

E2F1 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=E2F1*#gephebase-summary-title)	Gephebase Gene	GP00002400	GepheID
Published	Entry Status	Courtier	Main curator

Trait Category		Trait	
Physiology (#https://www.gephebase.org/search-criteria?/and+TraitCategory=~Physiology)			
Silk yield (#https://www.gephebase.org/search-criteria?/and+Trait=~Silk yield)			
Bombyx mori - local breed	Trait State in Taxon A		
Bombyx mori - breeds with improved silk yield	Trait State in Taxon B		
	Ancestral State		
Taxon A			
	Taxonomic Status		
Domesticated (#https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~Domesticated)			
Taxon A	Latin Name	Taxon B	Latin Name
Bombyx mori (#https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=~Bombyx mori)		Bombyx mori (#https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=~Bombyx mori)	
	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 Intraspecies?		is Taxon B an Intraspecies?	
No		No	

Generic Gene Name	UniProtKB Drosophila melanogaster
E2f1	Q27368 (http://www.uniprot.org/uniprot/Q27368)
Synonyms	GenebankID or UniProtKB Drosophila melanogaster
CG6376; dE2f; dE2F; de2f1; dE2f1; dE2F1; def21; DmE2F-1; Dmel\CG6376; Dp; drosE2F1; DRTF1/E2F; E(Sev-CycE)3A; E(var)3-93E; E(var)3-95E; E(var)93E; e2f; E2f; E2F; E2F-1; e2f1; E2F1; Evar(3)164; l(3)07172; l(3)j3B1; l(3)j3C2; l(3)rM729	Q27368 (https://www.ncbi.nlm.nih.gov/nuccore/Q27368)
String	
7227.FBpp0083516 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=7227.FBpp0083516)	
Sequence Similarities	
Belongs to the E2F/DP family.	
GO - Molecular Function	
GO:0046983 : protein dimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0046983)	
GO:0001228 : DNA-binding transcription activator activity, RNA polymerase II-specific (https://www.ebi.ac.uk/QuickGO/term/GO:0001228)	

GO:0003700 : DNA-binding transcription factor activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0003700>)
GO:0000977 : RNA polymerase II regulatory region sequence-specific DNA binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0000977>)
GO:0008134 : transcription factor binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0008134>)
GO:0003677 : DNA binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0003677>)
GO:0000978 : RNA polymerase II proximal promoter sequence-specific DNA binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0000978>)
GO:0001227 : DNA-binding transcription repressor activity, RNA polymerase II-specific
(<https://www.ebi.ac.uk/QuickGO/term/GO:0001227>)

GO - Biological Process

GO:0007419 : ventral cord development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007419>)
GO:0045944 : positive regulation of transcription by RNA polymerase II
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045944>)
GO:0006357 : regulation of transcription by RNA polymerase II
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006357>)
GO:0000122 : negative regulation of transcription by RNA polymerase II
(<https://www.ebi.ac.uk/QuickGO/term/GO:0000122>)
GO:0010628 : positive regulation of gene expression
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010628>)
GO:0000082 : G1/S transition of mitotic cell cycle
(<https://www.ebi.ac.uk/QuickGO/term/GO:0000082>)
GO:0035206 : regulation of hemocyte proliferation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0035206>)
GO:0042023 : DNA endoreduplication
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042023>)
GO:0010468 : regulation of gene expression
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010468>)
GO:0043065 : positive regulation of apoptotic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043065>)
GO:0051726 : regulation of cell cycle (<https://www.ebi.ac.uk/QuickGO/term/GO:0051726>)
GO:0035167 : larval lymph gland hemopoiesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0035167>)
GO:0007307 : eggshell chorion gene amplification
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007307>)
GO:0032877 : positive regulation of DNA endoreduplication
(<https://www.ebi.ac.uk/QuickGO/term/GO:0032877>)
GO:0045850 : positive regulation of nurse cell apoptotic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045850>)
GO:1900117 : regulation of execution phase of apoptosis
(<https://www.ebi.ac.uk/QuickGO/term/GO:1900117>)

GO - Cellular Component

GO:0005654 : nucleoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005654>)
GO:0005634 : nucleus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005634>)
GO:0090575 : RNA polymerase II transcription factor complex
(<https://www.ebi.ac.uk/QuickGO/term/GO:0090575>)
GO:0035189 : Rb-E2F complex (<https://www.ebi.ac.uk/QuickGO/term/GO:0035189>)

Presumptive Null

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

Molecular Type

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

Aberration Type

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

Molecular Details of the Mutation

There are one deletion and three insertions in the cis-regulatory region and introns of the E2F1 gene of the improved strain. Higher expression in the improves strain. CRISPR-cas9 mediated knockout of BmE2F1 reduces the number of silk gland cells by 7.68% and silk yield by 22%.

Experimental Evidence

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

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.

RELATED GEPHE

Related Genes

6 (asparagine synthetase (AS), Fkh, glutamate dehydrogenase (GDH), glutamate synthase (GOGAT), glutamine synthetase 2 (GS), sage) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=^7091^/and+Trait=Silk yield/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS