

Wnt1 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~Wnt1^#gephebase-summary-title)	Gephebase Gene	GP00002403	GepheID
Published	Entry Status	Courtier	Main curator

	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 <i>Bombyx mori</i> strains (p50 and N4) and non-domesticated <i>Bombyx mandarina</i>	
	Trait State in Taxon B
<i>Bombyx mori</i> - Caltrop-type multilunar (LC) phenotype with periodic patterns	
	Ancestral State
Taxon A	
	Taxonomic Status
Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Domesticated^#gephebase-summary-title)	

GENOTYPIC CHANGE

wg	Generic Gene Name	P09615 (http://www.uniprot.org/uniprot/P09615)	UniProtKB Drosophila melanogaster
	Synonyms		GenebankID or UniProtKB
I; 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)			

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

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

Deletion Size

100-1000 kb

Molecular Details of the Mutation

A specific large deletion (271â€kb) is present in the 3â€flanking region of Wnt1. Wnt1 expression is significantly higher in the epidermis of heterozygous LC (LC/+) mutants than in normal strains (+/+).

Experimental Evidence

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

Main Reference

High-resolution silkmoth pan-genome provides genetic insights into artificial selection and ecological adaptation. (2022) (<https://pubmed.ncbi.nlm.nih.gov/36153338>)

Authors

Tong X; Han MJ; Lu K; Tai S; Liang S; Liu Y; Hu H; Shen J; Long A; Zhan C; Ding X; Liu S; Gao Q; Zhang B; Zhou L; Tan D; Yuan Y; Guo N; Li YH; Wu Z; Liu L; Li C; Lu Y; Gai T; Zhang Y; Yang R; Qian H; Liu Y; Luo J; Zheng L; Lou J; Peng Y; Zuo W; Song J; He S; Wu S; Zou Y; Zhou L; Cheng L; Tang Y; Cheng G; Yuan L; He W; Xu J; Fu T; Xiao Y; Lei T; Xu A; Yin Y; Wang J; Monteiro A; Westhof E; Lu C; Tian Z; Wang W; Xiang Z; Dai F

Abstract

The silkmoth *Bombyx mori* is an important economic insect for producing silk, the "queen of fabrics". The currently available genomes limit the understanding of its genetic diversity and the discovery of valuable alleles for breeding. Here, we deeply re-sequence 1,078 silkworms and assemble long-read genomes for 545 representatives. We construct a high-resolution pan-genome dataset representing almost the entire genomic content in the silkworm. We find that the silkworm population harbors a high density of genomic variants and identify 7308 new genes, 4260

(22%) core genes, and 3,432,266 non-redundant structure variations (SVs). We reveal hundreds of genes and SVs that may contribute to the artificial selection (domestication and breeding) of silkworm. Further, we focus on four genes responsible, respectively, for two economic (silk yield and silk fineness) and two ecologically adaptive traits (egg diapause and aposematic coloration). Taken together, our population-scale genomic resources will promote functional genomics studies and breeding improvement for silkworm.

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Additional References

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