulation of stem cell proliferation
(https://www.ebi.ac.uk/QuickGO/term/GO:2000648)
GO:0010942 : positive regulation of cell death
(https://www.ebi.ac.uk/QuickGO/term/GO:0010942)
GO:0048754 : branching morphogenesis of an epithelial tube
(https://www.ebi.ac.uk/QuickGO/term/GO:0048754)
GO:0007442 : hindgut morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0007442)
GO:0001745 : compound eye morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0001745)
GO:0044719 : regulation of imaginal disc-derived wing size
(https://www.ebi.ac.uk/QuickGO/term/GO:0044719)
GO:0007448 : anterior/posterior pattern specification, imaginal disc
(https://www.ebi.ac.uk/QuickGO/term/GO:0007448)
GO:0035147 : branch fusion, open tracheal system
(https://www.ebi.ac.uk/QuickGO/term/GO:0035147)
GO:0060070 : canonical Wnt signaling pathway
(https://www.ebi.ac.uk/QuickGO/term/GO:0060070)
GO:0061316 : canonical Wnt signaling pathway involved in heart development
(https://www.ebi.ac.uk/QuickGO/term/GO:0061316)
GO:0090254 : cell elongation involved in imaginal disc-derived wing morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0090254)
GO:0035293 : chitin-based larval cuticle pattern formation
(https://www.ebi.ac.uk/QuickGO/term/GO:0035293)
GO:0007450 : dorsal/ventral pattern formation, imaginal disc
(https://www.ebi.ac.uk/QuickGO/term/GO:0007450)
GO:0035153 : epithelial cell type specification, open tracheal system
(https://www.ebi.ac.uk/QuickGO/term/GO:0035153)
GO:0035224 : genital disc anterior/posterior pattern formation
(https://www.ebi.ac.uk/QuickGO/term/GO:0035224)
GO:0035263 : genital disc sexually dimorphic development
(https://www.ebi.ac.uk/QuickGO/term/GO:0035263)
GO:0060914 : heart formation (https://www.ebi.ac.uk/QuickGO/term/GO:0060914)

GO:0007488 : histoblast morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0007488)
GO:0035217 : labial disc development (https://www.ebi.ac.uk/QuickGO/term/GO:0035217)
GO:0035167 : larval lymph gland hemopoiesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0035167)
GO:0007523 : larval visceral muscle development
(https://www.ebi.ac.uk/QuickGO/term/GO:0007523)
GO:0035170 : lymph gland crystal cell differentiation
(https://www.ebi.ac.uk/QuickGO/term/GO:0035170)
GO:0048542 : lymph gland development
(https://www.ebi.ac.uk/QuickGO/term/GO:0048542)
GO:0061332 : Malpighian tubule bud morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0061332)
GO:0048332 : mesoderm morphogenesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0048332)
GO:0009996 : negative regulation of cell fate specification
(https://www.ebi.ac.uk/QuickGO/term/GO:0009996)
GO:0032876 : negative regulation of DNA endoreduplication
(https://www.ebi.ac.uk/QuickGO/term/GO:0032876)
GO:0045611 : negative regulation of hemocyte differentiation
(https://www.ebi.ac.uk/QuickGO/term/GO:0045611)
GO:0014019 : neuroblast development
(https://www.ebi.ac.uk/QuickGO/term/GO:0014019)
GO:0061320 : pericardial nephrocyte differentiation
(https://www.ebi.ac.uk/QuickGO/term/GO:0061320)
GO:0046672 : positive regulation of compound eye retinal cell programmed cell death
(https://www.ebi.ac.uk/QuickGO/term/GO:0046672)
GO:0042691 : positive regulation of crystal cell differentiation
(https://www.ebi.ac.uk/QuickGO/term/GO:0042691)
GO:0061328 : posterior Malpighian tubule development
(https://www.ebi.ac.uk/QuickGO/term/GO:0061328)
GO:0048076 : regulation of compound eye pigmentation
(https://www.ebi.ac.uk/QuickGO/term/GO:0048076)
GO:0072091 : regulation of stem cell proliferation
(https://www.ebi.ac.uk/QuickGO/term/GO:0072091)
GO:0060061 : Spemann organizer formation
(https://www.ebi.ac.uk/QuickGO/term/GO:0060061)
GO:0050808 : synapse organization (https://www.ebi.ac.uk/QuickGO/term/GO:0050808)
GO:0051124 : synaptic growth at neuromuscular junction
(https://www.ebi.ac.uk/QuickGO/term/GO:0051124)
GO:0007418 : ventral midline development
(https://www.ebi.ac.uk/QuickGO/term/GO:0007418)
GO:0035311 : wing cell fate specification
(https://www.ebi.ac.uk/QuickGO/term/GO:0035311)

