

GEPHE SUMMARY

sage (<a +sage+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+sage+"#gephebase-summary-title)	Gephebase Gene	GP00002410	GepheID
Published	Entry Status	Courtier	Main curator

PHENOTYPIC CHANGE

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 Category		
Silk yield (<a +silk+yield+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait="+Silk+yield+"#gephebase-summary-title)	Trait		
Bombyx mori - local breed	Trait State in Taxon A		
Bombyx mori - breeds with improved silk yield	Trait State in Taxon B		
Taxon A	Ancestral State		
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)	Taxonomic Status		
	Taxon A		Taxon B
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)	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)	Latin Name
domestic silkworm	Common Name	domestic silkworm	Common Name
domestic silkworm; silk moth; silkworm; Bombyx mori Linnaeus, 1758	Synonyms	domestic silkworm; silk moth; silkworm; Bombyx mori Linnaeus, 1758	Synonyms
species	Rank	species	Rank
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	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	Lineage
Bombyx () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7090)	Parent	Bombyx () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7090)	Parent
7091 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7091)	NCBI Taxonomy ID	7091 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7091)	NCBI Taxonomy ID
No	is Taxon A an Intraspecies?	No	is Taxon B an Intraspecies?

GENOTYPIC CHANGE

sage	Generic Gene Name	Q9VHG3 (http://www.uniprot.org/uniprot/Q9VHG3)	UniProtKB Drosophila melanogaster
bHLHc7; CG12952; Dmel\CG12952; Sage; Dmel_LCG12952	Synonyms	()	GenebankID or UniProtKB
7227.FBpp0081462 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=7227.FBpp0081462)	String		
-	Sequence Similarities		
	GO - Molecular Function		
GO:0046983 : protein dimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0046983)			
GO:0003700 : DNA-binding transcription factor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003700)			
GO:0000981 : DNA-binding transcription factor activity, RNA polymerase II-specific (https://www.ebi.ac.uk/QuickGO/term/GO:0000981)			

GO:0000978 : RNA polymerase II proximal promoter sequence-specific DNA binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0000978>)

GO - Biological Process

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:0006355 : regulation of transcription, DNA-templated
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006355>)

GO:0001707 : mesoderm formation (<https://www.ebi.ac.uk/QuickGO/term/GO:0001707>)

GO:0007431 : salivary gland development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007431>)

GO - Cellular Component

GO:0005634 : nucleus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005634>)

GO:0005700 : polytene chromosome
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005700>)

Presumptive Null

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

Molecular Type

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

Aberration Type

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

Molecular Details of the Mutation

Increased expression in high yield strains. The sage gene encodes a transcription factor that activates glue genes in salivary glands of *Drosophila melanogaster*.

Experimental Evidence

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

Main Reference

Complete resequencing of 40 genomes reveals domestication events and genes in silkworm (*Bombyx*). (2009) (<https://pubmed.ncbi.nlm.nih.gov/19713493>)

Authors

Xia Q; Guo Y; Zhang Z; Li D; Xuan Z; Li Z; Dai F; Li Y; Cheng D; Li R; Cheng T; Jiang T; Becquet C; Xu X; Liu C; Zha X; Fan W; Lin Y; Shen Y; Jiang L; Jensen J; Hellmann I; Tang S; Zhao P; Xu H; Yu C; Zhang G; Li J; Cao J; Liu S; He N; Zhou Y; Liu H; Zhao J; Ye C; Du Z; Pan G; Zhao A; Shao H; Zeng W; Wu P; Li C; Pan M; Li J; Yin X; Li D; Wang J; Zheng H; Wang W; Zhang X; Li S; Yang H; Lu C; Nielsen R; Zhou Z; Wang J; Xiang Z; Wang J

Abstract

A single-base pair resolution silkworm genetic variation map was constructed from 40 domesticated and wild silkworms, each sequenced to approximately threefold coverage, representing 99.88% of the genome. We identified ~16 million single-nucleotide polymorphisms, many indels, and structural variations. We find that the domesticated silkworms are clearly genetically differentiated from the wild ones, but they have maintained large levels of genetic variability, suggesting a short domestication event involving a large number of individuals. We also identified signals of selection at 354 candidate genes that may have been important during domestication, some of which have enriched expression in the silk gland, midgut, and testis. These data add to our understanding of the domestication processes and may have applications in devising pest control strategies and advancing the use of silkworms as efficient bioreactors.

Additional References

RELATED GEPHE

Related Genes

6 (asparagine synthetase (AS), E2F1, Fkh, glutamate dehydrogenase (GDH), glutamate synthase (GOGAT), glutamine synthetase 2 (GS)) (<https://www.gephebase.org/search-criteria?/or+Taxon+ID=7091+and+Trait=Silk+yield+and+groupHaplotypes=true#gpepbase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS