

GEPHE SUMMARY

		Gephebase Gene		GepheID
Tret1-like (<a +tret1-like+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+Tret1-like+"#gephebase-summary-title)			GP00002402	
		Entry Status	Courtier	Main curator
Published				

PHENOTYPIC CHANGE

		Trait Category	
Physiology (<a +physiology+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait+Category=">https://www.gephebase.org/search-criteria?/and+Trait+Category="+Physiology+"#gephebase-summary-title)			
		Trait	
Diapause (<a +diapause+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+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 (<a +domesticated+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=">https://www.gephebase.org/search-criteria?/and+Taxonomic+Status="+Domesticated+"#gephebase-summary-title)			
Taxon A		Taxon B	
		Latin Name	
Bombyx mori (<a +bombyx+mori+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Bombyx+mori+"#gephebase-summary-title)		Bombyx mori (<a +bombyx+mori+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Bombyx+mori+"#gephebase-summary-title)	
		Common Name	
domestic silkworm		domestic silkworm	
		Synonyms	
domestic silkworm; silk moth; silkworm; Bombyx mori Linnaeus, 1758		domestic silkworm; silk moth; silkworm; Bombyx mori Linnaeus, 1758	
		Rank	
species		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		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)		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)		7091 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7091)	
		is Taxon A an Intraspecies?	
No		No	

GENOTYPIC CHANGE

		Generic Gene Name	UniProtKB Drosophila melanogaster
Tret1-1		A1Z8N1 (http://www.uniprot.org/uniprot/A1Z8N1)	
		Synonyms	GenebankID or UniProtKB Drosophila melanogaster
CG30035; CG7797; CG7801; Dmel\CG30035; DmTret1-1; Tre T1; Tret-1			
		String	A1Z8N1 (https://www.ncbi.nlm.nih.gov/nuccore/A1Z8N1)
7227.FBpp0087178 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=7227.FBpp0087178)			
		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			

(<https://www.ebi.ac.uk/QuickGO/term/GO:0015574>)

GO - Biological Process

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 (<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

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

Experimental Evidence

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

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