GO - Cellular Component

GO:0005886 : plasma membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005886)
GO:0045121 : membrane raft (https://www.ebi.ac.uk/QuickGO/term/GO:0045121)
GO:0005576 : extracellular region (https://www.ebi.ac.uk/QuickGO/term/GO:0005576)
GO:0030054 : cell junction (https://www.ebi.ac.uk/QuickGO/term/GO:0030054)
GO:0005615 : extracellular space (https://www.ebi.ac.uk/QuickGO/term/GO:0005615)
GO:0005783 : endoplasmic reticulum
(https://www.ebi.ac.uk/QuickGO/term/GO:0005783)
GO:0009986 : cell surface (https://www.ebi.ac.uk/QuickGO/term/GO:0009986)
GO:0005771 : multivesicular body (https://www.ebi.ac.uk/QuickGO/term/GO:0005771)
GO:0043195 : terminal bouton (https://www.ebi.ac.uk/QuickGO/term/GO:0043195)

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

Complex Change (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Complex Change^#gephebase-summary-title)

Molecular Details of the Mutation

Fine-resolution mapping of a 34kb regulatory region driving Ecdysteroid-dependent Wnt gain-of-function. The L-specific structural variations upstream of Wnt1-1 may cause its ectopic expression in the spot marking region of the epidermis, resulting in the L phenotype.

Experimental Evidence

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

Main Reference

Periodic Wnt1 expression in response to ecdysteroid generates twin-spot markings on caterpillars. (2013) (https://pubmed.ncbi.nlm.nih.gov/23673642)

Authors

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

Abstract

Among various pigmentation patterns on caterpillars, sequential spot markings are often observed and used for aposematic colouration. In contrast to adult wings, caterpillar cuticle markings are repeatedly generated at each moult, but little is known about how the patterns are formed and maintained periodically. Here we focus on a silkworm mutant, multi lunar (L), with twin-spot markings on sequential segments. Positional cloning of L and expression analyses reveal that cis-regulatory change in Wnt1 is responsible for the spot patterning. The periodical upregulation of Wnt1 in response to ecdysteroid is detected only in epidermis within spot marking area. We verify by transgenic expression that the ectopic Wnt1 induces the additional pigmentation. Furthermore, the association of Wnt1 expression with spot markings is observed in the wild Bombyx species and swallowtail butterfly Papilio machaon. Taken together, we anticipate that periodic Wnt1 expression may contribute to natural variations of spot patterning on caterpillar cuticle.

Additional References

Protruding structures on caterpillars are controlled by ectopic Wnt1 expression. (2015) (https://pubmed.ncbi.nlm.nih.gov/25815728)
High-resolution silkworm pan-genome provides genetic insights into artificial selection and ecological adaptation. (2022) (https://pubmed.ncbi.nlm.nih.gov/36153338)

RELATED GEPHE

Related Genes

9 (apontic-like, Bm-iAANAT, cardinal, cortex, SCARB1, SCRB15, 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

1 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^Wnt1^/and+Taxon ID=^7091^/or+Gene Gephebase=^Wnt1^/and+Taxon ID=^7091^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS

Electroporation-mediated somatic transgenesis confirms that an ectopically expressed Wnt1 transgene is sufficient for additional larval pigmentation both in B. mori and B. mandarina ; see 25815728 for additional data on the role of Wnt1 in the induction of larval protruding structures