

GEPHE SUMMARY

	Gephebase Gene	GephelD
Tret1-like (#gephebase-summary-title)	GP00002402	Main curator
Entry Status	Courtier	
Published		

PHENOTYPIC CHANGE

	Trait Category		
Physiology (#gephebase-summary-title)	Trait		
Diapause (#gephebase-summary-title)	Trait State in Taxon A		
Bombyx mori - diapause	Trait State in Taxon B		
Bombyx mori - non-diapause (ndp) mutant	Ancestral State		
Taxon A	Taxonomic Status		
Domesticated (#gephebase-summary-title)			
	Taxon A	Taxon B	
	Latin Name	Latin Name	
Bombyx mori (#gephebase-summary-title)	Bombyx mori (#gephebase-summary-title)		
	Common Name	Common Name	
domestic silkworm	domestic silkworm		
	Synonyms	Synonyms	
domestic silkworm; silk moth; silkworm; Bombyx mori Linnaeus, 1758	domestic silkworm; silk moth; silkworm; Bombyx mori Linnaeus, 1758		
	Rank	Rank	
species	species		
	Lineage	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	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	Parent	
Bombyx () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7090)	Bombyx () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7090)		
	NCBI Taxonomy ID	NCBI Taxonomy ID	
7091 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7091)	7091 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7091)		
	is Taxon A an Infraspecies?	is Taxon B an Infraspecies?	
No	No		

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Drosophila melanogaster
Tret1-1		
CG30035; CG7797; CG7801; Dmel\CG30035; DmTret1-1; Tre T1; Tret-1	Synonyms	GenebankID or UniProtKB Drosophila melanogaster
7227.FBpp0087178 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=7227.FBpp0087178)	String	A1Z8N1 (https://www.ncbi.nlm.nih.gov/nuccore/A1Z8N1)
	Sequence Similarities	
Belongs to the major facilitator superfamily. Sugar transporter (TC 2.A.1.1) family. Trehalose transporter subfamily.		
	GO - Molecular Function	
GO:0005355 : glucose transmembrane transporter activity (https://www.ebi.ac.uk/QuickGO/term/GO:0005355)		
GO:0022857 : transmembrane transporter activity (https://www.ebi.ac.uk/QuickGO/term/GO:0022857)		
GO:0015574 : trehalose transmembrane transporter activity		

GO:0055085 : transmembrane transport

(<https://www.ebi.ac.uk/QuickGO/term/GO:0055085>)

GO:1904659 : glucose transmembrane transport

(<https://www.ebi.ac.uk/QuickGO/term/GO:1904659>)

GO:0015771 : trehalose transport (<https://www.ebi.ac.uk/QuickGO/term/GO:0015771>)

GO - Cellular Component

GO:0016021 : integral component of membrane

(<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)

GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)

GO:0016020 : membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0016020>)

Presumptive Null

No ([#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive+Null=^No))

Molecular Type

Cis-regulatory ([#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular+Type=^Cis-regulatory))

Aberration Type

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

Molecular Details of the Mutation

The expression level of BmTret1-like in homozygotes (pnd/pnd) is significantly lower ($p < 0.01$, t test) than that in heterozygotes (pnd/+). CRISPR BmTret1-like knockout lines generate non-diapause eggs. A 747 bp deletion is present in the 3'-untranslated region (3'-UTR) of BmTret1-like in pnd homozygotes

Experimental Evidence

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

Main Reference

High-resolution silkworm 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 silkworm *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

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS